

The Wiley-IUBMB Series on Biochemistry and Molecular Biology

PLANT PHENOLICS and HUMAN HEALTH

Biochemistry, Nutrition, and Pharmacology

Edited by

Cesar G. Fraga

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Published by John Wiley & Sons, Inc., Hoboken, New Jersey.
Published simultaneously in Canada.

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Library of Congress Cataloging-in-Publication Data:

Plant phenolics and human health : biochemistry, nutrition, and pharmacology /
edited, Cesar G. Fraga.
p. ; cm.

Includes bibliographical references and index.

ISBN 978-0-470-28721-7 (cloth)

1. Phenols—Physiological effect. 2. Flavonoids—Physiological effect.
3. Phytochemicals—Physiological effect. 4. Nutrition. I. Fraga, Cesar G. [DNLM:
1. Phenols—pharmacology. 2. Phenols—therapeutic use. 3. Flavonoids—pharmacology.
4. Flavonoids—therapeutic use. 5. Nutritive Value. 6. Plant Extracts—pharmacology.
7. Plant Extracts—therapeutic use. 8. Review Literature as Topic. QV 223 P541 2009]

QP801.P4P46 2009

547'.632—dc22

2009009328

Printed in the United States of America

10 9 8 7 6 5 4 3 2 1

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PREFACE

In association with well-known health benefits related to the consumption of fruit- and vegetable-rich diets, research on the protective effects of plant-derived phenolic compounds (polyphenols) has developed notably in recent years. In particular, their antioxidant properties have been the objective of extensive research. However these phenolics are the target of an array of chemical reactions that, if confirmed to occur *in vivo*, would contribute to their health promoting effects. It is now emerging that both parent compounds and their metabolites produced after ingestion can regulate cell and tissue functions by both antioxidant and nonantioxidant mechanisms. This volume provides the latest evidence supporting these concepts.

The strategy behind the selection of the themes was to provide a comprehensive overview of the basic and applied research on phenolic compounds and their potential protective effects on health. The first chapters are on the identification, metabolism, and basic mechanisms affecting phenolic actions in biological systems. The book then develops in a series of pivotal chapters addressing the effects of flavonoids, stilbenes, and curcuminoids on cardiovascular disease, cancer, and neurodegeneration. The final chapter is on the complex functions that phenolics perform in plants, as a model that can help to better understand their effects on animal physiology. Explanations are essentially centered in applying basic biochemical mechanisms to improve nutrition and/or developing pharmacological strategies.

As being part of a series launched under the umbrella of the IUBMB, the volume was planned to tackle not only the cutting edge research, but also to provide a source for basic, educational information. The target audience includes not only scientists and health professionals but also educators and students, policymakers, food and pharmaceutical developers, and many others interested in understanding how plant-derived phenolic compounds can affect human health and so, in part, explains how fruit and vegetables play a key role in enhancing human health.

The color Figures in this title are posted on the following ftp site: ftp://ftp.wiley.com/public/sci_tech_med/phenolic_compounds.

I want to especially thank the group of outstanding scientist that provided chapters of the highest quality and readability. Particular appreciation is due to prof. Angelo Azzi who was central in the planning and concretion of the book.

I dedicate this volume to my four children,
MAGGIE, MARTÍN, JOAQUÍN, AND IGNACIO

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**THE WILEY–IUBMB SERIES ON BIOCHEMISTRY
AND MOLECULAR BIOLOGY**

Plant Phenolics and Human Health: Biochemistry, Nutrition, and Pharmacology

Editor: Cesar G. Fraga

1 Dietary Flavonoids and Phenolic Compounds

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INTRODUCTION

Plants synthesize a vast range of secondary metabolites with a significant portion consisting of phenolic compounds and flavonoid compounds [Crozier et al., 2006a]. These phytochemicals are structurally diverse, and many are distributed among a very limited number of species within the plant kingdom. This character allows them to act as biodiagnostic markers in chemotaxonomic studies. Phenolic compounds and flavonoids accumulate in relatively high amounts in plants and appear to have a myriad of supplemental functions in a plant's life cycle. These include structural roles in different supporting or protective tissues, involvement in defense strategies, as attractants for pollinators and seed-dispersing animals, and as allelopathic agents, ultra violet (UV) protectants and signal molecules in the interactions between plants and their environment. One of the most versatile classes of flavonoids, the anthocyanins, protect chloroplasts from photodegradation by absorbing high-energy quanta, while scavenging free radicals and reactive oxygen species (ROS) [Gould, 2004]. Flavonols, as well as providing protection against the damaging effects of UV-B light, are also involved in promoting the growth of pollen tubes down the style to facilitate fertilization. In addition, isoflavonoids play important defense roles against pathogen and insect attack and are key signal molecules in the formation of nitrogen-fixing root nodules in legumes. After the death of plants, phenolic compounds may persist for weeks or months and affect decomposer organisms and decomposition processes in soils. Therefore, their effects are not restricted to only the plant itself but may extend to the functioning of whole ecosystems [Horner et al., 1988].

Secondary metabolites, other than providing plants with unique survival or adaptive strategies, are of commercial significance to humankind. They have been used as dyes, fibers, glues, oils, waxes, flavoring agents, drugs, and perfumes and are viewed as potential sources of new natural drugs, antibiotics, insecticides, and herbicides [Croteau et al., 2000; Dewick, 2002]. In recent years the role of phenolic compounds and flavonoids as protective dietary constituents has become an increasingly important area of human nutrition research. Unlike the traditional vitamins, they are not essential for short-term well-being, but there is increasing evidence that modest long-term intakes may exhibit a potential for modulating human metabolism in a manner favorable for the prevention or reduction in the risk of degenerative diseases such as cardiovascular diseases, diabetes, obesity, and cancer [Anderson et al., 1999].

HEALTH BENEFITS AND MODE OF ACTION OF FLAVONOIDS AND PHENOLIC COMPOUNDS

The rapid rise of degenerative diseases worldwide is threatening economic and social development as well as the lives and health of millions of people. It represents a major health challenge to global development in the coming century.

It is estimated that up to 80% of cardiovascular disease, 90% of Type II diabetes, and one third of cancers can be avoided by changing lifestyle, including diet [WHO, 2003]. Diet-related high cholesterol, high blood pressure, obesity, and insufficient consumption of fruits and vegetables have been cited as significant interlinking risk factors that cause the majority of these diseases. There is, therefore, increasing interest in the role of nutrition and specific dietary constituents in the prevention of such diseases. Flavonoids and phenolic compounds are prominent among dietary constituents that are the focus of such interest.

Since the 1990s a number of epidemiological studies have been carried out attempting to correlate high dietary phenolic compounds and flavonoid intake, through the consumption of fruits and vegetables, with reduced risk of degenerative diseases. Many, but not all, of these studies have indicated some degree of inverse associations between high dietary phenolic/flavonoid intake and reduction of degenerative diseases [Steinmetz and Potter, 1996; Law and Morris, 1998; Riboli and Norat, 2003]. Since oxidative stress imposed by ROS is known to play a crucial role in the pathophysiology associated with neoplasia, atherosclerosis, and neurodegenerative diseases, the potential mechanism of the protective effects of phenolic compounds and flavonoids were thought to be due to direct scavenging of free radicals [see Heim et al., 2002].

Accumulating evidence now indicates the importance of interactions between various phytochemicals in reducing the risk of various degenerative diseases [Chan et al., 2000; Mouria et al., 2002; Mertens-Talcott et al., 2003]. The combination of antioxidative agents with different modes of action is thought to increase efficacy and minimize toxicity. In a recent review by Lee and Lee [2006], the abilities of phenolic-based antioxidant therapies to decrease ROS levels was shown to produce the best health benefits through a diet rich in multiple antioxidants rather than a high dosage of a single supplement. Evidence of the potential benefits of food synergy was provided by Liu et al. [2000] when they demonstrated that a combination of fruits, such as orange, apple, grape, and blueberry, displayed a synergistic effect on antioxidant activity *in vitro*. The median effective dose (EC_{50}) of each fruit in combination was five times lower than the EC_{50} of each fruit alone, suggesting synergistic effects due to the combination of the four fruits. In another study, Sakamoto [2000] emphasized the importance of consuming black tea together with soybean products as commonly occurs in a typical Japanese diet. In this study, thearubigen in black tea did not alter the *in vitro* growth of human prostate cancer cells. However, a small amount of thearubigen ($0.5 \mu\text{g mL}^{-1}$) administered with genistein ($20 \mu\text{g mL}^{-1}$), the major isoflavone in soybean, synergistically inhibited cell growth and increased the DNA distribution at the G2 M phase of the cell division cycle by 34% compared with genistein alone [Sakamoto, 2000]. Similar conclusions were reached by Temple and Gladwin [2003] when they reviewed 200 cohort and case-control studies that provided risk ratios concerning intake of fruits

and vegetables and risk of cancer. Their studies showed that the cancer-preventing action of fruits and vegetables is most probably due to the many bioactive compounds that act in concert to prevent cancer rather than being due to one or two potent anticarcinogens.

Nutrients generally have very specific functions such as being an enzyme cofactor. In contrast, in addition to their additive and synergistic effects, phenolic compounds and flavonoids, often exhibit pleiotropic effects that in combination may reduce the risk of chronic disease. For instance, curcumin, the active constituent of turmeric (*Curcuma longa*), a root vegetable, has been shown to be beneficial in all three stages of carcinogenesis [Thangapazham et al., 2006]. Isoflavones, the bioactive ingredient in leguminous vegetables, not only cause a small reduction in blood cholesterol but also reduce blood pressure, arterial dimensions, and oxidative stress [Anderson et al., 1999]. This combined effect may cause a reduction in the risk of coronary heart disease [Kris-Etherton et al., 2004].

In addition to the complexity mentioned above, the health implications of dietary phenolic compounds and flavonoids are also dependent on the composition of the components of the diet and the bioavailability of the individual compounds under study. Accumulating evidence on the absorption and bioavailability of phenolic compounds and flavonoids in humans reveals that most of these phytochemicals are modified during absorption from the small intestine, through conjugation and metabolism, and by the large intestine, mainly through the actions of the colonic microflora, and by subsequent hepatic metabolism [Graefe et al., 2001; Manach et al., 2004; Mullen et al., 2004, 2006, 2008; Jaganath et al., 2006]. Thus, metabolites that reach the cells and tissues are chemically, and, in many instances, functionally distinct from the dietary form, and such features underlie their bioactivity [Kroon et al., 2004]. This, in addition to the fact that in most instances very low levels of dietary phenolic compounds and flavonoids are actually absorbed and appear in the bloodstream ($<10 \mu\text{M}$), implies that the concept of these compounds functioning as hydrogen-donating antioxidants in vivo appear to be an oversimplified view of their mode of action [Williams et al., 2004; Williamson and Manach, 2005; Fraga, 2007].

It has been hypothesized that cells respond to phytochemicals through direct interactions with receptors or enzymes involved in signal transduction, or through modifying gene expressions that may result in alteration of the redox status of the cell that may trigger a series of redox-dependent reactions [Williams et al., 2004]. There is now emerging evidence that flavonoids may play an important role in molecular processes especially as modulators of intracellular signaling cascades, which are vital to cellular function [Williams et al., 2004]. For example, in a recent study carried out by Mackenzie and associates (2008), a naturally occurring phenolic compound, curcumin [1,7-bis(4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione,1] was found to deregulate signaling cascades, such as NF- κ B, leading to a decreased expression of proteins involved in cell proliferation and apoptosis. In another study on Caco-2 cells, hexameric

procyanidins was found to inhibit TNF α -induced NF- κ B activation, which is believed to play a central role in inflammation including human intestinal bowel disease [Erlejman et al., 2008].

There is growing evidence from human feeding studies that the absorption and bioavailability and thus bioactivity of phenolic compounds and flavonoids are very much dependent on the nature of their chemical structure. Their chemical classification and dietary occurrence is briefly discussed in the following section.

FLAVONOIDS—STRUCTURE AND THEIR DIETARY OCCURRENCE

To date, more than 6000 different flavonoids have been described and the number continues to increase [Harborne and Williams, 2000]. Flavonoids are polyphenolic compounds comprising of 15 carbons, with 2 aromatic rings connected by a 3-carbon bridge. According to the modifications of the central C-ring, they can be divided into different structural classes including flavonols, flavones, flavan-3-ols, flavanones, isoflavones, and anthocyanidins (Fig. 1.1). In a few cases, the 6-membered heterocyclic ring C occurs in an isomeric open form or is replaced by a 5-membered ring as in the case of chalcone. Other flavonoid groups, which quantitatively are relatively minor dietary components, are dihydroflavones, flavan-3,4-diols, coumarins, and aurones.

Flavonols

The flavonols are the most widespread of the flavonoids in plant food. They vary in color from white to yellow and are closely related in structure to the flavones. They are represented mainly by quercetin, kaempferol, and myricetin while the methylated derivative isorhamnetin is also quite common (Fig. 1.2). Of the various flavonols found in the diet, quercetin is the most ubiquitous. It is present in various fruits and vegetables, with especially high concentrations, 200–1000 $\mu\text{g g}^{-1}$ fresh weight, occurring in onions (*Allium cepa*) [Hertog et al., 1992; Crozier et al. 1997]. In a recent study by Sultana and Anwar [2008], flavonol levels were determined in 22 plant materials (9 vegetables, 5 fruits, and 8 medicinal plants). The highest concentrations were detected in the medicinal plant, moringa (*Moringa oleifera*) (68 $\mu\text{g g}^{-1}$ fresh weight), followed by strawberry (*Fragaria* spp.) (40 $\mu\text{g g}^{-1}$), peepal (*Ficus religiosa*) (12 $\mu\text{g g}^{-1}$), spinach (*Spinaceae oleraceae*) (19 $\mu\text{g g}^{-1}$), and cauliflower (*Brassica oleraceae*) (18 $\mu\text{g g}^{-1}$).

Flavonols that accumulate in plant tissues are almost always in the form of glycosylated conjugates. The main flavonols in onions are quercetin-4'-O-glucoside and quercetin-3,4'-O-,diglucoside with smaller amounts of isorhamnetin-4'-O-glucoside (Fig. 1.3) [Mullen et al., 2004].

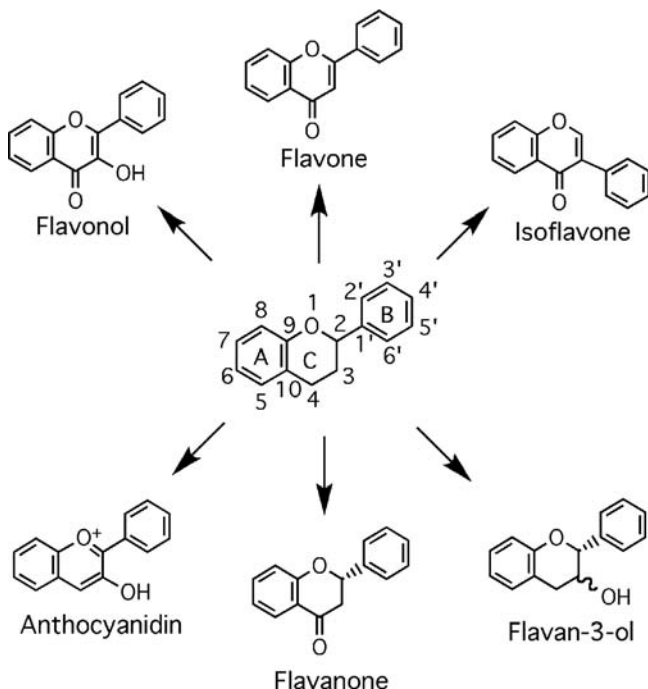


Figure 1.1 Structures of the main flavonoid subgroups.

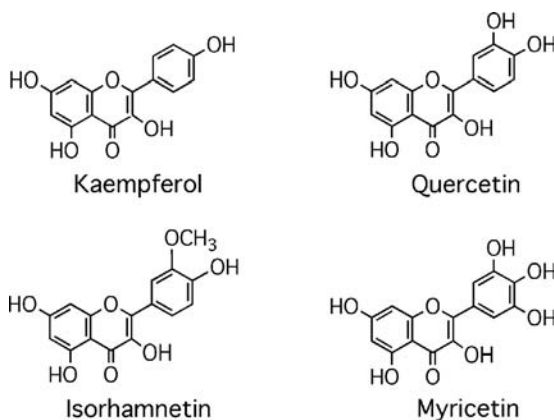


Figure 1.2 Structures of common flavonol aglycones.

A whole range of other quercetin conjugates such as quercetin-3-*O*-galactoside, quercetin-3-*O*-rhamnoside, quercetin-3-*O*-xyloside, quercetin-3-*O*-rutinoside, quercetin-3-*O*-arabinopyranoside, and quercetin-3-*O*-arabinofuranoside are found in apples (*Malus x domestica*) (Fig. 1.4) [Marks et al., 2008].

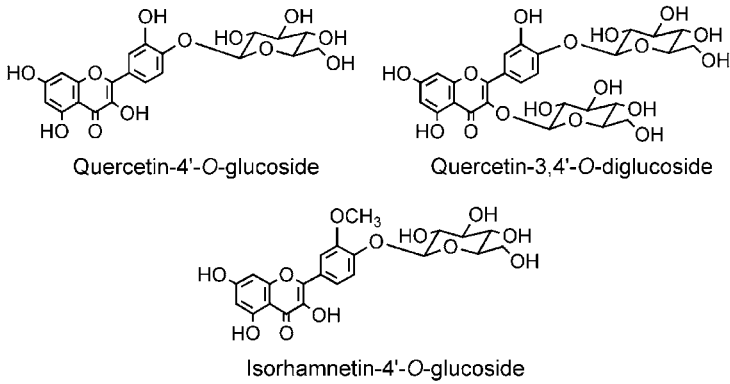


Figure 1.3 Main flavonol glucosides in onion.

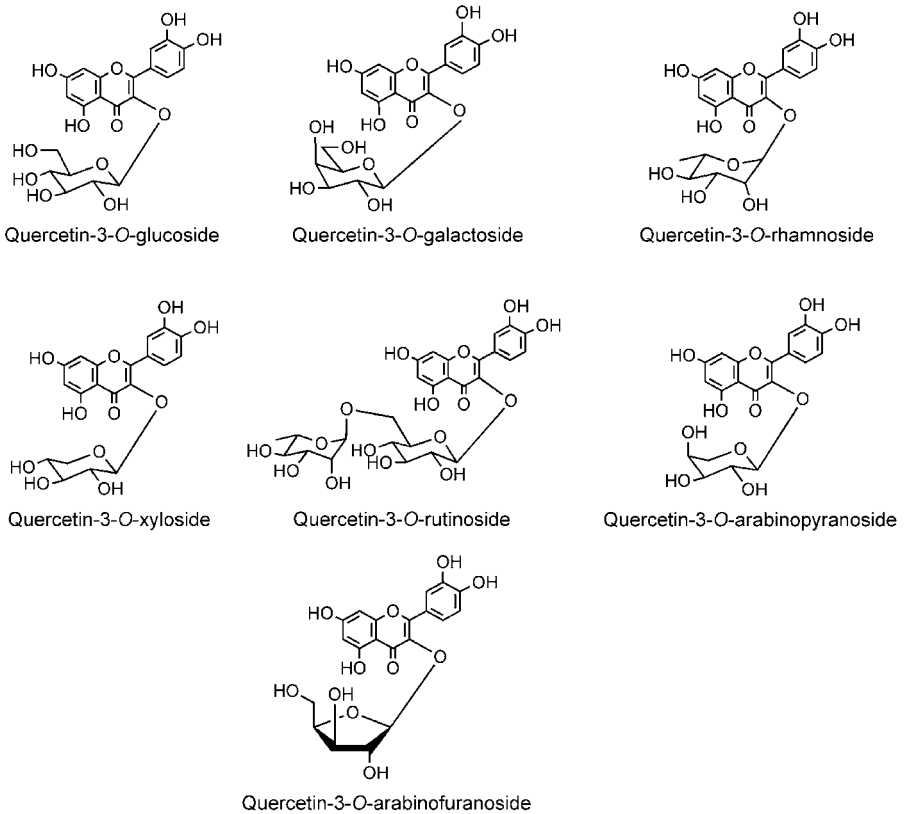


Figure 1.4 Principal flavonol glucosides in apples.

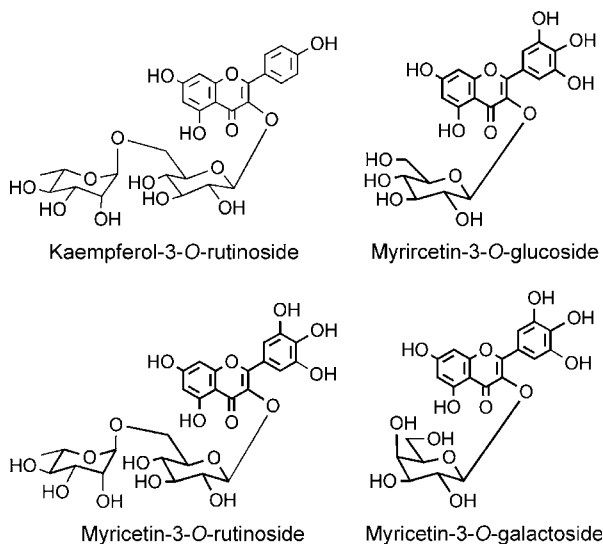


Figure 1.5 Flavonol conjugates found in berries.

Quercetin-3-*O*-rutinoside, on the other hand, is the main flavonol in tomatoes (*Lycopersicon esculentum*), asparagus (*Asparagus officinalis*), peaches (*Prunus persica*), and nectarines (*Prunus persica* var. *nectarina*) [Makris and Rossiter, 2001; Crozier et al., 2006c]. Quercetin-3-*O*-glucoside, quercetin-3-galactoside, and aquercetin arabinoside has also been detected in mangos (*Mangifera indica*) [Schieber et al., 2000]. Other flavonols in the diet include kaempferol-3-*O*-rutinoside in kiwi fruit (*Actinidia deliciosa*) and conjugates of myricetin in berries (Fig. 1.5) (Peterson and Dwyer, 1998).

Grapes of *Vitis vinifera*, grape products, and wines contain a wide range of flavonols such as quercetin, myricetin, kaempferol, isorhamnetin, quercetin-3-*O*-glucoside, quercetin-3-*O*-glucuronide, quercetin-3-*O*-glucoside, quercetin-3-*O*-galactoside, kaempferol-3-*O*-glucoside, and kaempferol-3-*O*-galactoside [Makris et al., 2006]. Tea (*Camellia sinensis*) infusions also contain a diverse spectrum of flavonols linked to mono-, di- and tri-saccharides [Del Rio et al., 2004].

Flavones

Flavones are structurally very similar to flavonols and differ only in the absence of hydroxylation at the 3-position on the C-ring. Flavones are mainly represented in the diet by apigenin and luteolin. Unlike flavonols, they are not widely distributed with significant concentrations being reported in only celery (*Apium graveolens*), parsley (*Petroselinum crispum*), and artichoke (*Cynara scolymus*) [Crozier et al., 2006a]. As a consequence their dietary intake

is very low. Flavone conjugates such as the 7-*O*-(2''-*O*-apiosyl)glucosides of apigenin, luteolin, and chrysoeriol (Fig. 1.6) are found in celery [Herrmann, 1976], while artichoke contains luteolin-7-*O*-glucoside, luteolin-7-*O*-rutinoside, and apigenin-7-*O*-rutinoside (Fig. 1.7) [Wang et al., 2003].

Substantial quantities of luteolin-7-*O*-glucuronide, luteolin-7-*O*-glucoside, and luteolin-7-*O*-rutinoside occur in Red Oak Leaf and Lollo Rosso, two red-leaved varieties of lettuce (*Lactuca sativa*) [Llorach et al., 2008]. Polymethoxylated flavones such as nobiletin, scutellarein, sinensetin, and tangeretin (Fig. 1.8) are found exclusively in citrus species [Crozier et al., 2006c], while diosmetin-7-*O*-glucuronide has been isolated from the fruits of a Chinese herb, *Luffa cylindrical*.

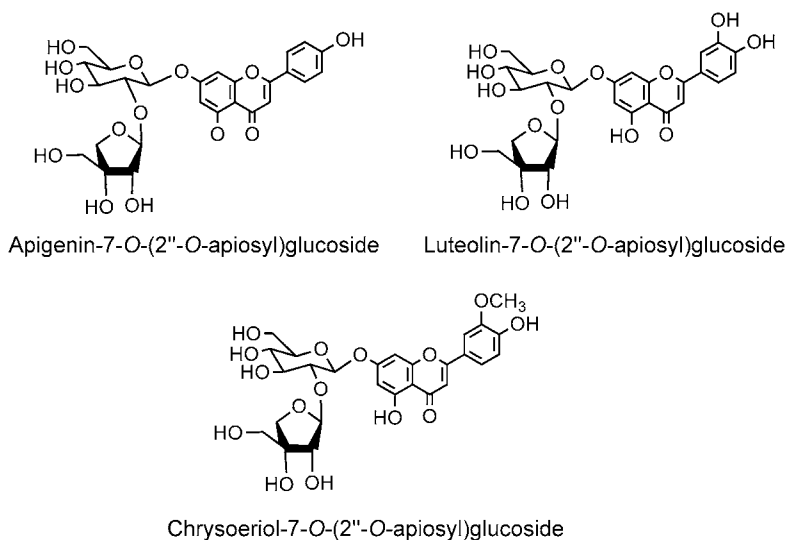


Figure 1.6 Flavone conjugates occurring in celery.

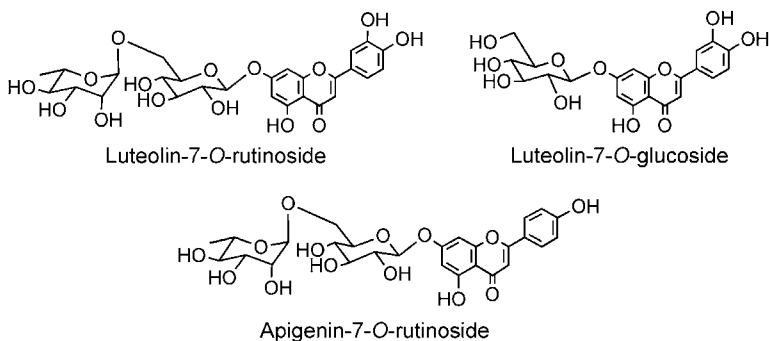


Figure 1.7 Flavone conjugates found in artichoke.

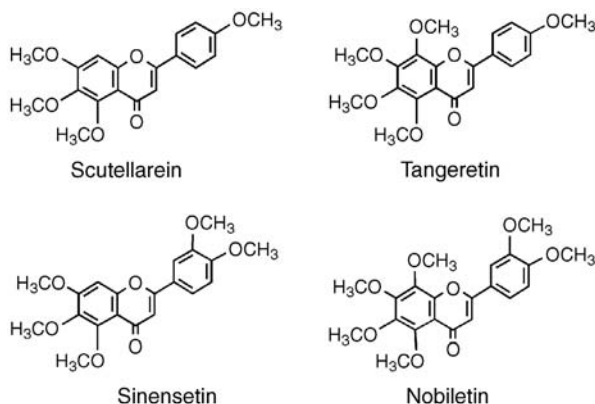


Figure 1.8 Polymethoxylated flavones found in citrus species.

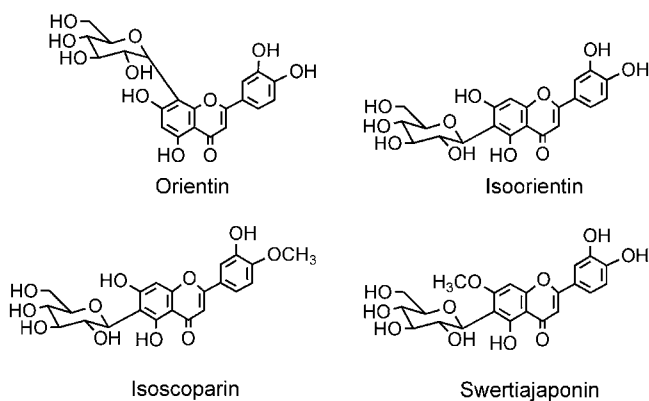


Figure 1.9 Flavones found in rooibos tea.

Red bush or rooibos tea, made from infusions of young leaves and shoots of the South African shrub *Aspalathus linearis*, and popularized by the *The No. 1 Ladies' Detective Agency* novels of the Edinburgh University Emeritus Professor of Medical Law, Alexander McColl Smith [1999, 2000], contains a number of compounds including C-flavone glycosides in the form of isoorientin (luteolin-6-C-glucoside) and orientin (luteolin-8-C-glucoside) [Bramati et al., 2003]. Orientin and isoorientin also occur in lemongrass (*Cymbopogon citratus*) along with two other flavone C-glycosides, chrysoeriol-6-C-glucoside (isoscoparin) and 7-O-methyl-luteolin-6-C-glucoside (swertiajaponin) (Fig. 1.9) [Cheel et al., 2005].

Recent observations reveal that when flavones are methoxylated, metabolic stability and membrane transport in the intestine/liver dramatically increases,

thus improving oral bioavailability. In addition, methoxyflavones also show increased cancer chemopreventive properties when compared to the more common unmethylated flavones [Walle, 2007].

Flavan-3-ols

Flavan-3-ols represent the most common flavonoid consumed in the American and, most probably, the Western diet and are regarded as functional ingredients in various beverages, whole and processed foods, herbal remedies, and supplements. Their presence in food affects quality parameters such as astringency, bitterness, sourness, sweetness, salivary viscosity, aroma, and color formation [Aron and Kennedy, 2007]. Flavan-3-ols are structurally the most complex subclass of flavonoids ranging from the simple monomers (+)-catechin and its isomer (−)-epicatechin to the oligomeric and polymeric proanthocyanidins (Fig. 1.10), which are also known as condensed tannins [Crozier et al., 2006b].

The most abundant type of proanthocyanidins in plants are the procyanidins, which consist exclusively of (epi)catechin units. The less common proanthocyanidins containing (epi)afzelechin (Fig. 1.11) and (epi)gallocatechin (Fig. 1.10) subunits are called propelargonidins and prodelphinidins, respectively [Balentine et al., 1997].

Flavan-3-ols are found abundantly in fruits such as apricots (*Prunus armeniaca*), sour cherries (*Prunus cerasus*), grapes and blackberries (*Rubus* spp.) [Porter, 1988]. The seeds of grapes contain substantial quantities of (+)-catechin, (−)-epicatechin, procyanidin oligomers, and polymers [Gu et al., 2004]. Apples, on the other hand, are a good source of (−)-epicatechin and procyanidin dimers B₁ and B₂ (Fig. 1.12), while peaches and nectarines contain (+)-catechin, (−)-epicatechin, and proanthocyanidins including procyanidin B₁ [Hong et al., 2004]. Barley, seemingly, is the only common cereal with a significant proanthocyanidin content (0.6–1.3 g kg⁻¹) [Santos-Buelga and Scalbert, 2000].

(+)-Catechin and the proanthocyanidin prodelphinidin B₃ are, respectively, the major monomeric and dimeric flavan-3-ols found in barley and malt where prodelphinidin B₃ is the main contributor for the radical scavenging activity [Dvoráková et al., 2007]. Proanthocyanidins have also been detected in nuts. Hazelnuts (*Corylus avellana*) and pecans (*Carya illinoensis*) are particularly rich in proanthocyanidins containing ca. 5 g kg⁻¹, whereas almonds (*Prunus dulcis*) and pistachios (*Pistachio vera*) contain 1.8–2.4 mg kg⁻¹, walnuts (*Juglans* spp.) ca. 0.67 g kg⁻¹, roasted peanuts (*Arachis hypogaea*) 0.16 g kg⁻¹, and cashews (*Anacardium occidentale*) 0.09 g kg⁻¹ [Crozier et al., 2006c]. Dark chocolate derived from the roasted seeds of cocoa (*Theobroma cacao*) is also a rich source of procyanidins [Gu et al., 2004]. Monomeric flavan-3-ols and the proanthocyanidin B₂, B₅ dimers, and C₁ trimer are found in fresh cocoa beans (Fig. 1.13). Flavan-3-ols have also been detected in mint

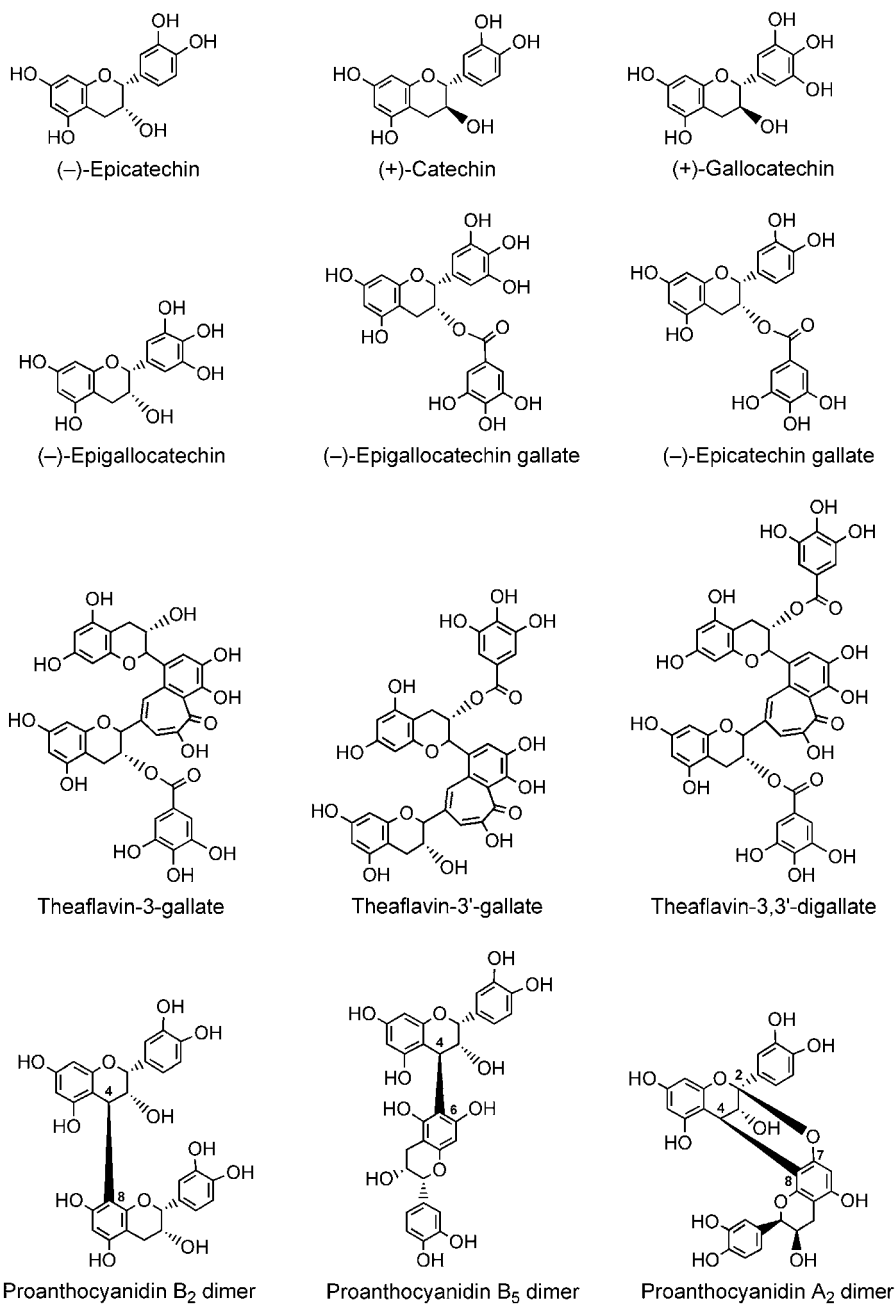


Figure 1.10 Flavan-3-ol structures.

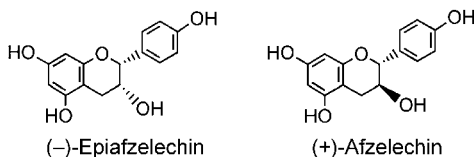


Figure 1.11 Less common flavan-3-ol monomers: (–)-epiafzelechin and (+)-afzelechin.

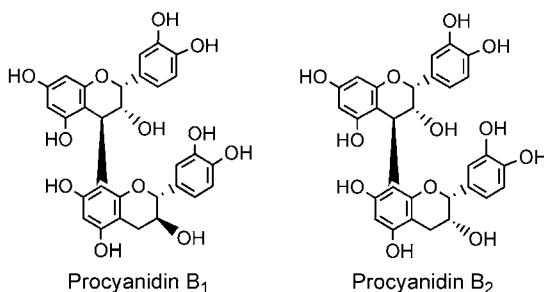


Figure 1.12 Procyanidin dimers occurring in apples.

(*Mentha rotundifolia*), basil (*Ocimum basilicum*), rosemary (*Rosemarinus officinalis*), sage (*Salvia officinalis*), and dill (*Anethum graveolens*) [Shan et al., 2005].

Flavan-3-ols can undergo esterification with gallic acid to form catechin gallates, and hydroxylation reactions to form gallo catechins (Fig. 1.10). Gallo catechins such as (–)-epigallocatechin, (–)-epigallocatechin gallate, and (–)-epicatechin gallate are abundant in green tea infusions [Stewart et al., 2005]. During fermentation to produce black tea, these compounds polymerize, giving rise to theaflavins and high-molecular-weight thearubigins (Fig. 1.14) [Crozier et al., 2006c]. Other beverages such as red wine and beer are also rich in flavan-3-ols. Red wines contain oligomeric procyanidins and prodelphinidins, originating mainly from the seeds of red grapes [Auger et al., 2004]. Flavan-3-ols such as (+)-catechin and (–)-epicatechin, and the dimers prodelphinidin B₃ and procyanidin B₃ have been detected in beer [Crozier et al., 2006c].

Flavanones and Chalcones

Flavanones are mainly represented by naringenin, hesperetin, and eriodictyol, while a number of minor compounds, including sakuranetin and isosakuranetin, also occur (Fig. 1.15). Two structural features—the absence of a $\Delta^{2,3}$ double

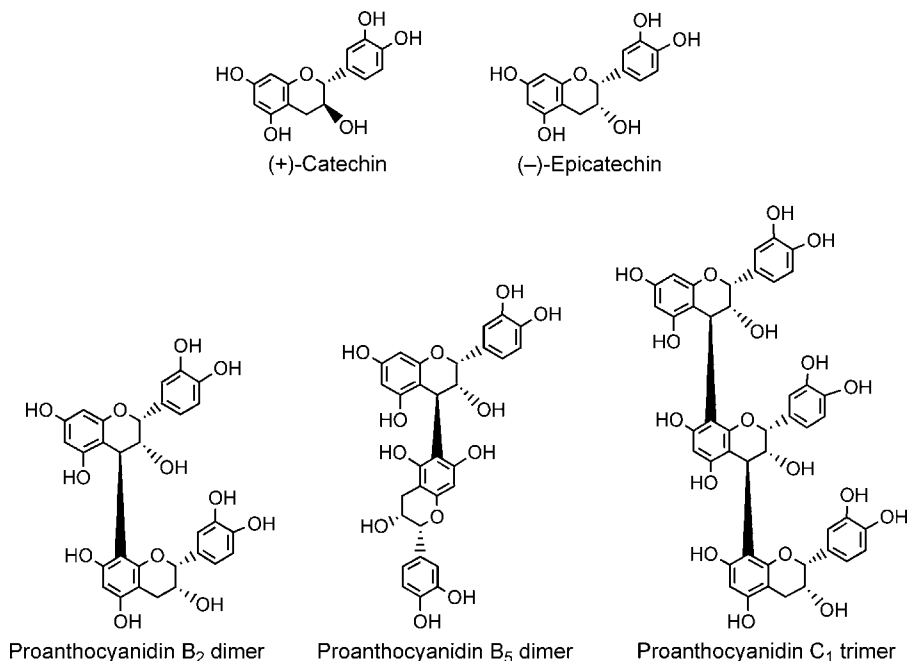


Figure 1.13 Monomeric flavan-3-ols and proanthocyanidin B₂, B₅ dimers, and C₁ trimer found in fresh cocoa beans.

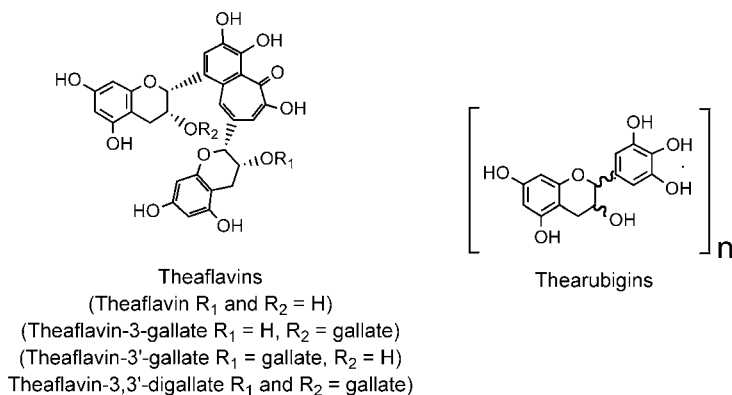


Figure 1.14 Theaflavins and thearubigins present in black tea.

bond and the presence of a chiral center at the carbon-2—characterize flavanones [Iwashina, 2000]. In the majority of naturally occurring flavanones, the C-ring is attached to the B-ring at C₂ in the α configuration.

The flavanone structure is highly reactive and has been reported to undergo hydroxylation, glycosylation, and *O*-methylation reactions. Flavanones are

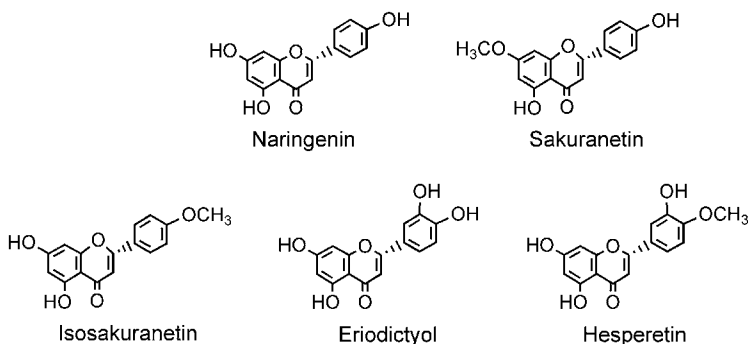


Figure 1.15 Structures of common flavanone aglycones.

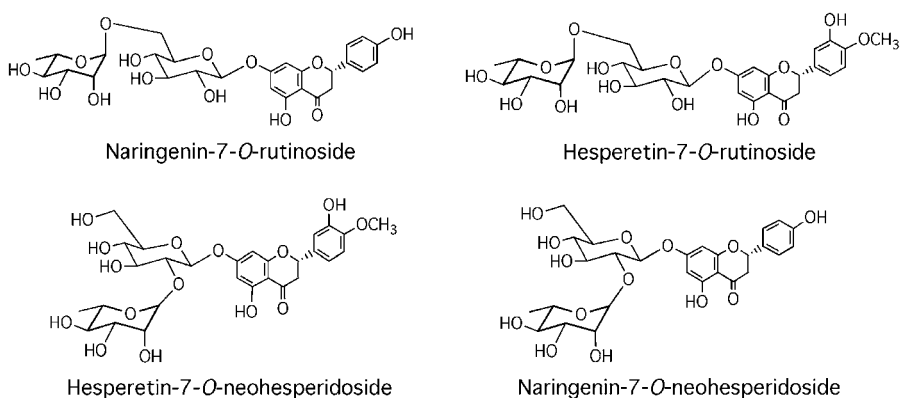


Figure 1.16 Flavanone conjugates in citrus fruit.

exclusively found in citrus fruits in their glycosidic forms. Grapefruit (*Citrus paradisi*) juice contains up to 377 mg L⁻¹ of naringin (naringenin-7-*O*-neohesperidoside) and orange juice, 16–84 mg L⁻¹ of narirutin (naringenin-7-*O*-rutinoside) [Manach et al., 2004; Tomás-Barberán and Clifford, 2000]. The peel is by far the richest part of citrus fruit in terms of its flavanone content. Substantial quantities of eriodictyol-7-*O*-rutinoside have been reported in lemon (*Citrus limon*) and lime (*Citrus aurantifolia*) [Peterson et al., 2006]. Flavanone rutinosides are tasteless, while neohesperidoside conjugates such as hesperetin-7-*O*-neohesperidoside (neohesperidin) from bitter orange (*Citrus aurantium*) and naringenin-7-*O*-neohesperidoside (naringin) from grapefruit peel (*Citrus paradisi*) have an intensely bitter taste (Fig. 1.16). Naringenin is also found in tomatoes and tomato-based products. Fresh tomatoes, especially the skin, also contain naringenin chalcone, which is converted to naringenin during the manufacture of tomato ketchup [Krause and Galensa, 1992]. Hesperetin-7-*O*-rutinoside has also been detected in kiwi fruit, while

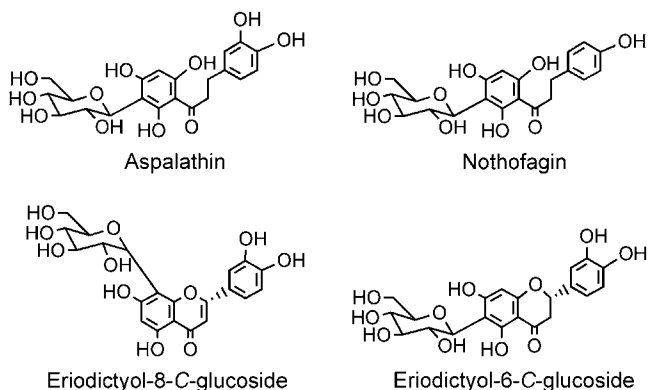


Figure 1.17 Hydroxychalcones occurring in unfermented rooibos tea and flavanone C-glycosides that accumulate during fermentation.

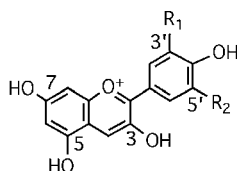
hesperetin-7-*O*-neohesperidoside was reported in bananas (*Musa cavendishii*) [Dégénéve 2004; Kanazawa and Sakakibara, 2000].

As mention earlier, rooibos tea, which is claimed to have a number of medicinal properties [Joubert and Ferreira, 1996; McKay and Blumberg, 2007], contains the flavone C-glycosides orientin and isoorientin. It also contains a number of rare dihydrochalcone C-glycosides, the main components being 2',3',4,4',6'-pentahydroxy-dihydrochalcone-3-*C*-glucoside (aspalathin) and 2',4,4',6'-tetrahydroxy-dihydrochalcone-3-*C*-glucoside (nothofagin). During fermentation aspalathin is oxidized to the flavanone C-glycosides eriodictyol-6-*C*-glucoside eriodictyol-8-*C*-glucoside (Fig. 1.17) [Krafczyk and Glomb 2008].

Anthocyanidins/Anthocyanins

Anthocyanins are water-soluble plant pigments and are particularly evident in fruit and flower tissue where they are responsible for a diverse range of red, blue, and purple colors. They occur primarily as glycosides of their respective aglycone anthocyanidin-chromophores (Fig. 1.18), with the sugar moiety typically attached at the 3-position on the C-ring or the 5-position on the A-ring [Prior and Wu, 2006]. They are involved in the protection of plants against excessive light by shading leaf mesophyll cells and also have an important role to play in attracting pollinating insects.

There are about 17 anthocyanidins found in nature, but only 6 — cyanidin, delphinidin, petunidin, peonidin, pelargonidin, and malvidin—are ubiquitously distributed and of dietary importance. The variation of anthocyanins are due to: (i) the number and position of hydroxyl and methoxy groups on the basic anthocyanidin skeleton; (ii) the identity, number, and positions at which sugars are attached; and (iii) the extent of sugar acylation and the identity of the



Anthocyanidin	R ₁	R ₂
Pelargonidin	H	H
Cyanidin	OH	H
Delphinidin	OH	OH
Peonidin	OCH ₃	H
Petunidin	OCH ₃	OH
Malvidin	OCH ₃	OCH ₃

Figure 1.18 Structures of major anthocyanins.

acylating agent [Prior and Wu, 2006]. Unlike other subgroups of flavonoids with the same C₆–C₃–C₆ skeleton, anthocyanins have a positive charge in their structure at acidic pH.

The most widespread anthocyanin in fruits is cyanidin-3-glucoside [Kong et al., 2003]. However, malvidin glycosides are the characteristic anthocyanins in red grapes and their derived products [Mazza and Miniati, 1993]. Other anthocyanins that occur in grapes include petunidin-3-*O*-glucoside, malvidin-3-*O*-(6''-*O*-*p*-coumaroyl)glucoside, malvidin-3-*O*-(6''-*O*-acetyl)glucoside, delphinidin-3-*O*-glucoside, and malvidin-3,5-*O*-diglucoside (Fig. 1.19) [Burns et al., 2001, 2002a].

Purple grape juice, from Concord grapes, a native American cultivar *Vitis labrusca*, which have a thicker skin and larger seeds than grapes of *Vitis vinifera*, is a rich source of more than 20 anthocyanins. The main components being 3-*O*-glucosides and 3,5-*O*-diglucosides of cyanidin, peonidin, delphinidin, and malvidin, delphinidin-3-*O*-(6''-*O*-acetyl)glucoside, delphinidin-3-*O*-(6''-*O*-*p*-coumaroyl)-5-*O*-diglucoside, and delphinidin-3-*O*-(6''-*O*-*p*-coumaroyl)glucoside (Fig. 1.20) [Wang et al., 2003; Mullen et al., 2007]

Anthocyanins occur in abundance in berries where they provide the fruits with their distinctive and vibrant palate of colors. Cranberry (*Vaccinium macrocarpon*), blackberry, and elderberry (*Sambucus nigra*) contain derivatives of only one type of anthocyanin (i.e., cyanidin), while a wide array of anthocyanins is found in blueberry (*Vaccinium corymbosum*) and blackcurrant (*Ribes nigrum*) (Fig. 1.21).

Anthocyanins such as cyanidin-3-*O*-rutinoside, cyanidin-3-*O*-glucoside, and peonidin-3-*O*-rutinoside (Fig. 1.22) have also been reported in sweet cherries (*Prunus avium*) and sour cherries (*Prunus cerasus*) [Wu et al., 2004].

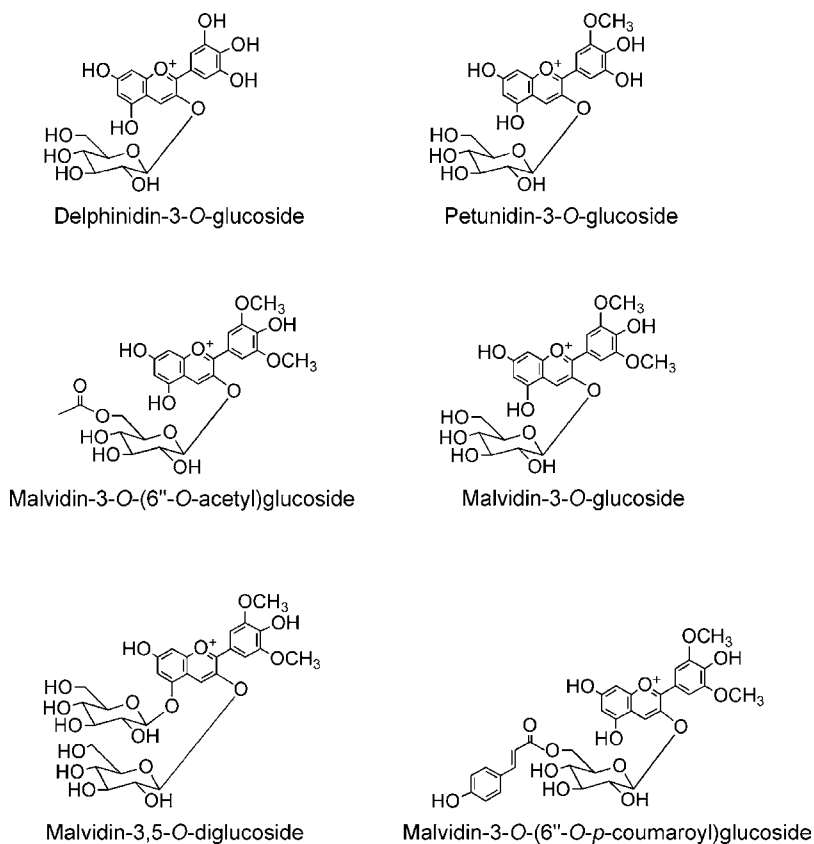


Figure 1.19 Anthocyanins found in red grapes.

Plums (*Prunus domestica*) and peaches are also a rich source of cyanidin-3-*O*-glucoside and cyanidin-3-*O*-rutinoside [Crozier et al., 2006c].

Red onions contain up to 250 mg kg⁻¹ anthocyanins [Clifford, 2000]; among the major components are cyanidin-3-*O*-(6''-malonyl)glucoside and cyanidin-3-*O*-(6''-malonyl)laminaribioside (Fig. 1.23) [Donner et al., 1997]. Cyanidin-3-*O*-(6''-malonyl)glucoside is also a component of the red-leaved Lollo Rosso lettuce [Ferreres et al., 1997], while 3-*O*-glucosides and 3,5-*O*-diglucosides of cyanidin and delphinidin have also been detected in pomegranate (*Punica granatum*) juice [Gil et al., 2000].

Isoflavones

In contrast to most other flavonoids, isoflavones are characterized by having the B-ring attached at C3 rather than the C2 position. They have a

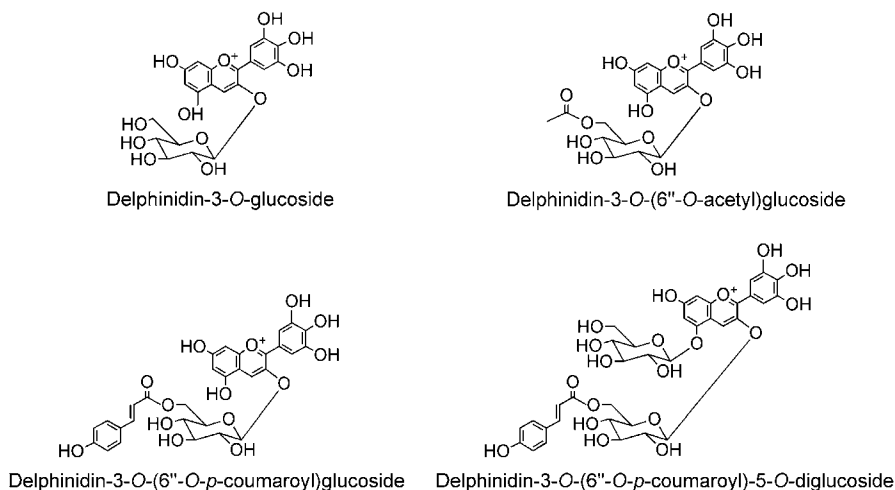


Figure 1.20 Purple grape juice anthocyanins.

very limited distribution in the plant kingdom with substantial quantities being found only in leguminous species [Graham, 1991; Dixon and Steele, 1999]. Isoflavones are known for their estrogenic activity due to their ability to bind to estrogen receptor and have received much attention due to their putative role in the prevention of breast cancer and osteoporosis [Barnes, 2003].

Worldwide, soybeans (*Glycine max*) are almost the sole dietary source of isoflavones. Common isoflavones such as genistein, daidzein, and glycitein (Fig. 1.24), also occur, albeit in low levels, in black beans (*Phaseolus vulgaris*) and green peas (*Pisum sativum*). In plants isoflavones occur predominantly as β -glucosides (genistin, daidzin, glycitin), or as acetyl- β -glucosides and malonyl- β -glucosides, and are therefore polar, water-soluble compounds [Coward et al., 1998]. Isoflavones also undergo various modifications, such as methylation, hydroxylation, or polymerization, and these modifications lead to simple isoflavonoids, such as isoflavanones, isoflavans, and isoflavanols, as well as more complex structures including rotenoids, pterocarpan, and coumestans [Dewick, 1993].

Isoflavones such as diadzein-7-O-(6''-O-malonyl)glucoside and diadzein-7-O-(6''-O-acetyl) glucoside (Fig. 1.25) occur in high concentrations in soybean [Barnes et al., 1994]. Formononetin and biochanin A (Fig. 1.24), present as 6''-O-malonyl-7-O-glucosides, 7-O-glucosides, and aglycones, are the most abundant isoflavones in red clover (*Trifolium pretense*), which is one of the ingredients used to extract isoflavones for dietary supplements [Delmonte

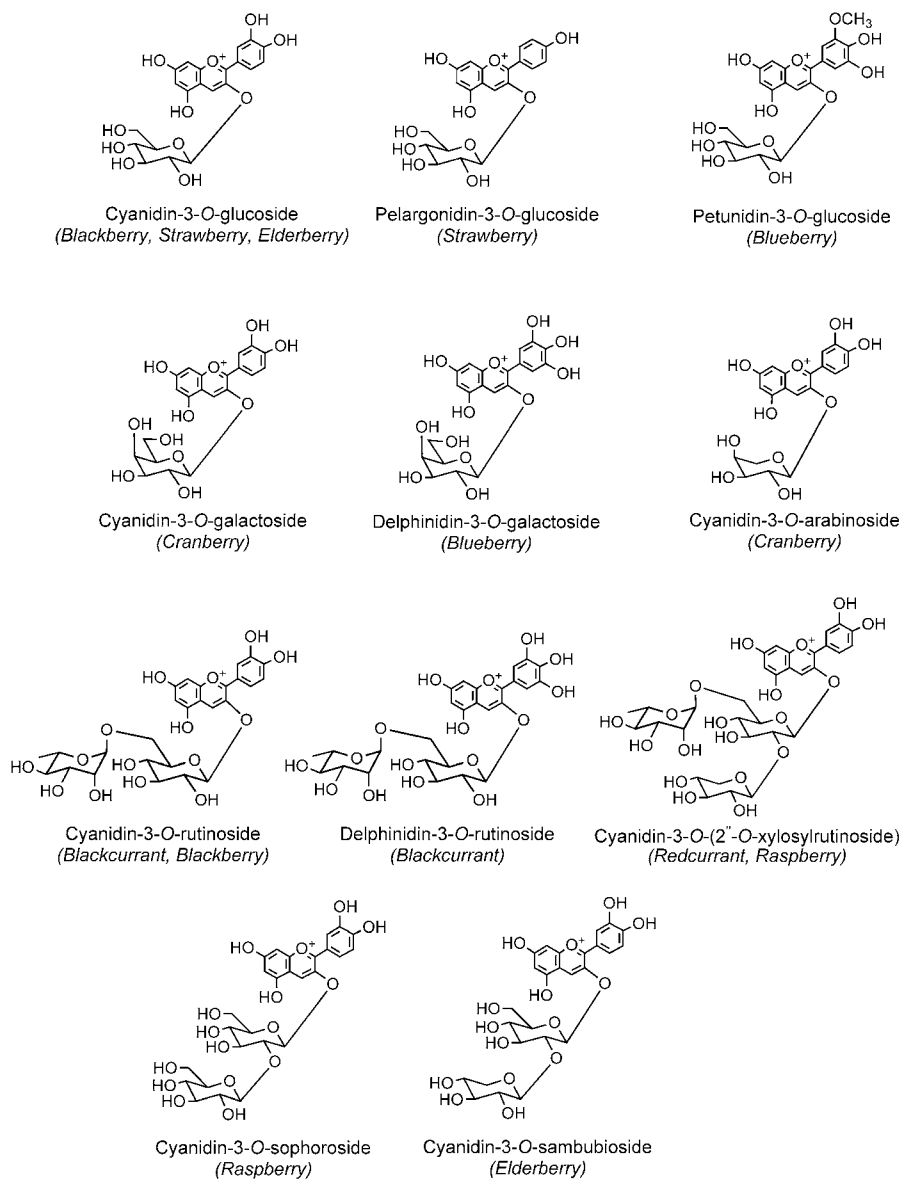


Figure 1.21 Major anthocyanins in berries.

et al., 2006]. Other than soya, *Pueraria lobata* (common name kudzu), a perennial vine native to Japan and China that also grows in the southeastern United States, is another commercial source of isoflavones for dietary supplements. Puerarin (daidzein-7-*C*-glucoside), daidzin (daidzein-7-*O*-glucoside), and daidzein are the main isoflavones in kudzu [Delmonte et al., 2006].

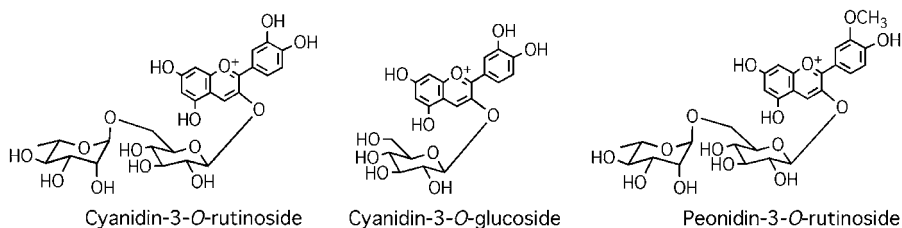


Figure 1.22 Anthocyanins present in cherries.

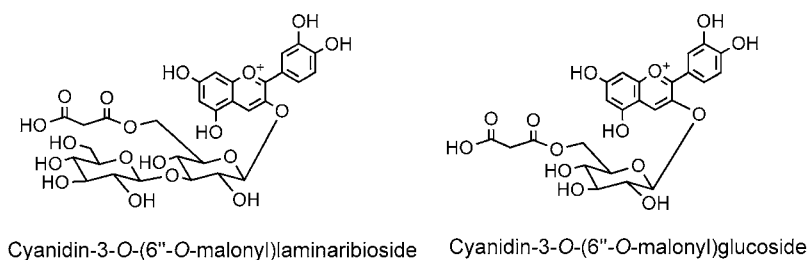


Figure 1.23 Main anthocyanins in red onions.

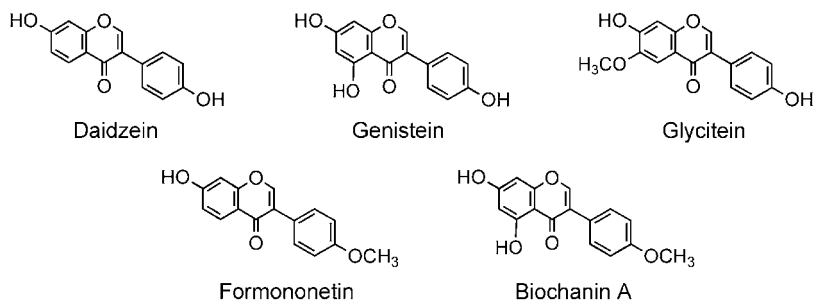


Figure 1.24 Structure of common isoflavone aglycones.

NONFLAVONOID PHENOLIC COMPOUNDS—STRUCTURE AND THEIR DIETARY OCCURRENCE

Phenolics are defined as compounds possessing one or more aromatic rings to which is attached at least one hydroxyl group. Phenolic compounds can be categorized as flavonoids and nonflavonoid phenolic compounds. The main nonflavonoid phenolic compounds of dietary significance are the C_6-C_1

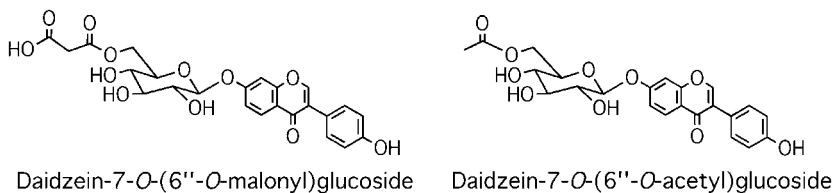


Figure 1.25 Legume isoflavone conjugates.

phenolic acids, the C₆–C₃ hydroxycinnamates and their conjugated derivatives, and the polyphenolic C₆–C₂–C₆ stilbenes.

Phenolic Acids

Phenolic acids are also known as hydroxybenzoates, and they are commonly represented by gallic, *p*-hydroxybenzoic, protocatechuic, vanillic, and syringic acids. Phenolic acids are usually present in the bound form and are typically components of complex structures such as lignins and hydrolyzable tannins. They can also be found as derivatives of sugars and organic acids in plant foods. Gallic acid is the base unit of gallotannins, whereas gallic acid and hexahydroxydiphenoyl moieties are both subunits of the ellagitannins, which are classified as hydrolysable tannins.

Ellagic acid has been reported to be present in berries, particularly raspberries (*Rubus idaeus*), strawberries, and blackberries [Amakura et al., 2000]. However, free ellagic acid is normally present in low levels in berries that more commonly contain ellagitannins, such as sanguin H-6 and lambertianin C, which release ellagic and gallic acid when treated with acid (Fig. 1.26) [Mullen et al., 2002].

Pomegranate juice is increasing in popularity and some, but far from all, commercial juices/drinks have a high ellagitannin and antioxidant content [Mullen et al., 2008]. Pomegranate juice contains gallagic acid, an analog of ellagic acid containing four gallic acid residues, and punicalagin, the principal monomeric, hydrolysable tannin, in which gallagic acid is bound to glucose (Fig. 1.27) [Gil et al., 2000]. Dates (*Phoenix dactylifera*), one of the oldest cultivated fruit, contain protocatechuic acid, vanillic acid, and syringic acid (Fig. 1.28) [Al-Farsi et al., 2005].

Free and bounded phenolic acids are also found in cereals. Different grains such as sorghum (*Sorghum bicolor*), millet (*Pennisetum americanum*), barley (*Hordeum vulgare*), wheat (*Triticum vulgare*), rice (*Oryza sativa*), oat (*Avena sativa*), and rye (*Secale cereale*) contain diverse phenolic acids such as gallic, protocatechuic, *p*-hydroxybenzoic, gentisic, salicylic, vanillic, and syringic acids [see Dykes and Rooney, 2007]. Hydroxybenzoic acid glycosides are also characteristic of some herbs and spices [Tomás-Barberán and Clifford, 2000]. After hydrolysis, protocatechuic acid is the dominant hydroxybenzoate in

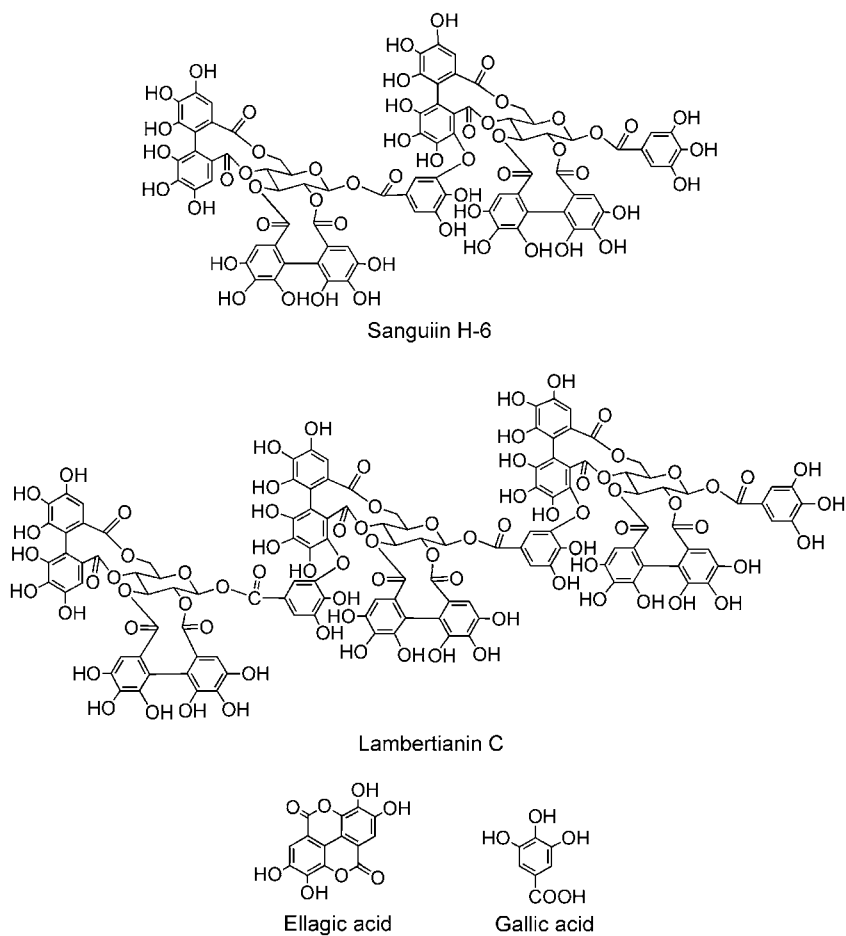


Figure 1.26 Ellagitannins and trace amounts of gallic acid and ellagic acid occur in raspberries.

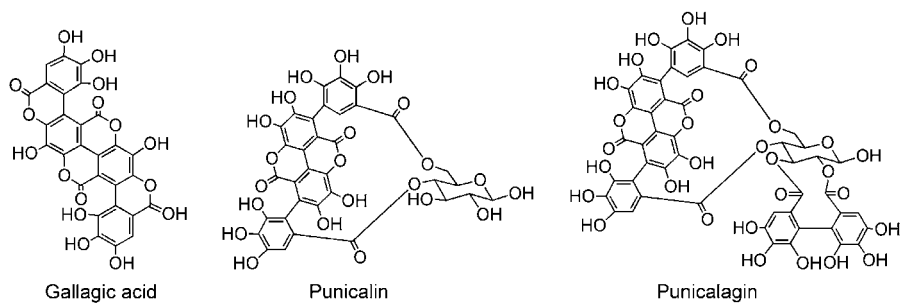


Figure 1.27 Ellagitannins detected in pomegranate juice.

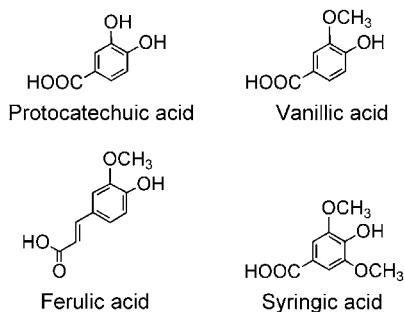


Figure 1.28 Phenolic acids in dates.

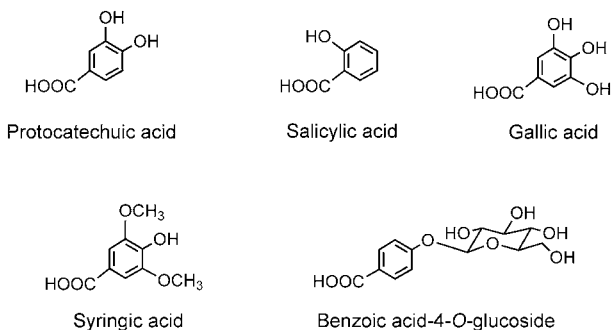


Figure 1.29 Some hydroxybenzoates derivative compounds found in herbs.

cinnamon bark accompanied by salicylic and syringic acid. Gallic acid occurs in clove buds (*Eugenia caryophyllata* Thunb.) along with protocatechuic and syringic acid (Fig. 1.29). Benzoic acid-4-*O*-glucoside is the common phenolic acid in many herbs such as in anise (*Pimpinella anisum*), star anise (*Illicium verum*), dill (*Anethum graveolens*), fennel (*Foeniculum vulgare*), caraway (*Carum carvi*), and parsley (*Petroselinum crispum*) (Fig. 1.25) [Crozier et al., 2006c].

Hydroxycinnammates

The most common hydroxycinnammates, *p*-coumaric, caffeic, and ferulic acids, frequently accumulate as their respective tartrate esters, coumaric, caftaric, and fertaric acids. Quinic acid conjugates of caffeic acid, namely 3-, 4-, and 5-*O*-caffeoylquinic acid, which belong to a family of hydroxycinnamate-quinic acid conjugates known as chlorogenic acids, are commonly found in fruits and vegetables. Fruits such as apples and dates (*Phoenix dactylifera*) are a good source of diverse phenolic compounds. 5-*O*-Caffeoylquinic acid, 4-*O*-*p*-coumaroylquinic acid, and caffeic acid have been detected in apples [Clifford et al., 2003; Kahle et al., 2005], while dates contain ferulic acid [Crozier et al., 2006c].

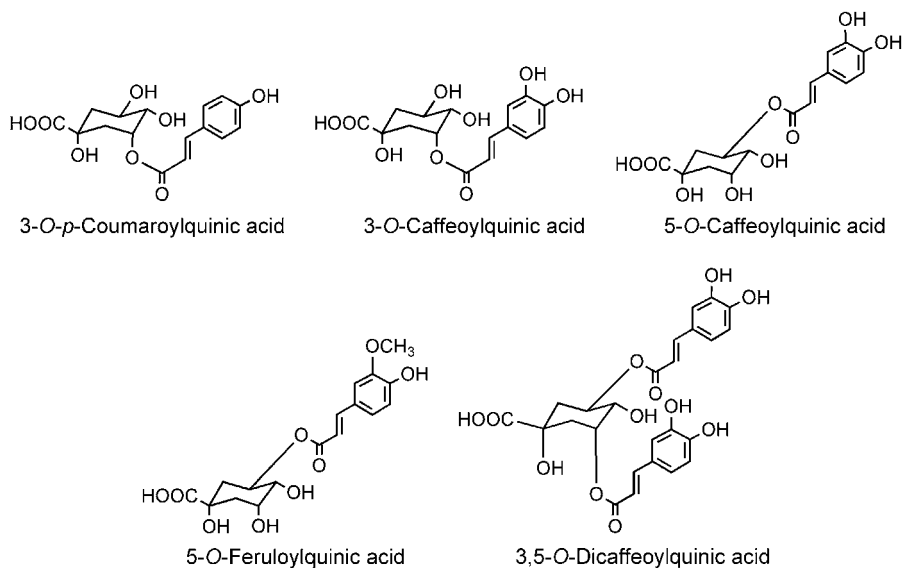


Figure 1.30 Chlorogenic acids in carrots.

Carrots (*Daucus carota*) contain a range of chlorogenic acids including 3-*O*- and 5-*O*-caffeoylquinic acids, 3-*O*-*p*-coumaroylquinic acid, 5-*O*-feruloylquinic acid, and 3,5-*O*-dicaffeoylquinic acids (Fig. 1.30). These chlorogenic acids are found in almost all varieties of carrot with a 10-fold higher level of 5-*O*-caffeoylquinic acid in purple carrots [Alasalvar et al., 2001].

The red-leaved lettuce Lollo Rosso contains the hydroxycinnammates caffeoyltartaric acid, dicaffeoyltartaric acid, 5-*O*-caffeoylquinic acid, and 3,5-*O*-dicaffeoylquinic acid (Fig. 1.31) [Ferrerres et al., 1997]. 5-*O*-Caffeoylquinic acid has also been detected in tomatoes [Paganga et al., 1999].

Green coffee beans (*Coffea arabica*) are one of the richest dietary sources of chlorogenic acids. 5-*O*-Caffeoylquinic acid is the dominant chlorogenic acid accounting for 50% of the total. This is followed by 3-*O*- and 4-*O*-caffeoylquinic acid, the three analogous feruloylquinic acids and 3,4-*O*-, 3,5-*O*- and 4,5-*O*-dicaffeoylquinic acids (Fig. 1.32) [Clifford, 1999]. Levels decline ca. 80% during the roasting of coffee beans, but sizable amounts with substantial antioxidant activity are still found in the typical cup of coffee.

There is also dietary interest in the curcuminoids, which are cinnamoyl-methanes (diaryl-heptenoids), are characteristic of ginger (*Zingiber officinale*), cardamon (*Elettara cardamonum*), and turmeric (*Curcuma longa*). Curcumin is a diferuloylmethane. Three curcuminoids, curcumin, demethoxycurcumin, and bisdemethoxycurcumin (Fig. 1.33), are the principal components in tumeric, and all three impart the yellow pigmentation that is a hallmark of the spice [Jayaprakasha et al., 2005].

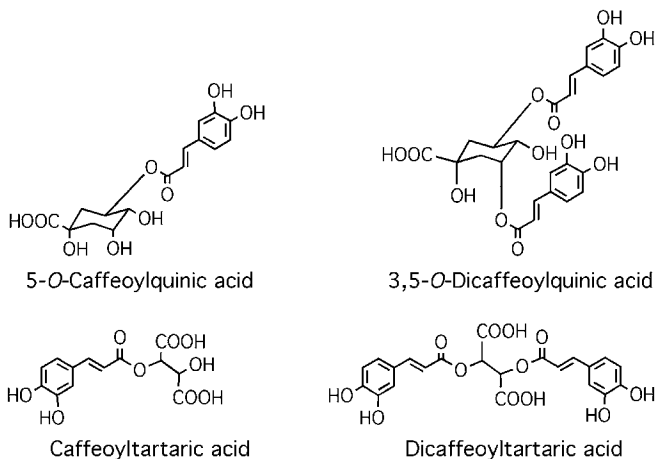


Figure 1.31 Hydroxycinnammates in Lollo Rosso lettuce.

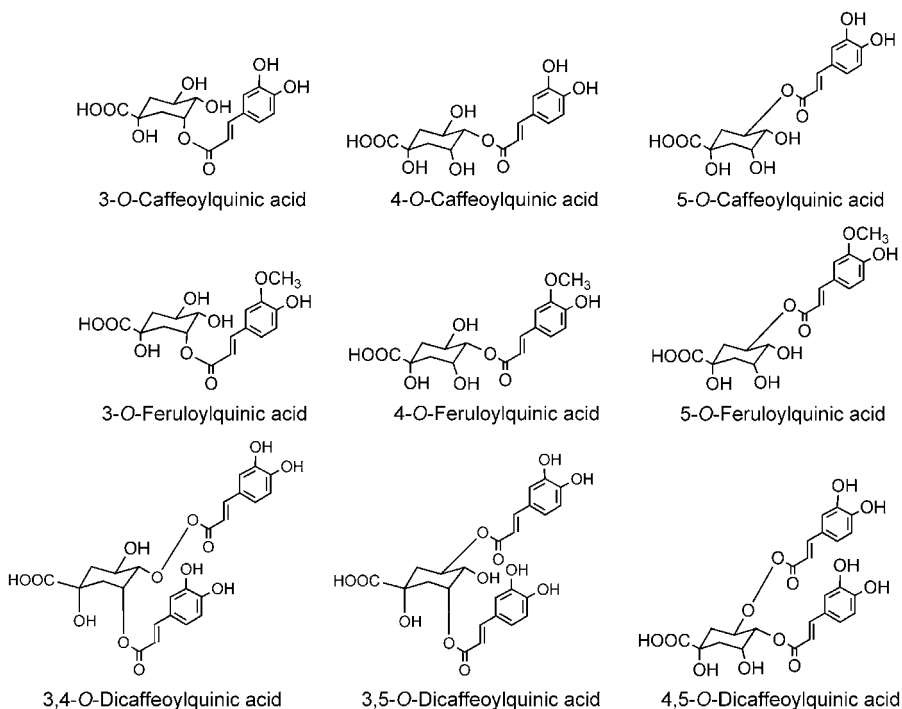


Figure 1.32 Main chlorogenic acids in green coffee beans.

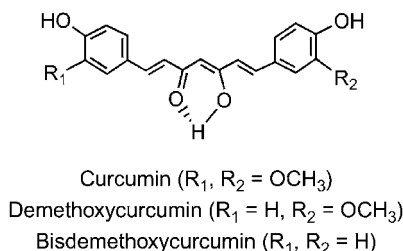


Figure 1.33 Curcuminoids accumulate in the rhizomes of turmeric.

Stilbenes

Members of the stilbene family have the $\text{C}_6\text{--C}_2\text{--C}_6$ structure and are phytoalexins produced by plants in response to disease, injury, and stress (Fig. 1.34) [Langcake and Pryce, 1977]. The main dietary source of stilbenes is resveratrol (3,5,4'-trihydroxystilbene) from red wine and peanuts (*Arachis hypogaea*) [Burns et al., 2002b] with lesser amounts found in berries, red cabbage (*Brassica oleraceae*), spinach, and certain herbs. Resveratrol occurs as *cis* and *trans* isomers and *trans*-resveratrol and *trans*-resveratrol-3-*O*-glucoside (*trans*-piceid) have recently been detected in pistachio nuts (*Pistacia vera* L.) [Grippi et al., 2008].

The woody root of the noxious weed *Polygonum cuspidatum* (Japanese knotweed or Mexican bamboo) has been shown to contain very high levels of *trans*-resveratrol and its glucosides with concentrations of up to $377 \text{ mg } 100 \text{ g}^{-1}$ dry weight [Vastano et al., 2000]. As well as resveratrol, Brazilian red wines have been shown to contain *trans*-piceatannol (3,3',4,5'-tetrahydroxystilbene) and *trans*-astringin, its 3-*O*-glucoside [Vitrac et al., 2005] *trans*-resveratrol is transformed by *Botrytis cinerea*, a fungal grapevine pathogen, to pallidol and resveratrol *trans*-dehydrodimer, and both these compounds have been detected in grape cell cultures along with the 11-*O*- and 11'-*O*-glucosides of resveratrol *trans*-dehydrodimer [Waffo-Téguo et al., 2001]. Viniferins are another family of oxidized resveratrol dimers [Langcake and Pryce, 1977], and δ -viniferin and smaller amounts of its isomer δ -viniferin have been detected in *Vitis vinifera* leaves infected with *Plasmopara viticola* (downy mildew) [Pezet et al., 2003].

trans-Resveratrol that has gained significant worldwide attention because of its ability to inhibit or retard a wide variety of animal diseases [Baur and Sinclair, 2006] that include cardiovascular disease [Bradamante et al., 2004] and cancer [Jang et al., 1997]. It has also been reported to increase stress resistance and enhance longevity [Baur et al., 2006; Valenzano et al., 2006]. The protective effects of red wine consumption are regularly attributed to resveratrol [Kaeberlein and Rabinovitch, 2006]. However, this is highly unlikely as the levels of resveratrol in red wines are low, and for humans to ingest the quantity of resveratrol that affords protective effects in animals they would have to drink in excess of 100 L of red wine per day [Corder et al., 2003].

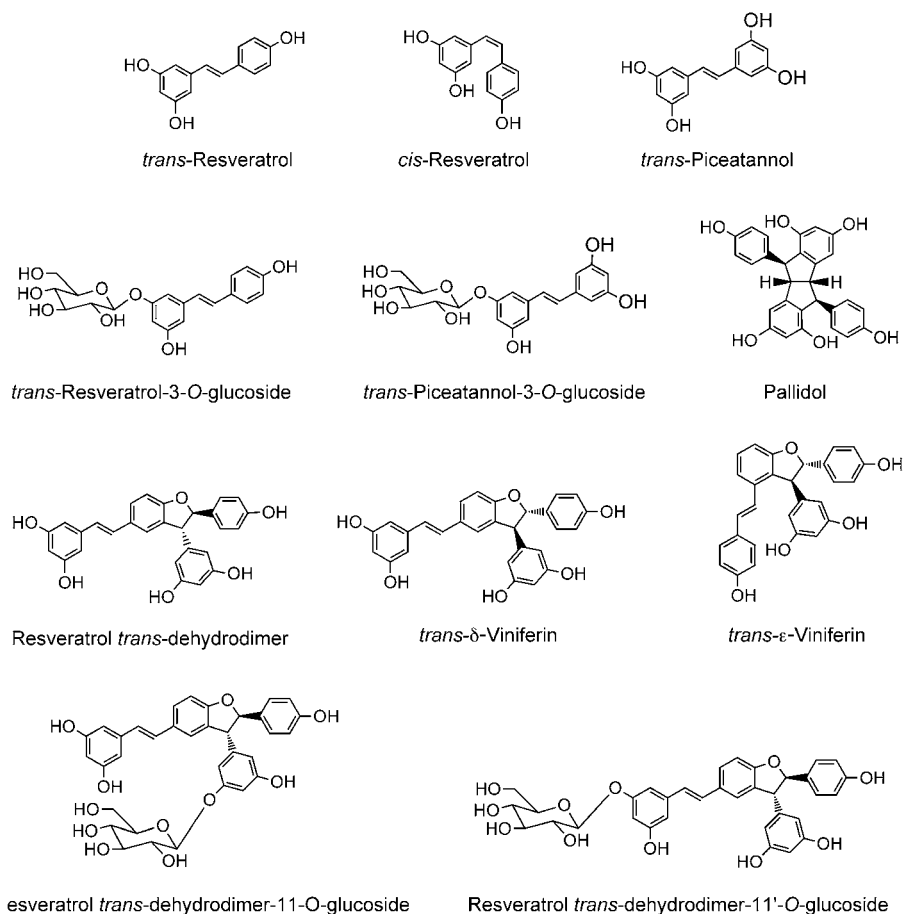


Figure 1.34 Structures of the *trans*- and *cis*-resveratrol and other stilbenes.

OVERVIEW OF FLAVONOID AND PHENOLIC BIOSYNTHETIC PATHWAYS

The biosynthesis of flavonoids, stilbenes, hydroxycinnamates, and phenolic acids involves a complex network of routes based principally on the shikimate, phenylpropanoid, and flavonoid pathways (Figs. 1.35 and 1.36). These biosynthetic pathways constitute a complex biological regulatory network that has evolved in vascular plants during their successful transition on land and that ultimately is essential for their growth, development, and survival [Costa et al., 2003].

From the 1970s to the 1990s, there was a rapid and substantial progress in the research on the phenylpropanoid pathway, focusing mainly on a broad understanding of the metabolic pathway [Hahlbrock and Grisebach, 1975; Ebel and Hahlbrock, 1982; Heller and Forkmann, 1988]. However, in more recent

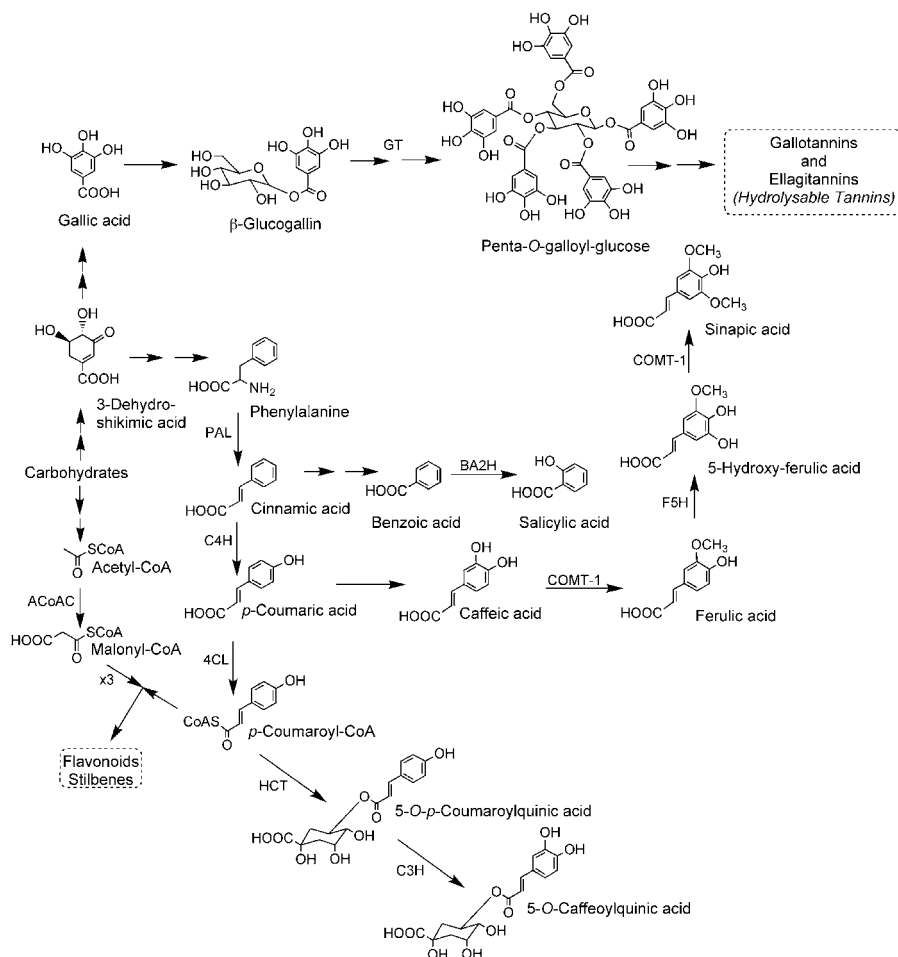


Figure 1.35 Schematic diagram of the phenolic biosynthetic pathway accompanied by the key enzymes involved. Enzyme abbreviations: PAL, phenylalanine ammonia-lyase; BA2H, benzoic acid 2-hydroxylase; C4H, cinnamate 4-hydroxylase; COMT-1, caffeic/5-hydroxyferulic acid *O*-methyltransferase; 4CL, *p*-coumarate:CoA ligase; F5H, ferulate 5-hydroxylase; GT, galloyltransferase; ACoAC, acetylCoA carboxylase.

years, much effort has been directed at elucidating the phenylpropanoid biosynthetic pathway from a biochemical and a molecular point of view by using approaches such as transposon tagging, positional cloning, co-immunoprecipitation, affinity chromatography, and two-hybrid experiments mainly utilizing *Arabidopsis thaliana* as a test system [Winkel-Shirley, 2001]. New information is also emerging regarding the regulation of the phenylpropanoid pathway. In the last few years, a great deal has been learned from studies in a variety of plant species, primarily about transcriptional regulation. A number of these studies were carried out using flavonoid mutants generated by

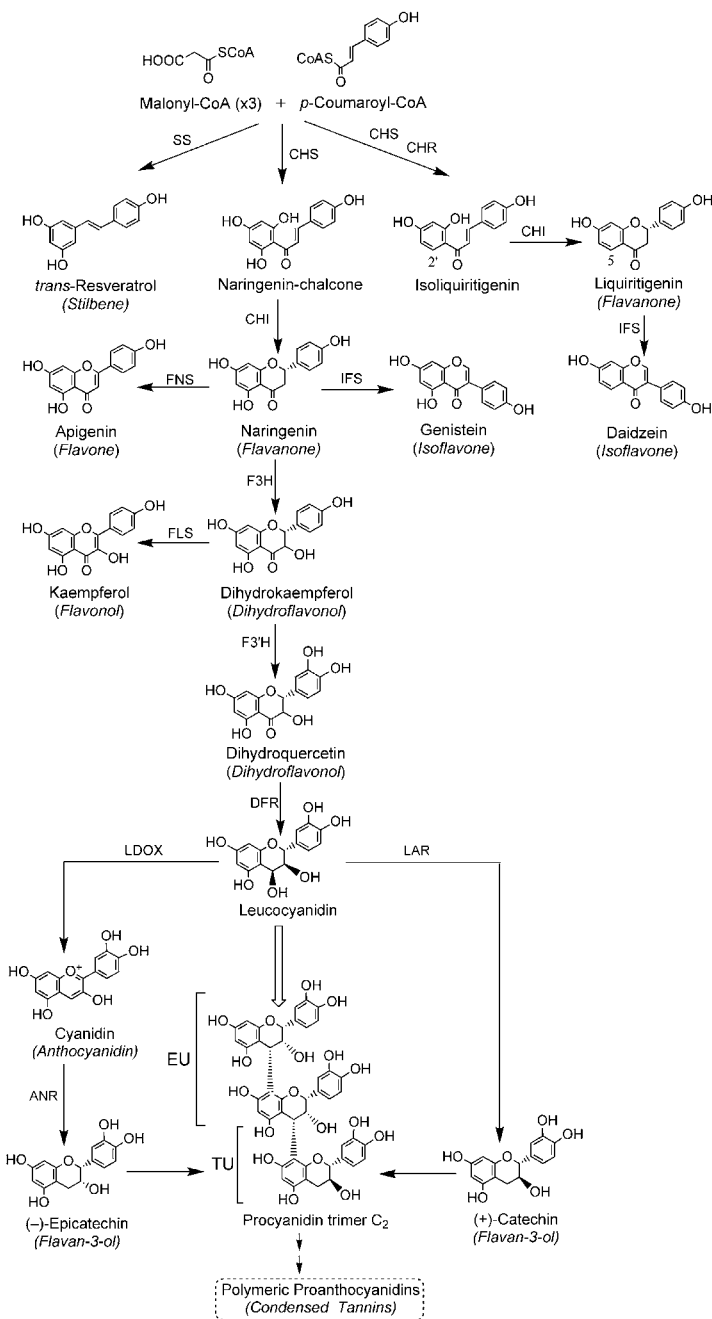


Figure 1.36 Schematic diagram of the stilbene and flavonoid biosynthetic pathway. Enzyme abbreviations: SS, stilbene synthase; CHS, chalcone synthase; CHR, chalcone reductase; CHI, chalcone isomerase; IFS, isoflavone synthase; FNS, flavone synthase; F3H, flavanone 3-hydroxylase; FLS, flavonol synthase; F3'H, flavonoid 3'-hydroxylase; DFR, dihydroflavonol 4-reductase; LAR, leucoanthocyanidin 4-reductase; LDOX, leucocyanidin deoxygenase; ANR, anthocyanidin reductase; EU, extension units; TU, terminal unit.

activation tagging [Borevitz et al., 2000; Mathews et al., 2003]. Characterization of flavonoid mutants in a variety of plant species has led to the identification of a number of novel regulatory proteins that are beginning to fill in the void between signals that induce the pathway and well-known flavonoid regulators such as the myb domain and basic helix–loop–helix transcription factors [Winkel-Shirley, 2001]. In addition, increasing evidence is being generated demonstrating that as well as inducing the phenylpropanoid pathway, these transcriptional regulators also influence the modification, transport, and deposition of metabolites in the vacuole [Broun, 2004].

In addition to the molecular techniques, technical advances both in chromatographic techniques and in identification tools, particularly the diverse forms of mass spectrometry, has allowed successful challenges to the separation and characterization of compounds of increasing complexity, poor stability, and low abundance [Whiting, 2001]. Information generated utilizing these techniques has resulted in characterization of a plethora of complex secondary metabolites that, in conjunction with the characterization of the enzymatic steps, has permitted the complete or partial elucidation of the flavonoid and the phenolic pathways present in many plants (Figs. 1.35 and 1.36).

Comprehensive information on the network of pathways responsible for the synthesis of numerous secondary metabolites can be found in Chapter 21. In addition, information on this aspect is also available in articles by Shimada et al. [2003], Toshiaki [2003], Tanner et al. [2003], Boatright et al. [2004], Hoffmann et al. [2004], Dixon et al. [2005], Niemetz and Gross [2005], Xie and Dixon [2005], and Ferrer et al. [2008]. Nonetheless, the complete dissection of phenolic metabolic pathway is far from being complete. For example, recent reports underline that important questions still remain to be answered in the field of protoanthocyanidins and tannins [Xie and Dixon, 2005], and that the exact nature of the biosynthetic pathway(s) leading to lignin monomers has not been fully elucidated [Boudet, 2007].

An example of the phenolic pathway, which produces secondary metabolites that have health benefiting effects, is the biosynthesis of curcuminoids. The initial investigations into the biosynthesis of curcuminoids were carried over 25 years ago [Denniff and Whiting, 1976; Macleod and Whiting, 1979; Denniff et al., 1980], although little has been done subsequently to elucidate fully the routes involved. The proposed biosynthetic pathway is presented in Figure 1.37. The curcuminoids are thought to be formed from condensation of two molecules of *p*-coumaroyl-CoA with one molecule of malonyl-CoA via the action of possibly a polyketide synthase. The resulting bisdemethoxycurcumin would then be transformed through demethoxycurcumin into curcumin via two sequential rounds of hydroxylation followed by *O*-methylation. Alternatively, it is possible that the curcuminoid synthase enzyme may utilize the CoA esters of both *p*-coumaric acid and ferulic acid as substrates [Ramirez-Ahumada et al., 2006].

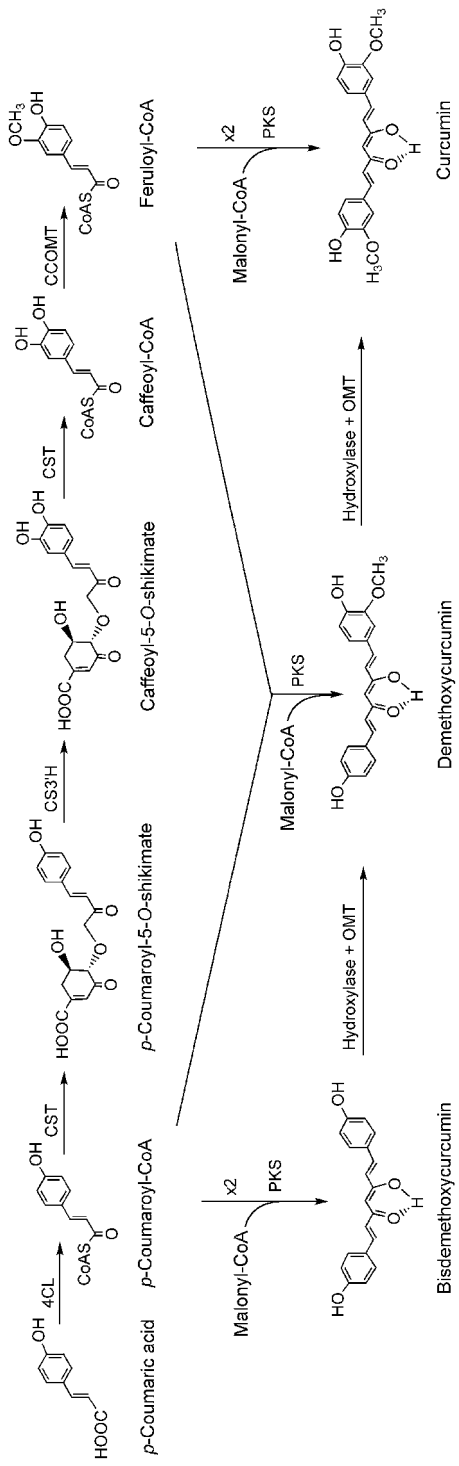


Figure 1.37 Proposed biosynthetic pathway of curcuminoids in tumeric. Enzyme abbreviations: CCOMT, caffeoyl-CoA *O*-methyltransferase; 4CL, 4-coumarate:CoA ligase; CST, shikimate transferase; CS³H, *p*-coumaroyl 5-*O*-shikimate 3'-hydroxylase; OMT, *O*-methyltransferase; PKS, polyketide synthase. [Adapted from Ramirez-Ahumada et al. (2006)]

OPTIMIZATION OF THE FLAVONOID AND PHENOLIC PROFILES IN CROP PLANTS

The recent increase in consumer awareness on the health benefits of dietary phytochemicals accompanied by the rapid progress in the field of molecular biology have provided the means and incentive to enhance the functional value of plant material. This enhancement of health-promoting compounds is being tackled using a variety of approaches, which are discussed in the ensuing sections.

Agronomical and Physiological Modifications

Abiotic and biotic stresses are known to induce the accumulation of phenolic and flavonoid compounds in many higher plants. As sessile organisms, plants rely on the accumulation of such chemicals for defense, protection, cell-to-cell signaling, and other stress adaptations. As such, wild-type berries from harsh environmental growing regimes were found to be among the most biologically potent in terms of antioxidant content compared to their commercially grown counterparts [Deighton et al., 2000; Reyes-Carmona et al., 2005]. Hence agronomic manipulation by the application of mild stress at defined points during the growing season may have generic effects on phenolic and flavonoid accumulation. This is why deliberate stress on the target plants that are specifically cultivated for their health-benefiting compounds is now becoming a popular research strategy. Environmental deprivation, such as exposure of plants to low temperatures, as well as heavy metals, wounding, desiccation, and high irradiance are typical triggers that switch on a biochemical pathway cascade leading to increased secondary product accumulation [Lila, 2006].

High temperature is known to reduce and low temperature to enhance anthocyanin synthesis [Saure, 1990; Leng et al., 2000]. This was observed in Starkrimson and Golden Delicious apples where there was rapid anthocyanin accumulation in the skin in cooler habitats compared to warmer climates [Li et al., 2004]. Similarly, when grapes were grown under low night temperatures, anthocyanin synthesis, L-phenylalanine ammonia-lyase activity and *chalcone synthase 3* transcript levels were all markedly higher [Mori et al., 2005]. Apart from temperature, it has long been known that UV radiation, specifically the UV-B, can up-regulate key genes such as the *phenylalanine ammonia-lyase* [Kuhn et al., 1984] and *chalcone synthase* [Christie and Jenkins, 1996]. This up-regulation of the genes in the phenylpropanoid pathway is part of the plant's ability to offset the absorption of excessive UV radiation by accumulating UV-filtering secondary metabolites such as flavonols [Cuadra et al., 1997] and anthocyanins [Oelmüller and Mohr, 1985]. Similarly, investigations with apples have shown that covering the orchard floor with metallic foil in an effort to reflect increased light into the canopy resulted in an increase in anthocyanin concentration in the skin of the fruit [Ju et al., 1999].

Agronomical manipulation has also been employed to improve the phytochemical content in plants. In a number of investigations, anthocyanins were observed to accumulate in plants deficient in nutrients such as phosphorus and nitrogen [Cobbina and Miller, 1987; Hodges and Nozzolillo, 1996; Close et al., 2000]. In another study, it was found that production of the isoflavones, daidzein and genistein, could be modulated by changing the ammonia/nitrate ratio. In bean plants cultured on phosphorus-deficient media, higher concentrations of anthocyanins were found in the leaves, and this may play a role in protecting the plant against oxidative stress [Juszczuk et al., 2004]. Substantial variability in the levels of caffeoylquinic, sinapic, and ferulic acid derivatives in eight broccoli (*Brassica oleracea*) cultivars grown under different agronomic conditions has also been reported by Vallejo et al. [2003]. In tomato, in addition to increasing flavonoid content, nitrogen stress also produces differential effects on expression of genes encoding anthocyanin biosynthetic enzymes [Bongue-Bartelsman and Phillips, 1995].

Another popular way to enhance the production of bioactive compounds is through elicitation. In this process, target plants are deliberately challenged with chemicals that trigger physiological responses that mimic the parallel environmental challenges. This in turn results in the accumulation of specific phytochemicals. This may include abiotic elicitors, such as metal ions and inorganic compounds, and biotic elicitors including fungi, bacteria, viruses or herbivores, plant cell wall components, as well as chemicals that are released by plants when they are subjected to pathogen or herbivore attack [Zhao et al., 2005]. Two well-known elicitors are salicylic acid and jasmonic acid, and these compounds have frequently been added to cell cultures to induce the accumulation of compounds with potential health benefits including flavonoids and phenylpropanoids [Zhao et al., 2005]. Other natural elicitors such as fish protein hydrolysates and lactoferrin have also been used. These elicitors stimulate the phenylpropanoid pathway in mung bean sprouts, probably through the pentose phosphate and shikimate pathways. This resulted in significant improvement of the phenolic content and antioxidant and antimicrobial properties of mung bean sprouts [Randhir et al., 2004]. In another study, preharvest treatment with benzothiadiazole increased *trans*-resveratrol and anthocyanin levels in grapevine [Iriti et al., 2004]. Further investigations revealed that five monoglucosides of delphinidin, cyanidin, petunidin, peonidin, and malvidin, accompanied by the corresponding acetylated and *p*-coumaroyl derivatives, were enhanced by benzothiadiazole treatment [Fumagalli et al., 2006]. Plant hormones can also affect the phenolic and flavonoid content of plants as revealed in a number studies [Jeong et al., 2004; Peppi et al., 2007; Kondo and Inoue, 1997].

Genetic Manipulation—Conventional Breeding and Genetic Engineering

The roles that dietary flavonoids and phenolic compounds play in promoting human health have stimulated intense interest in genetically manipulating their

accumulation in plants, through either conventional or molecular means. Genetic variability is one of the key factors in determining the amount of functional metabolites that accumulate in plants. Conventional breeding and cross-varietal screening tests have repeatedly revealed that genotypes within a plant species can have widely divergent levels of phytochemicals. For example, a number of different cultivars and species of blueberries exhibited varying levels of anthocyanins and proanthocyanidins, which were tightly correlated with the antioxidant capacity of fruit extracts [Kalt et al., 2001]. Enhanced lycopene and flavonoid levels have also been reported in some varieties of tomato and these lines are currently the preferred hosts for further genetic manipulation through conventional and molecular breeding [Long et al., 2006]. However, it is important to note that even though these genotypes are known to be capable of accumulating enhanced levels of specific phytochemicals, the final content is dependent on the selective pressure imposed by the environment. Genes are not always expressed, but instead can be triggered by environmental signals that may ultimately become the principal determinant for the accumulation of key secondary products. It is, therefore, important to note that gene–environment interactions are inherent as plants grow, which makes it difficult to predict phytochemical responses based on heritable traits and distinguish them from environmental influences [Lila, 2007]. The influences of the genome and the environment can be resolved through rigorous comparative tests of the identical plant genotypes in multiple environments followed by gene sequencing and phytochemical profiling of selected candidate plants [Taylor et al., 2002, Lim et al., 2005; Mpofu et al., 2006].

Due to the rapid speed at which knowledge of the genetic control of plant secondary metabolism has grown, it is hypothesized that over the next 25 years the most significant changes in the productivity and quality of crops will come about by applying genetic engineering tools. Normally, genetic engineering of a secondary metabolic pathway aims to increase the quantity of an individual or a group of specific compounds in the normal producing plant species or to transfer a pathway, or part of a pathway, to other plant species [Verpoorte and Memelink, 2002]. To increase the production of the compound(s) of interest, two general approaches have been followed. First, the structural genes encoding enzymes that participate directly in the formation of the compound of interest can be overexpressed. This is to enable the genetically modified plant to overcome specific rate-limiting steps in the pathway, to shut down competitive pathways, and to decrease catabolism of the product of interest. Secondly, attempts have been made to change the expression of regulatory genes that control the expression of the structural genes [Verpoorte and Memelink, 2002]. Regulatory genes control the expression of structural genes through the production of proteins called transcriptional factors. Transcriptional factors are believed to play an important role in regulating secondary metabolism pathways. Since transcriptional factors are able to control multiple steps within a pathway, they are potentially more powerful than structural genes that

control only a single step, when attempting to manipulate metabolic pathways in plants [Broun, 2004].

The best studied route at the genetic level is the flavonoid biosynthesis pathway leading to the formation of anthocyanins. Most of the structural and several regulatory genes involved in this pathway have now been cloned. The use of structural genes in metabolic engineering was used by Jung et al. [2000] who introduced the *isoflavone synthase* gene into the nonlegume arabidopsis (*Arabidopsis thaliana*) in order to convert naringenin, which is ubiquitous in higher plants, to the isoflavone genistein. In another study, chalcone isomerase (CHI), the key enzyme to increased flavonol production, was overexpressed in tomato. Results revealed a 78-fold increase of flavonol levels in the skin of tomatoes [Muir et al., 2001]. To date, several *leucoanthocyanidin reductase* (*LAR*) and/or *anthocyanidin reductase* (*ANR*) genes have been cloned and characterized from different plant species [Tanner et al., 2003; Xie et al., 2003; Bogs et al., 2005; Pang et al., 2007; Paolocci et al., 2007]. When the *ANR* gene was overexpressed in barrel clover (*Medicago truncatula*) and tobacco (*Nicotiana tabacum*), accumulation of proanthocyanidins was observed with a corresponding reduction of anthocyanin levels [Bogs et al., 2005; Xie et al., 2006]. Beyond the modified expression of one gene, more sophisticated strategies have been adopted such as the simultaneous introduction by cotransformation of a sense and an antisense construct to simultaneously up-regulate one enzyme and down-regulate another. For example, aspen trees (*Populus tremuloides*), expressing both antisense 4-coumarate-CoA ligase and sense coniferaldehyde 5-hydroxylase, had 52% reduced lignin content and a 64% higher syringyl/guaiacyl ratio [Li et al., 2003].

To control expression of structural genes, regulatory genes such as *LC*, *CI*, *MYB*, *HLH*, and the like are used. In an investigation where *LC* and *CI* genes were overexpressed in tomatoes, an increase in flavonols in the flesh of the fruit was observed. The total flavonol content of these overexpressed ripe transgenic tomatoes were ca. 20-fold higher than that of the controls where flavonol production occurred only in the skin [Bovy et al., 2002; Le Gall et al., 2003]. Similarly, when the *LC* gene was introduced into apple, both anthocyanin and proanthocyanidin accumulation was observed, and this was accompanied by induction of both the anthocyanin pathway genes and proanthocyanidin-specific pathway genes such as *LAR* and *ANR* [Li et al., 2007]. MYB and bHLH transcription factor is envisaged to be central to the control of proanthocyanidin biosynthesis. When two MYB transcription factors, AtTT2 and PAP1, together with one bHLH transcription factor, were introduced into Arabidopsis, the *ANR* gene was induced, which resulted in anthocyanin and proanthocyanidin accumulation [Sharma and Dixon, 2006].

Engineering of novel natural products by enzymatic modifications of core skeletons is another method where molecular tools are used to produce a range of novel products with enhanced/modified bioactivity. This is mainly carried out because the distribution of many of these compounds are either restricted or they accumulate at low levels, which is insufficient for large-scale extraction

[Tian et al., 2008]. Modifications to the ring structure and/or acyclic side structure of aglycones through the use of specific modification enzymes can be carried out to cause oxidation, *C*- or *O*-methylation, *C*- or *O*-glycosylation, and *C*- or *O*-prenylation to produce a range of phytochemical derivatives. Genes encoding some of the modification enzymes have been cloned and characterized in recent years using genetic, genomic, and biochemical approaches. The use of this method to produce a range of novel isoflavonoids has been reviewed in detail by Tian et al. [2008].

One of the major drawbacks of targeted induced modifications of key enzymes of phenolic and flavonoid metabolism, aiming to increase or decrease a specific phytochemical, is the observation of unexpected effects. This may be due partly to the effect of combined outcomes of a complex interplay of various metabolic pathways and variation between plant species. Other than the internetworking and regulation of endogenous pathways, the final result of metabolic engineering is also dependent on a number of factors such as the approach used, the encoded function of the introduced gene, and the type of promoter [Lessard et al., 2001; Broun, 2004]. Besseau et al. [2007] recently exhibited how network complexity and pathway interactions observed between different branches of phenolic biosynthesis resulted in an unexpected array of events. In arabidopsis plants silenced for hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase (HCT) expression lignin repression led to an increase in chalcone synthase activity, which resulted in a metabolic flux into flavonoid pathway. Correlated with this was a prominent reduction in plant growth. When this process was reversed through the repression of *chalcone synthase* expression in HCT-silenced plants, the wild-type plant growth was restored. The results suggest that the dwarf phenotype may be due to an indirect effect of ectopic flavonoid accumulation altering auxin transport [Boudet, 2007].

In several cases, studies on overexpression of genes have resulted in the production of unexpected products, as revealed by Bovy et al. [2002] when C1 and R transcriptional factors were cloned into tomato. Although several flavonoid genes were induced, they were not sufficient to induce flavonoid-3',5'-hydroxylase activity to enhance anthocyanin production by the fruit. Alternatively, the introduction of a new branch point into an existing pathway may interfere with endogenous flavonoid or phenolic biosynthesis and/or the transgenic enzyme may fail to compete with the native enzymes for the common substrate. This could, in part, be due to compartmentalization and metabolic channeling of substrates that may further complicate metabolic engineering strategies by limiting the access of substrates to introduced enzymes. This occurred when soybean-derived isoflavone synthase (IFS) was introduced into arabidopsis and tomato [Jaganath, 2005]. The nonleguminous species did not synthesize genistein despite expression of the IFS protein.

Based on these studies on biosynthetic pathways and metabolic engineering, it can be envisaged that once the plant cell factory has been assembled, the important determinants controlling the fluxes through the pathways are the

posttranslational regulation of enzyme activity, enzyme, and metabolite compartmentation and transport [Verpoorte and Memelink, 2002].

FUTURE TRENDS AND PROSPECTS

Phenolic compounds and flavonoids are a unique category of plant phytochemicals especially in terms of their vast potential health-benefiting properties. They represent the most abundant and the most widely represented class of plant natural products. A substantial amount of research has been carried out over the past two decades yet large information gaps still exist. For example, the inventory of these compounds is still incomplete, although there is continuous effort to provide new structures. In addition the dissection of the metabolic pathways for certain phenolic compounds remains to be resolved. Recent reports underline that important questions that still need to be answered in the field of proanthocyanidin and tannin biosynthesis [Xie and Dixon, 2005], and even the exact nature of the biosynthetic pathway(s) leading to lignin monomers is not fully elucidated.

Phenolic compounds and flavonoids are widely present in plant foods, and research in the last decade has increased dramatically. Two major objectives have been targeted: (i) to rationalize the potential health benefits of these phytochemicals and (ii) to redesign plants to enhance their production. The existing literature on biological activities suggests that polyphenol-rich products such as soya, teas, berries, red wine, and cocoa products may have positive effects on human health, especially by reducing the incidence of cardiovascular diseases and some types of cancer. Additional research is needed to substantiate whether it is a specific class of phenolic compounds and flavonoids present in plant foods that contributes to the observed bioactivities in man, or whether it is the consumption of a broad spectrum of phytochemicals that is more important. The exact mode of action of these phytochemicals still remains to be answered. Many earlier studies suggested that phenolic compounds and flavonoids protect cell constituents through direct scavenging of free radicals due to their antioxidant properties. However, recent data indicate that the protective effect of flavonoids and phenolic compounds may extend beyond their antioxidant activity. However, research in this field is still at its infancy as it has been carried out only on specific phytochemicals. Future research needs to focus on methods to better evaluate and optimize the *in vivo* effects of health-promoting compounds in biological system. Many promising results have been obtained to engineer or breed plants with enhanced levels of phenolic compounds and flavonoids. However, metabolomics and microarray analysis of global gene expression patterns have revealed that playing with a piece of the jigsaw may induce unfavorable changes in the fragile equilibrium of the interconnected pathways. Accurate controls should be envisaged in future studies to check for potential pitfalls. Once these setbacks are overcome there

remains the possibility to develop super crop varieties containing enhanced health-promoting flavonoid and phenolic compounds.

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2 Bioavailability of Flavanols and Phenolic Acids

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FLAVANOLS: STRUCTURE AND FOOD SOURCES

Flavanols consist of catechin and epicatechin monomers together with oligomeric tannins, which comprise the most abundant class of flavonoids in the human diet. The tannins are divided into three subclasses: the condensed

Plant Phenolics and Human Health: Biochemistry, Nutrition, and Pharmacology,

Edited by Cesar G. Fraga.

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tannins or proanthocyanidins, the derived tannins, and the hydrolysable tannins. Proanthocyanidins are present in fruits, bark, leaves, and seeds of many plants.

The procyanidins, the most abundant proanthocyanidins in plants, are composed of (epi)catechin units (Fig. 2.1) compared with the less common types of proanthocyanidins called propelargonidin and prodelfphinidin, which contain, respectively, (epi)afzelechin or (epi)gallocatechin subunits [Rasmussen et al., 2005]. The three forms of proanthocyanidins differ in the degree of hydroxylation of the B-ring. Prodelfphinidins possess a 3', 4', 5' -trihydroxy substitution on the B-ring, procyanidins have hydroxyl groups on the 3' - and 4' - positions, and propelargonidin on the 4' - position only [Dixon et al., 2005]. The monomeric units of proanthocyanidins are usually linked by C—C and occasionally by C—O—C bonds [Santos-Buelga and Scalbert, 2000]. The C—C bond is generally between the 4-position of the “upper” unit and the 8-position of the “lower” unit [Fine, 2000] (Fig. 2.1b), as in procyanidin B₁–B₄. However, an alternative linkage can be found between the C₄ of the “upper” unit and the

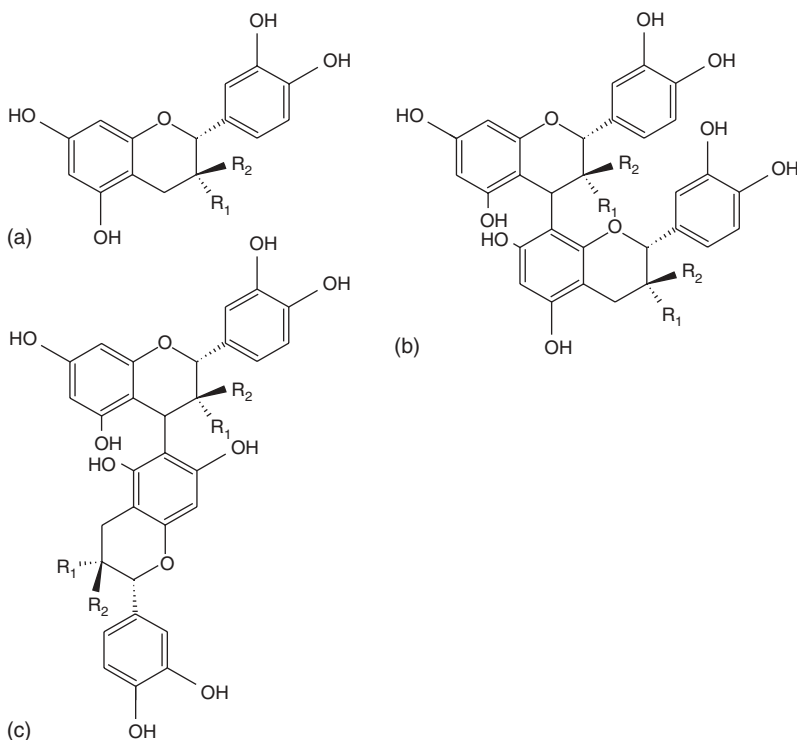


Figure 2.1 Structure of flavan-3-ol monomers and dimers. (A) (–)-Epicatechin with R₁=OH and R₂=H or (+)-catechin with R₁=H and R₂=OH; (B) procyanidin (4β→8)-dimer; (C) procyanidin (4β→6)-dimer.

C₆ of the “lower” one (Fig. 2.1c), as for the procyanidins B₅–B₈. Both of these are called a B-type linkage. Compounds with doubly linked units, by a B-linkage and a C₂–C₇ bond, or A-linkage, have also been reported in some foods such as cranberry fruits [Prior et al., 2001] and cinnamon [Anderson et al., 2004]. Many foods have been shown to contain proanthocyanidins—fruits and berries, nuts, beans, some cereals (barley and sorghum), spices such as curry and cinnamon, but also beverages such as wine and beer [Gu et al., 2004]. However, attention has been focused on the most abundant proanthocyanidins, the procyanidins. A good example of a food source of procyanidins is cocoa, which, apart from the monomeric units, contains dimeric to decameric (or larger) forms [Hammerstone et al., 1999]. Commonly consumed food, like dark chocolate or different varieties of apples and beverages, such as wine or cranberry juice, contain large amounts of procyanidins [Hammerstone et al., 2000].

PHENOLIC ACIDS: STRUCTURE AND FOOD SOURCES

Phenolic acids are generally divided into two classes, hydroxybenzoic (C₆–C₁) and hydroxycinnamic (C₆–C₃) derivatives [Clifford, 2000; Tomás-Barberán and Clifford, 2000], but phenylacetic (C₆–C₂) and phenylpropionic (C₆–C₃) also occur. The related phenylvaleric (C₆–C₅), phenyl-lactic (α -hydroxy C₆–C₃), phenylmandelic (β -hydroxy C₆–C₂), and phenyl-hydracrylic (β -hydroxy C₆–C₃) acids are gut flora/mammalian metabolites but rarely occur in food. Most have one or two substitutions on the phenyl ring, on the 3- and 4-positions (Fig. 2.2a). However, some derivatives can have three substitutions, the additional one being on the 5-position (Fig. 2.2b). Phenylacetic acids in foods are less common than benzoic, phenylpropionic, and cinnamic acids. While the content of hydroxybenzoic acids in edible plants is low, hydroxycinnamic acids are more abundant. The most commonly found hydroxycinnamic acids are 4-coumaric, ferulic, sinapic, and caffeic acids, the latter occurring the most extensively [Shahidi and Wanasundara, 1992]. Hydroxycinnamic acids are present in a wide range of berries, fruits, and beverages [Mattila et al., 2006] but also in many vegetables [Clifford, 1999] and cereals [Kern et al., 2003a]. In addition, phenolic acids are found in traditional herbal Chinese medicines and supplements [Cai et al., 2006].

Phenolic acids are rarely present as free forms, except in processed food, but occur more frequently as soluble or insoluble esters. These esters are formed with polysaccharides or simple sugars, with quinic acid or other carboxylic acids such as tartaric or shikimic acids [Herrmann, 1989], with other phenolic acids, with lipids [Clifford, 2000], with sterols or glycerol [Clifford, 1999], or with amino acids [Clifford and Knight, 2004]. To quinic acid, they can be conjugated as mono-, di-, tri-, and tetra-esters [Clifford, 2000]. The multiple esters can contain the same or different hydroxycinnamic acids. Among the hydroxycinnamic conjugates, caffeoylquinic and di-caffeoylquinic acids

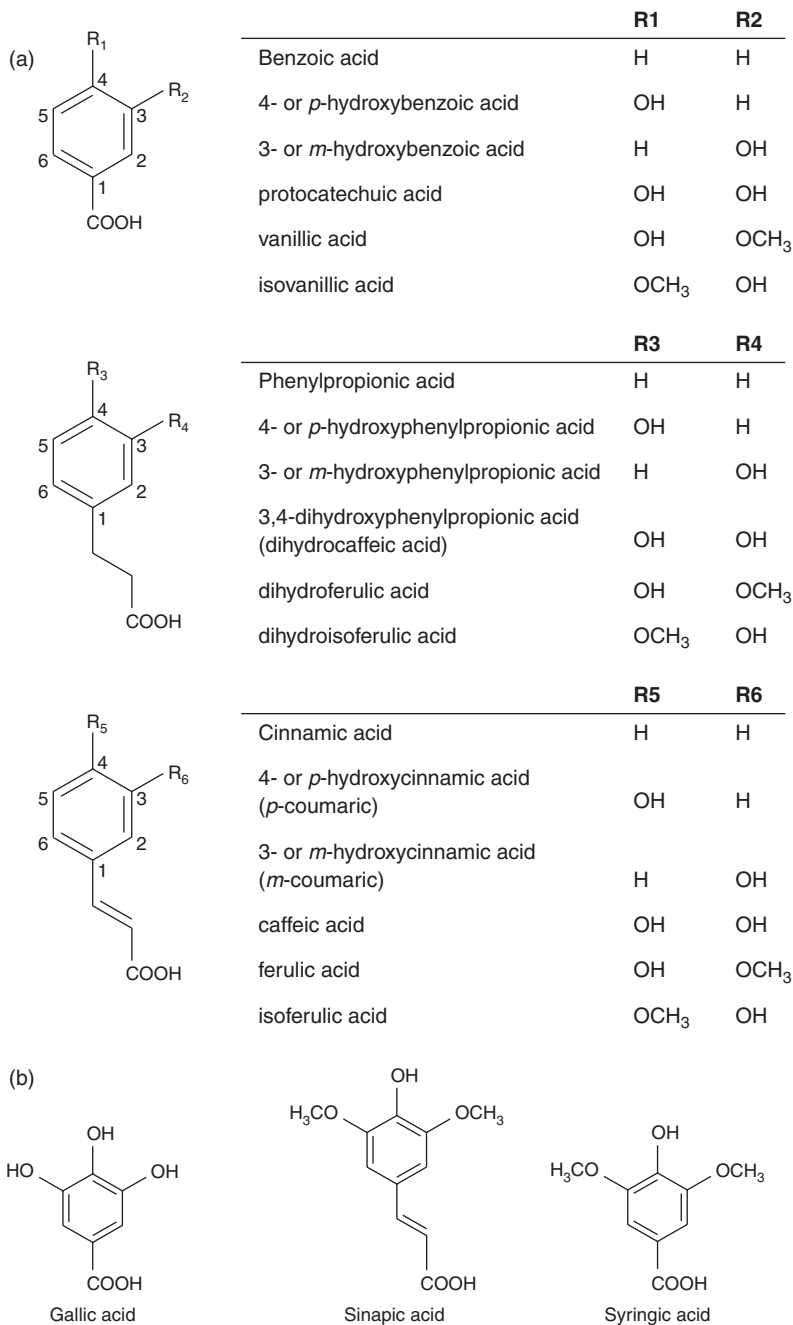


Figure 2.2 Chemical structure of phenolic acids. Phenolic acids commonly found with two substitutions on the (a) phenyl ring on the 3- and 4-positions and (b) some less commonly found with triple substitutions on the 3-, 4-, and 5-positions.

are the most ubiquitous [Clifford, 2000]. The best known quinic acid ester or chlorogenic acid is the 5-*O*-caffeoylquinic acid, a caffeic acid esterified to position 5 of a quinic acid moiety (Fig. 2.3).

Phenolic acids, and especially ferulic acid, which is abundantly present in cereals, is found esterified to the polysaccharides present in primary and secondary cell walls of plants. Ferulic acid is the major phenolic acid occurring in the cell walls of monocotyledons and appears as *cis* and the more abundant *trans* isomers (reviewed in [Klepacka and Fornal, 2006]). Ferulic acid is found in wheat, maize, rye, barley [Sun et al., 2001], oats, spinach, sugar beet, and water chestnuts [Clifford, 1999], generally esterified, and rarely as free form, such as in barley [Yu et al., 2001]. It is esterified in primary cell walls to arabinoxylans (Fig. 2.4) in the aleurone layer and pericarp [Clifford, 1999], as in spinach [Fry, 1982] or in wheat bran [Smith and Hartley, 1983]. Ferulic acid can also be found esterified to other hydroxycinnamic acids such as in Mongolian medicinal plants where it is found as feruloylodospermic acid, which is

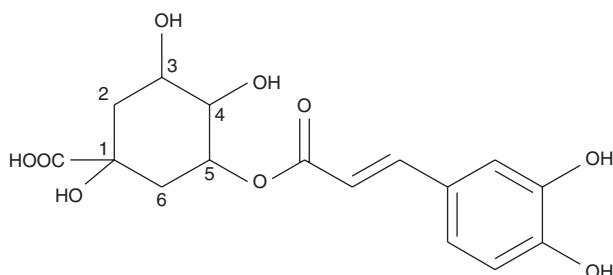


Figure 2.3 Example of chemical structure of a chlorogenic acid: 5-*O*-caffeoylquinic acid (with IUPAC numbering).

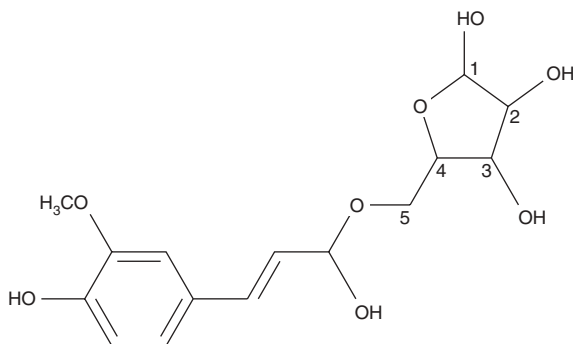


Figure 2.4 Example of chemical structure of 5-*O*-feruloyl-L-arabinofuranose a chlorogenic acid: 5-*O*-caffeoylquinic acid (with IUPAC numbering).

composed of two dihydrocaffeic acid units esterified at position 1 and 5 of a quinic acid moiety, with an additional feruloyl group being attached to position 3 [Tsevegsuren et al., 2007]. Dihydrocaffeic acid is also one of the major phenolic antioxidants abundantly present in black olive pericarp and in lower amounts in brined black olive, with traces in brined green olives [Owen et al., 2003].

ABSORPTION AND METABOLISM OF FLAVANOLS

Before reaching the systemic circulation, polyphenols orally administered will transit by the gastrointestinal tract (GIT) where they will be submitted to different biological and physiological parameters, which will participate to their bioavailability, such as the pH, the digestive enzymes, or the microflora.

Stability from the Mouth to the Small Intestine

The first fluid encountered by ingested procyanidins is saliva. Interaction between salivary proteins and flavan-3-ols has been investigated and demonstrated to be dependent on the chemical structure of the tested compounds, a gallate substitution on the position 3 on (–)-epicatechin or (–)-epigallocatechin, increasing their affinity to salivary proteins [Bacon and Rhodes, 1998]. Moreover, an extra hydroxyl group on the 5 -position of (–)-epicatechin gallate [(–)-epigallocatechin gallate] also favored interaction. However, epimerization of the hydroxyl group at position 3 seemed to have a less marked effect. The interactions between procyanidins and proline-rich proteins, optimum at two maxima at pH 3.5 and 5, were shown to lead to their precipitation [de Freitas and Mateus, 2001], the intraflavanol linkage and the structural monomeric units composing procyanidins influencing this precipitation, whereas the degree of polymerization had only a slight effect.

Different studies have investigated the effects of saliva and gastric fluid on the stability and, as a consequence, on the behavior of procyanidins during the first steps following their ingestion. Unpublished data, observed and mentioned by Spencer *et al.* in a review [Spencer et al., 2001a], showed that, incubated in human saliva for up to 30 min, procyanidins, from dimeric to hexameric forms, were not altered, 99% of the initial quantity being recovered at the end of the incubation period. Oligomeric procyanidins isolated from *Theobroma cacao* incubated in a phosphate buffer at pH 2 were degraded into monomeric and mainly into dimeric forms [Spencer et al., 2000]. After 2.5 hours at pH 2, 70% of the trimeric to hexameric forms were degraded compared with only 15% for the dimeric form during the same period of time. Since no difference was observed between the use of a phosphate buffer at pH 2 and a commercially available simulated gastric juice at the same pH without pepsin, the authors suggested that the pH was the only parameter responsible for the cleavage of oligomers. Another report mentioned that (–)-epicatechin and (+)-catechin

are stable in simulated gastric juice (0.24% hydrochloric acid – 0.2% sodium chloride solution, pH 1.8), whereas dimers B₂ and B₅ are unstable, producing epicatechin units and their respective isomers B₅ and B₂ [Zhu et al., 2002]. These results are in contradiction with data obtained from an *in vivo* study investigating the stability of procyanidins from a chocolate beverage during stomach transit [Rios et al., 2002]. The pH of the stomach was at about 5.4 ± 0.2 after intake of the cocoa beverage and not at 2, the latter corresponding more to the pH of an empty stomach. The percentage of each oligomer among the total amount of flavonoids present in the beverage was the same after stomach transit and the components were not degraded during the stay in the stomach. This supports the idea that all the ingested procyanidins should reach the small intestine without any pre-depolymerization in the stomach. However, the pH of the GIT from stomach to jejunum varies from 2 to 8.5. It is known that polyphenols such as flavanols oxidize rapidly at alkaline pH due to the catechol moiety of the B-ring [Spencer et al., 2001a]. Thus, oxidation of procyanidins could occur in the first part of the small intestine. In simulated intestinal juice [1.5% (w/v) sodium hydrogen carbonate solution, pH 8.5], monomers, as well as dimers, degraded almost completely within several hours, but neither epicatechin/catechin nor isomers were found to be produced from the dimers [Zhu et al., 2002]. At higher pH, monomers and dimers degraded within minutes. Studies have also shown that (epi)catechins are much more stable than the corresponding gallocatechins under digestive conditions (gastric or small intestinal), whereas the gallate substitutes had an intermediate stability [Neilson et al., 2007]. However, catechins were more stable in the gastric phase than in the intestinal phase. This stability was more linked to pH than to enzymatic activity, the sensitivity being for rather neutral or basic pH. The instability of epigallocatechin gallate, epicatechin, and epigallocatechin resulted in the formation of homodimers.

Absorption from the Small Intestine

Unlike some classes of polyphenols such as flavonols and flavones, flavanols are almost always present in the nonglycosylated form. Removal of glycoside from flavonoids, usually necessary before the transport across the intestinal barrier, is not required in the case of flavanols [Scalbert and Williamson, 2000]. The absorption of procyanidins by the small intestine was investigated by studying ¹⁴C-(+)-catechin, dimer, trimer, and procyanidin polymers permeation through Caco-2 cell cultures [Deprez et al., 2001]. There was little difference in permeability between monomer, dimer, and trimer, based on the measurement of radioactivity present on the basal side of the cultures, whereas the permeability of the polymers was 10 times lower. The authors reported the absence of catechin metabolism but did not determine whether the radioactivity measured on the basal side of the cultures was from the parent dimers to polymers or from their products of degradation or metabolites, which could have resulted from instability of the parent compounds in the culture

medium or from their metabolism by mammalian enzymes. From the results obtained, the authors suggested that procyanidins, from monomers to polymers, are poorly absorbed, transported via the paracellular pathway. The paracellular permeation of monomers does not fully support other studies reported in the literature, which rather suggested an absorption by intestinal cells of (epi)catechin in order to allow conjugation. For example, catechin glucuronide and 3'-*O*-methyl-catechin were found in the mesenteric vein after *in situ* perfusion of rat jejunum and ileum with catechin, indicating the intestinal origin of these conjugates [Donovan et al., 2001]. After oral administration of epicatechin by direct stomach intubation of rats, its free as well as its methylated forms were found in plasma of blood collected from the tail in addition to sulfated, glucuronidated, and sulfo-glucuronidated forms [Piskula and Terao, 1998]. Since the blood was taken from the tail 2 h after intake, it could not be concluded that conjugation took place in the intestinal cells. However, with isolated tissues, the authors reported a glucuronosyltransferase activity higher in the small and large intestinal mucosa than in the liver, kidney, and lung. In addition to global bioavailability of procyanidins, the mechanisms of transport have also been investigated, at least for the monomers. Indeed, an active transport, Na⁺ independent but stimulated by an outwardly directed gradient of protons, could be used by the flavan-3-ols monomers (–)-epicatechin and (+)-catechin to cross the intestinal barrier [Starp et al., 2005]. Based on their results, the authors also proposed that free diffusion would be favored by high concentrations of flavan-3-ols, whereas carrier-mediated uptake would be important for lower amounts.

If the mechanisms of absorption of monomeric forms of flavanols are better understood, the results obtained from the studies investigating the absorption of dimers are contradictory and make understanding their permeation mechanism more difficult. The absorption of dimers has been observed from *in vivo* data showing procyanidin B₁ detected in human serum after intake of procyanidin-rich grape seed extract [Sano et al., 2003]. After oral administration of procyanidin dimer B₂ to rats, 0.34% of the provided dose was detected in urine [Baba et al., 2002]. Besides dimer B₂, the presence of epicatechin and its 3'-*O*-methylated product were also excreted in urine. All the compounds found in urine were present in plasma, peaking at 30–60 min following the intake of procyanidin dimer. The absorption of pure dimers B₂ and B₅ from the perfusion of rat jejunum was also shown, with six different components having flavanol-like spectral characteristics detected on the serosal side of the intestinal epithelium, which represented a transfer of flavanol of 23% [Spencer et al., 2001b]. In addition to catechin, dimer, and *O*-methylated dimer, the major compound (95.8%) obtained on the serosal side had the characteristics of epicatechin, with no evidence for the presence of its glucuronides or 3'-*O*-methyl and 4'-*O*-methyl conjugates. The authors also suggested that the cleavage of the dimer into the monomeric form would be energy dependent, taking place in the intestinal cells. More recently, tetramethylated dimeric procyanidins were detected in rat plasma and liver 1 h after intake of synthetic

dimeric procyanidins [Garcia-Ramirez et al., 2006]. Appearance of procyanidin B₂ and B₃, purified from cinnamomonic cortex, has been measured in plasma, peaking, respectively, at 20 and 40 min after their oral administration to rats [Tanaka et al., 2003]. According to the chemical structure drawn and the mass reported in the study, the compound called dimer B₃ would be a trimer. This would be the first time that a trimer, found under the form of parent compound in plasma, is reported in the literature, which is unexpected due to its molecular weight.

Even if dimers and trimers are stable under GIT conditions and absorbed in their native form as seen for the monomers, the amount crossing the epithelial barrier of the small intestine and being further excreted in urine must be very low. The major part of the ingested procyanidins must reach the colon where an abundant microflora can metabolize them into smaller molecules, which are more readily absorbed. The general absorption and metabolism pathways of procyanidin monomers to oligomers in the GIT, from their ingestion to microbial metabolism, are summarized in Figure 2.5.

Formation of Phenolic Acids from Flavanols

Gut microflora account for a major part of the production of phenolic acids excreted in urine [Goodwin et al., 1994]. In addition, mammalian enzymes can also participate to the structural modification of these phenolic acids. Several studies have shown the presence of phenolic acids in plasma and/or urine after intake of different types of flavonoid-rich food, such as artichoke extract, apple cider, breakfast cereals, tomatoes, coffee, or beer, with 5-*O*-caffeoylquinic, caffeic, and ferulic acids being the most studied examples (as reviewed in [Manach et al., 2005]), but also after chocolate intake [Rios et al., 2003] or red wine consumption [Caccetta et al., 2000]. Several phenolic acids were identified in human urine after intake of a polyphenol-rich meal based on fruits and vegetables and comprising tomato and onion pasta sauce, pasta, cooked broccoli, cherry tomatoes, cucumber, continental leaf salad, pepper salad dressing, raspberries, red grape juice, and apple juice [Rechner et al., 2002]. Ferulic, isoferulic, sinapic, and 3-hydroxyphenylacetic acids were found glucuronidated, whereas vanillic and homovanillic acids were found as both free and glucuronidated forms. In plasma, dihydroferulic and 3-hydroxyphenylpropionic acids were present as free and glucuronidated forms with ferulic, isoferulic, 4-coumaric, hydroxybenzoic, and vanillic acids as glucuronide conjugates only. The authors proposed 3,4-dihydroxyphenylpropionic acid (dihydrocaffeic acid) as the first phenolic acid in the cascade of microbial metabolism of dietary flavonoids, based on their work and other reports from the literature. Monomeric units of procyanidins, which have not been absorbed through the small intestinal epithelium, can reach the colon to be metabolized by the intestinal microflora. 3-Hydroxyphenylpropionic acid has been proposed to be the major metabolite found in urine of rats after ingestion of (+)-catechin [Griffiths, 1962], in the free form but also conjugated [Griffiths, 1964],

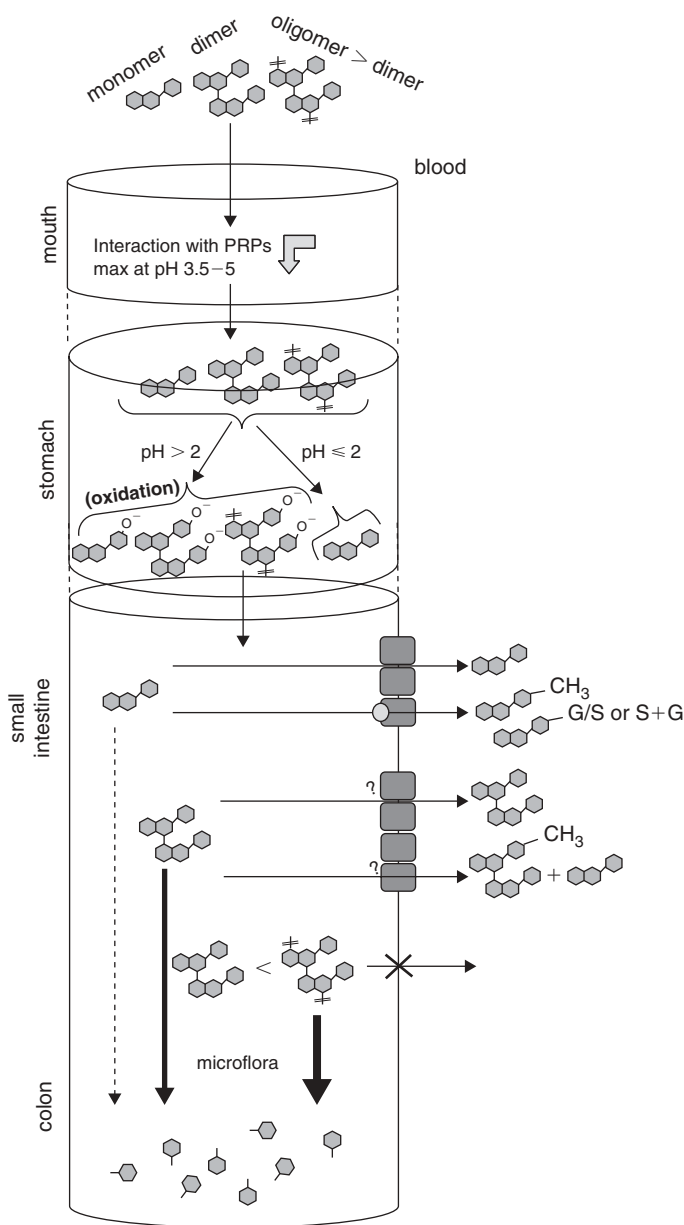


Figure 2.5 Summary of procyanidin behavior in the GIT. ↓ precipitation; ⬢ phenolic acid; CH_3 , methyl conjugate; G, glucuronic; O^+ , oxidized hydroxyl group; S, sulfate; S + G, sulphoglucuronide conjugate.

together with 4-hydroxyphenylpropionic acid, 5-(3-hydroxyphenyl)- γ -valerolactone, 5-(3,4-dihydroxyphenyl)- γ -valerolactone, and hydroxyphenylvaleric acids, as minor metabolites [Scheline, 1970]. 5-(3,4-Dihydroxyphenyl)- γ -valerolactone was also detected in urine of rats from the ring fission of (–)-epicatechin by microflora [Meng et al., 2002; Unno et al., 2003] and found together with 3,5-dihydroxyphenyl- γ -valerolactone in human urine after ingestion of green tea, epigallocatechingallate, or epigallocatechin [Meng et al., 2002].

Benzoic, isomeric 2-, 3-, and 4-hydroxybenzoic, phenylacetic, 4-hydroxyphenylacetic, phenylpropionic, isomeric 2-, 3-, and 4-hydroxyphenylpropionic, 3,4-dihydroxyphenylpropionic acids, δ -(3-hydroxyphenyl)- γ -valerolactone, and 1-(3-hydroxyphenyl)-3-(2,4,6-trihydroxyphenyl)-propan-2-ol have been detected after 5 days incubation of dimer B₃ with rat-cecal microflora [Groenewoud and Hundt, 1986]. In a more recent study, also investigating the *in vitro* microbial metabolism of a ¹⁴C-labeled procyanidins fraction, which did not contain monomer, dimer, and trimer, low-molecular-weight aromatic acids, differing by their hydroxylation status and the length of their aliphatic side chain, were detected [Deprez et al., 2000]. The six different compounds found were 3-hydroxyphenylacetic acid, and 3-hydroxyphenylpropionic acid, their isomers 4-hydroxyphenylacetic acid and 4-hydroxyphenylpropionic acid, 3-hydroxyphenylvaleric acid and phenylpropionic acid. Phenylacetic and benzoic acids were also detected, but their source was not clearly identified. *In vivo* work on rats or in human have also supported the results found *in vitro*, showing the presence of phenolic acids in plasma and urine after intake of isolated procyanidins, extracts, or food containing procyanidins. *In vivo* investigation of the metabolism of catechin monomer, dimer B₃, trimer C₂, and purified polymers using a rat model suggested that procyanidin degradation could start by a depolymerization into (epi)catechin monomers, due to similarities in the degradation products obtained from catechin and procyanidins, before further metabolism leading to the production of phenolic acids [Gonthier et al., 2003b]. Phenolic acids recovered in urine were also detected in humans after intake of a chocolate beverage [Rios et al., 2003] and in rats after intake of red wine powder [Gonthier et al., 2003a], food sources known to contain procyanidins. Phenolic acids can be expected to be found in plasma and urine after intake of procyanidin-rich foods such as grape seed extract [Ward et al., 2004], apples, cranberries, chocolate, and wine [Hammerstone et al., 2000]. The stability, as well as the microbial metabolism of monomeric and oligomeric/polypmeric procyanidins and the generation of the initial forms of hydroxycinnamic acids, are summarized in Figure 2.5. A nonexhaustive list of the phenolic acids found in plasma or urine *in vivo* after ingestion of flavonoid-rich foods or pure flavonoids is shown in Table 2.1.

Phenolic acids can come from the metabolism of polyphenols other than catechins and procyanidins. The degradation of flavonoid aglycones by microflora can be more or less rapid, the presence of a methoxyl group on the A- or B-ring of the flavonoid being protective against bacterial degradation by C-ring

Table 2.1 Summary of Phenolic Acids Found in Vivo and in Vitro from Different Food Sources and Flavonoids^a

Diet	Model	Phenolic acids	References
(+)-Catechin	Rats (urine)	major metabolites: 3-HPPA, free and C	Griffiths, 1962
(+)-Catechin		<ul style="list-style-type: none"> Major metabolite: 3-HPPA; minor metabolites: 4-HPPA, 5-(3-hydroxyphenyl)-γ-valerolactone, 5-(3,4-dihydroxyphenyl)-γ-valerolactone and HPVA 	Griffiths, 1964 Scheline, 1970
(-)-Epicatechin		5-(3,4-dihydroxyphenyl)- γ -valerolactone	Meng et al., 2002; Unno et al., 2003
<ul style="list-style-type: none"> 8-d diet supp. with 0.12 g catechin / 100 g 0.25 or 0.50 g red wine powder / 100 g 	Rats (urine)	<ul style="list-style-type: none"> Phenolic acids affected by the diet (represent 4.7 g/100 g catechin ingested): 3-HPPA (major), 3-HBA, 4-HBA, 3-HHA, 4-HBA, FA, 3,4-DHPAA, 3,4-DHPPA, 3-HPA 3-HBA, 4-HBA, HA, 3-HHA, 4-HHA, VA, PAA, 3-HPA, 3,4-DHPAA, 3-HPPA, 3,4-DHPPA, <i>p</i>-CA, CA, FA. 	Gonthier et al., 2003a
Catechin, dimer B3, trimer C2, and purified polymers	Rats (urine)	Phenolic Acids	Gonthier et al., 2003b
		From Dimer	Polymer
		3,4-DHPVA	nd
		3-HPVA	nd
		3,4-DHPPA	nd
		3-HPPA	×
		<i>m</i> -CA	×
		<i>p</i> -CA	×
		FA	×
		3,4-dHPAA	×
		3-HPAA	×
		PCA	×
		3-HBA	×
		4-HBA	×
		Trimer	Same as ctrl
		3,4-DHPVA	nd
		3-HPVA	×
		3,4-DHPPA	nd
		3-HPPA	×
		<i>m</i> -CA	×
		<i>p</i> -CA	×
		FA	×
		3,4-dHPAA	×
		3-HPAA	×
		PCA	×
		3-HBA	×
		4-HBA	×
		Same as ctrl	Same as ctrl
		Same as ctrl	×
		Same as ctrl	Same as ctrl
		Same as ctrl	Same as ctrl
		nd	nd
		Same as ctrl	Same as ctrl

(Continued)

Table 2.1 (Continued)

Diet	Model	Phenolic acids	References		
Green tea, epigallocatechingallate or epigallocatechin	Human (urine)	VA 3-HHA 4-HHA HA	× × × × × × × ×	× nd Same as ctrl ×	Meng et al., 2002
Polyphenol-rich meal based on fruits and vegetables	Human	<ul style="list-style-type: none"> urine: FA, isoFA, SA and 3-HPAA: G forms, VA and HVA: free and G forms plasma: DHFA and 3-HPPA: free and G forms; FA, isoFA, <i>p</i>-CA, HBA and VA: G forms 	× nd Same as ctrl Same as ctrl		Rechner et al., 2002
Chocolate intake	Human (urine)	3,4-DHPAA, 3-HPPA, FA, 3,4-dHPAA, 3-HPAA, PAA, VA, 3-HBA, 4-HBA, 4-HHA, HA			Rios et al., 2003
Proanthocyanidin dimer B3	5 d with rat-cecal microflora	BA, 2,3 and 4-HBA, PA, 4-HPAA, phenylpropionic, 2,3,4-HPPA, 3,4-diHPPA, -(3-hydroxyphenyl)- γ -valerolactone and 1-(3-hydroxyphenyl)-3-(2,4,6-trihydroxyphenyl)-propan-2-ol			Groenewoud and Hundt, 1986
¹⁴ C-labeled procyanidins fraction, without monomer, dimer, and trimer	Human colonic microflora	3-HPAA and 3-HPPA acid, 4-HPAA and 4-HPPA, 3-HPVA, PPA, PA, BA			Deprez et al., 2000

^aBA, benzoic acid; C, conjugated; CA, caffeic acid; *m* or *p*-CA, *m* or *p*-coumaric acid; DHFA, dihydroferulic acid; 3,4-DHPAA, 3,4-dihydroxyphenylacetic acid; 3,4-DHPAA, 3,4-dihydroxyphenylpropionic acid; 3,4-DHPVA, 3,4-dihydroxyphenylvaleric acid; FA, ferulic acid; G, glucuronide; HA, hippuric acid; 2-, 3- or 4-HBA, 2-, 3- or 4-hydroxybenzoic acid; 3- or 4-HHA, 3- or 4-hydroxyhippuric acid; 3- or 4-HPAA, 3- or 4-hydroxyphenylacetic acid; 3- or 4-HPPA, 3- or 4-hydroxyphenylpropionic acid; 3- or 4-HPVA, 3- or 4-hydroxyphenylvaleric acid; HVA, homovanillic acid; isoFA, isoferulic acid; nd, not detected; PAA, phenylacetic acid; PCA, protocatechuic acid; PPA, phenylpropionic acid; SA, sinapic acid; VA, vanillic acid.

cleavage [Lin et al., 2003]. 3-Hydroxyphenylpropionic acid results from ring fission followed by water elimination and dehydroxylation of quercetin [Rechner et al., 2004; Schoefer et al., 2003], which itself resulted from deglycosylation of rutin. However, quercetin has also been reported to be metabolized by C-ring fission into 3,4-dihydroxyphenylacetic acid (coming from the B-ring) and phloroglucinol (three hydroxyl groups on a phenyl ring, coming from the A-ring) [Winter et al., 1989]. 3-Hydroxyphenylpropionic acid also resulted from the ring fission of naringenin, itself the aglycone obtained by microbial deglycosylation of naringin, and could be further dehydroxylated to give phenylpropionic acid [Rechner et al., 2004]. Phenylhydracrylic acids are other metabolites that have been reported from the metabolism of flavanoids such as catechin [Baba et al., 1981] or rutin [Das, 1974].

Dihydrocaffeic acid, the metabolite of dihydroxyphenylvaleric acid in the cascade of microbial degradation of catechins and procyanidins (Fig. 2.6), is one of the major phenolic acids found in human fecal water [Jenner et al., 2005]. It was detected in the plasma of coffee drinkers [Goldstein et al., 1984], in urine as the free, form, and mainly conjugated in human plasma after ingestion of artichoke leaf extracts, which contain monocaffeoylquinic, dicaffeoylquinic, and caffeic acids as well as flavonoids [Wittmer et al., 2005], in human urine after chocolate intake [Rios et al., 2003], in rat urine after ingestion of polyphenol-rich red wine extract [Gonthier et al., 2003a], and produced by bacteria from luteolin and apigenin [Schoefer et al., 2003].

PHENOLIC ACIDS BIOAVAILABILITY

Release of Phenolic Acids from Esters

Phenolic acids, and most particularly ferulic acid, are mainly found in food as soluble or insoluble esters. For most of the insoluble esters, a preliminary hydrolysis and a release of the free form is required before absorption. In the gastrointestinal tract, the insoluble wheat bran fiber is first hydrolyzed by xylanase, releasing feruloylated oligosaccharides into the soluble phase, where cinnamoyl esterase can hydrolyze the ester bond and release ferulic acid [Kroon et al., 1997]. Human and rat colonic microflora contain an esterase activity able to release diferulic acids from dietary cereal brans [Andreasen et al., 2001b]. A small proportion of ferulic acid, as free form and esterified groups, has been shown to be released from wheat bran by *in vitro* gastric and small intestinal incubation, indicating the presence of enzymatic activities in the upper part of the GIT able to hydrolyze the xylan backbone and the ester bond of ferulic acid from the xylan backbone. However, 95% of the total release of feruloyl groups appear to take place in the colon, where xylanase and cinnamoyl esterase activities of microbial origin have been detected [Couteau et al., 2001]. Small amounts of cinnamoyl esterases of mammalian origin have been identified in the mucosa of the small intestine, which could possibly also come from

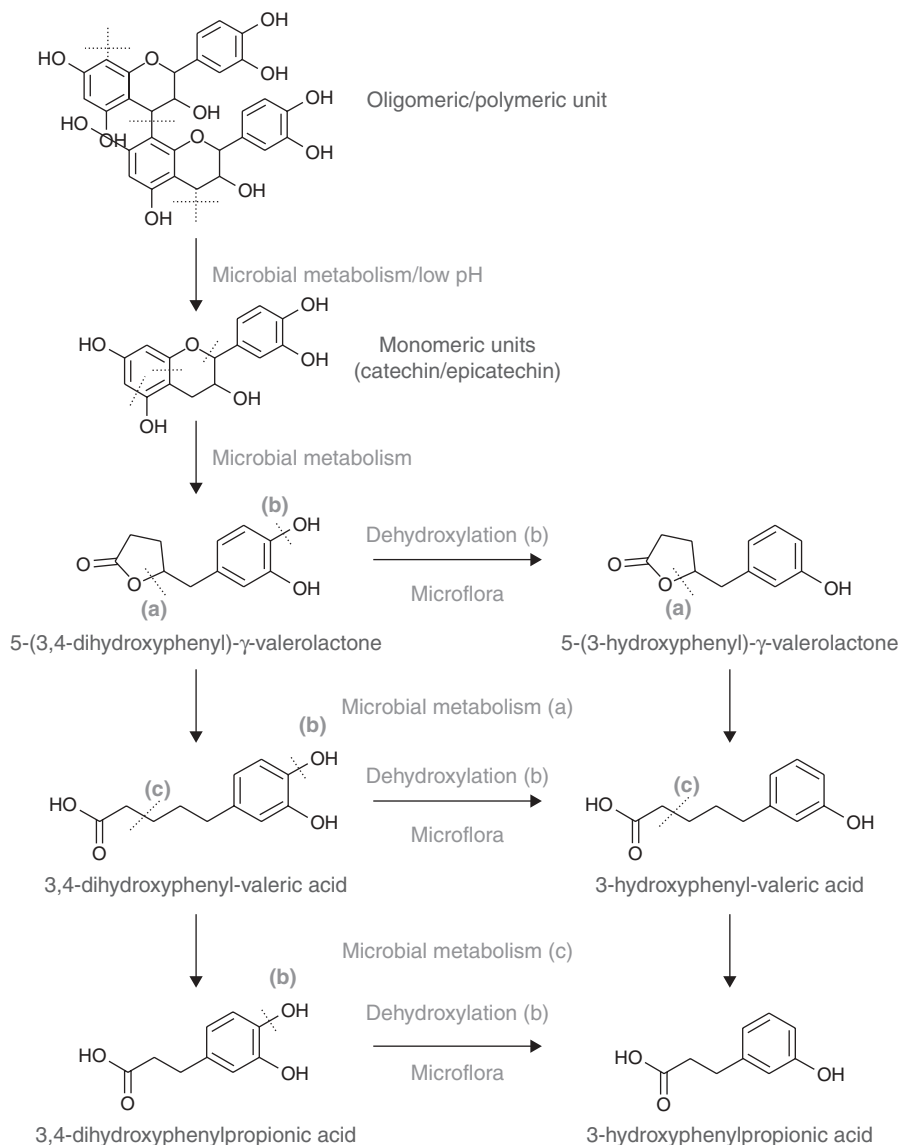


Figure 2.6 Summary of main possible interconversions between the different phenolic acids by microbial and mammalian enzymes, starting from dihydrocaffeic acid, the microbial metabolite of 3,4-dihydroxyphenylvaleric acid.

pancreatic secretions [Andreasen et al., 2001a, 2001b]. Recent findings of D-quinic acid in ileostomy bags of patients after consumption of apple juice containing 4- and 5-caffeoylquinic and 4-coumaroylquinic acids support this assumption of a possible small intestinal esterase activity [Kahle et al., 2007].

The enterocyte-like cells, Caco-2, also exhibited hydrolase activity toward esters of hydroxycinnamic acids and diferulates, part of the esterases produced by the cells being secreted in the culture medium [Kern et al., 2003b]. The hydrolysis of hydroxycinnamic acids by the intestinal esterases appeared, however, to be dependent on the substitution of the phenyl ring of the substrate, the activity decreasing with the number of substitutions and the substrate specificity being not as marked with microbial esterases [Andreasen et al., 2001a]. Interestingly, intestinal esterases are not active toward 5-*O*-caffeoylquinic acid, whereas microbial ones are able to produce caffeic acid [Plumb et al., 1999; Rechner et al., 2004]. Very low amounts of caffeic acid have been detected in gastric and small intestinal contents after ingestion by rats of a 5-*O*-caffeoylquinic-acid-supplemented diet, appearance of the free form being much more significant in the cecum [Lafay et al., 2006a]. From coffee consumption, the picture is uncertain. In one study, 5-*O*-caffeoylquinic acid was not found in human plasma but high amounts of caffeic acid were detected, suggesting no absorption of the ester and a requirement of precleavage of the ester bond before absorption in the gastrointestinal tract [Nardini et al., 2002]. However, another study showed high levels of chlorogenic acids in human plasma after intake of a large amount of coffee [Monteiro et al., 2007]. It can be extrapolated that ferulic acid, found esterified with carboxylic acids such as quinic acid in food [Herrmann, 1989] or with polysaccharides in cereals, for instance, could also reach the colon almost intact and be released by the action of xylanases and cinnamoyl esterases, mainly in the cecum and colon. Once ingested or released in the gastrointestinal tract, phenolic acids can be further metabolized by the microflora and/or by mammalian enzymes to produce new compounds.

Mammalian and Microbial Metabolism of Phenolic Acids

One of the first papers presenting microbial metabolism of phenolic acids was the report of Scheline who used rat intestinal microflora [Scheline, 1968]. This paper, covering most of the interconversions possible between phenolic acids by microflora, reported the reduction of the unsaturated side chain in 2-, 3- and 4-coumaric, caffeic, isoferulic and ferulic acids. Microflora were also capable of dehydroxylating position 4 of protocatechuic and dihydrocaffeic acids to form their respective 3-hydroxy acid forms. Dehydroxylation of hydroxycinnamic acids has also been demonstrated for human microflora, phenylpropionic acid obtained from 3-hydroxyphenylpropionic acid, itself resulting from dehydroxylation of dihydrocaffeic acid [Rechner et al., 2004]. Demethylation of the 3-hydroxy-4-methoxy- and 3-methoxy-4-hydroxy-phenylacetic, phenylpropionic, and cinnamic acids also occurred with rat intestinal microflora [Scheline, 1968]. In addition, the author showed decarboxylation of phenylacetic and cinnamic, but not phenylpropionic, acids that possessed a 4-hydroxyl group. Dihydrocaffeic and caffeic acids were later shown to be decarboxylated by α -oxidation to form, respectively, 4-vinyl-catechol and

4-ethylcatechol in vitro [Peppercorn and Goldman, 1971]. Vinyl-catechol was formed by *Lactobacillus* sp. 1 in vitro but not in vivo, in germ-free rats colonized by this strain [Peppercorn and Goldman, 1972]. The appearance of propionic and benzoic acids would be the result of progressive loss of carbons through β -oxidation from the phenylvaleric compounds [Deprez et al., 2000]. β -Oxidation, taking place in the liver by mammalian enzymes, was responsible for the production of vanillic acid from dihydroferulic acid, itself coming from the hydrogenation of ferulic acid [Rechner et al., 2002]. However, another report mentioned the production of vanillic acid from caffeic acid metabolism, with the detection of ferulic and isoferulic acid but not dihydroferulic acid, suggesting that vanillic acid could also directly come from ferulic acid instead of dihydroferulic acid [Jacobson et al., 1983]. This hydroxycinnamic metabolism seems to be similar to the β -oxidation of fatty acids. Indeed, vanillic acid has been proposed to result from ferulic acid via its reduction through the formation of feruloyl-SCoA, which is hydrogenated into 4-hydroxy-3-methoxyphenyl- β -hydroxypropionyl-SCoA further converted to vanillic acid and acetyl-SCoA by an enoyl-SCoA hydratase/lyase enzyme [Gasson et al., 1998]. This enzyme belongs to a superfamily, which includes bacterial, mitochondrial, peroxisomal, and glyoxysomal enzymes of the fatty acid oxidation pathway, suggesting that this enzymatic reaction can happen through bacterial or mammalian metabolism. The reduction, which has been shown to give dihydrocaffeic acid from caffeic acid by microflora [Peppercorn and Goldman, 1971; Rechner et al., 2004], could be an intermediate step in the β -oxidation. This reduction, which could also take place with mammalian enzymes due to the presence of the enzymes in mammalian cells, has never been clearly demonstrated. Indeed, gnotobiotic rats, germ-free rats harboring a strain of *Streptococcus*, were able to reduce caffeic into dihydrocaffeic acid, whereas germ-free rats were not [Peppercorn and Goldman, 1972]. It has also been shown more recently that hepatocytes reduced ferulic acid to dihydroferulic acid [Moridani et al., 2002].

Intestinal microflora is capable of demethylation, but not methylation, of phenolic acids, since dihydroferulic and ferulic acids were excreted in urine of germ-free rats after ingestion of, respectively, dihydrocaffeic and caffeic acids [Peppercorn and Goldman, 1972]. The mammalian enzyme catechol-*O*-methyl transferase catalyses the methylation of hydroxyl groups. Ferulic acid was an in vivo metabolite of caffeic acid [Azuma et al., 2000], as was its isomer isoferulic acid [Rechner et al., 2002], secreted back into the lumen by intestinal cells after caffeic acid perfusion of rat small intestine [Lafay et al., 2006b]. Ferulic and isoferulic acids, absent from the plasma samples, were detected in urine of rats, together with caffeic and 5-*O*-caffeoylquinic acids, 1.5 h after the beginning of a meal containing 5-*O*-caffeoylquinic acid [Lafay et al., 2006a]. Usually, ferulic acid is found in nature as the *trans* isomer. However, *cis* ferulic acid, found in biological samples [Zhao et al., 2004], was attributed to an isomerization of the form taking place during the storage of the samples, as already hypothesized [Graf, 1992].

In addition to different hydroxyl derivatives of cinnamic, phenylacetic, and benzoic acids, hydroxyl derivatives of hippuric acid are found as metabolites of flavonoids and phenolic acids. Hippuric acids come from the glycation (conjugation with glycine moiety) of benzoic acid derivatives in the liver and kidneys. The first step of this conjugation is the activation of benzoic acid by benzoyl-CoA ligase to form benzoyl-CoA, similarly to the first step of β -oxidation [Schwab et al., 2001]. However, benzoic acid, because of its short side chain, is not degraded by β -oxidation, but CoA is rather substituted by the amino acid glycine to form the hippuric conjugate. Hippuric acid derivatives are the end products of metabolism of phenolic acids and consequently of flavonoids. Indeed, they were detected in human urine after intake of a polyphenol-rich meal [Rechner et al., 2002], 3-hydroxyhippuric, 4-hydroxyhippuric, and hippuric acids present as both free and glucuronidated forms. Hippuric acid and/or its hydroxy derivatives were also detected in rat urine after intake of 5-*O*-caffeoylquinic acid [Gonthier et al., 2003c], dimer, trimer, and polymers of procyanidins [Gonthier et al., 2003b], of a diet supplemented with catechin or red wine powder [Gonthier et al., 2003a] and in human urine after chocolate intake [Rios et al., 2003] or black tea consumption [Clifford et al., 2000]. Figure 2.7 summarizes most of the possible interconversions of the commonly found phenolic acids.

Behavior and Absorption in the Gastrointestinal Tract

It is thought that the soluble esters of phenolic acids with carboxylic acids or sugars will be stable during their passage in the stomach, since acidic gastric juice was not sufficient to cleave the ester linkage in 5-*O*-caffeoylquinic acid [Rechner et al., 2001], nor was an incubation in HCl-NaOH (9 g/L) aqueous solution (pH 2.5) of the 5-*O*-feruloyl-L-arabinofuranose [Zhao et al., 2004]. In a study involving healthy ileostomy subjects, it was shown that 5-*O*-caffeoylquinic acid is absorbed as such and further metabolized in the liver, rather than hydrolyzed into caffeic acid before absorption in the stomach or in the small intestine, since it was fairly stable when incubated in gastrointestinal fluids [Olthof et al., 2001]. However, the absorption of the ester was lower (33% of the ingested dose) than the free form (95%). Other reports have also mentioned the absorption of the soluble ester 5-*O*-caffeoylquinic acid [Lafay et al., 2006a, 2006b] without a prelysis of the ester bond. Indeed, 5-*O*-caffeoylquinic acid was detected in urine [Gonthier et al., 2003c] or plasma [Lafay et al., 2006a] of rats after intake of a semipurified diet containing 5-*O*-caffeoylquinic acid. In a more recent study performed in humans, 3-, 4-, and 5-caffeoylquinic acids, as well as 3,4-, 3,5-, and 4,5-dicaffeoylquinic acids were identified in plasma, peaking at 1 or 3 h following ingestion of brewed coffee, depending on the subjects [Monteiro et al., 2007], one subject showing the additional presence of 4- and 5-feruloylquinic acid. Results on 5-*O*-caffeoylquinic acid absorption (summarized in Table 2.2) are, however, contradictory since some reports also indicated no detection of this ester in plasma of rats after direct stomach administration

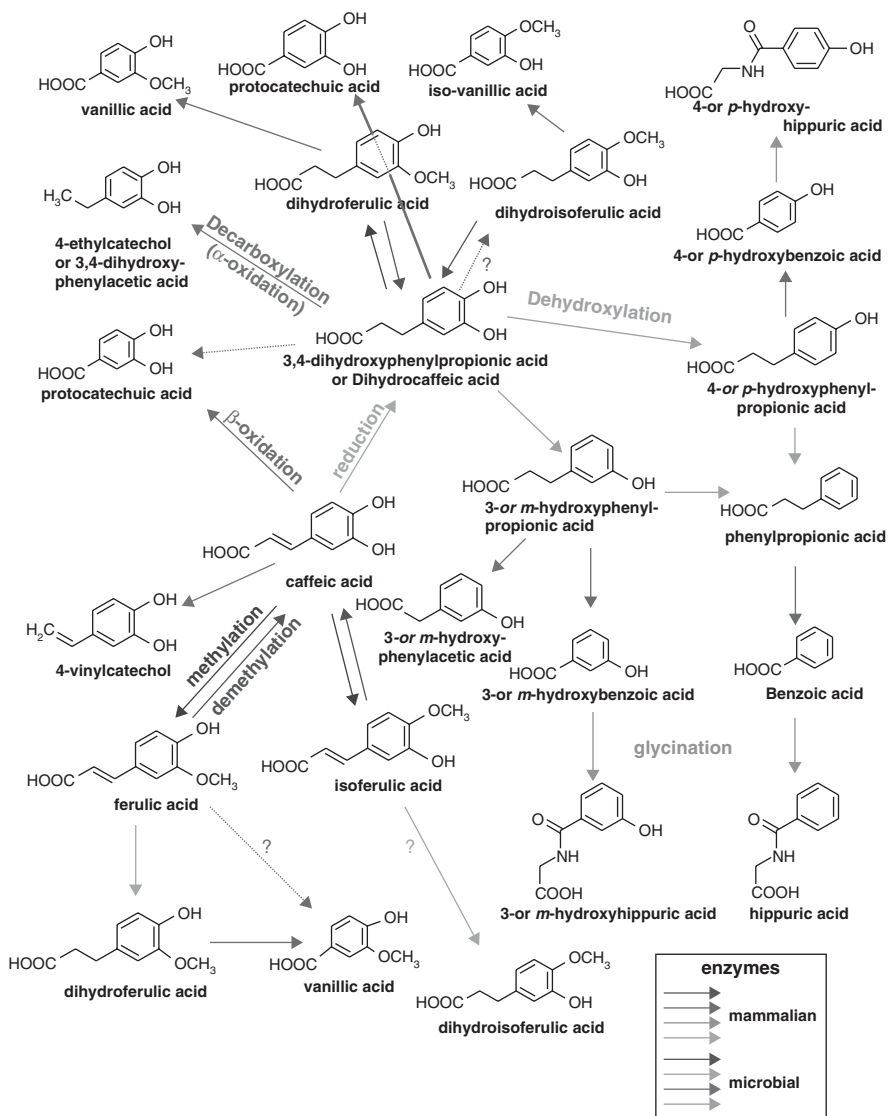


Figure 2.7 Summary of main possible interconversions between the different phenolic acids by microbial and mammalian enzymes, starting from dihydrocaffeic acid, the microbial metabolite of 3,4-dihydroxyphenylvaleric acid.

of a solution containing 5-*O*-caffeoylquinic acid [Azuma et al., 2000] or of humans after coffee consumption [Nardini et al., 2002]. These discrepancies could result from the methods used to detect chlorogenic acids in plasma, liquid chromatography–mass spectroscopy (LC–MS) with electrospray ionization appearing to be the most utilized [Matsui et al., 2007]. They could also result

from the instability of chlorogenic acids toward the methods of purification used to process plasma or urine, leading to the lysis of the ester bond and to the release of the free form. Interestingly, a recent report also proposed that isomerization of caffeoylquinic acids could occur in the human gastrointestinal tract as 1- and 3-caffeoylquinic acids were detected in ileostomy bags of patients after consumption of apple juice, which contained only the 4- and 5-caffeoylquinic acid forms, isomerization hypothesized by the authors to result from enterocyte esterase activity [Kahle et al., 2007].

Ferulic acid has often been reported as a model compound for the investigation of bioavailability of phenolic acids, as free or esterified forms (Table 2.3), since it is abundantly present in food. Absorption via the gastrointestinal tract has also been found for dimers of ferulic acid, or diferulic acids, released from cereal brans [Andreasen et al., 2001b].

A scheme of digestion and absorption of ferulic acid has been proposed, based on the study performed on rats fed ferulic acid sugar esters, 5-*O*-feruloyl-L-arabinofuranose and feruloyl-arabinoxylan [Zhao et al., 2003a]. Released from the ester, it would preferably be more absorbed by the small intestine and the cecum. The authors also proposed that 5-*O*-feruloyl-L-arabinofuranose could be absorbed as such and further hydrolyzed in the mucosa or in the circulation. The absorption of free phenolic acids is mainly expected to occur in the small and large intestine. However, a possible permeation of phenolic acids already in the stomach has been proposed in addition to the small intestine, such as for ferulic acid and its sugar ester, based on its rapid absorption observed with rats [Zhao et al., 2003a]. This hypothesis was later supported by a study using a rat *in situ* gastric perfusion model in which the pylorus was ligatured, followed by an injection of a solution of ferulic acid free or 5-*O*-feruloyl-L-arabinofuranose in the stomach before the ligature of the cardia [Zhao et al., 2004]. The authors showed a high absorption rate of ferulic acid from the stomach ($74 \pm 11\%$ of the administered dose), much higher than the absorption of its sugar ester ($19 \pm 4\%$ of the administered dose). Uptake of ferulic acid and of 5-*O*-feruloyl-L-arabinofuranose by the gastric cells only as unconjugated forms was shown *in vitro*. They were present in the gastric mucosa, after incubation in an excised stomach, even though the experiment was performed on ice, suggesting that the uptake by the gastric cells did not require any energy and was probably carrier independent. If the uptake was by a transcellular route, the incubation on ice must have lowered the amount uptaken by the cells, since the fluidity of the phospholipidic membranes would be reduced by lowering the temperature. Whereas ferulic acid was found in the gastric mucosa only as free form, it was also present as glucuronide, sulfate, and sulfoglucuronide in plasma, bile, and urine, in the portal vein after its perfusion in the stomach *in situ*, even though free ferulic acid was the major form. A further *in vivo* investigation confirmed the results obtained by Zhao *et al.* (above) and allowed the detection of metabolites of ferulic acid in the portal vein and abdominal artery, by using a more sensitive method of detection [coulometric instead of ultraviolet (UV)] [Konishi et al., 2006]. Based

Table 2.2 Summary of Different in Vivo Studies Investigating the Bioavailability of Chlorogenic Acid or 5-O-Caffeoylquinic Acid^b

Model	Vehicle/ Administration	Compound	Biological Fluid	Metabolites	Reference
Rat	Stomach intubation with 700 mol/kg	Chlorogenic acid Caffeic acid	Plasma (t_{max} 0.5–1h) Plasma (t_{max} within the first 2 h)	CA-G, CA-S/G, FA-S/G (small amounts) FA, FA-G, FA-S, FA-S/G (50% total CA conjugates = 34% total metabolites); CA, CA-G (41% total metabolites), CA-S/G	Azuma et al., 2000
Rat	Supplemented diets with 250 μ mol	With CLA or CA	Urine	% of the intake CLA, CA, FA, and isoFA Microbial metabolites: <i>m</i> -CA, derivatives of PPA, BA and HA From CLA From CA	Gonthier et al., 2003c
Rat	Duodeno-jejunal perfusion	50 μ M CA or CLA	Plasma 45 min after perfusion collection of:	FA, <i>m</i> -CA, <i>m</i> -HPPA, hippuric Parent (CA, CLA) and metabolites (FA, isoFA) (% ingested dose) From CLA From CA	Lafay et al., 2006b
Rat	Supplemented diet In situ gastric perfusion	CLA (0.25%) CLA (35 mols)	Bile Intestinal cells Secretion from cells Ileum effluent Net absorption Content in % of total phenolic acids at 1.5–7 h Plasma	traces 9.2 1.2 90.8 8 Stomach Traces CA (1%), CLA Small intestine Traces CLA CA (1%), CLA Cecum 15–32 % CA, CLA (peak at 4.5 h) 16% CLA absorption	Lafay et al., 2006a

(Continued)

Table 2.2 (Continued)

Model	Vehicle/ Administration	Compound	Biological Fluid	Metabolites	Reference
Human	Artichoke extract in 9 capsules	CLA (= 123 mg)	24 h urine	<ul style="list-style-type: none"> Estimation of CA absorption: 5.6% No CLA but FA, isoFA, DHFA, and VA (and their conjugates) 	Rechner et al., 2001
Healthy ileostomy subjects	Supplement	2.8 mmol	24 h urine	24 h ileostomy bag	Olthof et al., 2001
		CLA CA	Traces 11% ingested dose	67% ingested dose (estimated absorption: 33%) 5% ingested dose (estimated absorption: 95%)	
Human	Brewed coffee	96 mg CLA, 166 mg CA, 3 mg <i>p</i> -CA, 29 mg FA	Plasma, at 1 and 2 h after intake; t_{max} : 1 h	No CLA, <i>p</i> -CA and FA; CA and its glucuronide or sulfate conjugates	Nardini et al., 2002
Human	Brewed coffee	Containing (in mmol/serving): total CQA (2.9), total diCQA (0.24)	Plasma (%) Urine (%)	5-CQA: 40; 3- and 4-CQA: 18; di-CQA: 28FQA: present in 1 subject over 6; CA: 14 dHCA and GA: 56; <i>p</i> -HBA and <i>p</i> -CA: not in all subjects samples	Monteiro et al., 2007

Summary of the Different *in vivo* Studies Investigating Bioavailability of Ferulic Acid.^b

Models	Vehicle Administration	Compounds	Biological-fluids			Metabolites	References
		Absorption (% of ingested dose)	Foregut (small intestine/stomach)	Cecum	Colon	Residues	FA in plasma (µM)
Rat	Supplemented diet with (in g/kg):FA (1.5), FAA (2.5), FAXn (59.5)	FA FAA FAXn	~99 40 (6% as free FA) Traces (0.3% as free FA)	<1 57 (11% as free FA) 44 (0.7% as free FA)	23	3 33 (2% as free FA)	11 12 ~1

(Continued)

Table 2.2 (Continued)

Model	Vehicle/ Administration	Compound	Biological Fluid	Metabolites	Reference		
Rat	Supplemented water	FA, FAA, or FAXn at 70 mol/kg bw	Plasma (after 5, 15, 30, 60, 120 min)	Urine (over 24 h)	In % of total FA _{fmax} (min):FA- GFA-S/ GFA-SFA	Zhao et al., 2003a	
			FA	FA			
			FAA	FAA			
			FAXn	FAXn			
			4-23 [60']	6	18	5	
			60-70 [120']	87	76	91	
			4-6 [15 & 120']	2	2	1	
			1-34 [5']	4	4	3	
			Total FA excreted (% dose)				
			Relative BV of FA from diets				
			Urine	Feces			
			FA	1	72	1	
			FAA	0.56	54	1	
			FAXn	0.21	20	20	
Rat	Supplemented diet	FA at 5.15 mg/kg	In % of the total FA (30 min after ingestion)			Rondini et al., 2002	
			Plasma	Urine			
			24 (1.7 M)	11		FA	
			18 (0.9 M)	3		FA-G	
			58 (2.7 M)	86		FA-S and -S/G	
Rat	Small intestinal perfusion	Concentrations of FA from 10 to 50 μM	Absorption of FA	Biliary secretion of FA conjugates	Total excretion	No FA free but FA-G/ and FA-G/ S	Adam et al., 2002
			56 (for all doses)	~6	45-53	50	
			Plasma (μM)	Urine (% of intake)			No FA free but FA-G and FA-G/ S
			ND	42			
			1	52			
			7-8	39			
			0.25	Recovery quite limited (low absorption)			
Rat	Cereals with different amounts of FA	In mg/g: whole cereals (1.2) or bran (4.6)					

(Continued)

Table 2.2. (Continued)

Model	Vehicle/ Administration	Compound	Biological Fluid	Metabolites		Reference		
				% of total FA (over 24h)				
				Plasma	Urine			
Rat	26% bran-rich diet	Containing 95.8% bound and 4.2% of free FA (0.14 mg/g)		9	15	FA		
				19	11	FA-G		
				72	74	FA-S + FA-G/S		
Rat	Supplemented diet	5.05 mg/kg free ferulic acid		25	14	FA		
				17	2	FA-G		
				58	84	FA-S + FA-G/S		
Rat	Supplemented saline solution	2.25 mol(8 μmol/kg 25 min after BW) of/FA or FAA	gastric perfusion of	Gastric content		FA in % of the ingested dose Zhao et al., 2004		
				Gastric mucosa				
				in vitro	in situ		in vitro	in situ
				80	26		7	4
				91	81		2	2
				Plasma				
				Portal vein			Celiac arteria	
				Bile			Urine	
				49	6		8	5
				5	18		6	11
3	3	24	15					
43	72	62	70					
in % of total FAFAFA- SFA-GFA- G/S								

(Continued)

Table 2.2 (Continued)

Model	Vehicle/ Administration	Compound	Biological Fluid	Metabolites	Reference
Rat	Perfusion of jejunum + ileum	With 0.8 Ml/min of 1.5 or 120 M FA	Mesenteric vein Intestinal secretion: 5	Extracellular 75	Conjugates (% Silberberg et al., 2006) Conjugates (% of ingested dose)
Human	Tomato ingestion	21–44 mg FA	Urine (% of the ingested amount) 7–9 h after intake	Over 24 h 4–5	FA and conjugates (the major one being FA-G) Bourne and Rice- Evans, 1998

^aChlorogenic acid has been used as a name for 5-*O*-caffeoylquinic acid by the authors of the reports cited except [Monteiro et al., 2007]; 3-, 4-, or 5-CQA, 3-, 4- or 5-*O*-caffeoylquinic acid; BA, benzoic acid; CA, caffeic acid; CLA, chlorogenic acid or 5-*O*-caffeoylquinic acid; dHCA, dihydrocaffeic acid; diCQA, dicaffeoylquinic acid; FA, ferulic acid; FQA, feruloylquinic acid; GA, gallic acid; HA, hippuric; isoFA, isoferulic acid; *m*-CA, *m*-coumaric acid; *m*-HPPA, *m*-hydroxyphenylpropionic acid; *p*-CA, *p*-coumaric acid; *p*-HBA, *p*-hydroxybenzoic acid; PPA, phenylpropionic acid.

^bbw, body weight; FA: ferulic acid; FAA: 5-*O*-feruloyl-L-arabinofuranose; FA-G, feruloyl-glucuronide; FA-S, feruloyl-sulphate; FA-S/G, feruloyl-sulphoglucuronide; FAXn: feruloyl-arabinoxylan.

on their previous report [Zhao et al., 2004], the authors suggested that these metabolites would come from a further metabolism by the liver of the free form absorbed by the stomach, and/or reabsorption by the enterohepatic circulation rather than from a direct metabolism by the gastric cells. Ferulic acid and its sugar ester are not the only phenolic acids shown to be absorbed by the stomach. 5-*O*-Caffeoylquinic [Lafay et al., 2006a], but also gallic, caffeic, and 4-coumaric acids could also be absorbed at the gastric level, their absorption being dependent on their structure in the following order: 5-*O*-caffeoylquinic = gallic < caffeic < 4-coumaric acids [Konishi et al., 2006]. Indeed, caffeic acid has been shown to be three times better absorbed (95% of the ingested dose) than 5-*O*-caffeoylquinic acid (33%) [Olthof et al., 2001]. Figure 2.8 summarizes the behavior of phenolic acid esters and free forms in the GIT.

The Mechanisms of Uptake of Phenolic Acids

The partition coefficient ($\log P$, or \log octanol/water), which reflects the lipophilicity of a molecule, will determine its affinity for a biological membrane and its partitioning through and into a membrane. This coefficient has been shown to govern the capacity of different flavonoids to be absorbed by cells [Crespy et al., 2003], suggesting passive diffusion as a main mechanism of flavonoid transport. The partition coefficient determined for ferulic acid at 1.86 [Voisin-Chiret et al., 2007] rather suggests that the phenolic acid will have affinity for cytoplasmic membrane and permeate by transcellular diffusion. Moreover, the percentage of ferulic acid absorbed after perfusion of the rat small intestine was independent of the concentration perfused, indicating that there was no saturation of the permeation system involved [Silberberg et al., 2006], findings which do not support the existence of a specific transport system. However, some studies have attempted to discover other permeation mechanisms for phenolic acids.

Various drug transporters have been identified and characterized, among which are the monocarboxylate transporters (MCTs). The physiological role of these transporters is to co-transport the endogenous monocarboxylates such as pyruvate, lactate, acetoacetate, and β -hydroxybutyrate together with equimolar protons by a symport mechanism (as reviewed in [Enerson and Drewes, 2003]). MCTs may also have an important role in the transport of some exogenous compounds, which consist of weak organic acids that are monovalent, with the carboxyl group attached to a relatively small alkyl group having either hydrophobic or hydrophilic properties. These transporters are expressed by various tissues such as the intestine, heart, liver, kidney, and brain [Halestrap and Price, 1999]. Different isoforms of MCTs have recently been localized in the different regions of the human intestine and on the membrane of intestinal cells [Gill et al., 2005]. MCT1 expression is restricted to the luminal membranes of human intestinal cells, whereas MCT4 and MCT5 are present on the basolateral side. The isoform 3 is also expressed on the basolateral side but at a very low level compared with MCT4 and 5. However, no MCT6 is detected

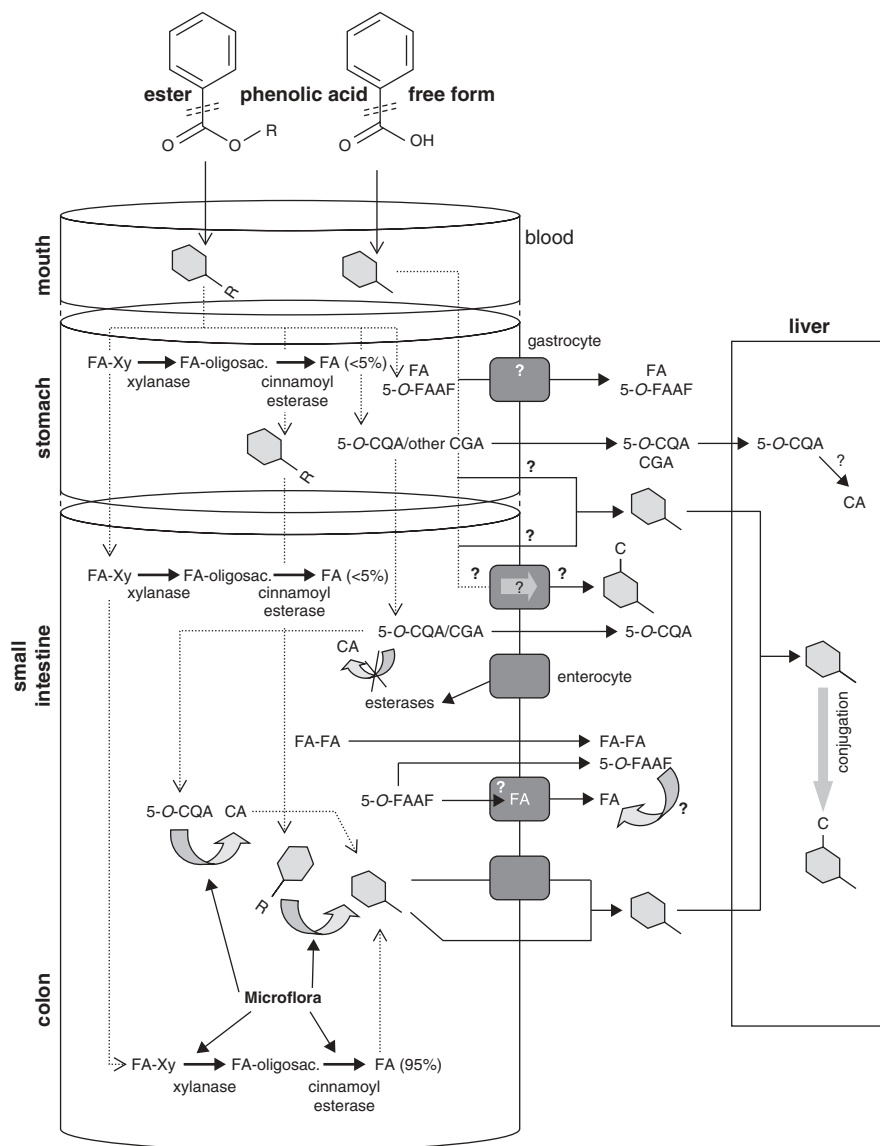


Figure 2.8 Summary of behavior of phenolic acid esters and free forms in the GIT and the liver. 5-O-CQA, 5-O-caffeoylquinic acid; 5-O-FAAF, 5-O-feruloyl-L-arabinofuranose; C, conjugate (sulfate, glucuronide or methyl); CA, caffeic acid; FA, ferulic acid; FA-FA, dimer of ferulic acid; FA-oligosac., ferulic acid esterified to an oligosaccharide; FA-Xy, ferulic acid esterified to xylan; R, alkyl group.

on either the basolateral or apical side of small intestinal or colonic cells. Expression of the transporters increases along the length of the intestine, being maximal in the distal colon and even absent in the jejunum for MCT4 and 5. MCT1, expressed on the luminal side of intestinal cells, is a potential candidate for the transport of phenolic acids.

An *in vitro* model of Caco-2 cells grown on semipermeable membranes was used to investigate the potential involvement of the MCTs in the transport of phenolic acids [Konishi et al., 2002]. The study was based on competition for transport between fluorescein, an MCT substrate [Kuwayama et al., 2002], and phenolic acids. Ferulic, cinnamic, 4-coumaric, and vanillic acids competitively inhibited the transport of fluorescein, with the following order of inhibition: cinnamic > ferulic \geq vanillic > 4-coumaric acids, suggesting the transport of these phenolic acids via MCTs. Caffeic acid had no effect, whereas ferulic and vanillic acids had a very similar effect (respectively, 49 and 45% of inhibition). However, it must be mentioned that the concentrations of phenolic acids used as competitors in this study were high (10 mM) and one could wonder, even though not mentioned by the authors, if phenolic acids used at such concentrations could be not fully dissolved and/or be toxic for the cells, the resulting percentage of inhibition influenced by the toxicity. Further studies aimed to better understand the mechanisms of phenolic acid transport. Using the same model, transport of 4-coumaric acid was shown to be pH dependent, higher, but saturable, in the presence of a proton gradient (basal side, pH 6; apical side, pH 7.4), and 10 times higher from the apical to the basal side compared with the opposite direction [Konishi et al., 2003b]. According to these results, the authors suggested that the permeation of 4-coumaric acid in the presence of a proton gradient would be dependent on an active transport mechanism, whereas in the absence of a proton gradient, it must be restricted by tight junctions. The active transport was proposed to be MCT mediated, since benzoic and acetic acids, substrates of MCTs, inhibited 4-coumaric acid permeation, although lactic acid, a good substrate for MCT1–MCT4, had no effect, suggesting the involvement of a different isoform. However, no metabolite of 4-coumaric acid could be detected on the basal side of the Caco-2 cell model. This model also served to study the permeation of ferulic acid, shown to be Na⁺-independent [Konishi and Shimizu, 2003], contrary to what has been proposed earlier for cinnamic acid [Ader et al., 1996; Wolfram et al., 1995]. As for 4-coumaric acid, ferulic acid was absorbed via an MCT system and was not conjugated by the *in vitro* model. The authors also proposed that tea polyphenols shared the same MCT transporter(s) with ferulic acid, since its permeation was inhibited by (+)-catechin, (–)-epicatechin, (–)-epicatechin-gallate, (–)-epigallocatechin, and (–)-epigallocatechingallate [Konishi et al., 2003a], the involvement of an MCT in the transport of electrocardiogram (ECG) also observed with Caco-2 cells as proposed by another report [Vaidyanathan and Walle, 2003]. Transport of caffeic, 3-coumaric, and 3-hydroxyphenylpropionic acids [Konishi and Kobayashi, 2004b], as well as dihydrocaffeic acid [Konishi and Kobayashi, 2004a], were also proposed to

occur via MCTs, as shown using Caco-2 cells, later proposed to be an isoform different from MCT1 [Konishi et al., 2006]. More recently, the mechanism of transport of phenolic acids through the epithelium of the colon, the major site of release of phenolic acids from esters and flavanol precursors, was clarified [Poquet et al., 2008b]. The initial purpose of investigation was to determine the eventual role of the mucus layer, much thicker in the colon than in the small intestine, which could influence the absorption of phenolic acids due to its property of maintaining the pH close to the mucosa around neutrality [McNeil et al., 1987]. However, the mucus layer secreted by the mucus secreting HT29-MTX cells in a co-culture with Caco-2 had only a slight negative role on the transport of ferulic acid. However, using this model and more physiological concentrations of phenolic acids, compared with studies reported in the literature, ferulic acid was shown to mainly (~80%) permeate through the intestinal epithelium by transcellular diffusion, which was dependent on the hydrophobicity and on the pK_a of the phenolic acid, and on the pH of the donor compartment. Moreover, the remaining 20% of ferulic acid seemed to be transported by a Na^+ -dependent carboxylic acid transporter (S-MCT) as well as by an MCT.

Circulating Metabolites and Conjugates

Free ferulic acid and its glucuronide were the forms excreted in human urine over the 7–9 h following ingestion of a meal based on fresh tomatoes, a source of ferulic, 5-*O*-caffeoylquinic, caffeic, and 4-coumaric acids [Bourne and Rice-Evans, 1998]. They represented 11–25% of the ingested amount, a considerable proportion as the glucuronide. Ferulic acid and its conjugates, glucuronide, sulfate, and sulfoglucuronide, peaked in rat plasma between 0 and 1 h, and lasted for at least 24 h after ingestion of a 26% bran-rich diet, which contained 95.8 and 4.2%, respectively, of bound and free ferulic acid [Rondini et al., 2004]. They also started to appear in urine only 30 min after the ingestion of bran, reaching a plateau after 4.5 h. In plasma, over the 24 h following intake of bran, the sulfate and sulfoglucuronide were the main metabolites (72% of total ferulic acid), followed by the glucuronide (19%) and the free form (9%). The free form was more abundant (25%) when animals received pure ferulic acid instead of the bran-based diet. Conjugated ferulic acid was also detected in the intestinal contents, suggesting a metabolism in the mucosa and a secretion back into the lumen via the bile duct. Free ferulic and its glucuronide, sulfate and sulfoglucuronide conjugates were detected in plasma after intake of ferulic acid or of 5-*O*-feruloyl-L-arabinofuranose [Zhao et al., 2003b]. Given as free form in a diet, the amount of ferulic acid in plasma peaked 30 min after ingestion of the meal and quickly decreased between 0.5 and 1.5 h and more slowly until 4.5 h [Rondini et al., 2002]. Ferulic acid was present in plasma and urine as the free form but also conjugated with glucuronide, sulfate, or both, the major form being the feruloyl-sulfate and feruloyl-sulfoglucuronide. Another study showed that, after oral administration of pure ferulic acid (1 mmol) to rats, three

metabolites, in addition to the parent compound, which was the main form excreted, were detected in urine 0–12 h after the intake [Zhang et al., 2005]. Two of the metabolites were identified as monoglucuronides of ferulic acid, the conjugation taking place on the 4-OH group or on the carboxylic function, as suggested by the authors. The third conjugate was proposed to be a diglucuronide, with one glucuronide on the free hydroxyl of the phenyl ring and the other one on the carboxylic function. This study also investigated the tissue distribution of ferulic acid in rats, found in the liver, spleen, kidney, and lungs, but not in the heart, 2 h after the oral administration. Free caffeic acid, together with ferulic acid, and their respective sulfate, glucuronide, and sulfoglucuronides were found in rat plasma following the oral administration of caffeic acid [Azuma et al., 2000; Plumb et al., 1999]. However, only caffeoyl-glucuronide, caffeoyl-sulfoglucuronide, and feruloyl-sulfoglucuronide were detected with a peak at 0.5–1 h in rat plasma after oral administration of 5-*O*-caffeoylquinic acid [Azuma et al., 2000]. In this study, interestingly, when caffeic acid was orally administered, caffeoyl-glucuronide, caffeoyl-sulfoglucuronide, and feruloyl-sulfoglucuronide peaked after 2 h instead of 0.5 h when 5-*O*-caffeoylquinic acid was administered. It is surprising to see that metabolites, which require microbial metabolism to be generated, appear quicker in plasma from 5-*O*-caffeoylquinic acid than when caffeic acid is absorbed. The results suggest that caffeic acid could be absorbed from the stomach but also in the upper part of the intestine, with a better absorption rate from the small intestine than from the stomach, explaining the delay of the peak of absorption. Even though not detected by the authors in plasma, 5-*O*-caffeoylquinic acid could be absorbed as such by the stomach, better than caffeic acid, and quickly hydrolyzed by gastric cells, intestinal cells, or liver, allowing the rapid presence of caffeic acid in plasma (0.5 h). Konishi et al. [2006] demonstrated that caffeic acid is better absorbed than 5-*O*-caffeoylquinic acid by the stomach, which does not support the above-mentioned hypothesis. 5-*O*-caffeoylquinic acid may be better absorbed than caffeic acid but, due to instability, its amount in biological fluids could be underestimated. The absorption by the stomach was also proposed for dihydrocaffeic acid, as the parent compound and its metabolites peaked in plasma before 30 min following its gastric administration to rats [Poquet et al., 2008a].

In situ perfusion of ferulic acid showed that ferulic acid could be absorbed from the small intestine and that the forms circulating in plasma were glucuronide and sulfate conjugates, ferulic acid being rapidly excreted in urine [Adam et al., 2002]. Dihydrocaffeic acid was rapidly excreted, detected in urine at 6 and 12 h, but not at 24 h, however, not detected in plasma at a time even as short as 30 min following its administration by gavage to rats, suggesting a quick absorption, before 30 min [Poquet et al., 2008a].

Caco-2 cells have also been used to study the metabolism of phenolic acids. Contrary to the transport studies, which usually use the cells grown on semipermeable filters (two compartments), the cultures used to study metabolism are prepared with cells grown and partially differentiated on dishes (one

compartment). The Caco-2 cell model could perform sulfation, glucuronidation, and methylation of various hydroxycinnamic acids [Kern et al., 2003b]. Ferulic, sinapic and 4-coumaric acids could enter the cells, be sulfated, but not glucuronidated, and then be effluxed back into the medium. However, the corresponding methyl esters were both sulfated and glucuronidated. The authors proposed that methyl esters could be more hydrophobic and as a consequence better access to the UGTs localized in the membrane of the endoplasmic reticulum, whereas the more polar corresponding hydroxycinnamic acids would remain in the cytosol where the sulfotransferases are located. When a co-culture of HT29-MTX and Caco-2 cells, differentiated on semipermeable membranes to study the metabolism and efflux of ferulic acid [Poquet et al., 2008b], was used, the parent compound was the major form excreted to the basal side of the culture, followed by the glucuronide conjugate, the reduced form (dihydroferulic acid) and the sulfate conjugate. The reduced metabolite was equally distributed to the apical and basal sides, whereas the concentrations of the conjugates were higher on the serosal side. An MRP transporter could contribute to the major part of the glucuronide efflux and also of some dihydroferulic acid at the serosal side, the strongest candidate being MRP3, without excluding the possible involvement of MRP6. Moreover, P-gp protein could be responsible for some of the efflux of these metabolites to the luminal side of the cells. Since the amount of sulfate conjugate effluxed was much lower, its mechanism of efflux could not be investigated. The pattern of dihydrocaffeic acid metabolism by HT29-MTX and Caco-2 cells suggested that Caco-2 cells do not possess the isoenzyme responsible for the glucuronidation of phenolic acids, proposed to be UGT1A7 [Poquet et al., 2008a]. Methylation of dihydrocaffeic acid was also proposed to be regioselective, favored on the 3-OH and dependent on the pK_a of the 4-OH. Apart from sulfation, methylation, or glucuronidation, a report mentioned the possible formation of mono- or biglutathione conjugates of caffeic, 5-*O*-caffeoylquinic and dihydrocaffeic acids by rat hepatocyte microsomes, the reaction taking place during peroxidase/ H_2O_2 -catalyzed oxidation of the phenolic acids [Moridani et al., 2001].

All these studies suggest that the metabolic pathway is the same for free and bound forms of ferulic acid. Whereas the free form is rapidly absorbed, metabolized and excreted in urine, the bound form allows a longer time period (free and conjugated) in plasma, as already suggested by the absence of free ferulic acid in rat plasma 18 h after intake from an enriched diet, whereas its metabolites were still present [Adam et al., 2002]. Even though its bioavailability, in terms of half-life in plasma and low excretion in urine, was improved when esterified, the absorption of ferulic acid from a wheat source was lower than if present as free form in a diet [Rondini et al., 2004]. This indicates that the amounts of ferulic acid circulating in plasma as well as its circulating metabolites are dependent on its form present in the food source.

Depending on the food source, the model used, the time points, the method of analysis, and the reports, phenolic acids and, especially ferulic acid can be detected under different forms in the biological samples. However, there is a

common tendency to suggest that phenolic acids can be absorbed through the gastrointestinal epithelium and be metabolized to circulate and be excreted as free and/or conjugated forms.

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3 Biochemical Actions of Plant Phenolics Compounds: Thermodynamic and Kinetic Aspects

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INTRODUCTION

Polyphenols are secondary metabolites of plants and include a myriad of chemical structures, from simple molecules such as phenolic acids to highly polymerized compounds such as condensed tannins. Considering this heterogeneity, we have focused this chapter on one of the most abundant family of polyphenols in human diets, the flavonoids. Flavonoids are a chemically defined family of polyphenols that have a basic structure of two aromatic rings (A and B) linked through three carbons that usually form an oxygenated heterocycle (ring C) and differ in the arrangements of hydroxy, methoxy, and glycosidic groups and in the conjugation between the B- and C-rings [Butkovic et al., 2004].

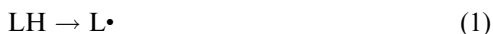
The benefits of polyphenols on human health are often ascribed to their potential ability to act as antioxidants. Such ability would be possible considering that polyphenols have chemical structures supporting antioxidant chemical reactions (i.e., scavenging of free radicals and chelation of redox-active metals). Importantly, many polyphenols retain key antioxidant features in their chemical structure after ingestion and metabolism by mammals. In parallel, it has been reported that certain polyphenols can provide benefits in pathological situations associated with high free-radical production, for example, hypertension and cardiovascular disease [Bazzano et al., 2002; Hung et al., 2004; Rimm, 2002]. However, the physiological mechanisms linking the antioxidant chemical characteristics of flavonoids with their health effects are still a subject of discussion.

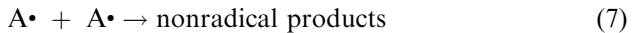
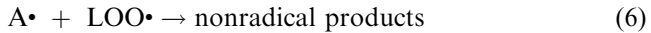
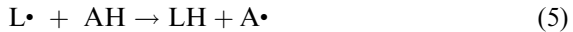
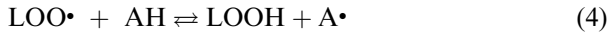
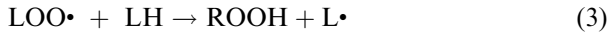
Based on chemical, thermodynamic, and kinetic data, this chapter will discuss the mechanisms proposed for polyphenol biological actions, especially antioxidant reactions. Although most of the points addressed in this chapter are valid for an important number of plant polyphenols, we will focus the analysis on flavonoids and, in particular, on flavanols.

POLYPHENOLS AS ANTIOXIDANTS

Polyphenols as Chain-Breaking Antioxidants

The inhibition of lipid (LH) oxidation may be considered as one of the most important chemical reaction mechanisms that could explain the antioxidant function of flavonoids. In general terms, chain-breaking antioxidants (AH) inhibit or retard lipid oxidation (reactions 1–7) by interfering with initiation [generically represented by reaction 1] or with chain propagating reactions (reactions 2 and 3) by readily donating hydrogen atoms to lipid peroxy radicals (LOO•) or lipid radicals (L•) (reactions 4 and 5) [Frankel, 1998]:

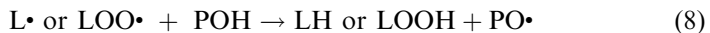




The analysis of the thermodynamic and kinetic characteristics of these reactions will allow a better understanding of the biological importance of chain breaking in the antioxidant actions of polyphenols.

Polyphenols as Chain-Breaking Antioxidants: Thermodynamics

Polyphenols could act as effective chain-breaking antioxidants ($AH = POH$) through the one-electron transfer reactions 4 and 5 if they produce a stable and relatively nonreactive "antioxidant radical" ($A\cdot = PO\cdot$) [Jovanovic et al., 1994]. Reactions 4 and 5 can be represented by the reaction 8, where $L\cdot$ or $LOO\cdot$ represents the oxidant free radical. This reaction can be decomposed in two half-reactions: one reduction (reaction 9) and one oxidation (reaction 10):



Thermodynamics is used to predict whether reactants have a spontaneous tendency to change into products. This tendency is associated with a decrease in the free energy or Gibbs energy of the system (G) to a minimum. As a consequence, the thermodynamic criterion for spontaneous change at constant temperature and pressure is $\Delta G < 0$. Under standard conditions (concentrations = 1 M, and $P = 1$ atm), the standard Gibbs energy variation (ΔG°) is related with the equilibrium constant (K) by equation 11:

$$\Delta G^\circ = -RT \ln K \quad (11)$$

To explore the spontaneity of electron/hydrogen atom transfer reactions ΔG° can be calculated by the following expression:

$$\Delta G^\circ = -nF \Delta E^\circ \quad (12)$$

where n is the number of electrons that are transferred from the reducing agent (antioxidant) to the oxidizing agent per mole of reaction events; F represents the Faraday constant (96485 C/mol of electrons); and ΔE° is the difference between the standard reduction potential of the involved couples (E° , for the reduction half-reaction and E° , for the oxidation half-reaction). Table 3.1 shows the E° , that is, E° under biological conditions (see footnote a in Table 3.1) of well-known antioxidant compounds and of select flavonoids. Table 3.1 also depicts the ΔG° obtained after applying equation 14 for the reactions of these flavonoids with HO•, LO•, and LOO•. The negative value of ΔG° observed for the processes indicate that these reactions are thermodynamically (energetically) favored, pointing out the feasibility of flavonoids as free-radical scavengers.

The possibility that some flavonoids can be prooxidant has also been suggested [Halliwell, 2008]. Such prooxidant activity is based on a sum of complex reactions involving the reaction between POH and O₂ to generate O₂•⁻, and the reaction of POH with O₂•⁻ yielding H₂O₂. The former process, that is, POH autoxidation, is thermodynamically unfavored (E° O₂/O₂•⁻ = -330 mV [Wardman, 1989] or -160 mV [Sawyer and Valentine, 1981]), although it has been claimed to occur under certain conditions [Miura et al., 1998; Nakayama et al., 1995]. By contrast, the latter reaction is energetically favored (E° O₂•⁻/H₂O₂ = 940 mV [Buettner, 1993]), but being dependent on the presence of a product of the first reaction has low possibilities to occur in a significant extent.

A strict approximation should take into consideration that in vivo conditions are usually nonstandard conditions, and the actual concentrations of the reactants (oxidants and antioxidants) are also important. This last situation will be considered in the subsequent kinetic analysis.

Polyphenols as Chain-Breaking Antioxidants: Kinetics

Thermodynamics only identify whether a particular reaction mixture has a tendency to form products, but do not indicate whether that tendency will ever occur in a biologically appropriate time scale. To have a real idea if that reaction occurs, it would be necessary to know the rate of the chemical reactions; that is, making a kinetic analysis. For a given reaction 13, the reaction rate (v) is proportional to the molar concentration of the reactants (A, B) raised to a simple power (α , β). These values are called partial orders with respect to each of the species participating in the reaction. The rate constant (k) is essentially defined by the thermodynamic characteristics of the species under reaction and

Table 3.1 Biological Standard Reduction Potentials (E°) for a Series of Antioxidant Compounds and Flavonoids and Biological Standard Free Energy Variation (ΔG°) for the Reactions between These Compounds and Oxygen Free Radicals

Compound (Redox Couple)	$(E^\circ)^a$ (mV)	$\Delta G^{\circ b}$ (kJ)		
		HO•/H ₂ O $E^\circ = 2310 \text{ mV}^{cc}$	LO•/LOH $E^\circ = 1600 \text{ mV}^{cd}$	LOO•/LOOH $E^\circ = 1000 \text{ mV}^c$
Glutathione-cysteine (RS•/RS ⁻)	920 ^e	-134	-66	-8
α -Tocopherol (α -TO•/ α -TOH)	500 ^f	-175	-106	-48
Trolox C (TO•/TOH)	480 ^f	-177	-108	-50
Ascorbate (A•/AH ⁻)	282 ^g	-196	-127	-69
Catechol (Cat-O•/Cat-OH)	530 ^h	-172	-103	-45
(-)-Epigallocatechin (EGC•/EGC)	430 ⁱ	-181	-113	-55
(-)-Epigallocatechin gallate (EGCG•/EGCG)	430 ^j	-181	-113	-55
(-)-Epicatechin (EC•/EC)	570 ^j	-168	-99	-41
(-)-Epicatechin gallate (ECG•/ECG)	550 ^j	-170	-101	-43
Quercetin (Q•/QH)	330 ^j	-191	-123	-65
Kaempferol (K•/KH)	750 ^j	-151	-82	-24
Rutin (R•/RH)	600 ^j	-165	-96	-39

^aSeveral considerations must be made about biological standard reduction potentials (E°) values. IUPAC convention of writing the involved couples always in the sense of the reduction is widely used. With this convention the potentials are presented in the form $E^\circ(A/B)$ where B is the one-electron reduction product of A. The standard reduction potentials (E°) are expressed in relation to the normal or standard hydrogen electrode (NHE or SHE) that has assigned the value zero [Atkins and de Paula, 2006]. Standard conditions refer to 1 M concentrations for all dissolved species [Atkins and de Paula, 2006]. As a consequence, E° corresponds to the reaction under these conditions, that includes $\text{pH} = 0$ when H^+ is involved. Considering that reactions in biological systems, E° (biological standard reduction potentials) is calculated for all dissolved species at 1 M concentration and $\text{pH} = 7$.

^b ΔG° for the reaction can be obtained by using equation 12 or by calculating the ΔG° of the overall reaction as the sum of the Gibbs energies of the reactions into which it can be divided ($\Delta G^\circ = \Delta G^\circ_1 + \Delta G^\circ_2$) (where 1 corresponds to the reduction half-reaction and 2 corresponds to the oxidation half-reaction). In general, we cannot combine the E° values directly because they depend on the value of n , which may be different for the two couples. In this case both of the approximations are valid because the E° considered correspond to one electron transferences.

^cBuettner, [1993].

^dKoppenol, [1990].

^e[Surdhar and Armstrong, 1986; Surdhar and Armstrong, 1987].

^f[Simic, 1990].

^g[Williams and Yandell, 1982].

^h[Scurlock et al., 1990]

ⁱ[Frei and Higdon, 2003].

^j[Jovanovic and Simic, 2000].

is independent of the concentration of these species. The reaction rates are experimentally determined.



$$v = k[A]^\alpha[B]^\beta \quad (14)$$

Reactions can be classified on the basis of their order, which is the sum of the powers to which the concentrations of the participating species are raised in the rate law. If $\alpha = \beta = 1$ in equation 14, the reaction is first-order in A, first-order in B, and is globally of second order. Reactions 4 and 5 respond to this kind of second-order reaction rate law, and the k values have been established for the reactions between several oxidant species and antioxidants.

Table 3.2 shows the relative reaction rates of two well-known antioxidants (ascorbic acid and α -tocopherol) and of the flavanol (–)-epicatechin, with different radicals, that is, hydroxyl radical ($\text{HO}\bullet$), alcoxyl radical ($\text{LO}\bullet$), and peroxy radical ($\text{LOO}\bullet$). These calculated values provide a relevant limitation for the “free-radical scavenging” hypothesis. The relatively low plasma concentrations of flavanols, which occur even after the consumption of foods rich in these compounds [Holt et al., 2002], leads to a situation kinetically unfavorable with respect to that of other compounds with similar thermodynamic free-radical scavenging capabilities. These compounds, that is, α -tocopherol and ascorbate, are present in blood and/or in the intracellular milieu in micromolar and even millimolar ranges. The bioavailability of flavonoids is generally low; the actual concentrations that can be reached in plasma of humans subjected to realistic polyphenol consumption are in the nanomolar range. These concentrations are transient in nature, peaking at 2–4 h after consumption [Holt et al., 2002; Rein et al., 2000; Schroeter et al., 2006]. Even assuming the highest flavanol concentration found in plasma (low micromolar values), the relative physiological reaction rate with the more common radicals does not support the *in vivo* free-radical scavenging effects proposed for polyphenols. Nevertheless, this kinetic limitation implies the existence of other mechanisms, compatible with the tissue levels reached by polyphenols, that may explain the observed changes in cell or tissue oxidation [Fraga, 2007]. Taking into consideration these limitations, a direct effect should be possible only in tissues directly exposed to polyphenols after their consumption, but unlikely to occur in other tissues in which polyphenols are present at significantly lower (nanomolar) concentrations.

It is possible to further expand this scenario considering that, in cells, flavonoids (or other polyphenols) should be competing with other relevant antioxidants, as glutathione. Glutathione is able to function as both a direct antioxidant (scavenging free radicals) and an indirect antioxidant, being the reducing cofactor of glutathione peroxidase, one of the main enzymatic antioxidant defenses. Additionally, most of biological systems are able to synthesize reduced glutathione and

Table 3.2 Relative Reaction Rates for the Reactions between Oxygen Free Radicals and Selected Antioxidant Compounds and (-)-Epicatechin

Compound concentration (M)	Relative reaction rate (s ⁻¹)	
	v/[HO•] ^a	v/[ROO•] ^c
Plasma		
Ascorbate = [50 × 10 ⁻⁶] ^d	500,000	80,000
α-Tocopherol = [28 × 10 ⁻⁶] ^e	280,000	2,800
(-)-Epicatechin ≈ [0.3 × 10 ⁻⁶] ^f	2,000	40
Cells		
Ascorbate = [5 × 10 ⁻³] ^d	50,000,000	8,000,000
(-)-Epicatechin ≈ [2 × 10 ⁻⁶] ^f	13,000	270

^aRelative reaction rates between HO• and ascorbate (AH⁻) are based on equation 3: v = k [HO•] M × [AH⁻] M assuming k = 1 × 10¹⁰ M⁻¹ s⁻¹ [Buettnner and Jurkiewicz, 1996]. Idem for α-tocopherol assuming k as 1 × 10¹⁰ M⁻¹ s⁻¹ [Niki, 1996]. Idem for (-)-epicatechin assuming k_{(-)-epicatechin} ~ k_{(+)-epicatechin} = 66 × 10⁸ M⁻¹ s⁻¹ [Bors et al., 1990].

^bRelative reaction rates between ROO• and AH⁻ are based on equation 3: v = k [ROO•] M × [AH⁻] M assuming k = 1.6 × 10⁹ M⁻¹ s⁻¹ [Buettnner and Jurkiewicz, 1996]. Idem for α-tocopherol assuming k = 1 × 10⁸ M⁻¹ s⁻¹ [Niki, 1996]. Idem for (-)-epicatechin assuming k_{(-)-epicatechin} ~ k_{(+)-epicatechin} as 1.35 × 10⁸ M⁻¹ s⁻¹ [Bors et al., 1990].

^cRelative reaction rates between ROO• and AH⁻ are based on equation 3: v = k [ROO•] M × [AH⁻] M assuming k = 1 × 10⁶ M⁻¹ s⁻¹ [Buettnner and Jurkiewicz, 1996]. Idem for α-tocopherol assuming k = 1 × 10⁶ M⁻¹ s⁻¹ [Niki, 1996]. Idem for (-)-epicatechin assuming k = 7.3 × 10⁶ M⁻¹ s⁻¹ [Scott et al., 1993]

^d[Frei and Higdon, 2003];

^e[Fraga et al., 2005];

^f[Rein et al., 2000].

reduce oxidized glutathione allowing the maintenance of an adequate steady-state concentration of reduced glutathione. By contrast, polyphenols are not synthesized, and there is no known recycling in animals. Furthermore, polyphenol levels in the organism have been reported to be transient, requiring a permanent consumption of polyphenol-rich foods to maintain a steady-state concentration. As a consequence, cells would have 10^7 – 10^{10} molecules of glutathione and less than 10^3 molecules of flavonoids as a protection from the oxidative injury. These considerations are not always taken into account in *in vitro* studies, where the number of molecules per cell present to exert a function is manipulated at concentrations that exceed biologically relevant ranges. The described considerations open the possibility for ascribing the well-documented beneficial health effects of flavonoids to other mechanisms, antioxidant or not, beyond the free-radical scavenger and metal chelation activity.

Other Physicochemical Aspects Associated to the Chain-Breaking Antioxidant Effect: The Stability of the Polyphenol-Derived Free Radicals

The reactions between free radicals and flavonoids (or polyphenols) are assumed to form aroxyl radicals ($\text{PO}\cdot$) (reaction 8). The stability of these secondary radical species is an important element to be considered in their antioxidant actions. Flavonoids with similar reduction potentials can originate radicals with very different reactivity toward other molecules present in biological systems. While a stable and relatively nonreactive $\text{PO}\cdot$ is also nonreactive to propagate the chain reaction, a high reactive $\text{PO}\cdot$ would propagate rather than interrupt a chain reaction.

To compare the stability of aroxyl radicals derived from different flavonoids, the rate constants for the disproportionation reaction between two $\text{PO}\cdot$ to render nonradical species (reaction 15) can be used:



The rate of reaction 15 can be described by the following equations:

$$v = -\frac{1}{2}d[\text{PO}\cdot]/dt = k_D[\text{PO}\cdot]^2 \quad (16)$$

$$-d[\text{PO}\cdot]/dt = 2k_D[\text{PO}\cdot]^2 \quad (17)$$

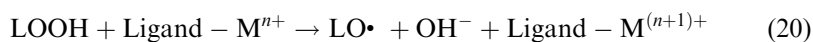
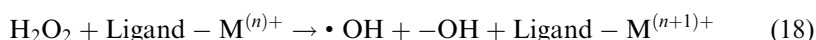
When a series of flavonoids were compared through the analysis of the second-order rate constants (k_D), it was concluded that (i) k_D values differ considerably, ranging from $10^5 \text{ M}^{-1} \text{ s}^{-1}$ (the most stable) to $10^8 \text{ M}^{-1} \text{ s}^{-1}$ (the less stable), and (ii) these data, together with the spectral characteristics of transient aroxyl radicals, were used to establish the structural requirements for

radical stabilization (the presence of the catechol moiety, the 2,3-double bond in conjugation with a 4-oxo function, and the additional presence of 3- and 5-hydroxyl groups) [Bors et al., 1990].

POLYPHENOLS AS METAL CHELATORS

Polyphenols as Metal Chelators: Thermodynamics

Redox active metals (M) such as iron, manganese, and copper can promote free radical formation by catalyzing otherwise slow reactions in biological settings: (i) catalyzing the decomposition of hydrogen peroxide (H_2O_2) into hydroxyl radicals ($\bullet\text{OH}$) (reaction 18), and (ii) catalyzing the decomposition of other hydroperoxides, mostly lipid hydroperoxides yielding peroxy and alkoxy radicals (reactions 19 and 20):



As a consequence, metal chelation is an alternative antioxidant strategy based on sequestering metal ions to prevent metal-catalyzed free radical formation [Brown et al., 1998; Guo et al., 1996; Morel et al., 1998]. To have an antioxidant action by metal chelation, a compound should be: (i) able to complex the metal and yield a stable product, and (ii) the resultant complex should be a poor catalyst for the free radical generating reactions where the metal is involved.

Some polyphenols, and specially flavonoids, have a strong affinity for metal ions due to the presence and position of several hydroxyl groups: the 3'- 4'-hydroxyl groups in the catechol unit, together with the hydroxyl groups at positions 3 and 5 and the 4-oxo function, have been postulated as metal-complexing sites within a flavonoid molecule [van Acker et al., 1996]. In addition, the electronic properties of the ring system make flavonoids good ligands for the *d* electrons of the elements of the fourth period, for example, iron [Havsteen, 1983]. Because of its biological relevance, there are numerous *in vitro* studies using iron as the transition metal. By defining the chelation strength as the ability to release Fe^{2+} from the $\text{EDTA}-\text{Fe}^{2+}$ complex, a wide range of chelating activities for flavonoids were reported, including those that act as efficient chelators, for example, apigenin, and those with nonchelating possibilities, for example, naringenin [van Acker et al., 1996].

The used experimental designs very often do not allow discriminating if the inhibitory effects on metal-catalyzed free radical reactions are mediated by metal chelation or by the scavenging of the resulting free radical. In this regard, Arora et al. [1998] analyzed the effects of a series of flavonoids on lipid oxidation comparing a metal-initiated process versus a metal-independent process. Results showed that flavonoids were less effective inhibiting metal-independent than metal-initiated lipid oxidation, suggesting that metal chelation would play a role in determining the antioxidant activities of these compounds. The large differences observed in the antioxidant action based on the iron-chelating capacity of different flavonoids can be explained by flavonoid-metal complex thermodynamic aspects, for example, stabilities and redox properties [Thompson et al., 1976] that involved the flavonoid chemical structure.

The stability of metal complex is also given by the number of chelate rings formed in the resultant ligand-metal complex. For example, desferrioxamine, the most widely used iron chelator, minimizes $\bullet\text{OH}$ production by acting as a hexadentate ligand [Liu and Hider, 2002]. Unfortunately, there is not enough information on the denticity of polyphenols as metal chelators to assess the relevance of the stability of the flavonoid-metal complex formed.

From the point of view of the redox properties of the formed complex, Merkofer et al. [2006] have studied the Fenton reaction 18 catalyzed by different iron chelators and concluded that a Fe-complex can participate in cell redox cycling only when two conditions are fulfilled: (i) the oxidized complex (ligand- $\text{M}^{(n+1)+}$) can be reduced by a physiologically relevant compound [e.g., NAD(P)H] [Pierre et al., 2002], then the $E^{\circ'}_{(\text{Ligand}-\text{M}^{(n+1)+}/\text{Ligand}-\text{M}^{n+})}$ is higher than -320 mV; and (ii) the reduced complex (ligand- M^{n+}) can transfer an electron to H_2O_2 , thus the $E^{\circ'}_{(\text{Ligand}-\text{M}^{(n+1)+}/\text{Ligand}-\text{M}^{n+})}$ should be smaller than $320\text{--}390$ mV [Buettner, 1993; Merkofer et al., 2006]. Then, complexes $E^{\circ'}$ in the -320 mV/ $320\text{--}390$ mV range could participate in the Fenton reaction promoting free radical generation. Complexes that are out of such range could act as good chelators and avoid free radical production. As was explained in a previous section, a strict approximation should take into consideration that in vivo conditions are not standard conditions as those used for defining the range of potentials.

Polyphenols as Metal Chelators: Kinetics

The actual biological concentrations of the reactants (ligands, iron, complexes, H_2O_2) are also important and need to be considered when assessing the redox properties of the formed complex.

When assessing the in vivo relevance of metal chelation to explain the antioxidant capacity of polyphenols, another physiological fact that should be considered is the very modest amount of metals available to catalyze free

radical formation. A basic kinetic analysis of an *in vivo* Fenton reaction mediated by Fe^{2+} reaction 18, in which M is iron], would include a second-order rate equation (equation 21) [Halliwell and Gutteridge, 1989]:

$$v = k[\text{H}_2\text{O}_2][\text{ligand} - \text{Fe}^{2+}] \quad (21)$$

The iron involved in this process, usually called “redox active iron” or “labile iron pool,” has been estimated to be $\leq 5 \mu\text{M}$ in the cell cytosol and $\leq 1 \mu\text{M}$ in human plasma [Woodmansee and Imlay, 2002]. Polyphenols should be able to diminish the rate of H_2O_2 decomposition (or $\bullet\text{OH}$ generation) by chelating a fraction of the “redox active iron” pool generating a flavonoid–iron complex with a very low rate constant (k) for Fenton reaction (reaction 18, equation 21). Nevertheless, considering that the physiological rate of $\bullet\text{OH}$ generation is indeed estimated to range between 2.5×10^{-10} and $1 \times 10^{-9} \text{M s}^{-1}$; and that the polyphenol concentrations in human and animal tissues are not enough to displace physiological metal chelators, the antioxidant actions of flavonoids could be only relevant in conditions in which “redox active iron”, and/or other redox active metal, are in excess.

Note: The $\bullet\text{OH}$ generation rate was calculated considering $[\text{citrate}-\text{Fe}^{2+}] = 5 \mu\text{M}$; k_{citrate} with $\text{H}_2\text{O}_2 = 4.9 \times 10^3 \text{M}^{-1} \text{s}^{-1}$ [Rush et al., 1990]; $[\text{H}_2\text{O}_2]$ steady state = 10–100 nM [Boveris et al., 1999; Merkofer et al., 2006]

POLYPHENOL INTERACTIONS WITH MEMBRANES

Flavonoids and other polyphenols can interact with lipids and proteins. The interactions with proteins could be both unspecific or specific, meanwhile the interactions with lipids seems to be rather unspecific, based essentially on physical adsorption. This physical adsorption would mostly depend on the hydrophobic/hydrophilic characteristics of the flavonoid molecule, the number of hydroxyl substituents, and the polymerization degree [Erlejman et al., 2004; Verstraeten et al., 2005, 2003, 2004].

Adsorption is the process of accumulation at an interface and should be distinguished from absorption, which implies the penetration of one component, for example, the polyphenol molecule, throughout the mass of a second, for example, membrane [Florence and Attwood, 1998]. Additionally, it is possible to distinguish two types of adsorption: (i) physical adsorption: the adsorbate is bound to the surface through weak van der Waals forces; and (ii) chemical adsorption: involves stronger interactions, usually covalent bonds [Florence and Attwood, 1998]. The theoretical study of this type of process has been originally developed for the adsorption of gases on solids, for example, Langmuir equation. Experimentally, this equation can be applied to flavonoid adsorption on membranes, which based on such processes, occurs as described by reaction 22. In this reaction, S represents the available sites on the

membrane surface; and k_a and k_d are the adsorption and desorption rate constants, respectively:



Adsorption rates can be described by (equation 23) and depend on [POH] and the number of available sites in the membrane. Being N the total number of surface active sites and θ the fraction of surface sites occupied by a single molecule of the adsorbent, the number of empty active sites will be $N(1 - \theta)$ (equation 24). Desorption rate is directly proportional to the number of adsorbed species ($N\theta$) [(Eq. (3.8)]:

$$V_{\text{adsorption}} = k_a[\text{POH}]N(1-\theta) \quad (23)$$

$$V_{\text{desorption}} = -k_dN\theta \quad (24)$$

At equilibrium, both rates are equal and it is possible to obtain the Langmuir equation (equation 25), in which K is the equilibrium constant ($K = k_a/k_d$):

$$1 + K[\text{POH}]_{\text{eq}} \theta = K[\text{POH}]_{\text{eq}} \quad (25)$$

The use of this type of equation to evaluate the interaction between tea catechins and lipid bilayers of dimyristoylphosphatidylcholine revealed that the affinities of (–)-epicatechin gallate and (–)-epigallocatechin gallate for the bilayers are similar, and 1000 times stronger than the affinity of (–)-epicatechin or (–)-epigallocatechin. These results indicate that the presence of the galloyl groups should be responsible for defining the extent of the interaction [Kamihira et al., 2008].

Polyphenol–protein interactions have been epitomized as similar to antigen–antibody interactions in that a binding agent and a ligand associate through single or multiple moieties to form a complex. For polyphenol–protein interactions, the chemical characteristics of such “multivalent” associations are mainly related to: (i) the hydrophobicity of the aromatic nuclei of polyphenols and (ii) the availability of multiple phenolic hydroxyl groups that allow hydrogen bonding [Hagerman and Butler, 1981]. Recently, it has been suggested that the inhibitory activity of flavonoids toward human α -amilase depends on the formation of hydrogen bonds between the OH groups in R7 and/or R4' of the flavonoid ligand, and the side chains of Asp¹⁹⁷ and Glu²³³, and a possible conjugated π -system between either the AC or the B ring system and Trp⁵⁹ [Lo Piparo et al., 2008]. By contrast, ligands without inhibitory activity (flavanols, flavanones, and isoflavones) do not interact at the same time with the catalytic residues as well as with Trp⁵⁹. Flavanols and

flavanones possess a C2–C3 single bond that prevents electron delocalization over the AC condensate ring system, and the isoflavone genistein may form a π -bond to Trp⁵⁹ but is unable to form a hydrogen bond to the catalytic residues because of the different position of the aromatic B-ring in the ligand structure. Proline-rich proteins are preferential targets for polyphenol interactions, that is, the precipitation of proline-rich proteins present in saliva by the tannins (polymers of flavanols) from wine, chocolate, tea, and other flavanol-containing foods [Luck et al., 1994]. It has also been reported that a significant number of enzyme activities are inhibited by polyphenols, flavonoids, and flavanols [Middleton et al., 2000].

CONCLUSIONS

The capacity of flavonoids, as well as other plant polyphenols, to scavenge free radicals and/or chelate metals has been often claimed as responsible for the antioxidant actions of these phytochemicals. This action is assumed based on some thermodynamic properties of polyphenols to react with free radicals and metals. Nevertheless, the physiological concentrations reached by polyphenols in animals and human tissues are incompatible with the kinetic requirements necessary to reach reaction rates of physiological relevance. Other biochemical mechanisms can explain the observed *in vitro* and *in vivo* antioxidant effects. These mechanisms are related to polyphenol–lipid and polyphenol–protein interactions and are based on the presence of OH groups that give polyphenols high possibilities for physical and chemical interactions. These mechanisms do not preclude direct free radical scavenging or metal chelating actions but are more consistent with the polyphenol levels observed in human and animal tissues. Furthermore, the actual occurrence of these potential actions *in vivo* should be considered when linking an antioxidant action to a polyphenol, or to any other molecule, whose metabolic fate and biological actions are not firmly established.

ACKNOWLEDGMENTS

This work was supported by NIH AT2966; UC Davis CHNR (State of California Vitamin Price Fixing Consumer Settlement fund); and UBACyT (B801 and B802). MG and CGF are members of the CIC, CONICET, Argentina. GSC has a postdoctoral fellowship from TUBITAK, Turkey.

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4 Flavonoid–Membrane Interactions: Consequences for Biological Actions

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INTRODUCTION

Flavonoids constitute one of the most common forms of phenolic compounds present in plants. Multiple health benefits have been proposed for flavonoids, although the biochemical and physiological mechanisms are not fully defined. Among others, the existence of a large number of flavonoids bearing different chemical substituent and the limited knowledge of their tissue distribution and concentration are factors that complicate the understanding of their biological effects.

The interactions of flavonoids with membranes emerge as an important mechanism involved in their biological effects. Importantly, certain flavonoids that, due to their chemical properties, cannot be absorbed by cells could still exert certain biological actions at the membrane level. Flavonoids can interact with different membrane components. As a consequence of a direct interaction with membrane lipids, flavonoids can alter membrane physical properties, modulating enzyme activity, ligand–receptor interactions, ion fluxes, signal transduction, transport, and other membrane-associated functions. These membrane–flavonoid interactions can affect the occurrence and extent of deleterious events, for example, lipid oxidation and membrane disruption. Flavonoids can also interact with membrane proteins and modify their biological function. While the interactions of flavonoids with proteins may have a specific requirement of flavonoid structure and conformation, the interactions with membrane lipids could be in general driven by the hydrophobic/hydrophilic character of the molecule, the number of hydroxyl substituent, and the degree of polymerization. This chapter will address current knowledge on the interactions of flavonoids with membrane lipids and proteins, the nature of these interactions, and their biological consequences.

INTERACTIONS OF FLAVONOIDS WITH MEMBRANE LIPIDS

Flavonoids bear different degrees of hydroxylation, polymerization, and methylation that define both specific and nonspecific interactions with membrane lipids. Molecule size, tridimensional structure, and hydrophilicity/hydrophobicity are chemical parameters that determine the nature and extent of flavonoid interactions with lipid bilayers. The hydrophilic character of certain flavonoids and their oligomers endows these molecules with the ability to bind to the polar headgroups of lipids localized at the water–lipid interface of membranes. On the other hand, flavonoids with hydrophobic character can reach and cross the lipid bilayer. In this section, we will discuss current experimental evidences on the consequences of flavonoid interactions with both the surface and the hydrophobic core of the lipid bilayer.

Interaction of Flavonoids and Procyanidins at Membrane Water–Lipid Interfaces

Flavonoids are a family of compounds that present subtle variations in the number and location of hydroxyl groups (Crozier et al., this volume). Considering that most flavonoids have $pK_a > 8$ [Jovanovic et al., 1994], these compounds will mainly make contact with polar surfaces through hydrogen bonds rather than ionic interactions [Singleton, 1987]. This is especially relevant in biological environments, where flavonoids could interact with the polar headgroup of phospholipids, e.g. phosphatidylcholine (PC) and adsorb to the cell surface. Using dipalmitoyl-PC vesicles as membrane models, Yoshioka et al. [2006] demonstrated that (+)-catechin, which is a highly hydrophilic molecule, adsorbs to the vesicle surface. As a result, (+)-catechin prevented membrane defects as it evolved from gel to liquid-crystalline phase transition and increased lipids transition temperature [Yoshioka et al., 2006]. The adsorption of catechin to dipalmitoyl-PC liposomes extended to the membrane core, decreasing the mobility of dipalmitoyl-PC acyl chains [Yoshioka et al., 2006]. It is noteworthy that not only the number of hydroxyl moieties but their distribution is determinant of the degree of flavonoid adsorption to membranes. Supporting this, it has been demonstrated that (–)-epicatechin, which is slightly more hydrophobic than its geometrical isomer (+)-catechin, has higher affinity for membrane lipids [Tsuchiya, 2001]. Additionally, the oligomerization degree of procyanidins built on catechin and epicatechin monomers (dimers A1, A2, B2, and trimers A, and C2) is also important in determining their adsorption to membranes, as the number of flavonoid–membrane contacts increases with the number of monomers present in these molecules [Verstraeten et al., 2005]. Similarly, the adsorption of procyanidins to PC liposomes affected the fluidity of the bilayer not only when evaluated with a probe located at the membrane water–lipid interface, but also in the hydrophobic region of the bilayer [Verstraeten et al., 2005]. Together, these findings demonstrate that upon their interaction with lipid polar headgroups, both, flavanol monomers and their oligomers cause the tightening of the liposome surface, which leads to the immobilization of phospholipids acyl chains and to the loss of membrane fluidity.

The interactions of flavonoids with polar surfaces can also be predicted using simpler membranes. Using a phosphatidyl choline-coated high-pressure liquid chromatography (HPLC) column, it has been observed that the surface interaction (measured as the retention delay) of eight different flavonoids with phospholipids was positively correlated with the number of hydroxyl groups in the flavonoids [Ollila et al., 2002]. To investigate the nature of the interactions between certain flavonoids and polar surfaces, Cartalade and Vernhet [2006] used three artificial membranes with a different degree of hydrophobicity. Interestingly, both, (+)-catechin and (–)-epicatechin mainly adsorbed to polar membranes, while (–)-epigallocatechin gallate (EGCG) adsorbed to both, polar and nonpolar membranes [Cartalade and Vernhet, 2006]. These flavanols

were easily desorbed by dilution, indicating the reversibility of their adsorption. Larger procyanidins, with an oligomerization degree that ranged from 3 to 10, adsorbed to all the studied membranes, regardless of their polar character. In addition, the desorption of these oligomers showed large hysteresis, indicating that the strength of their interactions with membranes was higher than that of the monomeric units [Cartalade and Vernhet, 2006]. By contrast, hexameric procyanidins presented a reversible adsorption to Caco-2 cell monolayers [Erlejman et al., 2006]. Similar findings in Caco-2 cells were observed for high-molecular-weight procyanidins isolated from willow shoots [Deprez et al., 2001]. Large amounts of hydroxyl groups in small flavonoid molecules can prevent their adsorption by causing a large increase in their hydrophylicity. For example, two highly hydroxylated flavonoids, myricetin and rutin, did not interact with a probe located in the polar region of PC liposomes—indicating the lack of penetration into the bilayer even at the most superficial membrane level, the polar region [Ratty et al., 1988]. Accordingly, Kayika et al. [2001] reported that green tea flavanols, which can be adsorbed to the membrane surface, interact with probes shallowly located at the water–lipid interface whereas no interaction was found with probes deeply buried into the bilayer.

The relevance of hydroxyl groups in flavonoid binding was also studied by Yano et al. [2007], who investigated how methylation at different positions of the gallate ring in EGCG affects its binding to biological membranes. Methylation at 3'- and/or 4'-positions of EGCG markedly reduced its affinity for membranes, which was abolished when EGCG was simultaneously methylated at the 4'- and 4''-positions. These findings stress the importance of flavonoid hydroxylation degree and of hydroxyl group location to define flavonoid–membrane interactions [Yano et al., 2007]. Using nuclear magnetic resonance (NMR) in both, solid-state and in bicelle systems, it was recently demonstrated that the gallate moiety of EGCG inserts into lipid bilayers and interacts with the choline moiety of the PC [Uekusa et al., 2007; Kajijiya et al., 2008]. Although methylation decreases the affinity of the flavonoids for lipid polar headgroups, it does not preclude the flavonoid capacity to interact with membrane proteins.

Another flavonoid characteristic that will determine the extent of flavonoid adsorption to the bilayer is their tridimensional structure. Van Dijk et al. [2000] evaluated the affinity of several flavonoids for liposomes, measuring their capacity to quench the fluorescence of a probe inserted in the lipid bilayer. The planar structure adopted by flavanols morin and quercetin confers to these molecules a markedly higher affinity for membranes than that of the flavanones pinocembrin, naringenin, eriodictyol, and hesperetin which adopt a tilted configuration. Accordingly, glycosylation at position 7 of naringenin and eriodictyol significantly increased their affinity for membranes when compared with their respective aglycons, effect that was associated with a molecule torsion due to glycosylation [van Dijk et al., 2000].

As a consequence of flavonoid–lipid interactions, flavonoids affect several physical properties of the bilayer. Studies from our laboratory demonstrated

that procyanidins isolated from cocoa adsorb to the surface of liposomes, preventing the disruption of the bilayer caused by the incorporation of Triton X-100 [Verstraeten et al., 2003]. Interestingly, the effect of oligomerization was not the additive for the number of monomer units but synergistic [Verstraeten et al., 2003]. These observations were extended to the plasma membranes of Caco-2 cells, in which the incubation with micromolar concentrations of procyanidins (dimer to hexamer) prevented bile-induced cell damage [Erlejman et al., 2006]. Both in liposomes and in Caco-2 cells the protective effects of procyanidins on detergent-mediated membrane disruption depended on the oligomerization degree, being more effective as the number of monomers increased [Verstraeten et al., 2003; Erlejman et al., 2006]. On the contrary, in giant unilamellar vesicles EGCG increases per se membrane permeability and promoted the interaction between vesicles (aggregation) and structural changes in vesicles topology, generating small lumps [Tamba et al., 2007]. As previously discussed, this effect could be due to the fact that EGCG is a relatively small molecule that could partially penetrate the bilayer and induce the formation of membrane pores. Through these nonspecific pores, molecules present in the inner liposomes aqueous space could reach the external milieu. In this regard, a strong dependence between flavonoid-mediated release of the water-soluble probe calcein and flavonoid hydrophobicity was reported by Olilla et al. [2002]. Thus, flavonoids could exert different effects on membrane permeability strictly based on their hydrophobicity: while the adsorption of highly hydrophilic molecules onto the membrane surface has a protective effect on the permeabilization induced by external agents, more hydrophobic flavonoids can incorporate into the bilayer and increase permeability by favoring the creation of unspecific pores.

Isoflavones obtained from different *Leguminosae* species were demonstrated to promote dipalmitoyl-PC liposomes aggregation [Hendrich et al., 2002]. Similarly, purified daidzein promoted liposome aggregation, with a magnitude that relied on the chemical nature of the phospholipid polar headgroup and that followed the order: phosphatidylinositol > phosphatidylserine (PS) > phosphatidylglycerol > phosphatidic acid > PC [Lehtonen et al., 1996]. Huh et al. [1996] proposed that flavonoids could generate polyphenol bridges between adjacent lipid surfaces and, by decreasing surface hydration, reduce the repulsion among them, leading to membrane aggregation. The ability of EGCG to promote membrane aggregation was postulated to have beneficial health effects by inducing Gram-positive bacteria death [Ikigai et al., 1993]. This bactericidal effect was ascribed to EGCG interactions with negatively charged lipopolysaccharides, whose absence in Gram-negative bacteria results in the resistance against the action of EGCG. By contrast, (–)-epicatechin, which has a poor capability to induce membrane aggregation, also has low bactericidal action [Ikigai et al., 1993]. However, the bactericidal properties of flavonoids should be carefully considered. Recently, the flavonol galangin, which has been proposed as a potent agent against *Staphylococcus aureus*, *Enterococcus* spp., and *Pseudomonas aeruginosa* [Pepeljnjak and Kosalec,

2004], was shown to cause bacteria clumping but not to decrease cell viability [Cushnie et al., 2007].

Another membrane property physically affected by flavonoids is the surface potential. Working with liposomes composed of PC and PS, we found that (–)-epicatechin and certain procyanidins (dimer to hexamer) decreased liposome surface potential. This effect relied on both, procyanidin concentration and number of monomeric units [Verstraeten et al., 2003]. On the other hand, when liposomes were composed exclusively of PC, it was found that (–)-epicatechin dimers A1 and B2, and the trimers A and C2 increased liposome surface potential in a concentration-dependent manner [Verstraeten et al., 2005]. In PC liposomes, the distance between two neighbor polar headgroups would allow a partial penetration of the oligomers into the polar region of the bilayer. Meanwhile, in PC:PS liposomes, the membrane is tightly packed due to ionic interactions between PC and PS headgroups, making the interactions with flavonoids shallower than in PC vesicles. As a consequence, differences in flavonoid penetration into the bilayer could lead to differences in their effects on membrane surface potential.

Partitioning of Flavonoids in the Hydrophobic Portion of Membranes

As previously mentioned, certain flavonoids can penetrate into the hydrophobic core of membranes, a feature that mainly relies on their hydrophobic character, which is dictated by flavonoid chemical structure and spatial conformation. When flavonoid hydrophobicity was assessed from the partition coefficient between *n*-octanol and an aqueous solution, the following order of hydrophobicity was observed: flavone, genistein > eriodictyol, myricetin, quercetin, kaempferol, hesperetin, daidzein >> galangin, morin, flavanone, naringenin, taxifolin (Table 4.1).

Interestingly, the partition of flavanols into *n*-octanol was almost negligible, with the exception of (–)-epicatechin gallate [Erlejman et al., 2004]. Using the partition system water:olive oil, van Dijk et al. [2000] found that flavonoids followed the hydrophobicity order: flavones > flavanones > flavanols. The authors concluded that at the same hydroxylation degree, flavones are more hydrophobic than flavanones, an effect that could be related to differences in their tridimensional structure. Accordingly, they observed that the capacity of flavonoids to affect transmembrane potential and to dissipate pH between inner and outer liposome aqueous spaces is restricted to the more hydrophobic flavones and flavanones, while the flavonols quercetin and morin do not affect these parameters [van Dijk et al., 2000]. Working with palmitoly-oleoyl-PC vesicles, Scheidt et al. [2004] demonstrated, by high-resolution magic angle spinning NMR spectroscopy, that flavonoids show a broad bilayer distribution determined by their hydrophobicity (flavone, chrysin > luteolin, myricetin). Furthermore, flavonoids deeply buried into the bilayer have similar motilities to that of fatty acids, by contrast more polar flavonoids are bound at the water–lipid interface having motilities similar to water molecules [Scheidt et al., 2004].

Table 4.1 Partition Coefficients of Selected Flavonoids^a

Family	Compound	Partition Coefficient
Flavonols	Flavone	108.55 ± 7.07
	Flavonol	0.70 ± 0.21
	Galangin	4.62 ± 4.65
	Kaempferol	23.65 ± 2.04
	Morin	4.59 ± 0.14
	Quercetin	20.65 ± 2.84
	Myricetin	39.34 ± 1.94
Flavanols	(+)-Catechin	1.80 ± 0.40
	(-)-Epicatechin	1.53 ± 0.03
	(-)-Epigallocatechin	0.14 ± 0.01
	(-)-Epicatechin gallate	13.47 ± 0.13
	(-)-Epigallocatechin gallate	5.22 ± 0.49
	Dimer	0.42 ± 0.03
	Hexamer	0.01 ± 0.001
Flavanones	Flavanone	7.87 ± 0.66
	Naringenin	6.70 ± 0.30
	Eriodictyol	61.94 ± 6.27
	Hesperetin	20.60 ± 1.53
	Taxifolin	5.67 ± 0.05
Isoflavones	Daidzein	20.81 ± 0.20
	Genistein	109.25 ± 7.79

^a Flavonoid partition coefficients were evaluated in the solvents mixture *n*-octanol and 20 mM Tris-HCl (pH 7.4), 140 mM NaCl buffer.

Source: Data taken from Erlejan et al. [2004].

Additionally, the authors did not observe flavonoid-induced alterations in membrane structures, indicating that bilayers can easily accommodate a large number of flavonoid molecules.

Similar to hydrophilic flavonoids, hydrophobic flavonoids can affect membrane permeability. Alterations in this biophysical property of liposome bilayers lead to the release of bulky molecules entrapped into the inner aqueous space. As mentioned in the previous section, a strong correlation was found between flavonoid retention to a hydrophobic matrix and their capacity to induce membrane leakage [Ollila et al., 2002]. Interestingly, hydrophilic flavonoids, such as (-)-epicatechin and related procyanidins (dimer to hexamer) prevented Fe²⁺-mediated liposome permeabilization, although in this case the beneficial effect could be related to both their antioxidant and metal chelating capacities and their membrane stabilizing properties [Verstraeten et al., 2004].

In addition, some flavonoids can differentially interact with membrane polar surfaces or penetrate into the bilayer, depending on certain characteristics of the reaction milieu. This is the case of quercetin, a flavonoid that at acidic pH is deeply embedded into planar lipid bilayers [Movileanu et al., 2000], while at

physiological pH it mainly interacts with lipid polar headgroups [Terao et al., 1994; Movileanu et al., 2000; Pawlikowska-Pawlega et al., 2003]. At low concentrations (10 μM), the isoflavone puerarin locates at the inner region of cetyl-trimethyl-ammonium bromide micelles, while it displaces toward the outer region of these micelles as its concentration increases, effect that is associated with puerarin deprotonation [Xi and Guo, 2007].

As previously mentioned, flavonoids can modulate membrane fluidity, with polar flavonoids binding to the membrane surface and propagating their effects into the hydrophobic region of the bilayer. Also, and using a set of fluorescent probes that sense lipid packing at different depths of the bilayer, it has been demonstrated that upon their incorporation, hydrophobic flavonoids, such as naringenin, rutin, and a series of isoflavones, reduce membrane fluidity especially in its deepest region [Arora et al., 2000]. The isoflavones daidzein and genistein have differential effects on membrane fluidity. Daidzein increases the fluidity of membranes when in gel phase or close to their transition temperature and do not affect membranes in the liquid-crystalline phase [Lania-Pietrzak et al., 2005]. On the contrary, genistein, which only has one hydroxyl group more than daidzein, decreases membrane fluidity in membranes in liquid-crystalline phase without affecting those in gel phase or close to their transition temperature [Lania-Pietrzak et al., 2005]. Other hydrophobic flavonoids, such as hesperetin and naringenin, which incorporate into the bilayer, also decreased dipalmitoyl-PC liposomes transition temperature [Saija et al., 1995].

In summary, current evidence supports the interaction of flavonoids with membrane lipids. The associated perturbations in membrane physical properties can have a significant impact on membrane-associated processes.

Interactions of Flavonoids with Membrane Proteins

Flavonoids can also interact with membrane proteins, such as those functioning as receptors, transporters, channels, and enzymes, and potentially affect their biological activities. A summary of recent advances on the study of flavonoid interactions with plasma membrane proteins is presented in Table 4.2.

Among plasma membrane transporters, the ABC [adenosine 5–triphosphate (ATP)-binding cassette] superfamily is especially important due to its involvement in the transmembrane movement of a myriad of organic and inorganic compounds, participating in the absorption of nutrients and the efflux of intracellular metabolites (for a review about ABC protein classifications and functions, see Pohl et al. [2005]). Several cancer cells present multidrug resistance through the overexpression of specific ABC proteins that extrude the chemotherapeutic agents. Since the use of specific ABC protein inhibitors that have adverse side effects on human health, flavonoids have risen as potential non-toxic inhibitors of these transporters [Brand et al., 2006].

Almost every known member of the ABC family can be inhibited by one or more flavonoids [Brand et al., 2006]. For example, in a human epidermal cell

Table 4.2 Effects of Interactions of Flavonoids and Selected Plasma Membrane Proteins

Function	Protein	Flavonoid	System	Effect	References
Broad range transporters	ABC transporters	Chrysin, quercetin, genistein, Silymarin	Caco-2 cells	Inhibition	Sergent et al., 2005
		Green tea catechins	Caco-2 cells	Inhibition	Zhang and Morris, 2003
Cl⁻ transport	CFTR		Various tissues	Stimulation and inhibition	Zhou et al., 2004
		32 flavonoids	K562 cells	Inhibition	Katayama et al., 2007
		16 flavonoids	MCF-7 cells	Inhibition	Zhang et al., 2005
		Silymarin, hesperetin, quercetin, and daidzein	MCF/MR cells	Inhibition	Cooray et al., 2004
		Kaempferol	Mice trachea	Stimulation	Sousa et al., 2007
			IB3-1 cells	Stimulation	Lim et al., 2004
		Genistein	Baby hamster kidney cells	Stimulation and inhibition	Schmidt et al., 2008
			Rat aorta	Stimulation	Valero et al., 2006
			epithelial cells	Stimulation and inhibition	Moran and Zegarra-Moran, 2005
			Renal epithelia	Stimulation	Lim et al., 2004
	Mouse jejunum	Stimulation	Baker and Hamilton, 2004		
	Airway epithelia	Stimulation	Andersson et al., 2003		
	CHO cells	Stimulation	Bulleau-Pignoux et al., 2002		
	Murine trachea and colon	Stimulation	Goddard et al., 2000		
	<i>Xenopus laevis</i> oocytes	Stimulation	Suaud et al., 2002		
	Mouse fibroblasts	Stimulation	Ferrera et al., 2007		

(Continued)

Table 4.2 (Continued)

Function	Protein	Flavonoid	System	Effect	References
			Human bronchial epithelial cells	Stimulation	Caci et al., 2003
		Cocoa flavanols	Human colon epithelia	Inhibition	Schuijer et al., 2005
		Apigenin	Renal epithelia	Stimulation	Lim et al., 2004
		<i>Opuntia ficus indica</i> polyphenols	<i>Xenopus laevis</i> oocytes	Inhibition	Lee et al., 2005
Ca ²⁺ transport	CRAC channel		Human Jurkat T-cells	Stimulation	Aires et al., 2004
	Voltage-gated Ca ²⁺ channels	Red wine polyphenols	Dorsal root ganglion neurons	Inhibition	Wu et al., 2005
		Quercetin	Rat pituitary GH3 cells	Stimulation	Wu et al., 2003
		Galangin	NG108-15 neuronal cells	Inhibition	Wu et al., 2003
		Myricetin	Rat urinary bladder	Inhibition	Capasso and Tavares, 2002
		Apigenin	Rat tail artery myocytes	Activation	Fusi et al., 2005
		Epigallocatechin gallate	Vascular smooth muscle	Activation	Fusi et al., 2003
K ⁺ transport	NMDA channels		HEK293 cells	Inhibition	Losi et al., 2004
	K _{ATP} channels		<i>Xenopus laevis</i> oocytes	Uncoupling	Jin et al., 2007
		<i>Aspalathus linearis</i> flavonoids	Rabbit jejunum	Inhibition	Baek et al., 2005
	K _v channels	Chatcones	HEK293 cells	Activation	Gilani et al., 2006
		Red wine polyphenols	Dorsal root ganglion neurons	Inhibition	Yarishkin et al., 2008
	BKCa channels	Isoliquiritigenin	Guinea-pig tracheal smooth muscle	Inhibition	Wu et al., 2005
		Naringenin	Rat thoracic aorta rings	Activation	Liu et al., 2008
		Quercetin	Rat coronary artery	Activation	Saponara et al., 2006

(Continued)

Table 4.2 (Continued)

Function	Protein	Flavonoid	System	Effect	References
Na ⁺ transport	Voltage-gated Na ⁺ channels	Quercetin	Human endothelial cells	Activation	Kuhlmann et al., 2005
		Quercetin, catechin	TSA201 cells	Inhibition	Wallace et al., 2006
Glucose transport	Na ⁺ /K ⁺ /2Cl ⁻ cotransporter GLUT1	Red wine polyphenols	Mouse dorsal root ganglionic neurons A6 cells	Inhibition	Wu et al., 2005
		Quercetin		Activation	Fujimoto et al., 2005
		Myricetin, quercetin, and catechin gallate	Rat adipocytes	Inhibition	Strobel et al., 2005
		Cinnamon polyphenols	Mouse macrophages	Increased expression	Cao et al., 2008
		Genistein Genistein Myricetin	Human erythrocytes 3T3-L1 adipocytes Insulin-resistant rats muscle	Inhibition Inhibition Stimulation	Afzal et al., 2002 Bazuine et al., 2005 Liu et al., 2007b
Phytoestrogen	GLUT1 + GLUT4 GLUT2 + GLUT5 Plasma membrane estrogen receptor	Green tea polyphenols	Obese Zucker rats Insulin-resistant rats muscle	stimulation Increased expression	Liu et al., 2007a Cao et al., 2007
		Epicatechin gallate Daizein	Caco-2 cells Bovine adrenal medullary cells	Inhibition Stimulation and inhibition	Shimizu et al., 2000 Liu et al., 2007c
Phytoestrogen	Naringenin Naringenin, quercetin <i>Ginkgo biloba</i> polyphenols	Embryonic rat and hippocampal neurons	Embryonic rat and hippocampal neurons	Increased expression	Wang et al., 2008
		HeLa cells	HeLa cells	Inhibition	Galluzzo et al., 2008
		MCF-7 cells	MCF-7 cells	Inhibition	Virgili et al., 2004
		MCF-7 cells	MCF-7 cells	Stimulation Inhibition	Oh and Chung, 2004 Oh and Chung, 2006

(Continued)

Table 4.2 (Continued)

Function	Protein	Flavonoid	System	Effect	References
Neurotransmission	Glutamate receptor	Quercetin, genistein	Brain synaptic membranes	Inhibition	Martini et al., 2007
	Dopamine receptor	Epigallocatechin gallate <i>Croton celtidifolius</i> proanthocyanidins	PC12 cells Swiss mice	Inhibition D ₂ -agonist	Li et al., 2006 DalBo et al., 2006
GABA receptor	Apigenin	Apigenin	Rat cerebellar granule cells	Inhibition	Avallone et al., 2000
	Apigenin, epigallocatechin gallate	Apigenin, epigallocatechin gallate	<i>Xenopus laevis</i> oocytes	Stimulation	Campbell et al., 2004
Glycine receptor	Quercetin	Quercetin	Rat hippocampal neurons	Desensitization	Sun et al., 2007
	Genistein	Genistein	<i>Xenopus laevis</i> oocytes Rat neurons Rat hypothalamic Neurons	Inhibition Inhibition Inhibition	Lee et al., 2008 Zhu et al., 2003 Huang and Dillon, 2000
5-HT receptor	Quercetin	Quercetin	<i>Xenopus laevis</i> oocytes	Inhibition	Lee et al., 2005
	Puerarin <i>Scutellaria lateriflora</i> flavonoids extract	Puerarin <i>Scutellaria lateriflora</i> flavonoids extract	Rat cerebral cortex CHO cells	Inhibition Inhibition	Overstreet et al., 2003 Gafner et al., 2003
Adrenergic receptor	Quercetin	Quercetin	Rats	α_2 -agonist	Kaur et al., 2007
	Genistein	Genistein	C2C12 cells Canine ventricular myocardium	α_1 -agonist β -agonist	Jou et al., 2004 Chu et al., 2005
Acetylcholine receptor	Genistein	Genistein	Bovine adrenal chromaffin cells	Nicotinic antagonist	Matsumura et al., 2007
	Daidzein	Daidzein	Bovine adrenal medulla	Nicotinic antagonist	Liu et al., 2007c

line (KB-C2 cells) that overexpresses P-glycoprotein (also known as ABCB1 protein, or MDR1), it has been demonstrated that select flavonoids, inhibit P-glycoprotein-mediated rhodamine 123 efflux [Kitagawa et al., 2005]. Among the flavonols assessed, the magnitude of the inhibitory effect followed the order: kaempferol > quercetin, baicalein > myricetin > fisetin and morin, which is in accordance with their hydrophobicity [Kitagawa et al., 2005]. On the contrary, in MCF-7 cells, flavanols stimulated P-glycoprotein-mediated transport of the carcinogen 7,12-dimethylbenz(a)anthracene [Phang et al., 1993]. As hypothesized by Morris and Zhang [2006], this conflictive behaviour could be explained based on the relative affinity of flavonoids for either the R or H sites of the protein, responsible for rhodamine 123 or Hoechst 33342 transport, respectively. Binding to one of these sites stimulates the transport activity of the other one. Supporting that, quercetin stimulates rhodamine 123 efflux through its binding to the H site, an effect that strongly depends on quercetin concentration [Shapiro and Ling, 1997]. At low concentrations (5 μM) quercetin stimulates P-glycoprotein phosphorylation and activation, while at high concentrations (50 μM) it causes P-glycoprotein inhibition [Mitsunaga et al., 2000]. Even when not all the flavonoids biologically tested were investigated in silico for the assignment of their specific binding sites in ABC proteins, a recent study [Badhan and Penny, 2006] located flavones, flavonols, flavanones, and chalcones binding sites to the nucleotide binding domain of P-glycoprotein. It was demonstrated that in the flavonoid-P-glycoprotein complex, flavonoids' B ring is oriented in a manner similar to the spatial disposition adopted by the adenine base of ATP, and thus, they can compete with the ATP for its binding to the binding domain [Badhan and Penny, 2006].

Another member of the ABC superfamily is cystic fibrosis transmembrane conductance regulator (CFTR, ABCC7), a plasma membrane channel involved in chloride transport. Recently, Sousa et al. [2007] demonstrated that an extract from the medicinal plant *Phyllanthus acidus* composed mainly by kaempferol, adenosine, and hypogallic acid, significantly stimulated the CFTR channel, increasing chloride transport. This effect was due to the activation of multiple events, including the modulation of intracellular Ca^{2+} concentration, cyclic adenosine 5-monophosphate (cAMP) generation, and CFTR redistribution. Individually, all three components of the extract activate the CFTR. Kaempferol has a direct effect on CFTR with a magnitude lower than that of adenosine [Sousa et al., 2007]. Accordingly, working with IB3-1 cells that bear the ΔF508 mutation that accounts for $\sim 70\%$ of the mutations found in patients with cystic fibrosis, Lim et al. [2004] demonstrated that kaempferol, apigenin, and genistein cause the redistribution of the mutant CFTR, restoring the usual location in the plasma membrane instead of the abnormal perinuclear location. These findings open a promising therapeutic strategy to ameliorate the progression of cystic fibrosis by using plant products.

Another key group of transporters present in the cell plasma membrane is integrated by Na^+ , K^+ , and Ca^{2+} channels. Among them, there are

ligand- and voltage-gated ion channels. The latter comprises a group of channels, all of them being transmembrane proteins with a central ion-conducting pore. These channels are operationally relevant in excitable cells, such as neurons and muscle cells, in which changes in the surrounding electrical potential lead to transmembrane movement of ions responsible for neurotransmitter release and action potentials, among other events. These channels can be also found in nonexcitable cells, although their biological function in this kind of cells is not established. The activities of several voltage-gated ion channels can be modulated by flavonoids (Table 4.2). For these channels, flavonoids do not show a unique behavior; depending on the cell model and the flavonoid assessed, the reported results are dissimilar. Wu et al. [2005] demonstrated that red wine polyphenols inhibit voltage-gated Ca^{2+} currents in dorsal root ganglion neurons. Conversely, L-type Ca^{2+} channels are specifically activated by myricetin [Fusi et al., 2003, 2005]. Quercetin has a stimulatory effect on these channels, although its effects also depend on the cell type. For example, working with rat pituitary GH3 cells, Wu et al. [2003] found that quercetin stimulates L-type Ca^{2+} channels, while it has an opposed effect on the same channels from NG108–15 neuronal cells. These differential effects of quercetin could be related to the various isoforms of L-type channels present in different cells.

Several lines of investigation demonstrated that flavonoids can also affect glucose uptake (Table 4.2). This process occurs through two groups of transporters, the Na^+ -coupled carrier system (SGLT) and the facilitative glucose transporters (GLUT) (reviewed in Scheepers et al. [2004]). Given the relevance of GLUT activities in the context of human pathologies such as obesity and insulin resistance, it is very important to elucidate if flavonoids could act as natural modulators of glucose uptake in muscle and adipose tissues. Most of the flavonoids studied have stimulatory properties on GLUT expression and/or activities (Table 4.2). However, the behavior of isoflavones should be analyzed separately. Genistein inhibit GLUT1 and GLUT4 activities in different experimental models [Afzal et al., 2002; Bazuine et al., 2005]. On one side, GLUT1 needs non-hydrolytic ATP binding to exert its biological effects [Carruthers and Helgerson, 1989; Cloherty et al., 2002,] which is prevented by genistein [Vera et al., 1996]. On the other hand, the signaling cascade that ends in GLUT4 translocation to the plasma membrane and to glucose uptake depends on the tyrosine kinase activity of the insulin receptor. Other non-insulin receptor-related tyrosine kinases can also stimulate GLUT4 translocation in adipocytes [Chen et al., 1997; Bazuine et al., 2003]. Genistein is a potent tyrosine kinase inhibitor [Akiyama et al., 1987] that raises a plausible explanation for its inhibitory effect on GLUT4 activation. In addition, Bazuine et al. [2005] found in 3T3-L1 adipocytes that genistein can also inhibit per se GLUT4 activity. Therefore, genistein has a dual inhibitory effects on GLUT4, impairing insulin-dependent GLUT4 translocation to the plasma membrane, and inhibiting GLUT4 once the transporter reaches the cell membrane, both events leading to a lower glucose uptake.

Other important effects of isoflavones is their capability to act as phytoestrogens. The finding that their regular consumption reduced osteoporosis and arteriosclerosis symptoms in postmenopausal women, and presumably, the incidence of certain cancers [Wuttke et al., 2007], fueled extensive research. Given that genistein structure and spatial topology highly resembles those of estradiol 17β [Vaya and Tamir, 2004], genistein could bind to the estrogen receptors α and β (ER α and ER β) and mimic some biological effects of estradiol, although with weaker transcriptional potency [Wuttke et al., 2007]. Since human mammary tissue is highly enriched in ER α , and the stimulation of ER α enhances cell proliferation, a controversy exists on the advice of increasing the consumption of isoflavones and the potential risk of breast cancer development [Warner et al., 2000]. Besides isoflavones, other flavonoids have been recently reported as phytoestrogens, including naringenin, quercetin, and certain polyphenols present in *Ginkgo biloba* extracts (Table 4.2). The flavanone naringenin inhibited ER α through a different mechanism than that of isoflavones. Naringenin inhibitory effect takes place at the plasma membrane level where it induces a rapid ER α depalmitoylation event that results in ER α redistribution in the cell membrane and in the inability to activate extracellular signal-regulated kinase (ERK) and protein kinase B (Akt) phosphorylation [Galluzzo et al., 2008]. On the other hand, *Ginkgo biloba* polyphenols, which include kaempferol, quercetin, and isorhamnetin, could have both estrogenic effects through their binding to ER β [Oh and Chung, 2004] and antiestrogenic effects by stimulating ER α catabolism and inhibiting its synthesis [Oh and Chung, 2006].

Finally, we will briefly focus on plasma membrane receptors involved in neurotransmission and on how flavonoids can affect their activity (Table 4.2). In general, the interactions of flavonoids with these receptors result in an inhibition of their biological response involving multiple mechanisms. As an example, genistein blocks glycine receptor-mediated electrical current but strictly requires glycine prebinding to the receptor, suggesting that genistein binds to the open state of the channel not competing with glycine for its binding site [Zhu et al., 2003]. Genistein can also act as a β -adrenergic agonist, which is due to its tyrosine kinase inhibitor properties [Chu et al., 2005]. Finally, genistein inhibits long-term potentiation in rat brain dentate gyrus, through the inhibition of the phosphorylation of presynaptic α -subunits of Ca^{2+} channels involved in glutamate release [Casey et al., 2002].

Flavonoids can also regulate the activity of postsynaptic neurotransmitter receptors. It has been demonstrated that apigenin has neuroprotective effects against glutamate-mediated neurotoxicity in cortical and cerebellar neurons antagonizing γ -aminobutyric acid (GABA) and *N*-methyl *D*-aspartate (NMDA) receptors, thus reducing the overall excitability of the neuronal network [Losi et al., 2004]. These effects of apigenin are closely related to its sedative effects, which have been recognized for a long time and used with therapeutic purposes against anxiety (for a review see Johnston et al. [2006]). Based on the capacity of apigenin, its dimer amentoflavone, and of other

flavonoids to inhibit GABA receptors through their binding to benzodiazepine's binding site [Marder and Paladini, 2002], several compounds have been synthesized and assessed as sedatives, with the purpose to develop better anxiolytic and sleep-enhancing compounds.

The above evidence shows that flavonoids can interact and modulate the activity of several membrane proteins. These effects can in part explain the beneficial health properties of flavonoids and could also help develop new therapeutic approaches for major human diseases.

CONSEQUENCES OF FLAVONOID INTERACTIONS ON MEMBRANE-ASSOCIATED PROCESSES

Antioxidant Actions of Flavonoids at the Membrane Level

Flavonoids are well-recognized antioxidant molecules with proven antioxidant activity in numerous biological systems [Lotito and Fraga, 1998; Lotito et al., 2000; Rice-Evans, 2001]. Chemically, flavonoid antioxidant ability relies mostly on three characteristics: (a) the number and location of hydroxyl groups; (b) the presence of a 2,3 double bond conjugated with a 4-oxo group in ring C; and (c) the presence of 3- and 5-OH groups [Bors et al., 1990]. The presence of an *o*-catechol group in the B-ring [Burda and Oleszek, 2001; Silva et al., 2002] could also be important, as it is the degree of oligomerization when flavonoids form oligomers [Verstraeten et al., 2003, 2004, 2005; Erlejman et al., 2004, 2006].

Several structure–activity studies have been performed to find the best antioxidant at the membrane level [Amic et al., 2007; Om and Kim, 2008; Ray et al., 2008]. Analyzing a set of 12 different flavonoids, Rackova et al. [2005] found a close association between flavonoid-mediated inhibition of dioleoyl-PC liposome oxidation by the azo-compound 2,2'-azobis-(2-amidino-propane)hydrochloride (AAPH) and flavonoid hydration energy, a parameter that evaluates their hydrophilicity. Given the fact that the initiator used for the experiments is a water-soluble compound, the observed relationship between flavonoids hydration energy and their antioxidant activity could be due mainly to the free-radical scavenger properties of the flavonoids OH groups. Thus, even when these findings are valuable in the prediction of certain flavonoid antioxidant ability, the assay leaves aside the flavonoids with hydrophobic character.

Besides their free-radical trapping properties, flavonoids can interfere with the capacity of oxidants to reach the bilayer. A study from our laboratory demonstrated that the adsorption of water-soluble (–)-epicatechin oligomers (dimer to hexamer) to membranes prevents lipid oxidation initiated by the azo-compound 2,2'-azobis (2,4-dimethylvaleronitrile), (AMVN), a hydrophobic molecule that upon its incorporation into the bilayer decomposes yielding peroxy radicals [Verstraeten et al., 2003]. In this case, given that the oxidant

species are generated in a membrane region relatively far from the adsorption sites of flavonoids, a direct scavenging action of these molecules should not be expected. These effect of (–)-epicatechin oligomers can be explained in terms of a protection to membranes by large oligomers adsorbed to the membrane surface limiting the accessibility of AMVN to the membrane interior. Supporting this hypothesis, a significant correlation between oligomers antioxidant capacity and the prevention of membrane disruption by a nonionic detergent was observed [Verstraeten et al., 2003]. Similarly, Aldini and co-workers [2003] observed that procyanidins isolated from *Vitis vinifera* bind to endothelial cell membrane and prevented peroxynitrite-mediated oxidative damage, an effect that the authors partially ascribed to procyanidin-mediated prevention of peroxynitrite diffusion into the cells.

The procyanidin structure further determines the extent of the protection to membranes. In this regard, dimers A1 and A2 had higher protective effects than dimer B2 against both, liposome membrane damage induced by the detergent Triton X-100 and AMVN-initiated lipid oxidation [Verstraeten et al., 2005]. This differential effect of the dimers could be due to a different molecule folding. Mackenzie et al. [2004] showed by using computational modelling that dimer B2 can establish internal hydrogen bonds, allowing epicatechin monomers the possibility to be stacked over each other. On the contrary, the monomeric units in the dimers A1 and A2 are connected by two covalent bonds that bring higher rigidity to the dimer and that could impede their folding and confer an elongated shape [Mackenzie et al., 2009]. Therefore, the molecules of dimers A1 and A2 will have higher membrane surface coverage per molecule compared to dimer B2.

The finding that water-soluble flavonoids could exert their beneficial properties at the hydrophobic portion of the membrane was also observed in in vivo studies and in cells in culture. For example, erythrocytes obtained from animals fed a flavanol- and procyanidin-rich meal showed reduced susceptibility to free-radical-mediated hemolysis [Zhu et al., 2002]. Consistently, we demonstrated that procyanidin hexamers, which interact with membranes but would not be internalized, protected Caco-2 cells from AMVN- and bile-induced oxidation [Erlejman et al., 2006]. When liposomes were preincubated with a series of flavonoids with diverse hydrophobicity, not only hydrophobic flavonoids prevented AMVN-mediated lipid oxidation but also the more hydrophilic ones [Erlejman et al., 2004]. Similarly to what was previously found in liposomes, the protective effects of flavonoids against AMVN-supported oxidation was strongly associated with their capacity to prevent membrane disruption by detergents, supporting the hypothesis of a physical protection of membranes by preventing oxidants to reach fatty acids.

A different mechanism should account for the antioxidant ability of hydrophobic flavonoids, which can be incorporated into the bilayer where they can affect certain membrane physical properties. It is well-known that alterations in membrane rheology will affect the extension and rate of lipid oxidation. For example, increased lipid oxidation rates have been observed

when membranes are incubated at temperatures below the transition temperature of their lipids [Mowri et al., 1984; Cervato et al., 1988]. In this situation, lipids are tightly packed with their acyl chains located in close vicinity, hence creating an environment where lipid oxidation will easily propagate [McLean and Hagaman, 1992]. As mentioned in a previous section, the isoflavones daidzein and genistein have differential effects on membrane fluidity; however, both genistein and daidzein act like antioxidants in membranes above lipid transition temperature [Erlejman et al., 2004]. These findings indicate that daidzein and genistein antioxidant properties reside in both their capacity to modulate membrane physical properties and their ability to trap oxidant species.

Modulation of Cell Signals by Flavonoids at the Membrane Level

Flavonoids could play a key role in the regulation of certain cell signals triggered at the plasma membrane level. As mentioned before, the flavanone naringenin inhibited ER α by inducing its rapid depalmitoylation, causing ER α detachment from the plasma membrane [Galluzzo et al., 2008]. It has been demonstrated that through cycles of palmitoylation–depalmitoylation catalyzed by protein acyltransferases and thioesterases [Linder and Deschenes, 2006], cells regulate the amount of ER α protein in the membrane. ER α Cys₄₄₇ palmitoylation leads to a strong protein association with caveolin-1 followed by its specific translocation to lipid rafts and to the triggering of numerous cell signals [Levin, 2005]. Even when the molecular mechanisms involved in naringenin-mediated ER α depalmitoylation is still under elucidation, it was hypothesized that naringenin could directly bind to ER α and promote changes in protein conformation that makes it prone to deacylation [Galluzzo et al., 2008].

(–)-Epicatechin hexamer (Hex) reversibly adsorbs to Caco-2 cell surface [Erlejman et al., 2006] and prevents the deleterious effects of the biliary salt deoxycholate. Hex protects cells from deoxycholate-induced cytotoxicity, oxidant production, and permeabilization of Caco-2 cell monolayer surfaces [Erlejman et al., 2008]. Hex also prevents tumor necrosis alpha (TNF α) activation of the transcription factor NF- κ B [Erlejman et al., 2008]. Hex is not incorporated into cells and the inhibition of TNF α -mediated NF- κ B activation could be due to either a direct interaction of this procyanidin with the TNF α receptor or secondary to alterations of the physical properties of the lipids in the receptor's immediate surroundings that impede the normal binding of its specific ligand. In the same experimental conditions, 30 min of preincubation with the (–)-epicatechin or dimer B2 did not inhibit TNF α -induced NF- κ B activation. These findings, together with the observation that after 24 h incubation, epicatechin and dimer B2 inhibited phorbol myristate acetate-mediated NF- κ B activation and binding to DNA in Jurkat T cells [Mackenzie et al., 2004, 2009] suggest that epicatechin and dimer B2 internalization is necessary to inhibit NF- κ B activation.

Lipids such as phosphoinositides, sphingolipids, and eicosanoids have been recognized as signaling molecules that control important cellular events such as cell proliferation, metabolism, apoptosis, and others. Alterations in normal lipid-mediated cell signaling have been related to the development of cancer, and inflammatory and metabolic diseases (recently reviewed by Wymann and Scheiter [2008]). The flavonoid apigenin-7-glucoside and those from German chamomile extracts prevent carbon tetrachloride (CCl₄)-mediated activation of neutral sphingomyelinase [Babenko and Shakhova, 2008]. This plasma membrane protein is responsible for sphingomyelin hydrolysis with formation of a key signaling molecule, ceramide. By preventing sphingomyelinase activation, those flavonoids helped to maintain rat hepatocytes membrane integrity upon CCl₄- administration, and from the physiological membrane alterations caused by ageing [Babenko and Shakhova, 2006, 2008]. The modulatory effects of flavonoids on signaling lipids formation could also occur through indirect mechanisms. For example, luteolin and luteolin-7-glucoside inhibited platelet-derived growth factor beta (PDGFβ) receptor phosphorylation in vascular smooth muscle cells [Kim et al., 2005]. The activation of this receptor causes phospholipase C gamma (PLCγ) activation with the subsequent hydrolysis of phosphoinositides and Ca²⁺ mobilization. In addition, PDGFβ receptor activation leads to Akt and ERK 1/2 phosphorylation. All these events were prevented by luteolin and luteolin-7-glucoside and therefore, the mitogenic effects of PDGFβ were abolished by these flavonoids [Kim et al., 2005, 2006].

Finally, another possible mechanism that could explain the regulatory effects of certain flavonoids on membrane-associated events is the creation of a lipid environment that ultimately affects membrane protein functionality. Recently, Tarahovsky et al. [2008] proposed that quercetin and taxifolin may have a preferential affinity for some membrane proteins and lipids, and then accumulate and promote lipid segregation with formation of raftlike domains. Among these interactions, flavonoids carboxyl and hydroxyl residues could interact with sphingosine moiety in sphingolipids, in a similar fashion as the cholesterol-sphingomyelin interactions observed in lipid rafts [McConnell and Radhakrishnan, 2003; McConnell and Vrljic, 2003]. Also, as flavonoids can interact with annular lipids in proteins, it has been hypothesized that flavonoids “may serve as adaptors mediating the interactions between membrane proteins and surrounding annular lipids” [Tarahovsky et al., 2008]. If true, flavonoids possibly could modulate the activity of many different membrane proteins. However, further research is required to assess this hypothesis.

CONCLUSIONS

As flavonoids are ubiquitous components of fruits and vegetables, they are part of almost any human diet. The identification of potential targets for the beneficial health effects of flavonoids exponentially increased over the years. The physiological relevance of the interactions of flavonoids with cell

membranes is becoming of interest to explain at least part of their beneficial health effects. As presented in this chapter, the interactions of flavonoids with major membrane components, lipids and proteins, modulate a number of cellular events involved in both physiological and pathological conditions. The knowledge of the nature and biological consequences of flavonoid–membrane interactions will certainly contribute to develop nutritional and pharmacological strategies oriented to prevent major human diseases.

ACKNOWLEDGMENTS

This work was supported by grants from the University of Buenos Aires, Argentina (UBACYT 081); NIH, USA (R21AT2966); UC Davis CHNR-which was established with funding from the State of California Vitamin Price Fixing Consumer Settlement Fund, and Mars Incorporated.

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5 The Biochemistry Behind the Potential Cardiovascular Protection by Dietary Flavonoids

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INTRODUCTION

Flavonoids are natural dietary phytochemicals and are currently the focus of much nutritional and therapeutic interest. However, the benefit of dietary flavonoids as part of a diet or as supplements is unclear. Results of population studies suggest that adopting flavonoid-rich diets may protect against cardiovascular disease [Hertog et al., 1995; Keli et al., 1996; Knekt et al., 1996; Huxley et al., 2003; Sesso et al., 1999; Yochum et al., 1999; Hirvonen et al., 2001;

Plant Phenolics and Human Health: Biochemistry, Nutrition, and Pharmacology,

Edited by Cesar G. Fraga.

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Geleijnse et al., 2002; Mukamal et al., 2002]. Mechanisms by which these compounds exert their cardiovascular protective effects are still unknown. It is widely hypothesized that dietary flavonoids improve cardiovascular health and may help to prevent cardiovascular diseases/events by inhibiting pathogenic processes such as oxidative stress (lipid and protein peroxidation), inflammation, endothelial dysfunction, and platelet activation [Nijveldt et al., 2001].

Daily intake of flavonoids such as quercetin and (–)-epicatechin has been estimated at between 20 and 35 mg/day, in the form of various glycosides, although intact glycosides are not found in plasma [Scalbert and Williamson, 2000]. Following supplementation with flavonoid-rich foods (such as onions or apples), or various glucosides of the pure flavonoids, at doses of 50–200 mg equivalents, their plasma concentrations can reach between 0.5 and 7 μM [Manach et al., 2005 and references therein]. However, due to metabolic transformation, many flavonoids are not present as the aglycone form in plasma but in conjugated forms. For example, 20–40% of circulating quercetin is methylated at the 3'-position with other identified metabolites being the 3-*O*-glucuronide, 3'-*O*-sulfate or the 3'-*O*-methylquercetin-3-*O*-glucuronide [Manach et al., 2005] (see Fig. 5.1). In this chapter, we will discuss the results from recent studies regarding the possible protective roles of dietary flavonoids against cardiovascular diseases.

ANTIOXIDANT ACTIVITY

The biological activity of dietary flavonoids was thought to be due to their antioxidant activity. Lipid peroxidative damage may be a critical step in the pathogenesis of atherosclerosis [Stocker and Keaney, 2004] and the well recognized *in vitro* antioxidant activity of many flavonoids, has led to the proposal that the mechanism for this benefit may involve antioxidant effects [Duthie and Crozier, 2000]. Flavonoids can potentially prevent free-radical-related injury as they exhibit powerful antioxidant activities *in vitro*. They are able to scavenge a wide range of reactive oxygen, nitrogen, and chlorine species [Hanasaki et al., 1994; Santos and Mira, 2004; Sadeghipour et al., 2005] as well as being able to inhibit the production of such reactive species [Selloum et al., 2001; Pincemail et al., 1988]. Flavonoids can also chelate metal ions and often decrease metal ion pro-oxidant activity [Mira et al., 2002]. Ishige et al. [2001] proposed that flavonoids may protect against oxidative stress by increasing intracellular glutathione, directly reducing reactive oxygen species and preventing the influx of Ca^{2+} . However, the studies carried out in this area should be interpreted with caution as the native unmodified forms of flavonoids found in the diet were utilized in *in vitro* experiments instead of the metabolites found *in vivo*.

Recent evidence on the bioavailability and metabolism of these compounds *in vivo* suggests that dietary flavonoids are less likely to act as antioxidants. Most flavonoids may not have significant antioxidant activity *in vivo* for two reasons: (1) bioavailability of dietary flavonoids is very poor (their concentration *in vivo*

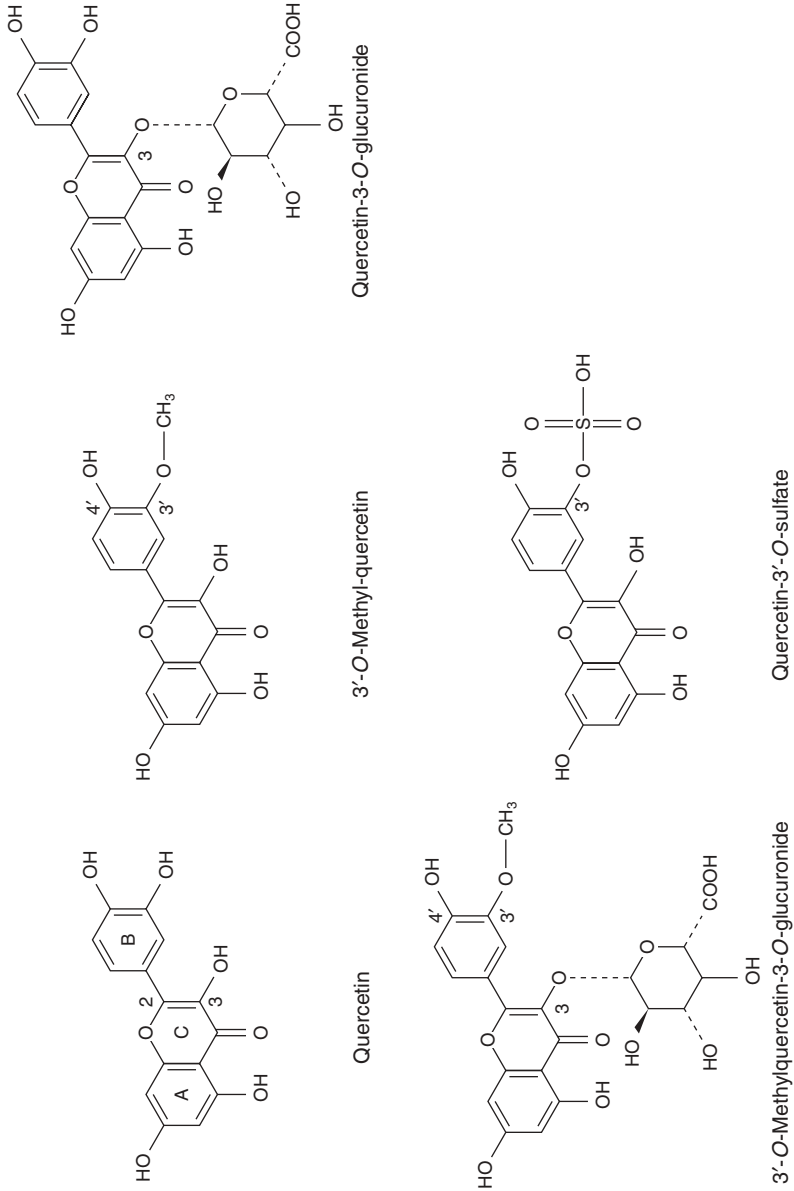


Figure 5.1 Backbone structure of dietary flavonoids.

is likely to be much lower than vitamin C or vitamin E, although they may act as co-antioxidants), and (2) biotransformation will lead to diminished antioxidant activity. Methylation, sulfation, and glucuronidation block the radical scavenging phenolic hydroxyl groups and may decrease antioxidant activity. It may be more useful to examine the antioxidant activity of the metabolites instead of the parent compounds. However, it has been suggested by some investigators that conjugated flavonoids may be hydrolyzed back to the free aglycones in certain cells [Kawai et al., 2008]. One pathway for low-density lipoprotein (LDL) modification *in vivo* is through reactive species generated by myeloperoxidase (MPO) [Zhang et al., 2002a; Podrez et al., 2000; Wang et al., 2007]. MPO has been suggested as a physiological catalyst for *in vivo* LDL modification in studies using monocytes and neutrophils isolated from humans [Hazen et al., 1999; Zhang et al., 2002b]. Previous reports of elevated plasma MPO in early adverse cardiac events [Brennan et al., 2003], in acute coronary syndrome [Baldus et al., 2003], and after acute myocardial infarction [Mocatta et al., 2007] provide further evidence that MPO may contribute to cardiovascular disease. More recently MPO has been implicated in the production of cyanate which can cause carbamylation of proteins [Wang et al., 2007].

We have recently concluded an *in vitro* study investigating and comparing the antioxidant activity of various major *in vivo* metabolites of quercetin against neutrophil-mediated LDL modification. The study showed that quercetin and its major metabolites at physiological realistic concentrations (1 μ M) significantly protect LDL against neutrophil-inflicted oxidative damage as well as peroxy radical-initiated oxidation, both measured by the formation of F₂-isoprostanes (a stable marker of lipid peroxidation) compared to the untreated control experiments [Loke et al., 2008a]. Quercetin acts predominantly through the inhibition of MPO as evidenced by reduction in both the MPO enzyme activity and 3-chlorotyrosine formation from LDL by freshly isolated human neutrophils in the presence of quercetin [Loke et al., 2008a]. Of the metabolites, only one (quercetin-3-*O*-glucuronide) showed comparable antioxidant activity as the parent molecule. Most structural activity relationship studies of flavonoids antioxidant action concluded that flavonoids owe their powerful antioxidant actions to the 2-phenyl-1,4-benzopyrone structure with multiple H-donating phenolic hydroxyl groups. Choi et al. [2002] reported that all flavonoids possessing the ortho dihydroxy functional group, whether on the A-ring or B-ring, and the OH group at position 3, containing either saturated or unsaturated C2–C3 double bonds, appear to have radical scavenging activities. While the 5-OH and 7-OH groups on the A-ring appear to have negligible radical scavenging abilities [Choi et al., 2002], they may enhance the radical scavenging activity of the 3-OH group on the C-ring [Heijnen et al., 2001]. Kettle et al. [2008] showed that myricitrin could irreversibly inactivate MPO and that the OH groups on the B-ring as well as the presence of a free *m*-phenol in the A-ring were important for the inhibitory effects. The catechol structure on the B-ring is widely reported to play a predominant role in scavenging free radicals [Santos and Mira, 2004; Justino et al. 2004].

Experiments carried out at physiological concentrations [Manach et al., 2005] showed that the 3'-OH and 3-OH groups on the B- and C-rings, respectively, played similar roles in both radical scavenging and MPO inhibiting activities [Loke et al., 2008a]. The 2,3 double bond on the B-ring played a negligible part in protecting LDL against oxidative damage because taxifolin (which lacks the 2,3 double bond) retained similar activity to quercetin (see Fig. 5.2). Similar observations were reported for cell-free Cu^{2+} and AAPH-mediated LDL oxidation under nonphysiological concentrations [Vaya et al., 2003; Hou et al., 2004]. Interestingly, conjugation at either 3- or 3'- positions did not significantly reduce quercetin activity against MPO-catalyzed events unlike that against radical scavenging activities. Therefore, metabolic transformation of quercetin may not render the molecule significantly less potent as a MPO inhibitor. These results are particularly interesting considering recent evidence that associates MPO with cardiovascular disease development and progression [Brennan et al., 2003; Baldus et al., 2003; Mocatta et al., 2007].

Studies examining whether dietary flavonoids exert antioxidant effects *in vivo* produced confusing and self-contradicting data. O'Reilly et al. [2001] reported that F_2 -isoprostane concentrations and plasma levels of oxidized LDL did not differ whether healthy subjects were on the flavonoid-rich diet or flavonoid-poor diet. A similar lack of effect was observed when rutin supplementation did not affect urinary concentrations of 8-hydroxy-2'-deoxyguanosine, F_2 -isoprostanes, or malondialdehyde in human volunteers [Boyle et al., 2000]. While the consumption of fruits and vegetables failed to decrease markers of oxidative damage, including F_2 -isoprostanes and DNA damage markers in some studies [Berg et al., 2001; M \ddot{u} ller et al., 2003], Thompson et al. (1999) reported decreased lipid peroxidation markers (F_2 -isoprostanes and malondialdehyde) among subjects who consumed more fruits and vegetables. Dietary intervention studies involving green tea [Freese et al., 1999; Hakim et al., 2003], black tea [Hodgson et al., 2002; Klaunig et al., 1999] and red wines [Young et al., 2000; Caccetta et al., 2000], which represent rich sources of flavonoids in human diets, produced similar contradicting results. These confusing data may result, in part, from the choice of the biomarkers of lipid and protein peroxidation, as they do not fulfill all of the criteria for ideal biomarkers [Halliwell et al., 2004]. Much more work must be done to establish more accurate *in vivo* biomarkers of oxidative damage in order to draw conclusions on the antioxidant effects of dietary flavonoids.

LIPIDS AND LIPOPROTEINS

Hypercholesterolemia is well established as a risk factor for atherosclerosis. Dietary flavonoids are thought to protect against the disease by exerting hypocholesterolemic effects. However, clinical studies are not conclusive enough to provide the supporting evidence. Recent clinical studies on both normo- and hypercholesterolemic subjects with different flavonoids sources lasting 1–13

weeks showed improvement or no change in lipid profiles. Consumption of black tea (5 servings/day) in hypercholesterolemic subjects over a period of 3 weeks resulted in significant reductions in total cholesterol, LDL cholesterol, and apolipoprotein B levels [Davies et al., 2003] (HDL) cholesterol levels in healthy volunteers were elevated, but LDL/HDL ratio remained unaffected after 4 weeks of intervention with cocoa powder and dark chocolate [Wan et al., 2001]. Two independent studies on healthy subjects and smokers showed no change in the levels of triglyceride, LDL, HDL, and total cholesterol after red wine intervention [Cartron et al., 2003; Caccetta et al., 2001]. Lyophilized grape powder significantly decreased triglyceride and LDL cholesterol concentrations in both pre- and postmenstrual women [Zern et al., 2005].

Mechanisms by which dietary flavonoids may influence plasma lipids are yet to be defined. Flavonoids may reduce cholesterol absorption via interaction with cholesterol carriers and transporters across the brush border membrane [Loest et al., 2002]. This reduction in cholesterol absorption decreases the delivery of cholesterol to the liver, which in turn up-regulates the expression of LDL receptor to compensate for less substrate availability and induces reductions in plasma cholesterol [Zern et al., 2003]. Dietary flavonoids were also shown to affect hepatic production of lipoproteins and inhibit cholesterol esterification through their binding with the plasma membrane transport P-glycoprotein [Debry et al., 1997]. Reductions in plasma triglyceride by the flavonoids may occur as a result of lower microsomal transfer protein activity and increased lipoprotein lipase activity, which may further alter the delipidation cascade, yielding less LDL in circulation [Zern et al., 2003]. The citrus flavonoid, naringenin has been shown to improve dyslipidemia and insulin resistance in a high-fat-fed animal model of LDL receptor knockout mouse [Borradaile et al., 2003]. The mechanism is via the inhibition of apoB100 secretion in the liver. Whether these benefits are observed in humans is yet to be established.

DIETARY FLAVONOIDS AND INFLAMMATION

Inflammation is now recognized as a key process in atherogenesis [Libby, 2002]. The potential for dietary flavonoids to inhibit inflammatory activities is of particular interest. A potential anti-inflammatory feature of the flavonoids is the ability to inhibit the biosynthesis of eicosanoids. Selected phenolic acids and some flavonoids have been shown to inhibit both cyclooxygenase (COX) and 5-lipoxygenase (5-LO) pathways [Nijveldt et al., 2001; Takano-Ishikawa et al., 2006]. Epicatechin and related flavonoids have been shown to inhibit the synthesis of pro-inflammatory cytokines *in vitro* [Sanbongi et al., 1997], and plasma metabolites of catechin and quercetin inhibit the adhesion of monocytes to cultured endothelial cells [Koga and Meydani, 2001]. Silymarin has been shown to inhibit the production of inflammatory cytokines, such as interleukin-1, interferon-, and tumor necrosis factor- α (TNF α), from macrophages and T-cells [Matsuda et al., 2005]. Some flavonoids can inhibit neutrophil

degranulation, diminishing the release of free arachidonic acid [Tordera et al., 1994]. These activities are of interest since the possible roles of COX-2 and leukotriene pathways in atherosclerosis are becoming more appreciated [Jala and Haribabu, 2004; Vila, 2004].

We have recently reported that although quercetin is a very potent inhibitor of LTB₄ production in human peripheral monocytes and neutrophils at a realistic physiological concentration ($\sim 2 \mu\text{M}$), some of its major metabolites show significantly diminished activity [Loke et al., 2008b]. Metabolism via conjugation at 3'-OH of quercetin's phenyl *benzopyrone* structure (3'-*O*-methylquercetin and quercetin-3'-*O*-sulfate) decreased LTB₄ inhibitory activity by up to 50% while conjugation at the 3-OH (quercetin-3-*O*-glucuronide and 3'-*O*-methylquercetin-3-*O*-glucuronide) greatly diminished LTB₄ inhibiting activity within the physiological concentration range (2–10 μM) tested. When quercetin was compared with structural analogs (luteolin, kaempferol, and taxifolin), it became apparent that the 3'-OH of the B-ring played a more critical role in LTB₄ inhibition than the 3-OH of the C-ring [Loke et al., 2008b]. This result is in agreement with a previous observation that formation of the 3-*O*-glucuronide by incubation of quercetin with liver cell-free extracts substantially reduces lipoxygenase inhibitory activity [Day et al., 2000]. Interestingly, glucuronide formation at other sites (3', 4', and 7) had little effect on soybean lipoxygenase inhibition in a cell-free preparation [Day et al., 2000]. These results also highlighted that the 2,3 double bond within the C-ring in quercetin is an essential structural requirement for inhibition of LTB₄ production in neutrophils, as its absence (as in taxifolin) totally diminished the inhibiting action. The results are consistent with previous reports that the 2,3 double bond of the C-ring in flavonols is essential for inhibition of adhesion molecule expression in endothelial cells [Lotito et al., 2006] and inflammatory cytokine production in mouse macrophages [Comalada et al., 2006; Takano-Ishikawa et al., 2006]. In addition, we have observed a remarkable dissociation between structural features that determine anti-inflammatory activity and antioxidant activity, which are illustrated in Figure 5.2 [Loke et al., 2008b]. Another factor that may influence the activity of quercetin metabolites is change in polarity and reduced cellular uptake. This is particularly noticeable with polar moieties such as glucuronide and sulfate, while methylation has little effect on cellular uptake. However, the actual mechanisms by which neutrophils sequester quercetin remain unknown at this time.

There is evidence that quercetin and other flavonols such as (–)-epicatechin can directly inhibit human 5-lipoxygenase. It has been established that quercetin does not suppress the hydrolysis of LTA₄ to LTB₄, indicating that quercetin acts directly on 5-lipoxygenase or possibly FLAP [Loke et al., 2008b]. Using a recombinant enzyme, Schewe et al. [2002] showed direct inhibition in a cell-free system with quercetin having $\text{IC}_{50} = 0.6 \mu\text{M}$ for 5-lipoxygenase and 4 μM for inhibition of 15-lipoxygenase. Since these were cell-membrane-free systems, the involvement of FLAP appears to be ruled out. Moreover, the flavonols appear to be nonspecific lipoxygenase inhibitors [Schewe et al., 2002].

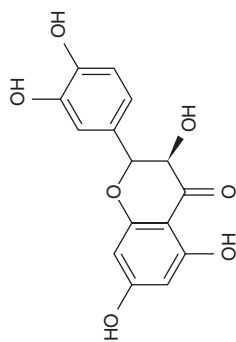
Whatever the mechanism of action for the inhibition of 5-lipoxygenase by flavonoids, it appears to be distinct from the antioxidant properties of these compounds. The results comparing antioxidant activity with leukotriene inhibitory activity clearly demonstrate this distinction. The profound effects of metabolic transformation on the anti-inflammation activity of dietary flavonoids such as quercetin must also be considered in relation to *in vitro* studies, and further highlights the need to use actual metabolic forms of flavonoids rather than the free aglycone or glycosides occurring in the diet.

While *in vitro* studies have provided extensive augments for anti-inflammatory effects of various dietary flavonoids, human studies provide only a few tangible results. Flavonoids may exert anti-inflammatory effects through modulation of immune processes involving cytokines, inflammatory mediators, as well as circulating adhesion molecules. TNF-induced adhesion of monocytes to endothelial cells was virtually abolished after red wine consumption [Badia et al., 2004]. Similar observations were made in another 11-week study with a crossover design comparing red wine and gin consumption in healthy men where adhesion molecules and monocyte adhesion to endothelial cells were significantly reduced due to red wine [Estruch et al., 2004]. Lyophilized grape powder treatment was shown to significantly decrease TNF and IL-6 concentrations in both pre- and postmenopausal women [Zern et al., 2005]. Circulating soluble P-selectin in healthy human volunteers was significantly reduced after black tea consumption [Hodgson et al., 2001]. However, supplementation with cocoa did not affect circulating concentrations of cytokines [Mathur et al., 2002] as well as urinary thromboxane B₂ and 6-keto-prostaglandin F_{1α} (a metabolite of prostacyclin) excretions [Wan et al., 2001] in healthy human volunteers. Circulating VCAM-1 concentrations were significantly reduced after 6 weeks administration of formononetin-enriched isoflavones [Teede et al., 2003]. This effect was totally absent in another human intervention study involving 6 weeks of soy isoflavones [Steinberg et al., 2003]. As the transcription factor, nuclear factor-kB (NF-kB) is responsible for activating cytokines, adhesion molecules and other pro-inflammatory mediators, flavonoids may act by inhibiting NF-kB [Murase et al., 1999]. The limited anti-inflammatory effects of flavonoids in these human studies may be due to the lack of inflammatory immune responses in healthy subjects.

In summary, while *in vitro* studies indicate that several flavonoids may have profound anti-inflammatory activity, results from human intervention studies are less consistent.

ENDOTHELIAL FUNCTION

Endothelial dysfunction is a critical event in the pathogenesis of atherosclerosis and its clinical manifestations [Mano et al., 1996; Cayatte et al., 1994]. It accelerates the development of atherosclerosis and may be one of the earliest



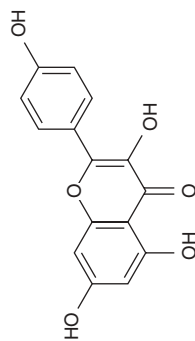
Taxifolin (T)

Absence of 2,3 double bond

Strong activity, similar to Q

Strong activity, similar to Q

No activity



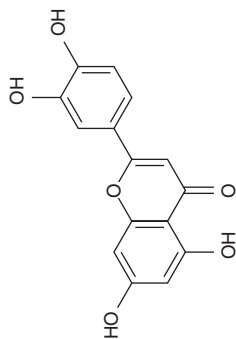
Kaempferol (K)

Absence of 3'-OH group

Diminished activity compared to Q,
similar to L

Diminished activity compared to Q,
similar to L

Some activity



Luteolin (L)

Absence of 3-OH group

Diminished activity compared to Q,
similar to K

Diminished activity compared to Q,
similar to K

Strong activity, similar to Q

Structural difference compared to Q

MPO inhibiting activity

Radical scavenging activity

Antiinflammatory activity

Figure 5.2 Structures of luteolin (L), kaempferol (K), and taxifolin (T). A comparison of the antioxidant (inhibition of MPO and radical scavenging activity) and anti-inflammatory (inhibition of LTB₄) activity with that of quercetin (Q) is summarized.

manifestations of this disease [Celermajer, 1997; Vogel, 1997]. The endothelium regulates vascular tone by balancing the production of vasodilators, most importantly nitric oxide (NO) [Rassaf et al., 2002] and vasoconstrictors, such as endothelin-1 (ET-1) [Strachan et al., 2002]. It maintains vascular homeostasis through multiple complex interactions with cells in the vessel wall. Therefore, endothelial function may serve as an indication for cardiovascular health and be used for evaluation of new therapeutic strategies [Ganz et al., 2003].

Flavonoid rich tea [Hirata et al., 2004], purple grape juice [Stein et al., 1999], and cocoa [Fisher et al., 2003] have all been found to improve endothelial function in acute and short-term intervention trials in humans [Hodgson et al., 2006]. Improving endothelium-dependent vasodilation is believed to be one possible mechanism by which flavonoids may improve cardiovascular risk [Heiss et al., 2006]. There are many hundreds of flavonoids in the human diet. However, it is likely that bioactivity relevant to endothelial function is limited to fewer compounds. Isolated (–)-epicatechin [Schroeter et al., 2006] and epigallocatechin gallate (EGCG) [Widlansky et al., 2005] have been found to acutely improve endothelial function in humans. Isolated (–)-epicatechin has also been shown to augment NO status in humans [Schroeter et al., 2006]. Resveratrol was able to up-regulate the expression of endothelial nitric oxide synthase (eNOS) messenger ribonucleic acid (mRNA) in a time- and dose-dependent manner and thereby increasing NO production in the cultured human endothelial cells [Wallerath et al., 2002]. Similar results were obtained with red wine polyphenol extract [Leikert et al., 2002]. Epicatechin was shown to protect endothelial cells against oxidized LDL and maintain NO synthase [Steffen et al., 2005]. It is therefore possible that flavonoids may improve endothelial function in vivo via NO production, explaining beneficial effects of dietary flavonoids in reducing atherosclerosis.

We have recently conducted a randomized, placebo controlled, crossover trial in healthy men to compare the acute effects on nitric oxide, ET-1, and oxidative stress after oral administration of 200 mg of quercetin, (–)-epicatechin, and EGCG [Loke et al., 2008c]. NO production was assessed by measuring plasma *S*-nitrosothiols, plasma and urinary nitrite and nitrate concentrations, while their effects on oxidative stress by measuring plasma and urinary F_2 -isoprostanes. Plasma and urinary concentrations of quercetin, (–)-epicatechin, and EGCG were measured to establish the absorption of these flavonoids. Relative to water (control), quercetin and (–)-epicatechin resulted in a significant increase in plasma *S*-nitrosothiols and nitrite and urinary nitrate concentrations, but not plasma nitrate or urinary nitrite. EGCG did not alter any of the measures of NO production. Only treatment with quercetin and epicatechin resulted in a significant reduction in plasma ET-1 concentration, and quercetin alone decreasing urinary ET-1. All three treatments did not significantly change plasma or urinary F_2 -isoprostane concentrations. Significant increases in the circulating levels of the three flavonoids were observed after each treatment, however, plasma levels of EGCG were very low (approx. 0.1 μ M) even after supplementation. Our results showed that dietary

flavonoids, such as quercetin and (–)-epicatechin augment NO status and may thereby improve endothelial function [Loke et al., 2008c]. The changes in plasma *S*-nitrosothiols concentrations were also shown to be significantly correlated to the changes in plasma quercetin and (–)-epicatechin concentrations [Loke et al., 2008c].

Quercetin may have increased NO production by enhancing the bioavailability of endothelium-derived NO [Machha et al., 2007] or increasing eNOS activity [Sanchez et al., 2006; Benito et al., 2002]. (–)-Epicatechin has been shown to elevate NO in endothelial cells *in vitro* via the inhibition of NADPH oxidase [Steffen et al., 2007]. Oral administration of pure (–)-epicatechin to humans closely emulated the acute vascular effects of the flavonol-rich cocoa [Schroeter et al., 2006]. Quercetin and (–)-epicatechin may also act as antioxidants, reducing nitrites and nitrates into free NO in the stomach [Gago et al., 2007]. ET-1 has been demonstrated to be associated with increased oxidative stress and endothelial dysfunction in humans. ET-1 stimulates superoxide production and vasoconstriction through activation of NADPH oxidase and uncoupled NOS in the rat aorta [Loomis et al., 2005]. It also reduces NO bioavailability via interference with the expression and activity of eNOS [Ramzy et al., 2006], indicating that diminished ET-1 level may be accompanied by elevated NO bioavailability. It has been reported that NO inhibits ET-1 production through the suppression of NF- κ B [Ohkita et al., 2002]. There seems to be an inverse relationship between NO and ET-1, which may serve to modulate the endothelial function in the vasculature. Quercetin was shown to decrease ET-1 production in thrombin-stimulated cultured human umbilical vein endothelial cells in a dose-dependent manner with an IC_{50} of 1.54 μ M [Zhao et al., 1999]. Red wine polyphenols have also been shown to prevent vascular oxidative stress by inhibiting NADPH oxidase activity and/or by reducing ET-1 release [Jimenez et al., 2007]. The potential mechanistic pathways by which dietary flavonoids may improve NO status and endothelial function are summarized in Figure 5.3.

Surprisingly, EGCG did not show the same augmentation of NO products as quercetin and (–)-epicatechin [Loke et al., 2008c]. It has been widely assumed to be the vasoactive flavonoid present in green tea that offers vascular protection against cardiovascular diseases [Demeule et al., 2002]. EGCG was shown to mediate NO-dependent vasodilation in rat aortic rings [Kim et al., 2007], and it works primarily by the rapid activation of eNOS and increase in eNOS activity, independent of an altered eNOS protein content [Lorenz et al., 2004]. However, it must be noted that these studies reported the effects of EGCG at nonphysiological concentrations. EGCG was present at much lower concentrations ($0.1 \pm 0.01 \mu$ M) in the circulation than quercetin ($3.54 \pm 1.57 \mu$ M) and (–)-epicatechin ($3.57 \pm 1.21 \mu$ M) after acute treatment. Similar circulating concentrations of EGCG was reported in a recent study in which 300 mg dose of EGCG acutely improves brachial artery flow-mediated dilation by vascular ultrasound in humans with coronary artery disease [Widlansky et al., 2005]. If improved endothelial function is brought about by EGCG, the

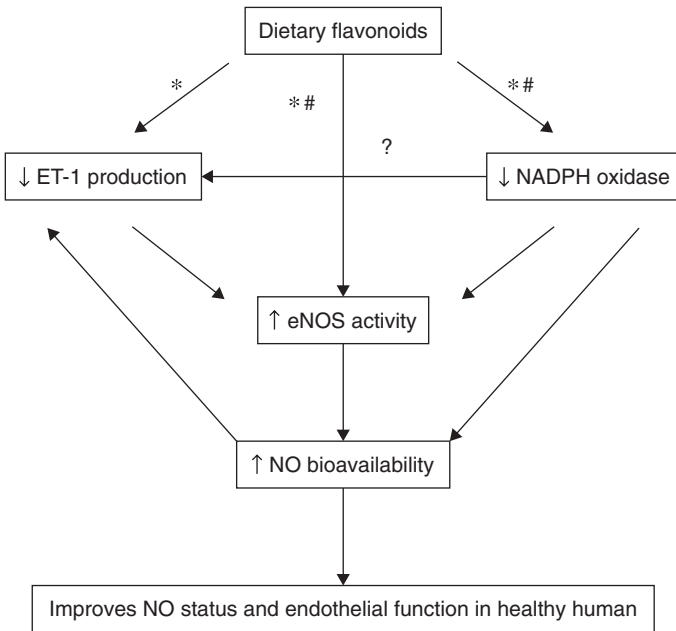


Figure 5.3 Potential mechanistic pathways by which dietary flavonoids may improve NO status and endothelial function. (*) Based on in vitro studies. (#) Evidence from animal studies.(?) Possible proposed action.

compound is likely to have exerted its effects through mechanisms other than those of NO or ET-1.

There is now emerging data that specific dietary flavonoids may improve endothelial function by increasing NO bioavailability. Longer term human intervention studies are required to establish a proven benefit on vascular function in healthy subjects as well as those who may be at increased risk of cardiovascular disease.

DIETARY FLAVONOIDS AND PLATELET REACTIVITY

Platelet aggregation plays a critical role in the pathogenesis of acute coronary syndromes with increasing evidence that antiplatelet therapy reduces cardiovascular disease risk [Awtry and Loscalzo, 2000]. The effect of dietary flavonoids to reduce platelet activity may provide an important mechanistic explanation for the available epidemiological data regarding flavonoids and cardiovascular disease.

Demrow et al. (1995) used the Folts model of unstable coronary stenosis, which closely mimics ruptured atherosclerotic plaque, causing unstable angina, to examine the effects of grape juice on platelet function in vivo. In this model,

transient platelet aggregation and release are reflected in cyclic variations in coronary blood flow. Acute intragastric administration of red wine or grape juice was associated with marked reductions in cyclic flow variations, which was indicative of an antiplatelet effect. Tea consumption reduced plasma concentrations of P-selectin (a marker of *in vivo* platelet activation) [Hodgson et al., 2001]. However, other studies that examined the effects of short-term and/or long-term tea consumption on *ex vivo* platelet aggregation did not demonstrate any effect on platelet function [Duffy et al., 2001; Hodgson et al., 2002]. More studies are required to define the effects of tea consumption on platelet function. Cocoa decreased epinephrine-stimulated or adenosine diphosphate-stimulated glycoprotein IIb/IIIa and P-selectin expression in human subjects 2 and 6 h after consumption [Rein et al., 2000]. When platelet-related primary homeostasis was measured as the time taken for epinephrine-stimulated or adenosine diphosphate-stimulated whole blood to occlude an aperture in a collagen membrane under stimulated small vessel shear condition, the respective closure time increased 6 h and 2 h after flavonoid-rich cocoa ingestion. Quercetin has been implicated as a dietary inhibitor of platelet cell signaling when a human acute intervention study showed that platelet aggregation was inhibited 30 and 120 min after ingestion of 150 and 300 mg of quercetin-4'-*O*- β -glucoside, accompanied by reduced tyrosine phosphorylation of the tyrosine kinase Syk and phospholipase C γ 2 components of the platelet glycoprotein VI collagen receptor signaling pathway [Hubbard et al., 2004].

The exact mechanisms by which flavonoids inhibit platelet activity are not yet fully understood, but it is possible that flavonoids effect changes in membrane fluidity, ligand-receptor affinity, and intracellular signaling pathways. Flavonoids may mediate their effects through antioxidant and NO-related pathways. Catechin was shown to reduce platelet aggregation and hydrogen peroxide *in vitro* [Pignatelli et al., 2000] and attenuate oxidant-induced platelet activation *in vivo* [Blache et al., 2002]. The addition of grape juice to platelets *ex vivo* reduced platelet aggregation, decreased platelet production of superoxide anion, and increased the platelet production of nitric oxide [Freedman et al., 2001]. Flavonoids or flavonoid-rich food can modulate different aspects of eicosanoid metabolism *in vivo* [Schramm et al., 2001] and were shown to inhibit platelet 12-lipoxygenase and 5-lipoxygenase *in vitro* [Sies et al., 2005]. Flavonoids can also modulate membrane fluidity by interacting with the lipid bilayer [Verstraeten et al., 2003], which in turn can result in changes in membrane receptor function and enzymatic activity [Oteiza et al., 2005]. Lipid rafts may be important membrane components involved in cell signaling [Simons et al., 1997; Bodin et al., 2003] and platelet activation [Gousset et al., 2002]. Recently, epigallocatechin-3-*O*-gallate was found to associate strongly with the cholesterol component of the lipid raft in human basophilic KU812 cells [Fujimura et al., 2004], suggesting that certain flavonoids may modulate cellular activation through interaction with lipid rafts.

CONCLUSIONS

If flavonoids are cardiovascular protective nutrients, the bioactivity must originate from their metabolites rather than from the native forms present in our food and beverages. These metabolites may be present in the circulation at sufficient concentrations to exert their protective actions. These include: (a) inhibition of MPO enzyme activity, which protects LDL against lipid peroxidation and protein modification; (b) inhibition of eicosanoid biosyntheses, especially from the COX and lipoxygenase pathways; (c) regulation of endothelial function by modulating the production of NO; and (d) platelet activity and thrombosis inhibition. Since NF- κ B is implicated in the transcriptional activation of numerous genes, including those relevant to atherosclerosis and inflammatory responses, its inhibition by these compounds may explain some of their potential properties. Flavonoids and their metabolites may also act in cells as signaling molecules through actions at protein kinase and lipid kinase signaling pathways [Williams et al., 2004].

To fully understand the actual mechanism of action of dietary flavonoids either as antioxidants, modulators of cell signalling, or inflammatory pathways, it is important to detect and identify their metabolites *in vivo* as well as to study the consequences of interaction of these circulating metabolites with cells. Animal models and human studies should also be conducted to identify the *in vivo* mechanism of action of dietary flavonoids. Results of such studies are crucial in the evaluation of their potential as cardiovascular protective agents and may eventually lead to specific advice regarding intake of foods and beverages rich in flavonoids and attempts to alter and enhance flavonoid content of a range of foods.

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6 Dietary Flavanols: Biochemical Basis of Short-Term and Longer-Term Vascular Responses

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INTRODUCTION

The literature on vascular responses to dietary components [e.g., Fitzpatrick et al., 1995] has increased substantially in recent years. Short-term and long-term consumption of black tea was shown to reverse endothelial dysfunction in patients with coronary artery disease [Duffy et al., 2001]. On the acute short-term time frame, which is taken here as the responses observed between 0 and 6 h, we demonstrated increases in flow-mediated dilation of the brachial artery upon intake of high-flavanol cocoa drink, but not of low-flavanol cocoa drink, in a crossover study [Heiss et al., 2003]. The effect of the flavanol-rich cocoa drink on flow-mediated dilation as well as the increase in circulating

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RNO [Heiss et al., 2003] was mimicked by isolated (–)-epicatechin administered to humans [Schroeter et al., 2006].

As in the studies on tea [Duffy et al., 2001], a chronic longer-term vascular response was identified with high-flavanol cocoa, when the flavanol-containing beverage was administered repetitively over several days [Heiss et al., 2007]. This effect was clinically characterized as continuously elevated baseline of flow-mediated dilation, on top of which the short-term effect was added on with every new dose; this additive effect was at about the same magnitude as without the pretreatment.

This chapter will summarize, in brief, results on the short-term and the longer-term responses, with emphasis on the former, where recent work led to some clarification and new perspectives [Schewe et al., 2008].

SHORT-TERM EFFECTS

Subsequent to ingestion of flavanol-rich cocoa products, the plasma levels of flavanols on their metabolites show a time course with increasing levels up to about 2 h, followed by a decrease toward the initial baseline, reached at about 4–6 h [Baba et al., 2000; Schroeter et al., 2006]. The vascular response, determined as an increase in flow-mediated dilation, follows a similar time course, as does the time course of the concentration of circulating nitric oxide (NO), assayed as RNO (RSNO and RNNO) [Heiss et al., 2003; Schroeter et al., 2006]. Several other studies also addressed these issues [Fisher et al., 2003; Engler et al., 2004; Heiss et al., 2005]. The responses on a time scale of only a few hours are not attributable to changes in gene expression followed by protein synthesis, but rather to more swift mechanisms like enhancement of flux through an enzyme reaction or to inhibitory effects directly influencing cellular and intercellular signaling.

Whereas enhancement of flux, that is, NO production, through the reaction catalyzed by endothelial nitric oxide synthase (eNOS) would be a straightforward explanation, our attempts to demonstrate such an activated flux through eNOS yielded no positive results, and we did not detect a potential short-term change in phosphorylation of serine-1177 of the enzyme, which would have led to an activation of the enzyme. However, we showed in cell culture experiments that indeed the steady-state level of cellular NO was increased in the presence of (–)-epicatechin, as visualized by DAF-2DA [Steffen et al., 2007]. A similar response was obtained with apocynin, 3-methoxy-4-hydroxyacetophenone, an efficient inhibitor of NADPH oxidase. When (–)-epicatechin was added in the presence of an inhibitor of the methylating enzyme, catechol-*O*-methyltransferase (COMT), the effect was blocked. Conversely, the methyl ether of (–)-epicatechin, 3'-*O*-methyl-epicatechin, was capable of elevating the fluorescence signal, indicating increased NO levels [Steffen et al., 2007]. Thus, it can be suggested that the effect of (–)-epicatechin is an indirect one, namely serving as precursor for the biologically active methyl ether, which acts as an inhibitor of

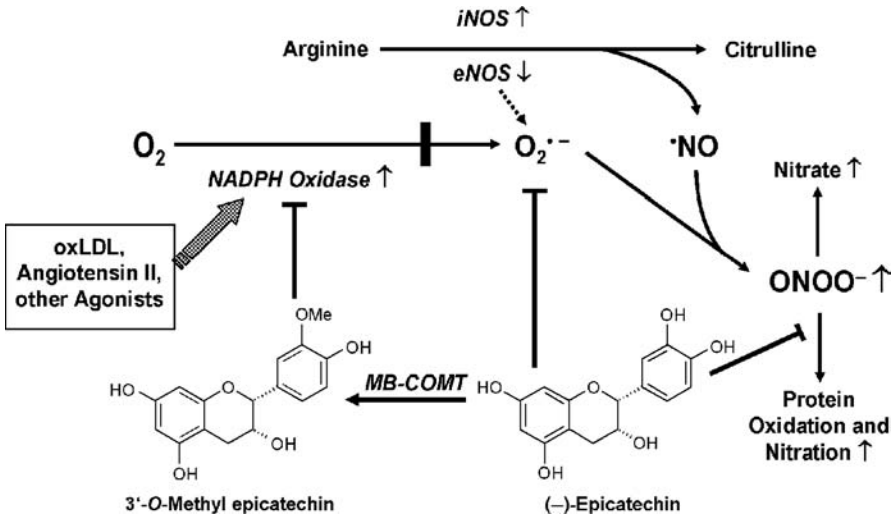


Figure 6.1 (-)-Epicatechin and 3'-O-methyl epicatechin increase NO levels in vascular endothelial cells via inhibition of NADPH-dependent formation of superoxide anions. Oxidized low-density lipoprotein (LDL), angiotensin II or other agonists evoke oxidative stress in vascular endothelial cells through activation of NADPH oxidase leading to elevated generation of $O_2^{\cdot-}$. Some $O_2^{\cdot-}$ may also arise from uncoupled eNOS (occurring, e.g. under conditions of tetrahydrobiopterin deficiency) (dotted arrow). $O_2^{\cdot-}$ reacts with NO generated by either eNOS or iNOS (the latter under proinflammatory conditions), forming peroxynitrite that, in turn, causes protein modifications or isomerizes to nitrate. (-)-Epicatechin is capable of scavenging $O_2^{\cdot-}$ and suppressing peroxynitrite-dependent reactions, but, more efficiently, serves as precursor of 3'-O-methyl epicatechin, which acts as inhibitor of NADPH oxidase. The methyl ether, generated by membrane-bound O-methyltransferase (MB-COMT), blocks NADPH oxidase-dependent $O_2^{\cdot-}$ generation, thus sparing NO.

NADPH oxidase in an apocynin-like fashion [Steffen et al., 2007, 2008; Schewe et al., 2008; Ximenes et al., 2007]. This is depicted schematically in Figure 6.1.

The occurrence of COMT in vascular cells has not been described so far. As shown in Figure 6.2, we confirm the presence of COMT by immunostaining of human umbilical vein endothelial cells. The localization is with intracellular membranes, and Western blots showed that the membrane-bound form, MB-COMT, is predominant by far over the soluble enzyme, S-COMT [Kravets, 2008]. Methylation of the B-ring of (-)-epicatechin exhibits some regioselectivity; the 3'-methyl ether was the preferred product, with the ratio of 3'- over 4'-O-methylepicatechin being about 2.0 [Kravets, 2008].

Among the metabolites circulating in human blood plasma after intake of (-)-epicatechin, the major one is the glucuronide [Natsume et al., 2003]. We suggest that the epicatechin glucuronide serves as transport metabolite, taken up into the cells and after deglucuronidation delivering the flavanol

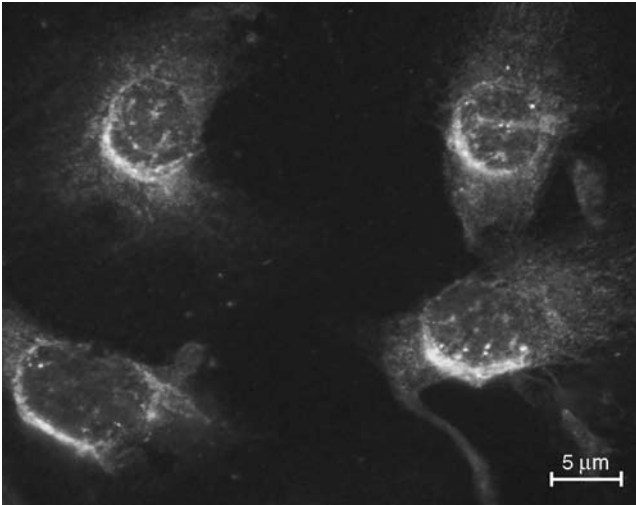


Figure 6.2 Immunocytochemical detection of catechol-*O*-methyltransferase (COMT) in human umbilical vein endothelial cells (HUVEC). Polyclonal COMT antibody from Chemicon Millipore, USA. (From Kravets E. [2008].)

intracellularly [Schewe et al., 2008]. These pathways will have to be worked out in more detail in the future.

The observations mentioned here suggest that short-term effects are correlated to metabolism of the flavanol moiety, potentially including a metabolic formation of a dimer, the procyanidin, and a main result being a modulation of the availability of circulating NO equivalents. In other words, there is an alternative pathway to induce a change in RNO levels without necessarily postulating an increase rate of production of NO through the NO synthase reaction. Abolition of the flavanol effects by inhibitors of eNOS, for example, L-NMMA, would not be in contradistinction, as the NO that is available is generated from eNOS, and only the disposition of it would be addressed.

LONGER-TERM EFFECTS

As mentioned above, repetitive ingestion over several days augments the baseline of flow-mediated dilation [Heiss et al., 2007]. The daily consumption of a flavanol-rich cocoa drink (3×306 mg flavanols/d) over 7 days ($n = 6$) resulted in continual FMD increases at baseline (after overnight fast and before flavanol ingestion) and in sustained FMD augmentation at 2 h after ingestion. Fasted FMD responses increased from $3.7 \pm 0.4\%$ on day 1 to $5.2 \pm 0.6\%$, $6.1 \pm 0.6\%$, and $6.6 \pm 0.5\%$ (each $P < 0.05$) on days 3, 5, and 8, respectively. FMD returned to $3.3 \pm 0.3\%$ after a washout week of cocoa-free diet (day 15). Increases observed in circulating nitrite, but not in circulating nitrate,

paralleled the observed FMD augmentations. The short-term response assayed each morning following application of the daily morning dose was unaffected; it remained at similar magnitude throughout the study [Heiss et al., 2007]. This established for the cocoa-derived responses what was also observed in the 30-day black tea study [Duffy et al., 2001]. More recently, a similar result was obtained on a group of diabetic patients [Balzer et al., 2008].

Thus, there are responses on the longer term that change the setpoints of responses, most likely involving changes in gene expression, enzyme patterns, or activity state of enzymes. Recently, we observed a decrease in arginase following treatment with cocoa [Schnorr et al., 2008], and there are numerous other observations relating to changes in eNOS level and activity. This longer-term time frame may be of importance for assessing health effects, which may have more of an impact on long-term degenerative disease prevention [see Ding et al., 2006] than the short-term responses on flow-mediated dilation. The currently available time range on longer term is 8 up to 30 days, and long-term studies over several months should be encouraged. A recent compilation of studies in this research area is available [Shenouda and Vita, 2007].

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7 Green Tea Catechins: Anticancer Effects and Molecular Targets

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INTRODUCTION

Tea is a popular beverage, derived from the plant *Camellia sinensis* and has been brewed for nearly 5000 years. There are three major commercial varieties of tea: green (20% of consumption), oolong (2% of consumption), and black tea (78% of consumption). In the production of black tea, the plant leaves are picked and then allowed to wither indoors, ferment, and oxidize. For green tea, the plant leaves are steamed and parched after picking to prevent oxidation of the catechins present in the leaf. Oolong tea is produced by “semifermenting” the green leaves, resulting in a tea that is chemically a mixture of green and black teas [Khan et al., 2007]. Although green tea is becoming popular worldwide, traditionally it is most commonly consumed in Asia, whereas black tea is more popular in the United States and Europe. Since ancient times green tea is a widely consumed beverage and, for centuries, has been regarded to possess significant health-promoting effects. The health-promoting effects of green tea are mainly attributed to its polyphenol content. Green tea is a rich source of polyphenols, especially flavanols, which represent approximately 30% dry weight of the fresh leaf. Catechins are the predominant flavanols in green tea and are mainly comprised of (–)-epigallocatechin gallate (EGCG), (–)-epigallocatechin (EGC), (–)-epicatechin gallate (ECG), and (–)-epicatechin (EC) (Fig. 7.1).

Catechins contain a benzopyran skeleton with a phenyl group substituted at the 2-position and a hydroxyl (or ester) function at the 3-position. Variations to the catechin structure include the stereochemistry of the 2,3-substituents and the number of hydroxyl groups in the B- and D-ring. More than 50% of the mass of this catechin combination is composed of EGCG, and a vast body of scientific research suggests that EGCG is responsible for the majority of the potential health benefits attributed to green tea consumption. Theaflavins, which include theaflavin, theaflavin-3-gallate, theaflavin-3' gallate, and theaflavin-3,3'-digallate, are key to the characteristic color and taste of black tea, and account for 2–6% of the solids in brewed black tea. The major fractions of black tea polyphenols, accounting for >20% of the solids in brewed black tea, are known as thearubigens [Khan et al., 2008]. In recent years, scientists throughout the world have investigated the potential benefits of green tea and its most abundant catechin, EGCG. The potential for use of EGCG in human cancer prevention and treatment seems very promising because EGCG acts against cancer through a variety of mechanisms. This potential is reflected by the growing number of *in vivo* and *in vitro* research studies on this topic. Tea is an important source of flavonoids in the diet with levels approaching 200 mg/cup for a typical brew of black tea. The flavonoids found in green and black tea are very effective antioxidants *in vitro* and may therefore be active as antioxidants in the body [Adhami and Mukhtar, 2007]. The mechanisms responsible for the anticancer actions of tea are not well understood but are being intensively investigated. Recent research findings indicate that tea polyphenols can protect against the multistages of carcinogenesis (Fig.7.2).

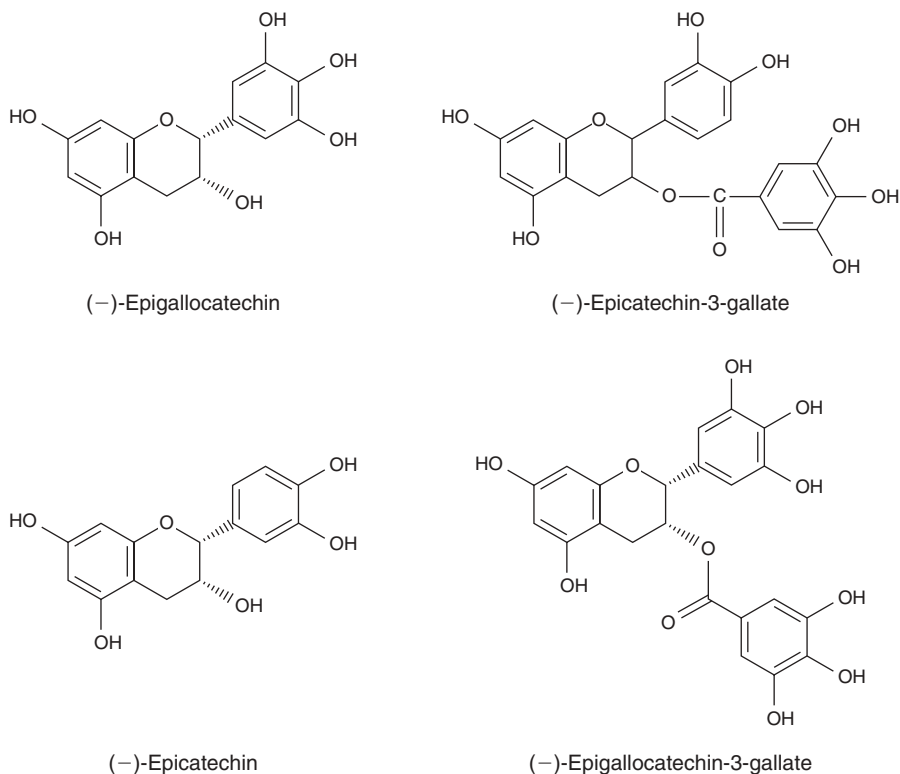


Figure 7.1 Chemical structures of major green tea catechins.

This chapter discusses the anticarcinogenic effects of green tea catechins, especially EGCG in different organ sites and effects on cellular signaling events.

BIOTRANSFORMATION AND BIOAVAILABILITY OF TEA POLYPHENOLS

Yang et al. [1998] have reported that administration of 1.5, 3.0, and 4.5 g of decaffeinated green tea solids to human volunteers resulted in maximal plasma concentrations (C_{\max}) of 326, 550, and 190 ng/L for EGCG, EGC, and EC, respectively. These C_{\max} values were observed 1.4–2.4 h after the ingestion of the tea preparation. The elimination half-life ($t_{1/2}$) of EGCG (5.0–5.5 h) was found to be higher than those of EGC and EC (2.5–3.4 h). EGC and EC, but not EGCG, were excreted in the urine. Within 8 h, over 90% of the total urinary EGC and EC was excreted [Yang et al., 1998].

The major metabolic pathways for tea catechins include glucuronidation, sulfation, and methylation. There are species and tissue-specific differences in

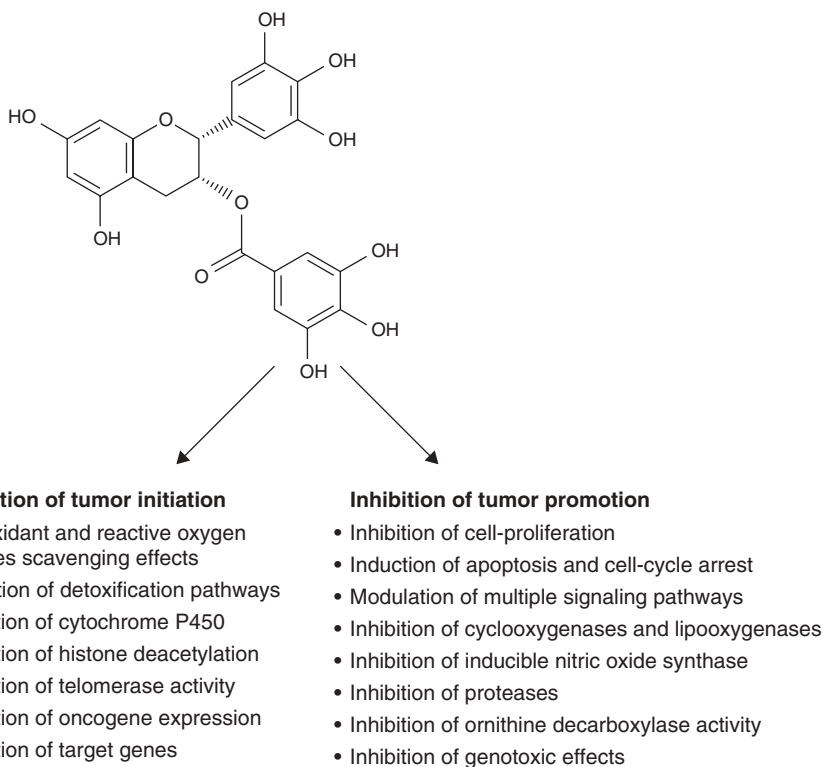


Figure 7.2 Mechanisms of inhibition of carcinogenesis by EGCG.

EGCG and EGC glucuronidation, with humans and mice being more similar than humans and rats. Methylated catechins have been observed in the rat including 3'- and 4'-*O*-methyl EC, 4'-*O*-methyl EGC, and 4''-*O*-methyl EGC and EGCG. Following oral EGCG administration, the major metabolite detected in the bile of the rat was 4', 4''-di-*O*-methyl-EGCG [Lambert and Yang, 2003]. The greatest catalytic efficiency for glucuronidation is in mouse intestinal microsomes followed in decreasing order by mouse liver, human liver, rat liver, and rat small intestine. EC undergoes sulfation catalyzed by human and rat intestinal and liver cytosol with the human liver being the most efficient [Vaidyanathan and Walle, 2002]. EGC is detected mainly as the glucuronidated form or sulfated form with only a small amount present as the free form in humans [Lee et al., 1995]. Tea catechins undergo metabolism in the gut to form the ring fission products 5-(3',4',5'-trihydroxyphenyl)- γ -valerolactone (M4), 5-(3',4'-dihydroxyphenyl)- γ -valerolactone (M6), and 5-(3',5'-dihydroxyphenyl)- γ -valerolactone (M6') [Li et al., 2000]. These metabolic intermediates are further broken down by gut flora to phenylacetic and phenylpropionic acids. M6 was previously shown to form during anaerobic incubation of ECG and EC with human intestinal bacteria [Meselhy et al., 1997].

Detailed pharmacokinetic and biotransformation studies of the tea catechins have been conducted in rats [Lambert and Yang, 2003]. It has been shown that treatment of rats with a green tea polyphenol (GTP) preparation in the drinking fluid result in increasing plasma levels over a 14-day period with levels of EGC and EC being higher than those of EGCG. EGCG levels are lower in the bladder, kidney, colon, lung, and prostate, whereas the levels of EGCG were found to be highest in the rat esophagus, intestine, and colon, which have direct contact with tea catechins. The EGCG levels in the plasma, lung, and liver are much higher than in rats when the same polyphenol preparation is given to mice. These levels appear to peak on day 4 and then decrease to $\leq 20\%$ of the peak values on days 8–10 [Kim et al., 2000]. The absolute bioavailability of EGCG, EGC, and EC, after intragastric administration of decaffeinated green tea is 0.1, 14, and 31%, respectively. After oral administration of 100 mg of EGCG, in studies with bile-duct-cannulated rats, 3.28% of the dose is recovered in the bile as EGCG (2.65%), 4'-*O*-methyl-EGCG (0.25%), 3''-*O*-methyl-EGCG (0.11%), 4'-*O*-methyl-EGCG (0.11%), 3''-*O*-methyl-EGCG (0.10%), and 4',4''-di-*O*-methyl-EGCG (0.06%) [Okushio et al., 1999].

ANTICARCINOGENIC EFFECTS OF GREEN TEA POLYPHENOLS

Green Tea Polyphenols and Lung Cancer

Green tea was also found to significantly inhibit benzo(*a*)pyrene-induced lung tumorigenesis in A/J mice [Wang et al., 1992]. There was reduction in lung tumor incidence and multiplicity in *N*-nitrosodiethylamine-treated A/J mice by green tea and decaffeinated green tea [Wang et al., 1992]. In LACA mice, green tea greatly reduced tumor incidence and multiplicity in *N*-methyl-*N*-nitrosoguanidine (MNNG)-induced lung cancers and precancerous lesions [Luo and Li, 1992]. Decaffeinated green and black tea showed a dose-dependent chemoprevention of lung tumors in dimethylnitrosamine-treated C3H mice [Cao et al., 1996]. Administration of polyphenon E, a standardized GTP preparation significantly reduced the NNK-induced lung tumor incidence and multiplicity in female A/J mice. Polyphenon E treatment inhibited cell proliferation and enhanced apoptosis in adenocarcinomas and adenomas and lowered levels of c-Jun and extracellular signal-regulated kinase (ERK) 1/2 phosphorylation [Lu et al., 2006]. There was significant reduction in tumor multiplicity in both $p53^{wt/wt}$ and $p53^{val135/wt}$ mice after the administration of green tea as the sole drinking source beginning 1 week after NNK administration [Zhang et al., 2000]. It has been reported that EGCG caused suppression of NF- κ B/PI3K/AKT/mTOR and MAPKs in normal human bronchial epithelial (NHBE) cells, which may contribute to its ability to suppress inflammation, proliferation, and angiogenesis induced by cigarette smoke [Syed et al., 2007]. Lu et al [2006]. analyzed the gene expression changes caused by the

administration of green tea or polyphenon E to chemically induced mouse model for lung tumorigenesis. They found that 88 genes that were differentially expressed in tumors (from the normal tissues) were reversed by the treatment and suggested that these genes may be used as markers for tea exposure [Lu et al., 2006].

Green Tea Polyphenols and Liver Cancer

It has been reported that EGCG inhibited the growth of hepatocellular carcinoma cell lines, induced apoptosis, and down-regulated Bcl-2 and Bcl-xL by inactivation of NF- κ B. Oral administration of EGCG showed similar effects in HLE xenograft tumors. Co-treatment with EGCG and necrosis factor-related apoptosis-inducing ligand (TRAIL) synergistically induced apoptosis in HLE cells [Nishikawa et al., 2006]. All four tea catechins (EC, EGC, ECG, EGCG), black tea extract, and oolong tea extract, significantly decreased the diethylnitrosamine and phenobarbital-induced number and area of preneoplastic glutathione *S*-transferase placental form-positive foci in the liver [Matsumoto et al., 1996]. EGCG inhibited the platelet-derived growth factor (PDGF)-BB-induced cell-proliferation and collagen α 1(I) and (IV) messenger ribonucleic acid (mRNA) expressions. EGCG also reduced the autophosphorylation of the PDGF receptor and blocked PDGF-BB binding to its receptor in a noncompetitive manner [Sakata et al., 2004]. In C3H mice, green and black tea treatment caused a significant decrease in the diethylnitrosamine-induced liver tumors [Cao et al., 1996]. There was inhibition of hepatic glucose-6-phosphatase system mediated through an elevated luminal glucose level by EGCG [Csala et al., 2007]. In mice, administration of green tea was able to prevent the increase in incidences and multiplicities of diethylnitrosamine-induced hepatocellular tumors and also arrest the progression of cholangiocellular tumors [Umemura et al., 2003].

Green Tea Polyphenols and Gastrointestinal Tract Cancer

The inhibitory effect of EGCG on MNNG-induced glandular stomach carcinogenesis in rats and on *N*-ethyl-*N*-nitro-*N*-nitrosoguanidine (ENNG)-induced duodenal carcinogenesis in mice has been reported [Yamane et al., 1996]. EGCG was found to inhibit growth and activation of the epidermal growth factor receptor (EGFR) and human EGFR-2 signaling pathways in human colon cancer cells [Shimizu et al., 2005]. Administration of EGCG in drinking fluid dose-dependently inhibited small intestinal tumorigenesis in ApcMin/+ mice. EGCG administration resulted in increased levels of E-cadherin as well as decreased levels of β -catechin in the nucleus, c-Myc, phospho-Akt, and phospho-ERK in the tumors [Ju et al., 2005]. IHC analysis showed that PPE or EGCG treatment increased apoptosis but decreased cell proliferation as well as levels of phospho-Akt and nuclear β -catenin. Green tea administration (0.6% in drinking fluid) inhibited the formation of

azoxymethane (AOM)-induced aberrant crypt foci in CF-1 mice on a high-fat diet [Ju et al., 2003]. Green tea extract administration also inhibited intestinal tumor formation in the Apc mutant Min mice, and the effect was enhanced synergistically when combined with sulindac [Suganuma et al., 2001].

Green Tea Polyphenols and Skin Cancer

It was reported that GTP acts as anti-initiating agent against the skin tumorigenicity induced by polycyclic aromatic hydrocarbons in mice. In a complete skin tumorigenesis protocol using 3-methylcholanthrene, the topical application of GTP to female BALB/c mice resulted in substantial protection against the onset and subsequent development of tumors. In the two-stage DMBA-TPA skin tumorigenesis protocol, topical application of GTP to female SENCAR mice afforded significant protection against skin tumorigenicity. Oral feeding of GTP in drinking water to female SENCAR mice also protected against skin tumorigenesis [Wang et al., 1989]. In SKH-1 mice, oral administration of GTP reduced ultraviolet-B (UVB)-induced skin tumor incidence, tumor multiplicity, and tumor growth. There was also reduced expression of the matrix metalloproteinases (MMP)-2 and MMP-9, CD31, vascular endothelial growth factor (VEGF), and proliferating cell nuclear antigen (PCNA) in the GTP-treated group. There were also more cytotoxic CD8(+) T cells and greater activation of caspase-3 in the tumors of the orally administered GTP group indicating the apoptotic death of the tumor cells [Mantena et al., 2005]. We have shown that topical application of a GTP fraction to the skin of DMBA-initiated mice, prior to that of TPA or mezerein, resulted in protection against skin tumor promotion as indicated by the decrease in tumor incidence, tumor multiplicity, and tumor volume. GTP also protected against the malignant conversion of papillomas to squamous cell carcinomas [Katiyar et al., 1997]. We have also shown that topical application of GTP resulted in significant decrease in UVB-induced bifold-skin thickness, skin edema, infiltration of leukocytes, and inhibition of MAPKs and NF- κ B pathways in SKH-1 hairless mice [Afaq et al., 2003]. Green tea, black tea, or EGCG when given orally inhibited the growth of well-established skin tumors and, in some cases, tumor regression was also observed. Complete regression was observed in papilloma-bearing mice [Conney et al., 1999]. In SKH-1 mice, there was enhancement in the rate and extent of disappearance of the mutant p53-positive patches by the oral administration of green tea as the sole source of drinking fluid starting immediately after discontinuation of UV-B treatment [Lu et al., 2005].

Green Tea Polyphenols and Prostate Cancer

It has been shown that EGCG-induced apoptosis, cell-growth inhibition, and cell-cycle dysregulation in human prostate cancer DU145 and LNCaP cells without producing similar effects in normal cells [Ahmad et al., 1997];

Adhami et al., 2003]. We have earlier reported that GTP consumption was found to significantly inhibit prostate cancer development and metastasis in transgenic adenocarcinoma of the mouse prostate (TRAMP) model. This was achieved by an oral infusion of GTP equivalent to six cups of green tea a day, that is, at an achievable dose in humans [Gupta et al., 2001]. Moreover, elevated levels of insulin-like growth factor (IGF)-1, coupled with lowering of IGF-binding protein-3 (IGFBP-3) are associated with a greater risk of developing prostate cancer. GTP infusion has been shown to reduce the levels of IGF-1 and concomitantly increase IGFBP-3 with marked inhibition of markers of angiogenesis and metastasis. This leads to a reduction in the downstream signaling and inhibition of protein expression, hence inhibiting prostate cancer development and progression [Adhami et al., 2004]. GTP feeding to TRAMP mice also resulted in marked inhibition of prostate cancer progression, which was associated with reduction of S100A4 and restoration of E-cadherin [Saleem et al., 2005]. It was reported recently that green and black tea inhibits CWR22Rv1 tumor growth and prostate-specific antigen (PSA) secretion in athymic nude mice [Siddiqui et al., 2006]. EGCG induced apoptosis in human prostate carcinoma LNCaP cells via stabilization of p53 by phosphorylation on critical serine residues and p14ARF-mediated down-regulation of murine double minute 2(MDM2) protein, negative regulation of NF- κ B activity, activation of caspases, causing a change in the ratio of Bax/Bcl-2 in a manner that favors apoptosis [Hastak et al., 2003]. In LNCaP and DU145 cells, EGCG treatment resulted in induction of G1 phase ckis, which inhibits the cyclin-cdk complexes operative in the G0/G1 phase of the cell cycle, thereby causing an arrest that ultimately leads to apoptotic cell death [Gupta et al., 2003]. We have recently reported that treatment of human prostate cancer cells LNCaP, PC-3, and CWR22Rv1 with a combination of EGCG and Cox-2 inhibitor resulted in enhanced cell growth inhibition, apoptosis induction, and inhibition of NF- κ B. In athymic nude mice, implanted with CWR22Rv1 cells, combination treatment with GTP and celecoxib resulted in enhanced tumor growth inhibition, lowering of PSA and IGF-1 levels, and increase in IGFBP-3 levels [Adhami et al., 2007]. It was demonstrated using isogenic cell lines that EGCG activates growth arrest and apoptosis in prostate carcinoma cells primarily via p53-dependent pathway that involves the function of both p21 and Bax such that down-regulation of either molecule confers a growth advantage to the cells [Hastak et al., 2005]. Recently, the stage(s) of prostate cancer development that is most vulnerable to chemopreventive intervention by GTP were identified. We selected animals and initiated oral feeding of GTP (0.2% in drinking water ad libitum) at ages representing different stages of the disease: (i) 6 weeks, mice with normal prostate pathology, (ii) 12 weeks, when mice histologically display hyperplasia, (iii) 18 weeks, when severe hyperplasia and adenocarcinoma are observed, and (iv) 28 weeks when mice display primary tumors and metastasis is common. It was found that the chemopreventive potential of GTP decreases with increasing tumor grade [Adhami et al., 2008].

EFFECTS ON SIGNAL TRANSDUCTION PATHWAYS

As shown in Figure 7.3, EGCG appears to afford protection against cancer through multiple biological mechanisms, although the specific molecular targets and intracellular pathways modulated by it remain incompletely defined as discussed in the following sections.

Inhibition of NF- κ B Signaling Pathway

Nuclear factor- κ B (NF- κ B) is a transcription factor important for the expression of numerous genes contributing to inflammation and innate and adaptive immune responses. Regulation of NF- κ B occurs at several different hierarchical levels. In most resting cells, NF- κ B is retained in the cytoplasm by binding to the inhibitory I κ B proteins, which blocks its nuclear localization sequences. NF- κ B is activated in response to a wide variety of stimuli that promote the dissociation of the I κ B α through phosphorylation, ubiquitination, and degradation, thus unmasking of the nuclear localization sequence of NF- κ B thereby allowing NF- κ B to enter the nucleus and bind κ B-regulatory elements [Richmond, 2002]. The activation of this transcription factor is affected by a number of parallel signaling pathways that cross-talk with NF- κ B activating signal cascades either positively or negatively. Because of the critical role of NF- κ B in cell survival, cell adhesion, inflammation, differentiation, and cell growth, it has been implicated in carcinogenesis. EGCG has been shown to

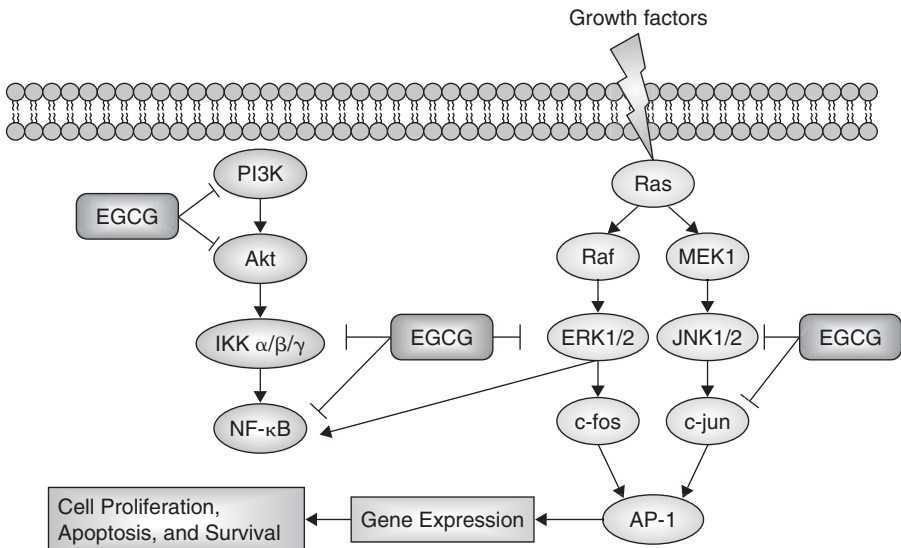


Figure 7.3 Effect of EGCG on the modulation of various signal transduction pathways.

inhibit TPA-induced DNA binding of NF- κ B and CREB in mouse skin *in vivo* and also suppressed TPA-induced phosphorylation and subsequent degradation of I κ B α , and prevented nuclear translocation of p65 [Kundu and Surh, 2007]. It has been reported that EGCG induced apoptosis in human prostate carcinoma LNCaP cells by negative regulation of NF- κ B activity, thereby decreasing the expression of the proapoptotic protein Bcl-2 [Hastak et al., 2003]. Study from our lab has shown that treatment of EGCG dose and time-dependently increased I κ B level, and inhibited NF- κ B nuclear translocation in A431 epidermoid carcinoma cells [Gupta et al., 2004]. It was shown that UVB irradiation-induced NF- κ B activation in NHEK was associated with increased I κ B phosphorylation and degradation and EGCG was shown to block NF- κ B activation and nuclear translocation [Afaq et al., 2003b]. Topical application of GTP to UV-B-irradiated SKH-1 hairless skin decreased phosphorylation and degradation of I κ B and the subsequent activation of NF- κ B [(Afaq et al., 2003a). It has also been reported that pretreatment of NHBE cells with EGCG suppressed cigarette smoke condensate (CSC)-induced phosphorylation of I κ B α and activation and nuclear translocation of NF- κ B/p65. NHBE cells transfected with a luciferase reporter plasmid containing an NF- κ B-inducible promoter sequence showed an increased reporter activity after CSC exposure that was specifically inhibited by EGCG pretreatment [Syed et al., 2007].

Inhibition of Mitogen-Activated Protein (MAP) Kinases and Activator Protein-1 (AP-1)

Mitogen-activated protein kinases (MAPKs) are major signaling transduction molecules that play an important role in regulating a variety of cellular responses, including cell proliferation, differentiation, and apoptosis. MAPKs pathways are comprised of a three-tier kinase module in which are MAPK is activated upon phosphorylation by a mitogen-activated protein kinase kinase (MAPKK), which in turn is activated when phosphorylated by a MAPKKK. Mammalian MAPKs mainly consist of three subfamilies; the Jun N-terminal kinases (JNKs), the p38 kinases, and the extracellular signal-related kinases (ERKs). MAPKs can be activated by diverse stimuli including growth factors and cellular/extracellular stresses. Once activated, MAPKs (ERK, JNK, and p38) can activate a variety of transcription factors, including ELK and c-Jun, a component of AP-1, thus leading to changes in the expression of genes that play critical roles in cell proliferation, migration, and apoptosis. It has been shown that treatment of H₂O₂ resulted in phosphorylation of extracellular signal-regulated kinases 1 and 2 (ERK1/2), JNK, and p38 in human epidermal keratinocytes. H₂O₂-induced phosphorylation of ERK1/2, JNK, and p38 was found to be significantly inhibited when these cells were pretreated with EGCG. These findings demonstrate that EGCG has the potential to inhibit oxidative stress-mediated phosphorylation of MAPK signaling pathways [Katiyar et al., 2001]. Recently, it has been reported that EGCG rapidly and substantially hampered UV-B irradiation-induced activation of ASK-1 and phosphorylation

of ERK1/2, JNK, and p38 in dermal fibroblasts. These results demonstrate that EGCG has abilities to hamper UV-B-induced collagenolytic MMP production via interfering with the MAPK-responsive pathways [Bae et al., 2008]. A study from our lab has reported that topically application of GTP decreased UV-B-induced phosphorylation of ERK1/2 and JNK and p38 proteins in SKH-1 mice [Afaq et al., 2003a]. It has been shown that tea polyphenols, EGCG, and theaflavins can effectively block arsenite-induced apoptosis of JB6 cells and inhibited arsenite-induced AP-1 transcription activity and AP-1 DNA binding activity. EGCG and theaflavins also potently inhibited arsenite-induced ERK1/2 activity but not p38 kinase activity [Chen et al., 2000].

Inhibition of Epidermal Growth Factor Receptor (EGFR)-Mediated Pathways

The epidermal growth factor receptor (EGFR) family of receptor tyrosine kinases (TKs) includes four members: EGFR (HER-1), HER-2/neu, HER-3, and HER-4. This family has been shown to be important for proper regulation of many developmental, metabolic, and physiologic processes mediated by EGF, transforming growth factor- α and multiple other ligands. In numerous cancers, including glioblastomas, breast cancer, and non-small-cell lung cancer (NSCLC), there is often a transforming deregulation of EGFR family kinase activity. EGFR is also expressed by various epithelial tumors; high levels of EGFR expression in these cells indicate a poor prognosis or a late stage of disease. In this context, EGFR has become a novel molecular target of cancer therapies [Yarden and Sliwkowski, 2001]. EGCG was found to inhibit the activation of the EGFR, HER2, and multiple downstream signaling pathways in colon cancer cell lines [Shimizu et al., 2005]. It was shown that GTP resulted in substantial reduction in the levels of IGF-I and significant increase in the levels of IGFBP-3 in TRAMP mice [Adhami et al., 2004]. It has also been shown that EGCG inhibits the binding of EGF to the EGFR and the subsequent dimerization and activation of the EGFR by altering membrane organization [Adachi et al., 2007]. It has been reported that EGCG binds to a specific metastasis associated 67-kDa laminin receptor that is expressed on a variety of tumor cells. It was shown using a subtraction cloning strategy involving cDNA libraries constructed from cells treated or untreated with all trans-retinoic acid that the anticancer action of EGCG is mediated by LR and it allows EGCG to bind to the cell surface [Tachibana et al., 2004]. EGCG has also been reported to suppress gene expression of EGFR in rat-activated hepatic stellate cells *in vitro* mediated by reducing the trans-activation activity of Egr-1 [Fu et al., 2006].

Inhibition of Insulin-like Growth Factor (IGF)-I Mediated Signal Transduction Pathway

The IGF system involves complex regulatory networks that operate at the whole organism, cellular and subcellular levels. Key molecules involved are the

ligands IGF1 and IGF2, the type 1 and type 2 IGF receptors (IGF1R and IGF2R, respectively), the IGF-binding proteins (IGFBPs), and the proteins involved in intracellular signalling distal to IGF1R, which include members of the insulin-receptor substrate (IRS) family, AKT, target of rapamycin (TOR), and S6 kinase. A final important determinant of IGF activity is through a family of at least six distinct IGFBPs that modulate bioavailability of IGFs in the circulation. Low circulating levels of IGFBPs favor an increased IGF mitogenic activity. IGF could be an appropriate target for cancer chemoprevention as increasing levels of IGF-I are associated with an increased risk of cancer [Adhami et al., 2006]. We have earlier reported that 0.1% GTP (wt/vol) provided as the sole source of drinking fluid to TRAMP mice from 8 to 32 weeks of age resulted in significant inhibition in serum IGF-1 and restoration of IGFBP-3 levels in the prostate compared with water-fed TRAMP mice [Gupta et al., 2001]. EGCG has been reported to abrogate anchorage-independent growth induced by IGF-IR overexpression and also prevented human breast and cervical cancer cell phenotype expression through inhibition of IGF-IR downstream signaling [Li et al., 2007]. We have reported that GTP resulted in substantial reduction in the levels of IGF-I and significant increase in the levels of IGFBP-3 in TRAMP mice [Adhami et al., 2004]. Recently, we have also shown that combination treatment with GTP and celecoxib resulted in enhanced tumor growth inhibition by lowering of IGF-1 levels and increase in circulating levels of serum IGFBP-3 compared with results of single-agent treatment [Adhami et al., 2007].

Induction of Apoptosis and Cell-Cycle Arrest

Apoptosis is a preferential way of elimination of damaged cells. Apoptosis is characterized by a set of morphologic changes including chromatin condensation, nuclear fragmentation, membrane blebbing, and cell shrinkage. Generally, the growth rates of preneoplastic or neoplastic cells outpace that of normal cells because of malfunctioning or dysregulation of their cell growth and cell death machineries. Therefore, induction of apoptosis or cell-cycle arrest by dietary chemopreventive compounds can be an excellent approach to inhibit the promotion and progression of carcinogenesis and to remove genetically damaged, preinitiated, or neoplastic cells from the body [Khan et al., 2007]. For the very first time, we have shown that EGCG induces apoptosis and cell-cycle arrest in many cancer cells without affecting normal cells [Ahmad et al., 1997]. This observation has been verified by many subsequent studies in several cell types including lung, colon, pancreas, skin, and prostate [Khan et al., 2006]. We have earlier reported that in EGCG-treated LNCaP cells, p53 protein was stabilized, and EGCG inhibited NF- κ B transcription activity. The balance between pro- and antiapoptotic Bcl-2 family proteins favored apoptosis, and LNCaP cells were arrested in the G0/G1 phase [Hastak et al., 2003]. EGCG induced expression of p21 and p27, inhibited the activity of CDK2 and CDK4, and caused Rb hypophosphorylation. EGCG increased the expression of p16,

p18, p21, and p53, which are associated with negative regulation of cell-cycle progression in prostate cancer cells [Gupta et al., 2003; 2000]. In the A/J mouse model, green tea in drinking fluid increased the apoptosis index in lung adenoma in chemically induced lung tumors [Liao et al., 2004].

Inhibition of Urokinase-Plasminogen Activator (uPA)

The urokinase plasminogen activator (uPA) system is believed to play a key role in tissue degradation, cell migration, angiogenesis, cancer invasion, and metastasis. uPA is a member of the serine protease family and is strongly implicated as a promoter of tumor progression in various human malignancies. It is synthesized and secreted as a pro-enzyme, whose activation is markedly accelerated upon binding with high affinity to specific membrane-bound or soluble cell surface uPA receptors (uPAR). Binding to uPAR, uPA efficiently converts the inactive zymogen, plasminogen, into the active serine protease, plasmin, which then directly or indirectly cleaves extracellular matrix components including laminin, fibronectin, fibrin, vitronectin, and collagen. Plasmin can activate latent elastase and MMPs, potent enzymes that can also digest a variety of ECM components. uPAR plays a key role not only in localizing uPA activity but also in mediating various signaling events essential for the differentiation and migration of cells within the tumor environment [Duffy et al., 2004]. EGCG has been reported to inhibit the activity of uPA. With the use of molecular modeling, it was shown that EGCG binds to urokinase, blocking His 57 and Ser 195 of the urokinase catalytic triad and extending toward Arg 35 from a positively charged loop of urokinase [Jankun et al., 1997]. We have reported that GTP infusion to TRAMP mice resulted in marked inhibition of uPA in the dorso-lateral prostate [Adhami et al., 2004]. Recently, we have shown that EGCG sensitizes TRAIL-resistant LNCaP cells to TRAIL-mediated apoptosis in part through inhibition in the protein expression of VEGF, uPA, and angiotensin 1 and 2 in prostate cancer cells [Siddiqui et al., 2008]. EGCG was found to decrease the expressions of MMP-2, MMP-9, and uPA in a concentration-dependent manner in human oral cancer cell line [Ho et al., 2007]. It has also been reported that GTP inhibited constitutively active transcription factors AP-1 and NF- κ B, which further suppressed secretion of uPA from breast cancer cells [Silvova et al., 2005].

INHIBITION OF PROTEASOME ACTIVITIES

The proteasome is a ubiquitous enzyme complex that plays a critical role in the degradation of many proteins involved in cell-cycle regulation, apoptosis, and angiogenesis. Since these pathways are fundamental for cell survival and proliferation, particularly in cancer cells, the inhibition of proteasome is an attractive potential anticancer therapy. The ubiquitin/proteasome pathway is the main nonlysosomal route for degradation and is responsible for the

turnover of > 80% of cellular proteins. This pathway involves the conjugation of multiple ubiquitin moieties to a substrate followed by the downstream degradation of the tagged protein by a multicatalytic proteasome complex [Montagut et al., 2006]. EGCG analogs with acetyl protected -OH groups were reported to be much more potent than natural EGCG in inhibiting the proteasome in cultured tumor cells. Consistently, these protected analogs showed much higher potency than EGCG to inhibit proliferation and transforming activity and to induce apoptosis in human leukemic, prostate, breast, and simian virus 40-transformed cells [Kuhn et al., 2005]. EGCG and ECG, but not EGC and EC, potently inhibited the chymotryptic activity of the 20s proteasome both in cell-free systems and in tumor cell lines at the concentrations found in the serum of green tea drinkers. This inhibition of the proteasome by EGCG in several tumor and transformed cell lines results in the accumulation of two natural proteasome substrates, p27(Kip1) and $\text{I}\kappa\text{B}\alpha$, followed by growth arrest in the G(1) phase of the cell cycle [Nam et al., 2001].

CONCLUSION AND FUTURE PROSPECTS

Green tea is an extremely popular beverage worldwide. Derivatives of green tea, particularly its major polyphenolic catechin, EGCG, have been proposed to have anticarcinogenic properties based on preclinical, observational, and clinical trial data. Furthermore, subsequent studies have shown that green tea can also prevent lifestyle-related diseases and that it has life-prolonging effects. Additional studies are required to determine how the active ingredients in green tea interact with environmental and genetic factors, as well as to identify mechanisms effective against given cancer types, so that these mechanisms can be fine-tuned or supplemented to increase the desired effects. The elucidation of the molecular mechanisms/targets associated with the antitumor effects exhibited by tea catechins will contribute greatly to the development and design of chemopreventive agents and more effective cancer chemoprevention trials.

ACKNOWLEDGMENT

The original work from the author's (HM) laboratory outlined in this review was supported by U.S. Public Health Service Grants RO1 CA 78809, RO1 CA 101039, RO1 CA 120451, and P50 DK065303.

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8 Flavonols: Metabolism, Bioavailability, and Health Impacts

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INTRODUCTION

Flavonols are a subclass of flavonoids, which are distributed ubiquitously in the plant kingdom. The most common flavonols are kaempferol, quercetin, isorhamnetin, and myricetin (Fig. 8.1). They are frequently found as *O*-glycosides, in which glycosidation occurs mainly at the 3-position of the C-ring, but substitution can also occur at the 5', 7', 4', 3', and 5'-positions [Crozier et al., 2006]. Many types of glycosides are derived from flavonol aglycones because various sugar groups can conjugate to the hydroxyl groups of flavonols at different positions. Flavonol glycosides are often found in commonly consumed plants. Figure 8.1 shows typical examples of quercetin glycosides. In 1936, Szent-Györgyi found that rutin (quercetin 3-*O*- β -rutinoside) had

vitamin properties and termed this flavonol “vitamin P” [Rusznayak and Szent-Györgyi, 1936]. Studies investigating deficiencies of dietary flavonols in humans were not reported. Dietary flavonols were believed to be little absorbed in the body due to their poor bioavailability. Nutritional scientists, therefore, excluded vitamin P from the category of vitamins at that time. In the 1970s, quercetin and other plant flavonols were suspected to be potential carcinogens because these polyphenolic compounds were found to possess mutagenic activity [Bjeldans and Chang, 1977; Sugimura et al., 1977]. A diet containing quercetin did not show a carcinogenic effect in animals. Recent studies strongly suggest that quercetin acts as a potential anticarcinogen in animal models of carcinogenesis [Murakami et al., 2008]. Epidemiological studies revealed that daily intake of flavonols from food is closely related to the prevention of atherosclerosis and other vascular diseases [Hertog et al., 1994]. The protective role of flavonols against oxidative damage in the central nervous system is thought to help prevent neurodegenerative diseases [Youdin et al., 2004]. Excessive intake of these polyphenolic compounds seems to exert an adverse effect on the body [Galati and O’Brien, 2004]. Studies on the bioavailability of plant flavonols, including intestinal absorption, metabolic conversion, and transport to target sites, are essential. Plant flavonols are recognized as xenobiotics by the body; they are subject to metabolic conversion, resulting in nontoxic compounds due to phase II enzymes [Spencer et al., 2004; Walle, 2004]. The mucosa of the small intestine and large intestine is the site for metabolic conversion of flavonols, as well as their absorption into the body [Scalbert and Williamson, 2000], that is, dietary flavonols are mostly converted into their conjugated metabolites before influx into the circulation. This conversion may be an effective tool for the attenuation of their toxicity and the regulation of their physiological function because some metabolites possess various biological activities [Williamson et al., 2005]. In this chapter, we focus on quercetin and its glycosides as typical flavonols originating from vegetables.

ANTIOXIDANT AND PRO-OXIDANT ACTIVITY

Flavonols are characterized by the substitution of a hydroxyl group at the 3-position and a double bond between the 2- and 3-position in diphenylpropane. These two structural characteristics contribute to the enhancement of the activity of flavonoids to scavenge free radicals. Flavonols are recognized as a subclass with strong antioxidant activity among flavonoids [Bors et al., 1990]. The essential part of flavonol structure for exerting such activity is the *o*-dihydroxyl structure at the 3'- and 4'-position of the B-ring [Bors, 1990; Terao and Piskula, 1997]. Hydroxyl groups at the 3'- and 4'-position scavenge free radicals by donation of hydrogen or an electron. Quercetin and myricetin can exert strong antioxidant activity because they possess an *o*-dihydroxyl structure, so-called

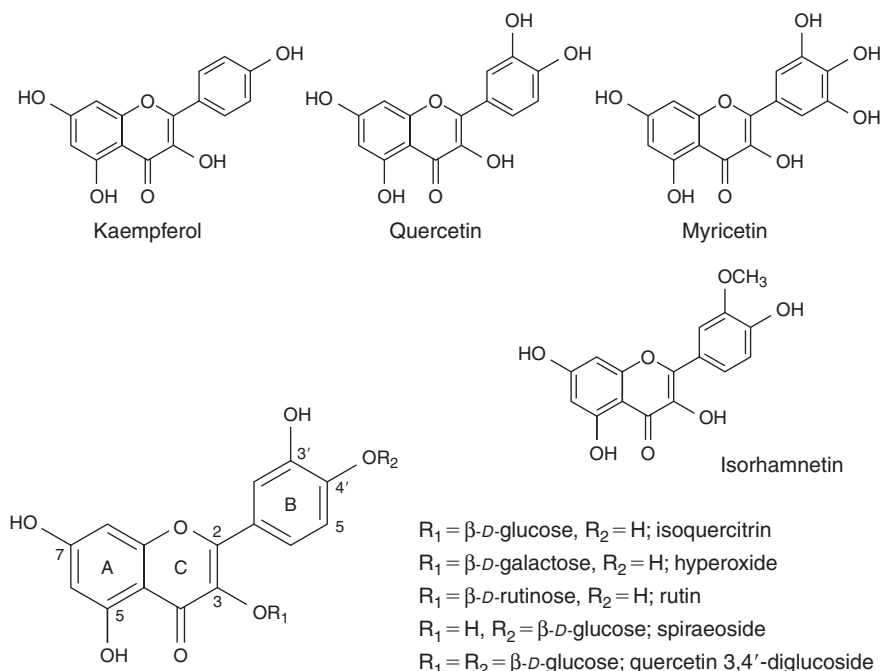


Figure 8.1 Structures of main flavonol aglycones and quercetin glycosides present in plant foods.

catechol and pyrogallol, respectively. Kaempferol is a weak antioxidant because of its monophenol structure in the B-ring [Terao and Piskula, 1997].

Figure 8.2 illustrates the potential reaction pathways for catechol. One catechol can scavenge two peroxy radicals, resulting in the formation of an *o*-semiquinone radical when receiving the first electron, and the formation of an *o*-quinone after receiving the second electron. Then, the *o*-dihydroxyl moiety possesses pro-oxidant properties [Gouphua et al., 1997] supported by the formation of an *o*-semiquinone radical that can react with an oxygen molecule to generate $\text{O}_2^{\bullet-}$, and also convert $\text{O}_2^{\bullet-}$ to H_2O_2 [Metodiewa et al., 1999; Kawanishi et al., 2005]. These reactive oxygen species (ROS) can act as both cellular redox signals for the expression of antioxidant enzymes and inducers of oxidative damage to cell components. Then, catechol/pyrogallol can yield antioxidant and pro-oxidant activity by scavenging or generating ROS depending on the environment of the reaction, and the relative concentration of other antioxidant or pro-oxidant molecules. Monophenol moieties in the B-ring do not show such a pro-oxidant effect. Loss of the *o*-dihydroxyl structure by conjugation of the hydroxyl group seems to help avoid the unfavorable pro-oxidant effect of flavonols on health. Physiologically, conjugation of the hydroxyl group in catechol/pyrogallol happens during intestinal absorption of flavonols by phase II enzymes.

ABSORPTION AND METABOLIC CONVERSION IN THE DIGESTIVE SYSTEM

Human saliva can hydrolyze glucose-bound quercetin glycosides, resulting in active aglycone within a few minutes [Walle et al., 2005]. This hydrolytic activity is suggested to be derived from bacterial colonies and epithelial cells in the mouth. Large interindividual variability was found in the hydrolytic activity of the oral cavity. Contribution of this activity is not obviously referred to the physiological function of dietary flavonols. Quercetin monoglucosides such as isoquercitrin (quercetin 3-*O*- β -D-glucoside) and spiraeoside (quercetin 4'- β -D-glucoside) are efficiently absorbed by the small intestine (Fig. 8.3) [Murota and Terao, 2003], that is, they are incorporated into the epithelial cells of the small intestine through independent pathways [Day et al., 2000a]. One is a sodium-dependent glucose transporter-1 (SGLT-1)-mediated cellular transport pathway in which glucosides are converted into aglycones by the activity of cellular β -glucosidase. In the other pathway, glucosides are first hydrolyzed by lactose-phlorizin hydrolase (LPH) on the surface of brush-border membranes, and the resulting lipophilic aglycone is readily transported into cells by passive absorption. LPH and cellular β -glucosidase prefer the glucoside bond at the 4'-position to that at the 3-position [Walle et al., 2000; Ioku et al., 1998]. Spiraeoside may therefore be more favorable than isoquercitrin in intestinal absorption.

Quercetin and other flavonols are subject to metabolic conversion during the absorption process in the small intestine. Phase II enzymes including uridine 5'-diphosphate glucuronosyl transferase (UGT), phenol-sulfotransferase (PST),

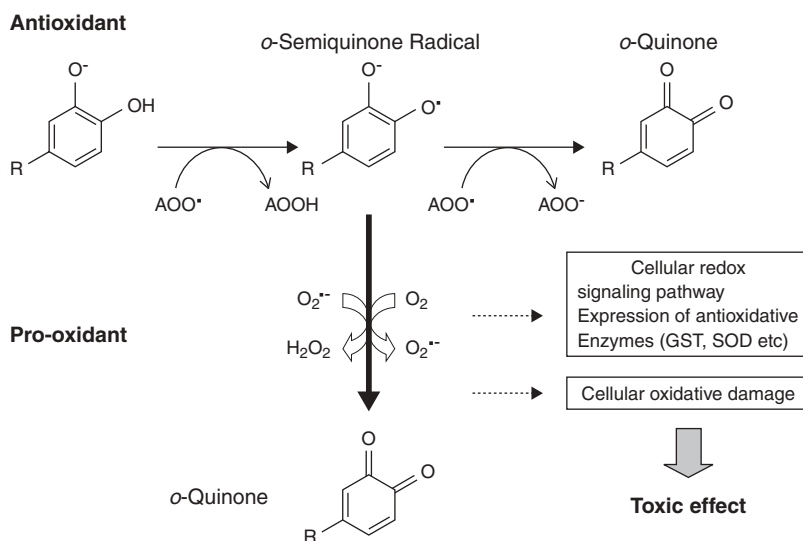


Figure 8.2 Free-radical scavenging and ROS-generating pathway of catechol-type flavonols (GST: glutathione-*S*-transferase; SOD: superoxidie dismutase).

and catechol-*O*-methyltransferase (COMT) are distributed in intestinal epithelial cells (Fig. 8.4) [Murota and Terao, 2003]. Quercetin aglycone is inevitably converted to its conjugated metabolites with or without *O*-methylation and then transferred to the liver through the portal vein. Some conjugated metabolites are likely to be transferred into the systemic circulation via lymph [Murota and Terao, 2005]. Most conjugated metabolites do not enter the body but return to the intestinal tract by the action of multidrug resistance-associated protein-2 (MRP-2).

Quercetin glycosides other than monoglucosides (e.g., rutin, hyperoside) reach the large intestine without absorption (Fig. 8.3). Quercetin glycosides from foods are mostly excreted into the feces without absorption. They are subject to hydrolysis by enterobacteria, resulting in their aglycone. Anaerobic bacteria such as *Bacteroides distasonis*, *Bacteroides uniforms*, and *Bacteroides ovatus* are known to possess β -glucosidase activity [Bokkenheuse et al., 1987]. Enterobacteria also decompose aglycone to produce its ring scission products such as 3,4-dihydroxyphenylacetic acid, *m*-hydroxyphenylacetic acid, and *m*-homovanilic acid [Terao, 1999]. These products can be absorbed into the body by the monocarboxylic acid transporter and/or paracellular diffusion pathway [Konishi, 2005]. Aglycone is partly absorbed by large intestinal

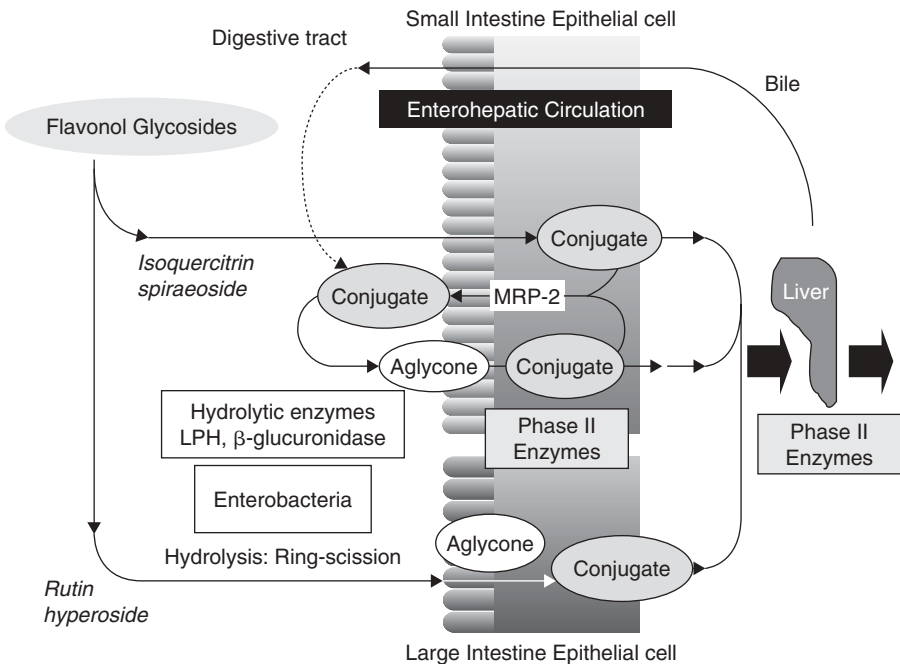
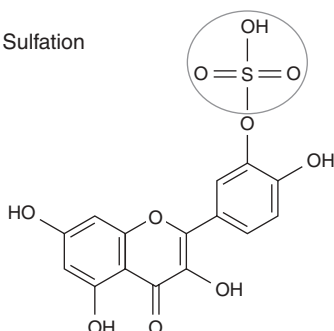


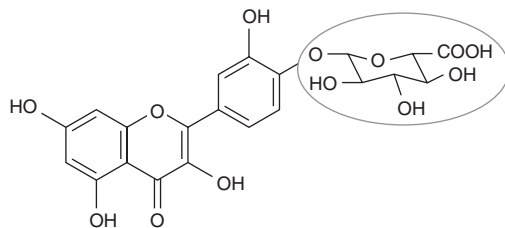
Figure 8.3 Pathway of absorption and metabolism of flavonols in the digestive system (MRP-2: multidrug resistance-associated protein-2; LPH: lactose phlorizin hydrolaze).

Phenol sulfotransferase (PST)

Sulfation

**Uridine 5'-diphosphate glucuronosyl transferase (UGT)**

Glucuronidation

**Catechol-O-methyl transferase (COMT)**

Methylation

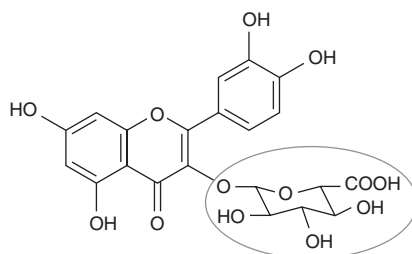
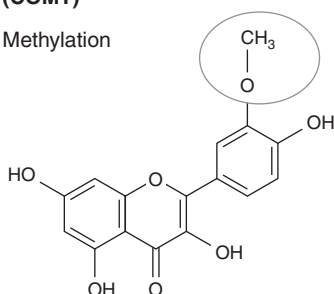


Figure 8.4 Metabolic conversion of quercetin in human epithelial cells of the small intestine.

mucosa and likely to be transferred into the circulation after metabolic conversion similar to that seen in the small intestine.

Conjugated metabolites delivered to the liver are metabolized by hepatic phase II enzymes. The latter were reported to convert conjugated quercetin metabolites to a wide variety of their conjugates with and without deconjugation [Day et al., 1998; van de Woude et al., 2004]. Conjugated metabolites are released into the circulation after secondary metabolism in the liver. Considerable amounts of conjugated metabolites also simultaneously enter bile and return to the intestinal tract together with bile components. This enterohepatic circulation should be considered if the overall bioavailability of flavonols is discussed.

DISTRIBUTION OF CONJUGATED METABOLITES IN THE CIRCULATION AND THEIR ACCUMULATION IN ORGANS

Day et al. [2001] detected >20 species of metabolites, including quercetin 3-*O*- β -D-glucuronide (Q3GA), quercetin 3'-*O*- β -D-glucuronide (Q3'GA), quercetin

4'-*O*- β -D-glucuronide (Q4'GA), quercetin 3'-*O*- β -sulphate (Q3'S), quercetin 3'-*O*-methyl 4'-*O*- β -D-glucuronide, and quercetin 3'-*O*-methyl 3'-*O*- β -D-glucuronide in human plasma fractions, but aglycone was not detected. These metabolites were found in human urine after the intake of flavonol-rich foods [Mullen et al., 2004; Hong and Mitchell, 2005]. Quercetin metabolites are suggested to be located in the bloodstream in an albumin-bound form [McAnlis et al., 1999]. Quercetin aglycone is tightly bound to plasma albumin by noncovalent bonds [Papadopoulou et al., 2005]. It was reported that the binding strength of its conjugated metabolites to albumin is much lower than that of aglycone [Dufour and Dangles, 2005]. This implies that conjugated metabolites can be readily delivered to tissues by release from the albumin fraction.

In human plasma, quercetin metabolites transiently increased at $\sim 1 \mu\text{M}$ after the intake of a flavonol-rich diet [Hollman et al., 1995], after which concentration gradually decreased to nearly zero in $< 8 \text{ h}$ [Manach et al., 1997]. Continuous ingestion of flavonol-rich foods may maintain a low level of quercetin metabolites in plasma, but this baseline level may be greatly influenced by individual differences [Moon et al., 2000].

Whether or not dietary quercetin and other flavonols can accumulate in internal organs is controversial. It is unclear if they accumulate in the human body, but dietary quercetin was found to be distributed in each organ in experimental animals [de Boer et al., 2005]. In rats fed 0.1% quercetin for 11 weeks, the highest accumulation was in the lungs. Low amounts of quercetin metabolites were detected in the brain. This indicates that quercetin metabolites can access the central nervous system by passing the blood-brain barrier, although the mechanism of this passage is incompletely understood.

POTENTIAL HEALTH EFFECTS OF CONJUGATED METABOLITES AT TARGET SITES

Whether or not the intake of plant flavonols increases the antioxidant activity of human blood plasma is interesting. It was found that Q3GA (one of the major quercetin metabolites detected in human plasma) possesses substantial activity for scavenging free radicals and inhibits *in vitro* low-density lipoprotein (LDL) oxidation at higher concentration [Moon et al., 2001]. Various small-molecule antioxidants, including uric acid (160–450 μM), ascorbic acid (30–150 μM), bilirubin (5–20 μM), α -tocopherol (15–40 μM), and carotenoids (1.0–2.0 μM) contribute to the antioxidant activity of plasma [Wayner et al., 1987; Frei et al., 1988]. Plasma albumin is known to be an effective scavenger of free radicals and to contribute to plasma antioxidant activity [Roche et al., 2008]. It is therefore unlikely that albumin-bound flavonol metabolites affect plasma antioxidant activity if flavonols are ingested from an ordinary diet. We recently carried out a study in which cooked onion was consumed by human volunteers [Murota et al., 2007]. Onion consumption failed to enhance antioxidant activity of the albumin fraction against LDL oxidation, although about 80% of quercetin metabolites

were in this fraction. Other major metabolites such as Q4'GA and Q3'S in human plasma seem to be devoid of antioxidant and pro-oxidant activity because they lack the catechol structure.

These metabolites are known to possess specific biological activities other than antioxidant activity in vitro (Table 8.1) [Yoshizumi et al., 2002; de Pascual-Teresa et al., 2004; Day et al., 2000b; O'leary et al., 2004; Mochizuki et al., 2004; Kim et al., 2007; Kawai et al., 2008; Shiba et al., 2008]. Steffen et al. [2008] recently demonstrated that isorhamnetin and its glucuronide conjugates, not quercetin aglycone, inhibit the activity of NADPH-oxidase of endothelial cells. Quercetin metabolites are likely to exert their physiological function at the target sites where they concentrate. Shimoi et al. [2005] demonstrated that conjugated metabolites of luteolin, a flavone-type flavonoid, were converted into their aglycone by the enhanced activity of plasma β -glucuronidase during inflammation when luteolin was orally administered to lipopolysaccharide-injected mice. This phenomenon implies that conjugated metabolites circulate as nontoxic forms in the bloodstream but can be converted to active aglycones to exert their function immediately. This effect was clarified using newly synthesized monoclonal antibody: Q3GA accumulated in atherosclerotic lesions but not in normal aorta (Fig. 8.5) [Kawai et al., 2008]. This finding indicates that quercetin metabolites translocate to the vascular target selectively when blood

Table 8.1 Biological Activities of Conjugated Quercetin Metabolites

Quercetin 3'-glucuronide (Q3GA)	• Prevention of vascular smooth muscle cell hypertrophy by angiotensin II via effects on JNK and AP-1	Yoshizumi et al., 2002
	• Decreased expression of COX-2 in human lymphocytes	de Pascual-Teresa et al., 2004
	• Increase expression of bone sialoprotein mRNA expression	Kim et al., 2007
	• Inhibition of scavenger receptor mRNA expression in murine macrophages	Kawai et al., 2008
	• Potent inhibition of myeloperoxidase	Shiba et al., 2008
Quercetin 3'-glucuronide (Q3'GA)	• Potent inhibition of bovine xanthine oxidase	Day et al., 2000b
	• Inhibition of soybean lipoxygenase	Day et al., 2000b
Quercetin 4'-glucuronide (Q4'GA)	• Potent inhibition of bovine xanthine oxidase	Day et al., 2000b
	• Inhibition of soybean lipoxygenase	Day et al., 2000
Quercetin 3'-sulfate (Q3'S)	• Inhibition of COX-2 mRNA expression in Caco-2 Cell	O'Leary et al., 2004
Quercetin 3-sulfate	• Inhibition of ICAM-1 expression in human aortic endothelial cells	Mochizuki et al., 2004
Isorhamnetin glucuronide	• Inhibition of endothelial NADPH oxidase	Steffen et al., 2008

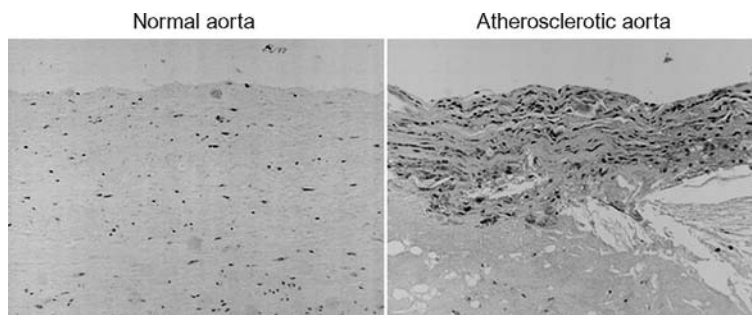


Figure 8.5 Detection of quercetin metabolites in human atherosclerotic aorta using Q3GA-specific monoclonal antibody mAb14A2. (Data from Kawai et al. [2008].)

vessels are injured by oxidation. It can be hypothesized that conjugated metabolites may exert specific activity by themselves or by conversion into their active aglycone under intolerable oxidative stress, for example, accelerated inflammation.

CONCLUSION

It is generally thought that plant flavonols have beneficial effects on human health by enhancing the antioxidant defense system. In recent years, their plasma metabolites were also found to possess various other biological activities, but excessive intake of plant flavonols may induce an adverse effect by generating ROS. Metabolic conversion of flavonols to their sulfate/glucuronide conjugates in the digestive system eliminates their toxic effects and, more importantly, regulates their biological activities. These conjugates may concentrate at the target site and exert their functions efficiently under oxidative stress.

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9 Flavonols: Biochemistry Behind Cardiovascular Effects

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INTRODUCTION

Flavonoids constitute a large class of polyphenols found in fruits and vegetables that share a common skeleton of phenylchromane. This basic structure allows a large number of substitution patterns leading to several subclasses of flavonoids, such as flavonols, flavones, flavanones, flavanols, anthocyanidins, isoflavones, dihydroflavonols, and chalcones. Among the diverse flavonoid subclasses, flavonols (especially quercetin) and flavanols (catechins) are the most abundant in our food. Flavonols are present in foods as diverse glycosides, whereas flavanols are usually found as aglycones.

Flavonols are present in considerable amounts in our normal diet and show a wide range of biological activities. Therefore, they are candidates to explain the advantageous effects of fruits and vegetables on cardiovascular health. Formerly considered vitamins, the term “vitamin P,” coined for their effect on capillary Permeability [Rusznayak and Szent-Györgyi, 1936] was discontinued in the 1950s [Joint Committee on Nomenclature of the American Society of Biological Chemists, 1950]. Some specific flavonols (e.g., quercetin) or flavonoid mixtures or extracts are commercialized as dietary supplements and recommended at doses that exceed by far the common daily intake. The health claims of these supplements are not clearly supported by clinical trials. As a rebound effect, for many within the academic community, the use of flavonoids, among other natural antioxidants used at high doses, have a certain whiff of the nonscientific. Within academic medicine they are only used as “venotonic” or “phlebotropic” drugs with limited results on several venous diseases [Lyseng-Williamson and Perry, 2003]. However, a glance at their pharmacology reveals that these compounds show a much wider therapeutic potential.

In this chapter, we will review the available evidence supporting a beneficial role of flavonols on cardiovascular disease and the potential molecular targets involved.

ARE FLAVONOLS REALLY EFFECTIVE IN CARDIOVASCULAR DISEASE?

Epidemiological Evidence

The interest in dietary flavonoids has grown in the last 15 years after the publication of the study of Hertog et al. [1993] showing an inverse correlation between dietary consumption of flavonols and flavones and reduced incidence and mortality from ischemic heart disease. Most prospective epidemiological studies carried out have found a similar relationship regarding ischemic heart disease while a possible inverse relationship with stroke is less clear [Hertog et al., 1997; Knekt et al., 1996; Rimm et al., 1996; Yochum et al., 1999; Hirvonen et al., 2001; Arai et al., 2000; Mursu et al., 2008]. The meta-analysis

of seven prospective cohort studies concluded that the individuals in the top third of dietary flavonol intake are associated with a reduced risk of mortality from coronary heart disease as compared with those in the bottom third, after adjustment for known risk factors and other dietary components [Huxley and Neil, 2003].

Intervention Studies

No intervention studies published so far have analyzed the effects of flavonols or flavonol-rich food on cardiovascular morbidity or mortality, which would require a large number of patients followed for several years. However, the above-mentioned epidemiological studies and the basic research has stimulated several intervention trials analyzing the short-term effects on selected cardiovascular risk factors, mainly hypertension and endothelial function. Endothelial dysfunction is an early manifestation common to several cardiovascular risk factors such as arterial hypertension, arteriosclerosis, smoking, diabetes, or aging [Endemann and Schiffrin, 2004; Widlansky et al., 2003]. The presence of endothelial dysfunction has prognostic value independently of the traditional cardiovascular risk factors. Recently, it has been reported that high doses of quercetin reduced blood pressure in patients with stage 1 hypertension [Edwards et al., 2007]. However, high doses of quercetin have no effect on blood pressure or other cardiovascular risk factors in normotensive healthy individuals [Conquer et al., 1998]. A number of studies have analyzed the effects of flavonoid-rich food and beverages such as cocoa, tea, or fruit juices. Consumption of flavanol-rich cocoa was found to lower blood pressure and improve endothelial function in short-term human intervention studies [Taubert et al., 2003; Grassi et al. 2005; Fraga et al. 2005]. A recent study has also shown reduction in blood pressure and improvement of endothelial function with low doses of dark chocolate in untreated upper-range prehypertension or stage 1 hypertension followed for 18 weeks [Taubert et al., 2007]. Another double-blind, crossover study conducted in 12 hypertensive patients who received alternately high-flavonoid sweetie juice and low-flavonoid sweetie juice for 5 weeks showed that the flavonoid-rich juice significantly reduced blood pressure [Reshef et al, 2005]. These results, interesting from a nutritional point of view, have an important limitation because the effects, which are normally attributed to the flavonoids present, could be due to any of the several hundred other substances present in these food and beverages or due to interactions among them.

Animal Studies

Studies from several laboratories including ours have revealed that quercetin is able to prevent or revert hypertension and endothelial dysfunction, and we believe that this is a fundamental mechanism involved in the protective effects of flavonoids on cardiovascular health. Oral administration of quercetin (5 or

10 mg/kg/day) prevents the development of hypertension or produces a gradual decrease in blood pressure in various experimental models in rats, such as genetic hypertension in spontaneously hypertension rats (SHRs) [Duarte et al., 2001; Sanchez et al., 2006], L-NAME-induced hypertension [Duarte et al., 2002], hypertension induced by the administration of mineralcorticoids plus NaCl (DOCA-salt) [Galisteo et al., 2004], hypertension induced by unilateral nephrectomy and stenosis of the contralateral renal artery [Goldblatt model; García-Saura et al., 2005], genetic salt-sensitive rats (Dahl rats) [Aoi et al., 2004], high-fat high-sucrose diet-induced hypertension [Yamamoto and Oue, 2006], and in rats with aortic constriction [Jalili et al., 2006]. Therefore, regardless of the status of the renin-angiotensin system, volume expansion, NO, renal injury, or oxidative stress, quercetin produced consistent antihypertensive effects *in vivo*. These antihypertensive effects are accompanied by a reduction of associated end-organ damage: cardiac hypertrophy, kidney histological alterations and proteinuria, vascular remodelling, and endothelial dysfunction, as well as a decrease in the markers of oxidative stress in plasma, liver, and urine. The effects on endothelial dysfunction has been recently reviewed [Perez-Vizcaino et al., 2006]. In a recent puzzling report, Carlstrom et al. [2007] observed that when quercetin is added to the diet, it did not prevent cardiovascular complications in SHRs while it was effective when given orally by gavage. In principle, this could not be attributed to different bioavailability since the levels of quercetin metabolites were higher in the former. In contrast, in another study by the same group, quercetin-supplemented diets lowered blood pressure and attenuated cardiac hypertrophy in rats with aortic constriction [Jalili et al., 2006].

Consumption of low doses of quercetin reduced the progression of atherosclerosis in apolipoprotein E-deficient mice [Hayek et al., 1997]. The reduction in the atherosclerotic lesion area was not associated with changes in plasma low-density or high-density lipoprotein (LDL or HDL) cholesterol levels in this study but with a reduced susceptibility to oxidation (induced by different modes such as copper ions, free-radical generator, or macrophages) of LDL. Quercetin also efficiently protected hypercholesterolemic hamsters against aortic fatty streak accumulation, an early manifestation of the atherosclerotic process [Auger et al., 2005]. In addition, quercetin attenuated the hyperlipidemia and the lipid peroxidation in the aorta in high-cholesterol-fed rabbits [Kamada et al., 2005].

ARE ANTIOXIDANTS USEFUL IN CARDIOVASCULAR DISEASE?

As discussed below, the biological effects of flavonoids include the interaction with many biochemical targets in addition to their effects on the antioxidant status. However, as the cardiovascular effects of flavonoids are commonly attributed to their antioxidant effects, it seems pertinent to address herein the

available evidence of the role of oxidative stress and the effectiveness of antioxidants in cardiovascular disease.

In the 1980s, when enthusiastic lecturers initiated us into the pathophysiological role of reactive oxygen species (ROS), the scientific community naively took for granted that, in a few years, the so-called antioxidants would be to cardiovascular diseases as antibiotics were to bacterial infections. Some years later, we are still in need of concrete evidence that allow the incorporation of antioxidants as pharmacologically accepted therapies. Nevertheless, the evidence from basic research studies in favor of the role of ROS in diseases such as atherosclerosis, ischemic heart disease, hypertension, heart failure, and diabetes has been continuously growing over the last three decades. Multiple epidemiological studies have suggested that increased intake of dietary antioxidant vitamins lowers the risk of atherosclerosis [Stampfer et al., 1993]. However, the scarce positive results with antioxidants—mainly with vitamin E, β -carotene, vitamin C, and cocktails—for the prevention of coronary heart disease are far outweighed by negative results in prospective controlled large-scale trials [Steinberg and Witztum, 2002]. A recent meta-analysis indicates that treatment with high doses of β -carotene, vitamin A, and vitamin E may even increase mortality while vitamin C and selenium had no effect [Bjelakovic et al., 2007].

On the other hand, it is becoming apparent that truly effective drugs such as statins, angiotensin-converting enzyme (ACE) inhibitors, angiotensin receptor antagonists, and possibly aspirin owe their clinical value, at least partly, to a direct or indirect reduction of oxidative stress. Besides the cholesterol-lowering effect, statins produce several alternative or pleiotropic beneficial effects. Among these pleiotropic effects they share the property of inhibiting LDL oxidation [Gotto, 2003]. ACE inhibitors and angiotensin receptor antagonists inhibit one of the most powerful triggers of oxidative status in cardiovascular disease, that is, angiotensin II [Reckelhoff and Romero, 2003]. Furthermore, these drugs have the advantage over classic antioxidant compounds that they target the signal transduction pathway leading to ROS formation in cells—rather than scavenging ROS already formed—which seems to be a more reasonable approach.

Several arguments have been used to answer why the ROS/antioxidant hypothesis is not translated into daily therapeutics [Heinecke, 2001]. First, ROS and antioxidants exhibit a complex chemistry, and there is an intricate interplay among the various ROS and antioxidant systems to produce or prevent damage and disease. A scavenger reacting with a radical species is converted into a radical itself, albeit less reactive. This radical could, under certain conditions, propagate lipid oxidation by attacking polyunsaturated fatty acids, or oxidize proteins or DNA. Thus, the behavior of a compound as antioxidant or pro-oxidant depends on the reaction conditions and available substrates. Second, claims of wrong antioxidant selection, dosages, and/or timing in clinical trials have been put forward. Notably, most clinical trials have analyzed the effects of antioxidants in established coronary artery disease while their effectiveness in primary prevention is unknown. Still, there is a general belief that some

appropriate antioxidant intervention has the potential to improve prognosis. It should be emphasized herein that each antioxidant shows a differential pharmacological profile, and its effects may go beyond the changes in cellular antioxidant status. This is specially the case of flavonoids.

In summary, the evidence for the preventive effect of flavonols in cardiovascular disease is growing based on mechanistic, animal, epidemiological, and short-term intervention studies. However, we must learn from the lessons with dietary antioxidants, the last word awaits large-scale intervention clinical trials.

MOLECULAR TARGETS

Complex Pharmacology of Flavonoids

Flavonoids constitute a very large class, which includes several thousand compounds as found in nature, plus the hemisynthetic or synthetic derivatives. Second, as a group, they are far from being specific. Flavonoids are regarded as antioxidants. However, the interference of flavonoids with the oxidant species seems to be a tiny part of the whole range of their biological activities. The reader is invited to have a look to the classic review of Middleton and colleagues [2000] showing that there is an impressive number of enzymes whose activity is modulated (mostly inhibited) by flavonoids. Thus, it might be predicted that a huge number of signaling pathways can be affected by flavonoids. Moreover, flavonoids can modify the expression of multiple genes. One may think that, as there are so many different flavonoids, these effects would not be produced by all of them or, at least, in the same range of concentrations. While this is undoubtedly true, it is still clear that within the low micromolar range, a prototypical flavonol such as quercetin inhibits numerous enzymes and scavenges several ROS. Thus, flavonoids should be regarded as “dirty drugs,” or, in other words, they present “pleiotropic effects.” When any given cellular function is modified by quercetin, it is relatively easy to find out a mechanism potentially implicated, but difficult to ascertain whether this proposed target is a true biochemical mechanism involved. This promiscuous behavior of quercetin has been attributed to nonspecific interactions, for example, the formation of aggregates [McGovern and Soichet, 2003]. In recent years it has also become clear that most flavonoids, especially flavonols, are undetected in plasma or are present at extremely low concentrations. Only glucuronosylated and sulfated conjugates of the parent aglycone (or methylated derivatives) are present in plasma following ingestion of quercetin or quercetin glycosides, and the plasma concentrations reached are in the low micromolar range [Kroon et al., 2004]. Unfortunately, the literature on the vascular effects of these metabolites is scarce, and it is presently unknown which of the effects obtained *in vitro* reported for the parent compounds are also pertinent to the metabolites. The biological activities of these metabolites have been only recently started to be

analyzed, which is complicated by the lack of commercial sources of these compounds. This issue is further complicated because the glucuronyl metabolites can be deglucuronidated at the target tissues rendering the original aglycone. There is some evidence that the activity of quercetin glucuronides depends on their deconjugation [Lee-Hilz et al., 2008].

In the following sections we will review some of the targets of flavonols that, in our opinion, are the most relevant to explain their cardiovascular effects.

Antioxidant Activity

The antioxidant activity of flavonols has been reviewed in detail elsewhere. Briefly, flavonols are good antioxidants *in vitro*, sometimes providing better protection than vitamin C or E. They are effective scavengers of superoxide, singlet oxygen, hydroxyl radicals, and peroxyinitite, and they are powerful inhibitors of *in vitro* LDL oxidation. [Naderi et al., 2003; Ozgova et al., 2003; Pollard et al., 2006]. The copper chelating properties of flavonols may also contribute to prevent LDL oxidation. In addition, they prevent cytotoxicity of oxidized LDL. Flavonoids can prevent vitamin E consumption in phospholipid bilayers and can regenerate it once consumed in a similar way to what ascorbic acid does. The hydrophilic properties of flavonoids facilitate their localization at the water phase–lipid bilayer interface and thereby protect lipids and vitamin E from the initial attack by aqueous radicals. By scavenging superoxide anions, quercetin may protect nitric oxide (NO) [Lopez-Lopez et al., 2004]. Interestingly, the glucuronidated metabolites of quercetin retain its antioxidant properties [Moon et al., 2001].

Pro-oxidant Effects

It is often ignored that flavonols can also autoxidize to generate free radicals, behaving as pro-oxidants. At physiological conditions of pH and O₂, quercetin effectively scavenged NO in the low micromolar range [Lopez-Lopez et al., 2004]. This reaction involves the autoxidation of quercetin and the subsequent production of O₂⁻, which rapidly reacts with NO to produce peroxyinitrite. However, quercetin was apparently a more effective scavenger of O₂⁻ than of NO under conditions of increased O₂ [Lopez-Lopez et al., 2004]. In addition, the glucuronidated metabolites lack a pro-oxidant effect at physiological concentrations [Lodi et al., 2008]. Therefore, even when the relevance of the pro-oxidant effect of flavonols *in vivo* may be limited, it should be taken into account when designing and analyzing *in vitro* studies.

NADPH Oxidase

Reduced nicotinamide adenine dinucleotide phosphate (NADPH) oxidase is an enzymatic complex considered the most important source of superoxide

production in the vascular wall [Azumi et al., 1999] as well as in other tissues. Several lines of evidence indicate that NADPH oxidase plays a pathophysiological role in patients with endothelial dysfunction, atherosclerosis, and other cardiovascular risk factors [Guzik et al., 2000]. Quercetin was originally shown to inhibit NADPH oxidase in neutrophils [Tauber et al., 1984]. More recently, it was found that quercetin inhibited Protein kinase C (PKC)-dependent NADPH oxidase activation in platelets [Pignatelli et al., 2006]. In the vessel wall, quercetin inhibited NADPH oxidase activity and the associated spontaneous tone in SHR [Lodi et al., 2006]. The activity of NADPH oxidase is often measured by the production of superoxide stimulated by addition of NADPH. The analysis in intact cells or tissues is commonly criticized because NADPH added exogenously may not reach the intracellular target in the enzyme. However, we have found that quercetin exerts a similar inhibitory effect in intact aorta or in aortic homogenates [Lodi et al., 2006]. Moreover, these methods are also criticized because they do not allow distinguishing between a true inhibitory effect on the enzyme activity and the scavenging of the product of the enzyme, that is, superoxide. Recently, Steffen et al. [2008] have suggested that only *O*-methylated flavonoids do inhibit the enzyme activity while nonmethylated ones behave as superoxide scavengers. They found a structural analogy between methylated compounds and the standard inhibitor of NADPH oxidase apocynin. More intriguingly is the recent report suggesting that even apocynin predominantly acts as a superoxide scavenger rather than an enzyme inhibitor in endothelial cells and vascular smooth muscle cells and should not be used as a NADPH oxidase inhibitor in vascular systems [Heumüller et al., 2008]. Interestingly, besides the direct scavenging or the inhibitory effect on the enzyme, quercetin down-regulated the expression of NADPH oxidase subunit p47^{phox} in SHR [Sanchez et al., 2006] and also prevented the overexpression of this subunit induced by angiotensin II [Sanchez et al., 2007] and endothelin-1 [Romero et al., 2008] in aortic rings. This mechanism of NADPH down-regulation is exerted at lower concentrations of quercetin, and it is also observed to occur with the glucuronosylated metabolites. Therefore, it seems that down-regulation of NADPH oxidase subunit expression is more important than the inhibitory effect on the enzyme or the superoxide scavenging effect.

Nitric Oxide

Nitric Oxide Synthase Expression and Activity; Nitric Oxide Synthase Uncoupling. Inhibitory effects of quercetin on the activity or expression of endothelial NO synthases (eNOS and iNOS) has been reported but only at high concentrations ($< 50 \mu\text{M}$) [Camuesco et al., 2004; Chiesi and Schwaller 1995]. Therefore, direct changes in endothelial NO expression or activity, even when relevant to other polyphenolics, do not appear to be physiologically relevant for quercetin. However, quercetin may restore NOS expression or activity when unpaired by pathological stimuli. In fact, eNOS expression, which is up-regulated in SHR, can be corrected by chronic quercetin administration

(Sanchez et al., 2006). Under conditions of oxidative stress, substrate or cofactor deficiency eNOS is uncoupled, that is, it switches from an NO producing enzyme to a superoxide producing enzyme. Quercetin, by reducing superoxide levels, can prevent the uncoupling of eNOS [Romero et al., 2008].

Nitric Oxide and cGMP Metabolism During the autoxidation process of quercetin in aqueous buffers, superoxide anions are generated and the half-life of NO is reduced [Lopez-Lopez et al., 2004]. However, the rate of NO scavenging by quercetin is lower than that of the physiological NO scavenger hemoglobin. On the other hand, by scavenging superoxide anions or by inhibiting their synthesis (see above), quercetin protects NO from superoxide-driven inactivation and increases its half-life and its biological activity under conditions of high oxidative stress [Lopez-Lopez et al., 2004; Shutenko et al., 1999]. This property plays a key role in the protective effects on endothelial dysfunction. Quercetin and related flavonoids also inhibit several cyclic nucleotide phosphodiesterases (PDEs) [Picq et al., 1989], and thus reduce the degradation of cyclic (guanosine 5-munophosphate (eGMP), the main downstream effector of NO. However, these effects are produced only at concentrations above 10 μ M.

Protein Kinases

Numerous signaling pathways involve the activation of serine-threonine protein kinases in both physiological and pathological conditions. Quercetin and related flavonoids, in the micromolar range, inhibit multiple serine-threonine kinases. Inhibition of protein kinases and the subsequent reduction in target phosphorylation is expected to affect multiple signaling pathways and, hence, numerous cellular functions. The inhibitory effects of quercetin on the activity of PKC and phosphatidylinositol-3 kinase (PI-3 kinase) are well known [Ferriola et al., 1989; Walker et al., 2000]. Quercetin also interacts with members of the family of mitogen-activated protein kinases [MAP kinases, ERK p38 and JNK] [Yoshizumi et al., 2002; Moon et al., 2003; Perez-Vizcaino et al., 2006a]. Akt/PKB, cyclin-dependent kinases (CDKs) and myosin light-chain kinase (MLCK) are also targets of quercetin. Quercetin has been crystallographically observed to specifically form an enzyme-inhibitor complex with PI-3 kinase [Walker et al., 2000]. The glucuronosylated metabolites of quercetin also inhibit the activity of JNK kinase [Yoshizumi et al., 2002]. In contrast to serine/threonine kinases, the inhibitory activity of quercetin on tyrosine kinases is generally weak and can only be observed at high concentrations of the flavonoid [Palmieri et al., 1999; Agullo et al., 1997].

Endothelin-1

A reduction in the gene expression of endothelin-1 (ET-1) has been observed with several polyphenols. The influence of quercetin on ET-1 production by

endothelial cells is controversial. Corder et al. [2001] found no effect of quercetin itself (but of other wine polyphenolics), while Zhao et al. [1999] and Nicholson et al. [2008] reported that quercetin is able to inhibit ET-1 release in human endothelial umbilical vein. The effects of quercetin or other flavonols on ET-1 in vivo has not been analyzed so far.

Ion Channels

The possible modulation of ion channels by flavonoids has been investigated by several groups. In rat tail artery smooth muscle, quercetin has been shown to activate L-type Ca^{2+} channels [Saponara et al., 2002]. This would lead to vascular smooth muscle contraction. However, mechanisms inducing vasodilation are more effective, and quercetin-activated Ca^{2+} entry does not appear to have a functional correlate [Fusi et al., 2003]. Much more attention has been paid on the possible modulation of potassium channels by quercetin and related flavonoids. Potassium channels do not seem to contribute to quercetin-induced relaxation in rat aorta and iliac arteries [Perez-Vizcaino et al., 2002]. However, in rat coronary arteries, quercetin has been shown to increase the current through large conductance calcium-activated potassium channels (BK_{Ca}), which contributes to its relaxant effect [Cogolludo et al., 2007]. Similar results have been reported with (+/-)-naringenin in rat tail arteries [Saponara et al., 2006]. Quercetin also increases the frequency of spontaneous transient outward currents (STOCs), which are carried by BK_{Ca} channels and triggered by Ca^{2+} sparks [Cogolludo et al., 2007]. Thus, quercetin potentiates a fundamental feedback mechanism in vascular function, limiting membrane depolarization and vasoconstriction. Notably, the modulation of BK_{Ca} channels by quercetin could be involved in its higher potency to relax coronary arteries as compared to aorta [Ibarra et al., 2002]. Interestingly, quercetin also increases endothelial NO production through the activation of endothelial BK_{Ca} channels, leading to hyperpolarization and subsequent Ca^{2+} influx [Kuhlmann et al., 2005].

Sirtuins

The sirtuins Sir2 and its mammalian analog SIRT1 have been implicated in the extended life span induced by caloric restriction [Cohen et al., 2004]. Regarding the cardiovascular system, activation of SIRT1 has been shown to promote endothelium-dependent vasodilation [Mattagajasingh et al., 2007] and to down-regulate angiotensin II receptor expression [Miyazaki et al., 2008]. The discovery of the role of sirtuins in oxidative stress and life span has led to a new and fascinating area of research in the field of polyphenols since several polyphenols can activate sirtuins [Howitz et al., 2003]. Resveratrol was the most potent sirtuin activator, but quercetin and other flavonoids were also active. Based on these ideas, it was proposed that sirtuin activators increase life span in several different organisms, mimicking the effects of caloric restriction.

In fact, resveratrol and quercetin extend the life spans of the yeast *Saccharomyces cerevisiae*, the worm *Caenorhabditis elegans*, and the fly *Drosophila melanogaster*, but only if the gene that encodes Sir2 is present in these organisms [Belinha et al., 2007]. In addition, resveratrol has been shown to improve health and survival of mice on a high-calorie diet [Baur et al., 2006].

Adhesion Molecules and Matrix Metalloproteinases

Adhesion molecules and matrix metalloproteinases are key proteins for several processes involved in atherosclerotic plaque formation such as infiltration of inflammatory cells. Furthermore, matrix degradation by matrix metalloproteinases may cause the plaque instability and rupture that leads to the clinical symptoms of atherosclerosis: unstable angina, myocardial infarction, and stroke. Quercetin inhibits the expression of the adhesion molecules such as monocyte chemoattractant protein-1 (MCP-1), intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and E-selectin and also the expression of matrix metalloproteinase-2 and matrix metalloproteinase-9, which are induced by proliferative/inflammatory stimuli (e.g., angiotensin II, epidermal growth factor, or TNF α) [Huang et al., 1999]. The inhibitory effect on ICAM-1 expression occurs through a down-regulation of the JNK/AP-1 pathway [Kobuchi et al., 1999]. In addition, quercetin metabolites inhibited VCAM-1 endothelial cell surface expression at low concentrations [Tribolo et al., 2008].

Other Inflammatory Signaling Pathways

Quercetin has been reported to affect a number of enzymes and transcription factors involved in inflammation at the vascular level. Thus, quercetin inhibits several enzymes involved in cellular signaling through lipid mediators such as phospholipase A₂, phospholipase C, cyclooxygenases (COXs), lipoxygenases (LOXs), and cytochrome P450 oxygenases [Middleton et al., 2000; Sadik et al., 2003]. In addition, it also inhibits the expression of inducible cyclooxygenase (COX-2) and iNOS (as mentioned above), which are up-regulated during inflammation [Garcia-Mediavilla et al., 2007]. These later effects are supposed to be due to the inhibition of the transcription factor NF- κ B. Quercetin may also decrease DNA binding of the transcription factor activator protein-1 (AP-1) [Yoshizumi et al., 2002]. On the other hand, quercetin up-regulates the expression of the anti-inflammatory enzyme heme oxygenase-1 [Chow et al., 2005].

Conclusions

Two fundamental questions regarding flavonols and cardiovascular disease remain open: (1) Are flavonols protective against human cardiovascular disease? and if so, (2) what is/are the molecular target(s) responsible of the

protective effect? Concerning the first question, evidence from animal and clinical studies continues growing to support a beneficial effect on vascular homeostasis preventing the development of cardiovascular complications. Yet, long-term clinical trials have to confirm or refute it. Concerning the second, flavonols can potentially interact with many of the molecular targets known to be involved in the pathophysiology of ischemic heart disease and stroke. Thus, they might act by multiple mechanisms operating simultaneously.

ACKNOWLEDGMENTS

The authors research is funded by a grant from CICYT (SAF AGL2007-66108).

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10 Metabolism, Bioavailability, and Analysis of Dietary Isoflavones

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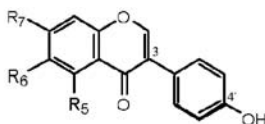
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INTRODUCTION

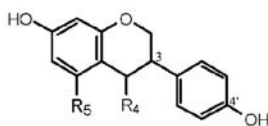
Considerable evidence exists from epidemiological and experimental studies for preventive effects of soy or isoflavones against chronic diseases including cancer (breast, prostate, colorectal, lung), osteoporosis, cardiovascular disorders, and menopausal symptoms, but this is not always consistent [Adlercreutz

and Mazur, 1997; Cassidy, 2005; Duncan et al., 2003; Kurzer and Xu, 1997; Magee and Rowland, 2004; Setchell and Lydeking-Olsen, 2003; Yan and Spitznagel, 2004, 2005]. In four recent epidemiologic studies strong preventive effects were observed against breast cancer later in life when soy was consumed at young age [Shu et al., 2001; Thanos et al., 2006; Wu et al., 2002; Korde et al., 2009], and animal studies had shown this before [Lamartiniere, 2002]. The structural similarity of isoflavones to steroidal estrogens (Fig. 10.1) and the potent binding of genistein, one of the most predominant soy isoflavones, to the estrogen receptor-beta, including its transactivation [Kuiper et al., 1997], are believed to be the basis for many effects of soy intake [Cotroneo et al., 2002]. Recent findings on higher isoflavone bioavailability in children versus adults [Halm et al., 2007] and on cardioprotective effects independent from lipid profiles [Walker et al., 2008] strengthen the hypothesis that isoflavones play an important role in the biological effects of soy intake [Wiseman, 2006].

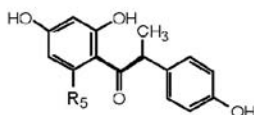


Aglycon	R ₅	R ₆	R ₇	Conjugates in soy foods	R ₇
Genistein	OH	H	OH	7-O-(6''-O-acetyl)-glucoside of daidzein of genistein of glycitein	
Glycitein	H	OCH ₃	OH	7-O-(6''-O-malonyl)-glucoside of daidzein of genistein of glycitein	
Daidzein	H	H	OH	7-O-glucoside ... of daidzein = Daidzin of genistein = Genistin of glycitein = Glycitin	

Metabolized isoflavonoids by intestinal bacteria



Aglycon	R ₄	R ₅
dihydrodaidzein	=O	H
dihydrogenistein	=O	OH
equol	H	H



Aglycon	R ₅
O-desmethylangolensin	H

Figure 10.1 Structures of Isoflavonoids Studied.

The basis for understanding the health benefits of isoflavones requires detailed knowledge on the absorption, distribution, metabolism, elimination, and bioavailability of these phytoestrogens that demands robust, precise, accurate, and affordable analyses from biological and other matrices.

OCCURRENCE

Isoflavone concentrations in foods are by far highest in soy and its products; therefore, but dependent on the population, dietary isoflavone exposure occurs mainly through intake of soy products. They typically contain a total of 0.01–0.3% isoflavones composed of glycosides of daidzein, genistein, and glycitein (Fig. 10.1) while fermented products contain predominantly aglycons [Adlercreutz and Mazur, 1997; Franke et al., 1995, 1999; Horn-Ross et al., 2000; Umphress et al., 2005]. Isoflavone concentrations in soy vary depending on a variety of factors such as environmental, genetic, harvesting, and processing conditions [Tsukamoto et al., 1995]. 7-*O*-malonylglucoside and 7-*O*-glucosides are the main native isoflavone conjugates in unprocessed soy, and 7-*O*-acetylglycosides are formed by dry heating [Barnes et al., 1994; Kudou et al., 1991]. Isoflavones occur in a variety of plants and are often used for chemotaxonomic purposes but are particularly concentrated in the Fabaceae [Andersen, 2006], for example, in kudzu (*Pueraria lobata*) or red clover (*Trifolium pratense*) or, of course, soy. Isoflavone-rich plants other than soy are often not consumed in large amounts or are not considered food plants at all. Updated databases for isoflavone content in commonly consumed foods became recently available [U.S. Department of Agriculture, 2007].

UPTAKE AND METABOLISM

As shown in Figure 10.2 isoflavonoid-*O*-glucosides require hydrolysis for absorption, which is followed by passive diffusion through the mucosa and reconjugation to glucuronides and sulfates on the basolateral side of the enterocyte and/or in the liver [Franke et al., 2004b; Setchell, 2000]. This hydrolytic step can happen either by lactate phloridzin hydrolase, an enzyme bound at the brush border of enterocytes, or by the gut bacteria. Hydrolysis could possibly occur in the oral cavity [Walle et al., 2005] or in the stomach but only to a small extent that is unlikely to contribute significantly to aglycon formation [Franke et al., 2004b]. Due to the absence of isoflavone-*O*-glucoside in the circulation [Setchell et al., 2002] or the bile [Prasain et al., 2006] transport of the intact glycoside through the apical membrane of the enterocyte via sodium-dependent glucose transporter 1 (SGLT1) does not take place. Whether the uptake can be interrupted by efflux of the aglycon from the enterocyte back into the lumen via multidrug resistance-associated protein 2 (MDRP2) is not known. To a minor extent further metabolism can take place in the liver to

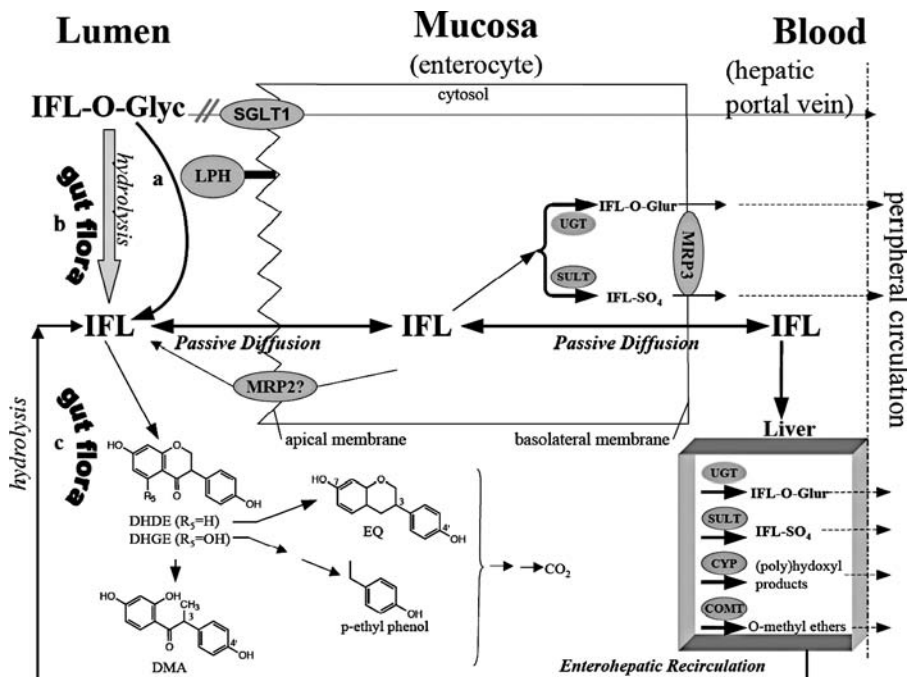


Figure 10.2 Absorption, transport, and metabolism of ingested isoflavone glycosides. See text for details. IFL-*O*-Glyc = isoflavone-*O*-glycoside; IFL = isoflavone aglycon; IFL-*O*-Glyc = isoflavone-*O*-glucuronides; IFL-*SO*₄ = isoflavone sulfates; LPH = lactate phloridzin hydrolase; SGLT1 = sodium-dependent glucose transporter 1; COMT = catecholamine ortho methyl transferase; MRP2/3 = multi-drug resistance-associated protein 2/3; UGT = UDP-glucuronyltransferase; SULT = sulfotransferases; DHDH = dihydrodaidzein; DHGE = dihydrogenistein; DMA = *O*-desmethylangetolensin.

mono- or polyhydroxylated or *O*-methylated isoflavonoids [Heinonen et al., 2003; Kulling et al., 2001] while enterohepatic recirculation of isoflavone glucuronides/sulfates directly from the liver to the lumen can also occur [Sfakianos et al., 1997] followed by bacterial hydrolysis and reabsorption.

It is important to note that gut bacteria play a vital role because they not only hydrolyze but also form the major known human isoflavone metabolites dihydrodaidzein, dihydrogenistein, equol, *O*-desmethylangetolensin, other minor compounds from isoflavones including *p*-ethyl phenol from genistein, and ultimately degrade isoflavones to CO₂ [Atkinson et al., 2005; Bannwart et al., 1984; Setchell et al., 2002]. This is highlighted by the extremely low levels of these metabolites in infants [Setchell et al., 1997] and germ-free animals [Bowey et al., 2003]. Urinary recovery of total isoflavones in humans including all major metabolites is usually in the range of 10–40% of ingested dose [Franke and Custer, 1994; Franke et al., 2004b; Setchell et al., 2003]. This, combined

with the minimal fecal isoflavone excretion [Xu et al., 1995], suggests bioconversion of isoflavones to yet unknown metabolites (or CO₂). In vitro experiments identified bacterial species responsible for the known conversions, particularly for that to equol [Decroos et al., 2005; Ueno and Uchiyama, 2001; Wang et al., 2005], which, however, have not been confirmed in humans.

All metabolic studies after intake of soy or isoflavone preparations show great interindividual variations of all absorption, distribution, metabolism, and elimination parameters for isoflavones [Franke and Custer, 1994] [reviewed in Cassidy, 2006; Nielsen and Williamson, 2007]. Of the population 30–60% possess a gut flora that can produce equol [reviewed in Atkinson et al., 2005; Yuan et al., 2007] occurring naturally as the optical S-isomer, which has higher biological effects than its other isomers [Setchell et al., 2005]. Exact cut-offs for equol production have only recently been suggested based on a urinary equol/daidzein ratio of 0.018 [Setchell and Cole, 2006], but the assignment to an equol excretor in the literature remains still somewhat arbitrary. A carbohydrate rich diet may increase equol production while fat may reduce it [Rowland et al., 2000]. Fiber was reported to diminish isoflavone uptake [Tew et al., 1996], and oral antibiotics were shown to lead to a trend of decreased equol and variable *O*-desmethylangolensin production [Halm et al., 2008]. Vegetarians [Setchell and Cole, 2006] and Asians [Arai et al., 2000; Watanabe et al., 1998] who are usually habitual soy consumers, seem to have a greater ability to convert daidzein to equol (ca. 60%) than Western populations (ca. 30%) [Lampe et al., 1998]. Whether men are more likely to produce equol than women [Setchell and Cole, 2006] remains to be confirmed in larger studies. In contrast, 80–90% of populations are *O*-desmethylangolensin producers [Frankenfeld et al., 2005], whereas all animals except pigs [Gu et al., 2006] are the opposite, namely extensive equol and small *O*-desmethylangolensin producers. The health effects caused by the ability of the gut flora to produce equol, which is more estrogenic, more present as “free” aglycon (ca. 50%), and less protein bound than its precursor daidzein, or *O*-desmethylangolensin by intestinal bacteria are so far unclear and inconsistent [Atkinson et al., 2005; Frankenfeld et al., 2004, 2006; Horn-Ross et al., 2000; Setchell and Cole, 2006].

Metabolic studies by us [Fanti et al., 1999; Franke et al., 1999] and others [Anupongsanugool et al., 2005; de Pascual-Teresa et al., 2005; Kano et al., 2006; King and Bursill, 1998; Setchell et al., 2003; Vergne et al., 2008; Zubik and Meydani, 2003],) observed consistently a biphasic isoflavone appearance pattern in plasma and urine (Fig. 10.3) when humans consume soy or purified isoflavone preparations. Peak levels occur at 1–2 h and again at 4–7 h after intake. When this was investigated by simultaneous soy challenge and drastic reduction of the intestinal microbiota through oral antibiotic therapy combined with mechanical bowel preparation, it was concluded that only approximately 10% of overall uptake occurs in the proximal small intestine where probably lactate phloridzin hydrolase deconjugates isoflavones to the bioavailable aglycon [Franke et al., 2004b]. The majority, however, is absorbed after hydrolysis by the gut bacteria that start to occur in significant amounts in

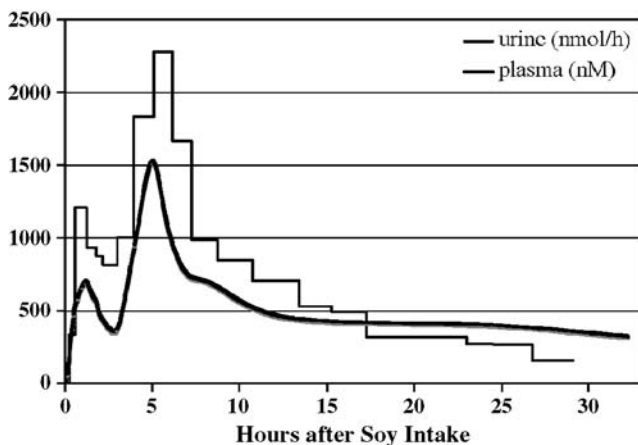


Figure 10.3 Typical pattern of isoflavone appearance in urine and plasma over time after soy intake. Plasma units are nanomole per liter and urine units are nanomole per hour. (From Franke et al. [2004b].)

the more distal intestine. Interestingly this biphasic isoflavone appearance pattern persisted with intake of aglycons indicating a saturation limit regarding uptake in the proximal small intestine and possibly preferred gut locations where absorption can take place.

BIOAVAILABILITY

Pharmacokinetic parameters from 16 studies summarized in Table 10.1 show greater bioavailability of genistein versus daidzein and of glycosides versus aglycons [reviewed in Nielsen and Williamson, 2007]. Relative to their *O*-glycosides, the aglycons daidzein and genistein show a C_{\max} smaller by 43 and 37%, respectively, and about a 17% shorter time to reach C_{\max} (t_{\max}) while the elimination half-lives ($t_{1/2}$) are similar. Relative to daidzein, genistein has a 28% higher C_{\max} when dosed on a molar and 20% higher when dosed on a milligram basis while t_{\max} is 8% shorter and $t_{1/2}$ 23% longer. The comparisons for genistin versus daidzin (the glucosides) show a similar trend (C_{\max} 16 and 9% higher, t_{\max} 9% shorter, $t_{1/2}$ 36% longer). According to these parameters doses of 25 mg of daidzein and genistein, or daidzin and genistin (these glucosides dosed in aglucon equivalents), applied to subjects weighing 50–75 kg would be expected to lead to peak plasma levels (C_{\max}) for daidzein of 980–660 nM and genistein of 1190–790 nM, or 1730–1150 nM and 1890–1260 nM, respectively. Accordingly, relative to C_{\max} , there will be residual isoflavone plasma levels of approximately 20–29%, 6–12%, and 2–5% 24, 36, and 48 h after isoflavone intake, respectively. As expected, isoflavone plasma accumulation over time

Table 10.1 Pharmacokinetic Parameters of Isoflavones

	C_{\max}^a (μM)	r^b	t_{\max}^c (h)	$t_{1/2}^d$ (h)	C_{24}^e Rel. to C_{\max}	C_{36}^f Rel. to C_{\max}	C_{48}^g Rel. to C_{\max}
Daidzein	1.97 ± 0.63	0.93	6.2 ± 1.5	7.7 ± 3.3	20%	7%	2%
Genistin	2.37 ± 0.41	0.71	5.7 ± 1.8	9.5 ± 3.2	26%	11%	5%
Daidzin ^h	3.46 ± 0.75	0.85	7.5 ± 1.6	7.0 ± 1.6	20%	6%	2%
Genistin ^h	3.78 ± 1.00	0.85	6.8 ± 1.4	9.5 ± 1.7	29%	12%	5%

^aPeak plasma levels in μM per mg isoflavone per kg body weight.

^bCorrelation between dose and plasma levels by linear regression.

^cTime to reach peak plasma levels.

^dTime to reach peak plasma levels.

^{a-d}Elimination half life mean of 16 studies [Nielsen and Williamson 2007].

^ePercent plasma level after 24 h relative to peak plasma levels.

^fPercent plasma level after 36 h relative to peak plasma levels.

^gPercent plasma level after 48 h relative to peak plasma levels.

^hWhen dosed in aglycon units.

was observed by dosing soy 1–2 times per day [Gardner et al., 2008]. The correlation between dose and expected plasma levels in the circulation is almost linear with only slight saturation effects [Setchell et al., 2003]. However, it is still unclear whether fermented soy foods containing mostly isoflavone aglycons or unfermented soy foods containing mostly isoflavone *O*-glucosides result in better bioavailability. Aglycons as present in fermented soy products were found to result in higher isoflavone uptake by some [Cassidy et al., 2006; Hutchins et al., 1995; Izumi et al., 2000; Kano et al., 2006] but not others [Franke et al., 2004b; Setchell et al., 2003; Tsangalis et al., 2005] including nondistinguishable differences [Maskarinec et al., 2008b; Richelle et al., 2002]. In contrast, isoflavones from liquid relative to solid foods were consistently found to be absorbed more quickly and more extensively [Cassidy et al., 2006], but the overall isoflavone exposure as measured by urine excretion or area under the plasma curve is often not significantly different [de Pascual-Teresa et al., 2005; Franke et al., 2004b].

Intake Compared to Urine or Plasma Values

We found in several populations significant linear correlations of soy or isoflavone intake with urinary isoflavones [Franke et al., 1999; Jaceldo-Siegl et al., 2008]. This was confirmed by others who found these correlations with either urinary isoflavones [Atkinson et al., 2002; Slavin et al., 1998], plasma isoflavones [Frankenfeld et al., 2003; Heald et al., 2007; Wu et al., 2004], or both [Arai et al., 2000; Grace et al., 2004; Low et al., 2006; Ritchie et al., 2004; Yamamoto et al., 2001]. The correlations were highest (up to $r = 0.6$) for recent intake data (food diaries) and weaker (approximately $r = 0.2$) or disappeared for long-term intake measures (food frequency questionnaires). This is expected

considering the fast elimination pattern of isoflavones. Very recent results indicate that fasting morning serum isoflavone estimates will provide a poor index of long-term soy intake, but that overnight urinary estimates perform much better [Fraser et al., 2008]. Therefore and due to high reproducibility within subjects over time [Frankenfeld et al., 2005; Maskarinec et al., 2008b], it is highly recommended to measure isoflavones in subjects, favorably urine (see below), as reliable biomarker for soy intake [Lampe, 2003].

Apparent Bioavailability

The same isoflavone appearance pattern (aglycon equivalents) was observed in plasma and urine [Fanti et al., 1999; Franke et al., 1998], and correlations between these matrices were very high [Arai et al., 2000; Grace et al., 2004; Low et al., 2006; Nettleton et al., 2004; Ritchie et al., 2004; Setchell and Cole, 2006; Yamamoto et al., 2001], particularly when the timing of sample collection was considered accurately [Franke et al., 2004b, 2006a; Halm et al., 2008]. The correlation between isoflavone values in urine and blood are much improved by using area under curve (AUC) units for both matrices instead of urinary isoflavone excretion rate (UIER) for urine, a time-based unit, and isoflavone level for plasma, a volume-based unit [Franke et al., 2004b; Halm et al., 2008]. This is largely due to the time domain being accurately considered by using the identical time intervals for the AUCs of both matrices. This is important to keep in mind because in living organisms isoflavone amounts in biological fluids change markedly over a given time period. It is vital to recognize that at similar doses more daidzein than genistein appears in urine while the opposite is true for plasma. Therefore, the AUC_{plasma} for daidzein is smaller than that for genistein (accordingly the bioavailability of daidzein is smaller than that of genistein) and the ratio $AUC_{\text{urine}}/AUC_{\text{plasma}}$ much greater for daidzein than for genistein, but most importantly, this ratio remains constant over any given time interval for each isoflavone [Franke et al., 2004b].

Advantages of using urine over plasma include its noninvasiveness (particularly important for research in children), its superiority at defining an equol producer [Setchell and Cole, 2006], as well as the ability to collect a more concentrated matrix (particularly overnight urine) and large amounts, which leads to low quantification limits. Also, collections can be performed by participants themselves without medical supervision, in private, and, most importantly, can be accumulated over many hours (even days), reflecting exposures over much longer time periods compared to data from blood, which only reflects one given point in time per collection. This is confirmed as mentioned above by experimental findings of urinary estimates being a much better index of long-term soy intake than plasma values [Fraser et al., 2008]. We suggest to use UIERs as a reliable surrogate to determine circulating isoflavones and thereby assess isoflavone bioavailability. Since bioavailability is defined based on circulating levels, we propose to use the term apparent bioavailability when using urinary excretion data.

It has been recently suggested by our group [Halm et al., 2007, Halm et al., 2008] to examine the accuracy of timed urine collections by comparing the measured urinary creatinine excretion with established daily creatinine excretion data for each gender and age group (Table 10.2). Urinary excretion expressed relative to time (hour) is more accurate than expressed relative to creatinine, but timed urine is often not feasible to collect [Franke et al., 2006b]. Since creatinine excretion depends mostly on muscle mass, it varies largely depending on body weight (BW), gender, and age [1993; Remer et al., 2002]. This is particularly relevant in growing children, not only due to marked changes of muscle mass in absolute terms, but also after adjustment for body weight [Barr et al., 2005; Kampmann et al., 1974; Kesteloot and Joossens, 1996; Remer et al., 2002]. Urinary excretions adjusted solely for creatinine underestimate true excretion in heavier individuals—for example, in males versus females, or in older children versus younger children. The lack of conversion to time-based urinary excretion rates might explain the lower UIE in older than in younger soy-exposed children [Hoey et al., 2004] or the loss of differences in urinary sex steroid excretion in females of different reproductive ages [Hall Moran et al., 2001]. Therefore, as a general rule, it is best to have the collection time interval and the volume of the urine specimen available. The second choice is to convert a creatinine-based excretion value into a time-based excretion (in hours) by multiplying the former with the creatinine/hour ratio as determined from any timed urine collection for a given subject since the creatinine excretion remains quite constant within a subject. The third choice is to multiply the nmol/mg creatinine value with the established mg creatinine/kg BW/day ratio as shown in Table 10.2 [Kampmann et al., 1974; Remer et al., 2002] to arrive at a time-based unit. We suggest using 22 mg/kg/day and 24 mg/kg/day for 20- to 30-year-old women and men, respectively, to adjust the original data (19.7 mg/kg/day for women and 23.8 mg/kg/day for men) [Kampmann et al., 1974] to the more recent values (20.9 mg/kg/day and 23.3 mg/kg/day for 17-year-old girls and boys, respectively) [Remer et al., 2002].

Following this approach it was determined that the apparent isoflavone bioavailability in healthy children relative to healthy adults is ca. 30–40% higher [Halm et al., 2007]. This is in excellent agreement with previous reports on healthy minors, such as infants [Franke et al., 2006a], school-aged children [Franke et al., 2008], and (pre)pubertal girls [Maskarinec et al., 2005]. These findings suggest a higher systemic isoflavone exposure in children versus adults at the same relative soy dose. When considering that children eat generally much more per kilogram body weight, the exposure in children is probably up to twofold higher relative to adults. This could result in children experiencing more benefits from the health effects of soy [Shu et al., 2001; Wu et al., 2002]. We believe that the isoflavone exposure after soy intake will stay far below levels that would give rise to concern regarding adverse effects. Toxic activity is usually observed at much higher isoflavone levels, and adverse effects have not been reported in populations with high soy intake.

Table 10.2 Daily Creatinine Excretion Per kg of Body Weight as Function of Age and Gender^a

Age (years)	Urinary Creatinine (mg/kg/d)		Age (years)	Urinary Creatinine (mg/kg/d)	
	Women	Men		Women	Men
3	14.5	15.2	25	22.0	24.0
4	15.7	17.1	30	20.4	21.9
5	15.7	17.1	35	20.4	21.9
6	17.9	19.3	40	17.6	19.7
7	17.9	19.3	45	17.6	19.7
8	17.9	19.3	50	14.9	19.3
9	18.9	20.7	55	14.9	19.3
10	18.9	20.7	60	12.9	16.9
11	18.9	20.7	65	12.9	16.9
12	18.9	20.7	70	11.8	14.2
13	18.9	20.7	75	11.8	14.2
14	20.9	23.3	80	10.7	11.7
15	20.9	23.3	85	10.7	11.7
16	20.9	23.3	90	8.4	9.4
17	20.9	23.3	95	8.4	9.4
20	22.0	24.0	30		

^aAges 3–17 from Remer et al. [2002]. Ages 20–95 Kampmann et al., [1974] except ages 20–25 where we suggest to use 22 mg/kg/d for women and 24 mg/kg/day for men to adjust the original Kampmann data (19.7 mg/kg/day for women and 23.8 mg/kg/day for men) to the more recently determined Remer values (20.9 mg/kg/day and 23.3 mg/kg/day for 17-year-old girls and boys, respectively).

Antibiotic Effects on Apparent Bioavailability

In soy intervention studies we found that children showed consistently a lower apparent isoflavone bioavailability when on oral antibiotics compared to when healthy; but the opposite was found in adults [Franke et al., 2004b; Halm et al., 2008]. We hypothesized that these observations can be explained by the changes in gut bacteria caused by oral antibiotics, or to unknown factors connected with the disease that led to oral antibiotic therapy. As pointed out above (Fig. 10.2), ingested isoflavone-*O*-glucosides are hydrolyzed to the bioavailable aglucons mainly by intestinal bacteria. However, gut bacteria also further metabolize the “free” bioavailable isoflavone aglucons to metabolic products such as equol, *O*-desmethylangolensin, *p*-ethylphenol, and other nonspecific phenolic agents [King, 2002]. Although definitive evidence is lacking, our seemingly paradoxical observation in adults versus children could be due to oral antibiotics in children reducing the isoflavone-hydrolyzing gut bacteria significantly (and possibly also the isoflavone aglycon degrading flora), which consequently leads to the isoflavones not becoming bioavailable. Vice versa, oral antibiotics in adults could possibly preferentially reduce the isoflavone aglycon degrading gut bacteria that are involved in isoflavone

degradation to unknown and nonspecific metabolites, while the bacteria that hydrolyze isoflavone glycosides are comparably little affected; thereby the time during which bioavailable isoflavone aglucons can be absorbed is increased. The participants we investigated were treated with broad-spectrum oral antibiotics, but no correlation between specific types of antibiotics used, type of illness, gender, age, and ethnicity of the participant and UIER changes was observed. This might be due to the overall small sample size and/or inter-individual differences and the small numbers in each ethnic group. Similarly, our protocol did not allow for detailed evaluation of isoflavone metabolites because a 12-h urine sampling after soy exposure is insufficient to allow for efficient metabolite formation by the gut bacteria. With our relatively small studies we were unable to differentiate effects due to the bacterial infection, the antibiotics, or both. To further investigate the role of inflammation and infection on the isoflavone metabolism in humans, we recently initiated studies with participants suffering from viral or other acute and chronic infections not requiring antibiotics.

ANALYSIS

For accurate analyses serious attention needs to be paid to calibration of analytical instrumentation. For this purpose it is recommended to prepare stock solutions of authentic standards by determining concentrations through absorbance readings followed by checking purity via high-pressure liquid chromatography (HPLC). This avoids problems with weighing inaccuracies (hygroscopy), allows the repeated checking of existing stock solutions, and assures simple interlaboratory comparability. While the determination of the molar extinction coefficient (ϵ , the absorbance of a one-molar concentration) is critical, it remains a reliable reference point even if it needs to be changed because all final values can be adjusted linearly if ϵ value changes should become necessary. Table 10.3 shows that reported ϵ values for isoflavones as a function of wavelength and solvent vary greatly, which warrants an agreement on the true value to use for all analysts. For the sake of consistency we continue to use values reported by Ollis [1962] (daidzein, genistein) and Kelly et al. [1993] (glycitein) due to the lack of other published data when we started our isoflavone work in 1990.

Traditionally HPLC methods were used for isoflavone analysis from foods [Wang et al., 1990], and gas chromatography/mass spectrometry (GC/MS) to determine isoflavones and their metabolites in human biological fluids including urine [Adlercreutz et al., 1991; Kelly et al., 1993], plasma [Adlercreutz et al., 1993], and feces [Adlercreutz et al., 1995; Kurzer et al., 1995]. HPLC with photodiode array (PDA) detection was introduced in 1994 to measure these analytes in human urine [Franke and Custer, 1994; Xu et al., 1994]. Compared to GC/MS, HPLC methods require fewer steps for sample preparation and analysis and demand less technician time and less expensive instrumentation.

Table 10.3 Molar Extinction Coefficients (ϵ) of Isoflavones as a Function of Wavelength and Solvent^a

	Solvent	λ (nm)	ϵ (L/mol/cm)	Reference
Daidzein	96% EtOH	250	20,893	Ollis, 1962
	100% EtOH	262	24,739	Wiseman et al., 2002
	NA	249	31,563	Murphy et al., 2002
	MeOH	248–249	27,100–27,200	Sigma-Aldrich 2006 ^b
	80% MeOH	250	27,542	Walz, 1931
Genistein	96% EtOH	263	37,154	Ollis, 1962
	100% EtOH	262	35,842	Wiseman et al., 2002
	NA	263	35,323	Murphy et al., 2002
	EtOH	263	35,000–38,400	Sigma-Aldrich 2006 ^b
	96% EtOH	262.5	37,291	Merck Index 10th ed.
	NA	261	33,113	Williams and Harborne, 1989
Glycitein	85% MeOH	261	24,435	Walter, 1941
	alcohol	256	22,387	Kelly et al., 1993
	NA	256	25,388	Murphy et al., 2002
Daidzin	NA	249	26,830	Murphy et al., 2002
	NA	NA	23,749	Univ. of St. Andrews ^b
	MeOH/Water	250	28,561	Purina/Nestle
Genistin	MeOH/Water	262.5	39,129	Nestle/Purina 2006 ^b
	NA	262.5	35,323	Hendrich and Murphy, 2001
	85% aq EtOH	262	39,000–40,000	Sigma-Aldrich 2006 ^b
Glycitin	NA	259	26,713	Murphy et al., 2002
Acetyldaidzin	NA	256	29,007	Murphy et al., 2002
Acetylgenistin	NA	261	38,946	Murphy et al., 2002
Acetylglycitin	NA	260	29,595	Murphy et al., 2002
Malonyldaidzin	NA	258	26,830	Murphy et al., 2002
Malonylgenistin	NA	260	29,895	Murphy et al., 2002
Malonylglycitin	NA	260	26,313	Murphy et al., 2002
Malonylglycitin	NA	260	26,313	Murphy et al., 2002
Dihydrodaidzein	NA	277	13,600	Wähälä et al., 1998 ^b
Dihydrogenistein	NA	290	18,300	Wähälä et al., 1998 ^b
<i>O</i> -desmethylangolensin	NA	280	12,023	Wähälä et al., 1998 ^b
Equol	NA	281	6,761	Wähälä et al., 1994 ^b
Formononetin	NA	256	29,512	Ollis, 1962
Biochanin-A	NA	263	27,542	Ollis, 1962

^a λ (nm) = wavelength of absorbance maximum in nm; ϵ = molar extinction coefficient in L/mol/cm.

^b Private communications; na = not available.

Higher sensitivity and selectivity for HPLC analyses can be achieved by detection with MS, which has gained extreme attention due to ease of use through electrospray ionization [Barnes et al., 1998; Franke et al., 2002; Twaddle et al., 2002]. For food isoflavone analyses we favor PDA monitoring

over fluorescence or electrochemical detection (ECD) due to its much better diagnostic value, and over MS due its more affordable operation and extreme robustness except when levels become very low [Franke et al., 2004a]. Although ECD results in higher sensitivity than PDA, it is much less selective and can result in wrong positive results [Franke et al., 1998]. HPLC with PDA was applied for the analysis of isoflavones from foods [Franke et al., 1994, 1999; Umphress et al., 2005], urine [Franke and Custer, 1994] including epidemiologic studies [Zheng et al., 1999], plasma [Franke et al., 1998], and breast milk [Franke et al., 1998]. In all cases later projects that applied MS detection confirmed the earlier findings [Dai et al., 2002; Franke et al., 2006b] and were extended for analyses of nipple aspirate fluid [Maskarinec et al., 2008a].

Food analyses of isoflavones were improved very recently in our laboratory by the application of ultra-HPLC technology, which reduced run times of 45 min to less than 9 min, a more than five-fold gain (Fig. 10.4), while reducing solvent consumption and waste generation by a factor of more than 8. In brief, homogenized material was extracted with 80% aqueous methanol (v/v) containing 20 ppm flavone as internal standard by sonication (10 min) and stirring (2 h) at room temperature, yielding isoflavone conjugates and originally present aglycons. After centrifugation a clear aliquot was diluted 1:1 with 0.2 M acetate buffer (pH 5) and 5 μ L were injected into a ultra-HPLC system (model Accela, ThermoFisher, San Jose, CA) using a Hypersil Gold C18 (100 \times 2.1 mm; 1.9 μ m) reversed-phase column (Waters; Milford, MA). Elution was performed at a flow rate of 0.5 mL/min (9600 psi) with the following linear gradient: $A = 0.1\%$ formic acid in 50/50 methanol/acetonitrile (v/v), $B = 0.1\%$ formic acid in water; A/B (v/v): from 22/78 to 35/65 in 6 min, then to 50/50 in 0.2 min, hold at the same ratio for 0.8 min, then change to 90/10 in 0.01 min, and hold at the same ratio for 1 min to eliminate hydrophobic components, then change back to the initial conditions in 0.01 min, and hold for 1 min for equilibration. Analytes were scanned between 200 and 400 nm by PDA detection for identification purposes and quantitated at 260 nm after adjustment of internal standard recovery. Further improvements of this method could include increasing the flow rate, applying a steeper gradient, or heating the column; but this was not warranted for our needs.

Isoflavone analyses from biological matrices including tissue are routinely analyzed in our laboratory by HPLC with electrospray ionization (negative mode) and has been improved by applying high-resolution tandem mass spectrometry (model TSQ Ultra, Thermo, San Jose, CA) (Fig. 10.5) [Blair et al., 2003; Franke et al., 2002a; Maskarinec et al., 2008a]. $^{13}\text{C}_3$ -labeled daidzein, equol, and enterolactone (University of St. Andrews, UK) and $^2\text{H}_4$ -labeled genistein (University of Helsinki, Finland) are added as internal standards to each homogenized specimen, and hydrolysis is performed with β -glucuronidase and arylsulfatase (Roche Applied Sciences, Indianapolis, IN) followed by phase separation with methyl tertiary butyl ether using a robotic extraction system (model Versa100, Aurora Biomed, Vancouver, Canada) [Franke et al., 1998]. The ether fractions are dried under nitrogen at room temperature and

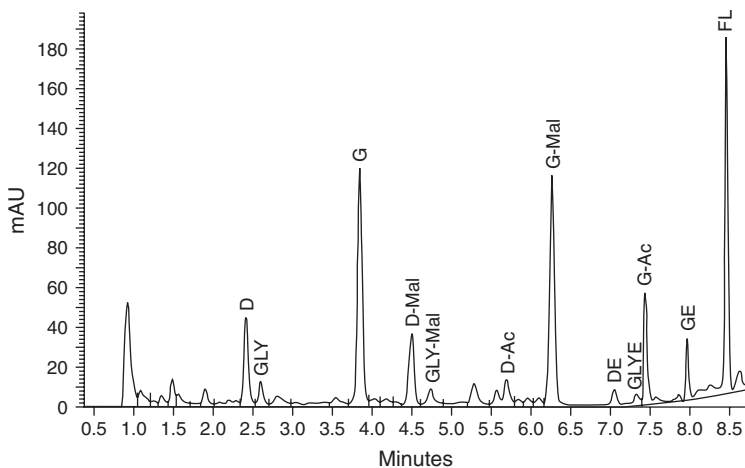


Figure 10.4 Typical UHPLC trace of isoflavones from a soy protein extract monitored at 260 nm using a Hypersil Gold C18 column (100 × 2.1 mm; 1.9 μm; Waters, Milford, MA) and a 0.5-mL/min flow rate (9600 psi) of a linear gradient of 0.1% aq. formic acid versus methanol/acetonitrile(1:1). FL = flavone (internal standard), other details in figure and in text. Concentrations of ISOFLAVONE peaks (μM): D = 17.66, GLY = 6.27, G = 26.49, D-Mal = 16.76, GLY-Mal = 3.62, D-Ac = 5.87, G-Mal = 26.70, DE = 3.37, GLYCITEIN = 1.74, G-Ac = 8.33, GE = 4.36.

redissolved in a 1:1 mixture of methanol:0.01% aq. formic acid. Of this extract 25 μL are separated on a Gemini C18 (150 × 2.0 mm; 5 μm) reversed-phase column coupled to a Gemini C18 (4.0 × 2.0 mm; 5 μm) direct-connect guard column (Phenomenex, Torrance, CA) using a linear gradient at 0.2 mL/min of MeOH/MeCN/Water = 15/15/70 to 30/30/40 in 2.5 min, to 40/40/20 in 5.5 min, and back to 15/15/70 in 0.1 min for equilibration before subsequent injections; 0.5% aq. ammonia at 40 μL/min is added postcolumn as dopant.

The general MS conditions we currently apply are as follows: source = electrospray ionization; ion polarity = negative; spray voltage = 3000 V; sheath and auxiliary and ion sweep gas = nitrogen; sheath gas pressure = 35 arbitrary units; auxiliary gas pressure = 10 arbitrary units; ion sweep gas pressure = 4 arbitrary units; ion transfer capillary temperature = 280°C; scan type = high-resolution selected reaction monitoring; collision gas = argon; collision gas pressure = 1.0 mTorr; source collision induced dissociation = 10V; scan width, 0.002u; scan time, 0.02–0.08 s; Q1 peak width = 0.1–0.3 u full width at half maximum (FWHM) and Q3 peak width at 0.70 u FWHM. Mass spectrometric monitoring is started 4.0 min after sample injection by multiple reaction monitoring as previously [Maskarinec et al., 2008a] using transitions (collision energies applied in brackets): daidzein from m/z 253.0 to m/z 223.0 (35 eV), 208.0 (33 eV), and 132.0 (40 eV); $^{13}\text{C}_3$ -daidzein from m/z 256.0 to m/z 226.0 (31 eV), 211.0 (31 eV), and 182.0 (15 eV); genistein from m/z 269.1 to m/z 159.1 (30 eV), 133.0 (33 eV), and 132.0 (43 eV);

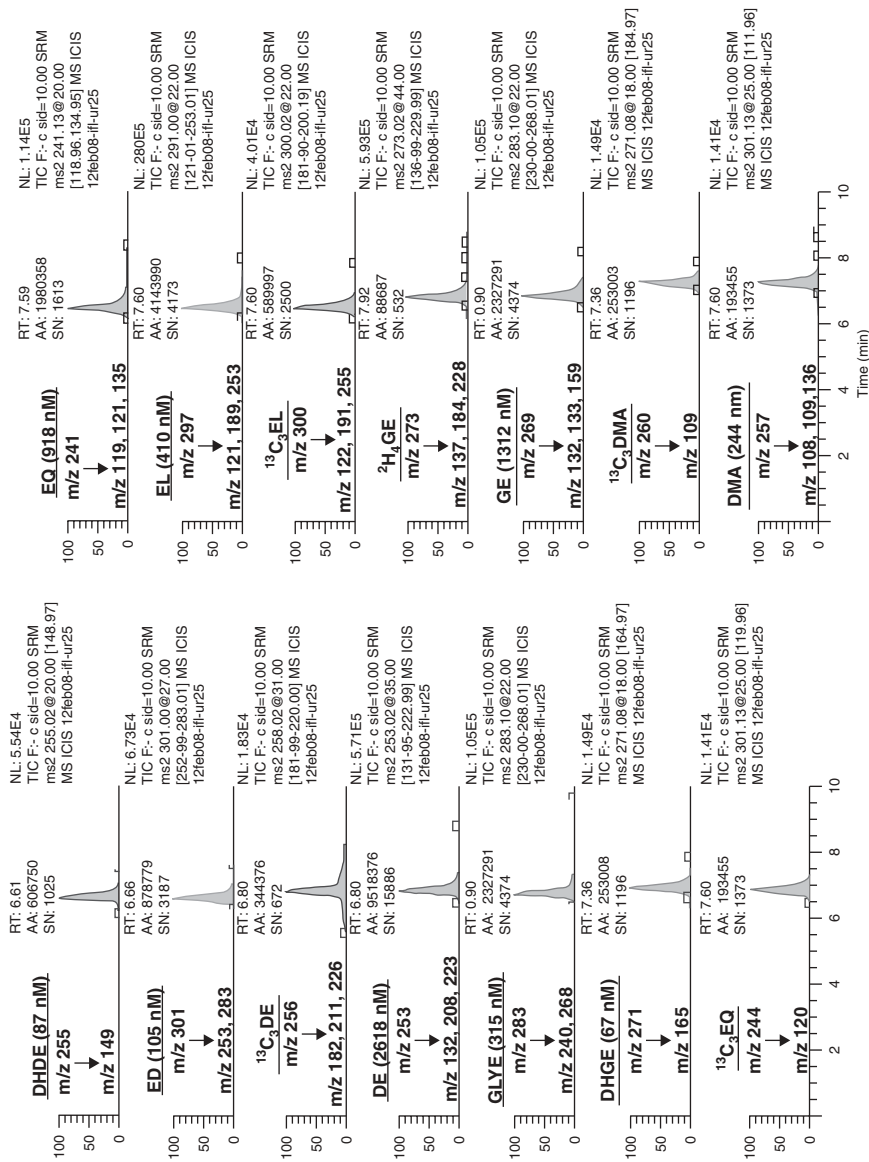


Figure 10.5 Typical LC-MS/MS trace by negative ESI of isoflavonoids from a urine extract. Measured concentrations in bracket. Y-axis units in relative intensity; EL = enterolactone, ED = enterodiol, other abbreviations see figure.

$^2\text{H}_4$ -genistein from m/z 273.0 to m/z 228.0 (44 eV), 184.0 (44 eV), and 137.0 (42 eV); equol from m/z 241.1 to m/z 135.0 (20 eV), 121.0 (16 eV), and 119.0 (20 eV); $^{13}\text{C}_3$ -equol from m/z 244.1 to m/z 120.0 (25 eV); *O*-desmethylangolensin from m/z 257.1 to m/z 135.9 (25 eV), m/z 109.0 (20 eV), and m/z 108.0 (28 eV); $^{13}\text{C}_3$ -*O*-desmethylangolensin from m/z 260.1 to m/z 109.0 (35 eV); for glycitein from m/z 283.1 to m/z 268.0 (22eV) and m/z 240.0 (25eV); for dihydrodaidzein from m/z 255.0 to m/z 149.0 (20eV); for dihydrogenistein from m/z 271.1 to m/z 165.0 (18eV); enterolactone from m/z 297.0 to m/z 253.0 (22 eV), 189.2 (39 eV), and 121.0 (39 eV); $^{13}\text{C}_3$ -enterolactone from m/z 300.0 to m/z 255.2 (22 eV), 191.0 (39 eV), and 121.9 (39 eV); and enterodiol from m/z 301.0 to m/z 283.0 (27 eV) and 253.0 (27 eV). Limits of quantitation (LOQ) for all analytes were approximately 1 nM for daidzein and genistein, 2 nM for equol, and 5 nM for enterolactone; between-day coefficients of variation ranged 4–18% for all analytes, while intraday variation was half or less of that.

CONCLUSIONS

Reemerging interest in soy and isoflavones is due to recent findings on their potential cancer- and other disease-preventing effects, particularly when exposure happens at a young age and when intake persists throughout adulthood. Accurate, precise, and affordable analytical techniques will be the basis for future research aimed at defining the details of the biological activity of isoflavones.

ACKNOWLEDGMENTS

Supported in part by Physicians Pharmaceuticals, Inc., and NIH grants RR020890 and CA71789 (there are no conflicts of interest).

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11 Phytoestrogens Up-regulate Antioxidant Genes

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SOURCES OF PHYTOESTROGENS IN FOOD

Phytoestrogens have been defined as any plant substance or metabolite that induces biological responses in vertebrates and can mimic or modulate the actions of endogenous estrogens, usually by binding to estrogen receptors [Madej et al., 2002]. The principal phytoestrogens in food are isoflavones, coumestrans, prenylated flavonoids, and lignans. Most of the available information on dietary phytoestrogen concentrations is related to isoflavones. Table 11.1 summarizes the principal dietary sources of each type of phytoestrogen and the concentrations found in them.

The most prevalent dietary isoflavones include genistein, daidzein, glycitein, biochanin A, and formononetin [Klejdus et al., 2007]. These compounds are primarily found in legumes where they occur as glucosides. This fact may affect the absorption rate of isoflavones and will be discussed in the next section.

Soybeans and soy-based products are a particularly rich source of isoflavones, especially genistein and daidzein [Fukutake et al., 1996; Bingham et al., 1998; Mazur, 1998], reaching concentrations of up to 198 mg of total isoflavones per 100 g of soy-based product (Table 11.1). When referring to bioavailability of isoflavones, it is very important to consider the effect of food processing and cooking. In fact, commercial processing of soy into food products lowers isoflavone concentrations and may lead to chemical alterations, such as deacetylation or deglycosylation [Coward et al., 1998; Genovese et al., 2007]. An example for deglycosylation of isoflavones occurs in fermented soy products where the isoflavone content is halved when compared with nonfermented soy products [Slavin et al., 1998]. Nevertheless, it is very important to take into account that fermentation can alternatively increase bioavailability of isoflavones in soy: Fermented soy products are better absorbed than nonfermented ones [Cassidy et al., 2006]. Cooking can reduce phytoestrogen concentrations and alter their chemical characteristics. It has been shown that boiling and roasting affect phytoestrogen concentration [Coward et al., 1998; Liggins et al., 2000]. However, baking or frying does not appear to modify the total isoflavone content [Coward et al., 1998].

Table 11.1 Principal Dietary Sources of Each Class of Phytoestrogen and Concentrations Found in Them

Phytoestrogen class	Dietary Source	Concentration (mg/100 g)
Isoflavones	Fruits, cereals, vegetables	<0.1
	Legumes	0–0.58
	Soy milk	5–10
	Soy flour, soybeans	~150
Coumestrans	Bread	0
	Soybeans	0.05
	Beans	3.6
	Bean sprouts, alfalfa	4.7
Lignans	Peas	0.2
	Cereals	0.5
	Teas	2.04
	Linseeds	60–370

Source: Data from USDA–Iowa State University Isoflavone Database, 2002.

PHARMACOKINETICS OF PHYTOESTROGENS

Pharmacokinetic data of phytoestrogens given are basically centered in their excretion profiles. In general, the conclusions are that genistein and daidzein begin to rise within 2 h of an ingested dose [King and Bursill, 1998] and reach peak concentrations within 5–8 h after ingestion [King and Bursill, 1998; Setchell et al., 2001].

It is not clear whether absorption of aglucones is better than glucosides or not. Piskula et al. [1999] reported that aglucones can be absorbed directly from the stomach unlike their glucoside forms. It has been showed that glucosides need gut microflora to be absorbed from the gut [Xu et al., 1995; Rowland et al., 2003; Turner et al., 2003]. However, germ-free rats fed a soy-isoflavone-containing diet excrete large quantities of daidzein and genistein in urine, indicating that gut microflora is not absolutely required for the absorption of isoflavones. Isoflavone metabolites equol, *O*-desmethylangolensin, and lignan enterolactone were not detectable in urine from the germ-free rats but were present in human flora-associated rat urine, indicating that they were products of gut microflora activity [Bowey et al., 2003]. Interindividual variation of gut microflora population may be one of the reasons for the different bioavailability found in different individuals [Rowland et al., 2003]. In this regard, when studying the pharmacokinetics of isoflavones, it is important to consider gender, age, and dietary habits.

EFFECTS OF PHYTOESTROGENS ON HEALTH AND DISEASE

The significance of the structural similarity of lignans and isoflavones to mammalian estrogens and possible effects on cancer prevention were first postulated in the early 1980s [Setchell et al., 1984; Adlercreutz et al., 1987]. Heart disease, osteoporosis, breast cancer, prostate cancer, and menopausal symptoms share a common epidemiology: They are rare in Far Eastern populations eating traditional diets containing soybean products when compared with Western populations [Bingham et al., 1998]. Cross-sectional studies have shown higher phytoestrogen levels in urine and plasma of populations at lower risk of these diseases [Adlercreutz et al., 1982, 1991]. It was concluded that beneficial effects of phytoestrogens on climacteric women are either very weak or barely noticeable [Wuttke et al., 2007]. Only a few double-blind placebo-controlled trials document any significant relief of the symptoms. The situation concerning the risk to the cardiovascular system is similar. Isoflavones share the beneficial effects on high-density (HDL) and low-density lipoproteins (LDL) with estrogens. Clearly, there is a current necessity of clinical endpoint studies investigating the influence of preparations containing isoflavones on cardiovascular events. Isoflavones are likely to have a mild bone protective (antiosteoporotic) effect [Atkinson et al., 2004].

CELLULAR AND MOLECULAR MECHANISMS OF PHYTOESTROGEN ACTION

Phytoestrogens have similar chemical structures to estrogens and have been found to bind to estrogen receptors [Cos et al., 2003]. Therefore, there is reason to believe they will elicit estrogenic effects by similar, if not identical, mechanisms.

Many, but not all, the classical physiological effects of estrogens are mediated by ligand-activated nuclear transcription factors, the estrogen receptors (ERs). ERs are predominantly located in the nucleus under normal conditions, but they can move between the nucleus and the cytoplasm bound to heat shock proteins (HSPs). Upon entering the cell, estrogens bind to ERs, causing the dissociation from the heat shock proteins. Subsequently, ERs form a dimer and bind to DNA containing estrogen responsive elements (ERE) Receptor, estrogen-responsive elements, and the corresponding coactivators and corepressors promote gene transcription and synthesis of proteins, which produces an estrogenic response [Parker, 1995].

Three estrogen receptor subtypes have been described: ER α , ER β , and recently ER γ [Hawkins et al., 2005], but the significance of this latter receptor is still unclear. Estrogen receptor subtypes can mediate different biological effects and display different intracellular and tissue distribution patterns [Parker, 1995]. The ER α and ER β subtypes can interact with a wide variety of different compounds, although some ligands have different affinities for the subtypes. Indeed, phytoestrogens bind preferentially to ER β , although they can also bind weakly to ER α [Kuiper et al., 1997; Pike et al., 1999; Branham et al., 2002]. Cell-surface forms of ER α and ER β coupled to cytosolic signal transduction pathways have been described [Collins and Webb, 1999] and are discussed in the next section.

PHYTOESTROGENS UP-REGULATE ANTIOXIDANT GENES

Estrogens were long ago recognized as *in vitro* antioxidants [Ruiz-Larrea et al., 1997]. However, at physiological concentrations it is very unlikely that they may act as such, especially due to their low concentration in plasma. A simple calculation indicates that if the recommended dose of estradiol in estrogen replacement therapy is 50 micrograms/day and the recommended dose of vitamin E as supplement is 500 mg/day, estrogen ought to be approximately 10,000 times more potent than vitamin E to have a similar antioxidant effect; and this is obviously not the case when chemical structures, that is, capacity to trap radicals, are compared.

Yet, *in vivo* experiments show that estrogens have a powerful antioxidant effect: Mitochondrial H₂O₂ production is significantly increased (by more than 50%) after ovariectomy, and this is completely prevented when ovariectomized rats are treated with estradiol at doses similar to those used in estrogen

replacement therapy [Borras et al., 2003]. Therefore, estrogens clearly do not act as chemical antioxidants *in vivo*, but rather they exert their antioxidant effect by up-regulating the expression of antioxidant genes and enzymes. *In vitro* studies using MCF-7 cells confirmed the results *in vivo* and demonstrated that estradiol up-regulates the expression of antioxidant genes by binding to estrogen receptors, which in turn activates mitogen-activated protein (MAP) kinases and nuclear factor kappa B (NF- κ B) signaling pathways [Borras et al., 2005].

The effect of estradiol as an up-regulator of antioxidant and longevity-related genes indicates that its administration might be beneficial to increase life span, particularly for males who should then have a life span similar to females. However, considerable evidence has shown that estrogen replacement therapy after menopause may have setbacks (on top of their obvious feminizing effects in males) [Kasai et al., 1986]. Phytoestrogens constitute an interesting alternative. Their beneficial health effects have been reported repeatedly [Munro et al., 2003; Mahn et al., 2005] and, to our knowledge, very few, if any, major reports have shown detrimental effects. Thus, to find the molecular mechanisms by which phytoestrogens exert their antioxidant action, we tested the effect of 0.5 μ M genistein on the H₂O₂ levels in MCF-7 cells [Vina et al., 2005; Borras et al., 2006]. This level of genistein can be considered as nutritionally relevant as it is the concentration normally found in plasma of people at the Far East, who eat relatively large quantities of soy in their normal diet. This concentration is, however, significantly higher than that found in people living in the Western world. When these cells were incubated with genistein, the levels of H₂O₂ were significantly decreased. However, when the cells were incubated with both genistein and tamoxifen (an estrogen receptor modulator) levels of H₂O₂ were similar to controls, thus confirming that the antioxidant effect of genistein is mediated by the interaction of genistein with the estrogen receptor. This observation posed the question about the intracellular mechanism by which genistein acts to increase the expression of mitochondrial antioxidant enzymes. A direct genomic effect of genistein was unlikely because neither Mn-SOD nor GPx has estrogen-responsive elements in their promoter region. Thus, it is likely that the action of genistein is mediated via intracellular signaling cascades. We tested the effect of mitogen-activated protein kinases (MAPK) by using UO126, an inhibitor of the phosphorylation of these kinases. Our experiments showed that UO126 completely inhibited the lowering effect of genistein on the level of H₂O₂ in cells. MAPK are known to activate the NF- κ B. Therefore, we tested whether genistein acts by activating NF- κ B in its up-regulation of the expression of both Mn-SOD and GPx genes, whose promoters contain putative NF- κ B-binding motifs. This was indeed the case: When cells were incubated with pyrrolidine dithiocarbamate, an inhibitor of the I- κ B degradation, and therefore an inhibitor of the NF- κ B translocation to the nucleus, the effect of genistein on the up-regulation of antioxidant enzyme expression was prevented. Integrating the observed effects of these pharmacological inhibitors of the signaling pathways, we concluded that genistein up-regulates the expression of

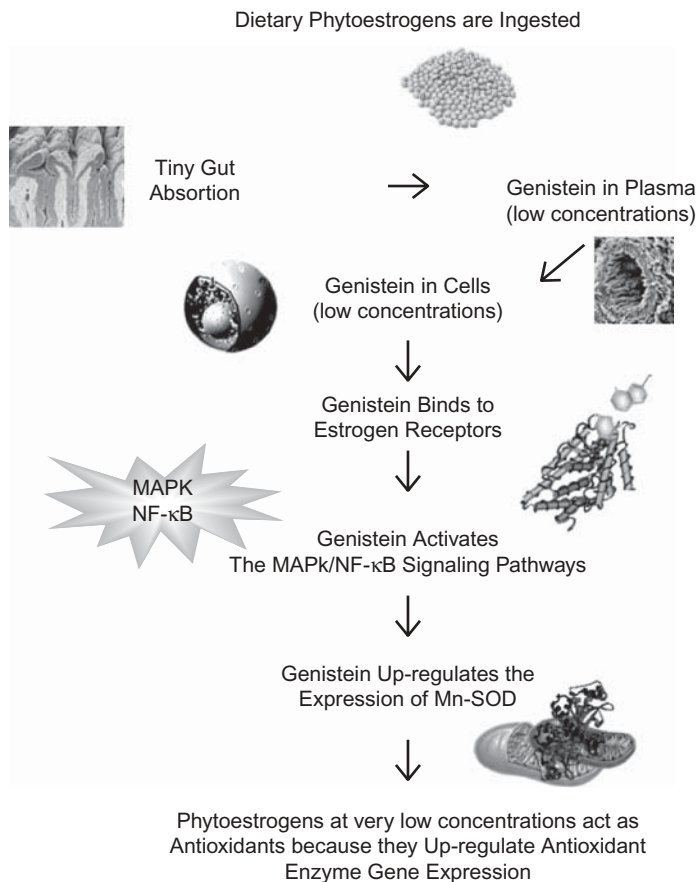


Figure 11.1 Mechanism of the up-regulation of antioxidant genes by phytoestrogens.

Mn-SOD mediated by the following pathway: interaction with membrane estrogen receptor, activation of MAPK, activation of NF-κB, and up-regulation of gene expression [Borras et al., 2006; Vina et al., 2008].

To sum up, we found that genistein significantly decreased H_2O_2 levels in cells and that effect, just as with estradiol, is mediated by estrogen receptors signaling pathways involving MAPK and NF-κB activations and up-regulation of the antioxidant gene for Mn-SOD. A schematic rendition of these pathways is shown in Figure 11.1.

CONCLUDING REMARKS

Work from our laboratory has shown that the difference in longevity between males and females may be traced to the beneficial effects of estrogens, which

up-regulate the expression of longevity-associated genes. However, estrogens present the obvious problems of their feminizing action in males, and, when given to postmenopausal women, they may increase the incidence of cardiovascular events. Phytoestrogens, especially isoflavones, offer an interesting alternative: They are not feminizing and their use has proved very safe. We have shown that phytoestrogens exert their antioxidant action by up-regulating the expression of antioxidant genes. A conclusion that can be drawn is that even if phytoestrogens are absorbed from the gut in tiny concentrations, since their effect is catalytic and mediated by interaction with specific receptors, it may be significant. The effect of the oral administration of phytoestrogens and, in general, of flavonoids has to be tested in specific experimental or clinical model. Low rates of absorption and/or metabolism should not deter from studying biological effects that, as stated above, may occur significantly at catalytic concentrations.

ACKNOWLEDGMENTS

This work was supported by grants SAF 2004-03755, BFU2007-65803/BFI, and ISCIII2006-RED13-027 from the “Red Temática de investigación cooperativa en envejecimiento y fragilidad (RETICEF)” to J.V. and by grant GV/2007/263 to C.B. C.B. is recipient of a Bancaja postdoctoral fellowship.

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12 Dietary Isoflavones: Cardiovascular Actions and Activation of Cellular Signaling Pathways

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INTRODUCTION

Cardiovascular diseases, such as hypertension, coronary heart disease (CHD), and atherosclerosis, are associated with increased oxidative stress and are more common in men than in premenopausal women of similar age, with the incidence of CHD increasing significantly after menopause, with loss of cardiovascular protection attributed to estrogen deficiency [Forte et al., 1998]. Differences in the regulation of blood pressure and vascular function between males and females have been investigated extensively over the past

decade, and female hormones are implicated in the protective effects of gender on the vasculature [Sader et al., 2002; Orshal et al., 2004; Mendelsohn et al., 2005] and expression of longevity associated genes [Viña et al., 2008]. Although estrogens and dietary phytoestrogen isoflavones have antioxidant properties due to the presence of a phenolic group in their steroid structure, these compounds can also activate intracellular kinase cascades and transcription of genes [Mann et al., 2007; Siow et al., 2007], potentially accounting for their beneficial effects on hypertension, thrombosis, and cardiovascular diseases [Chahoud et al., 2000; Visioli et al., 2000]. Nutrient–gene interactions have gained wide acceptance in the “postgenomic” era, and nutrigenomic approaches are yielding insights at genomic, proteomic, and metabolomic levels to evaluate the therapeutic potential of diets in the prevention and/or treatment of cardiovascular diseases [Muller and Kersten, 2003].

The cardiovascular benefits of naturally occurring diphenolic plant compounds, such as the isoflavones genistein, daidzein, and its metabolite equol, have recently been extensively examined in view of the lower incidence of CHD in populations consuming high amounts of soy-based foods. The U.S. Food and Drug Administration initially approved health claims for the addition of soy protein to foods for cardiovascular protection [Erdman, 2000], yet re-evaluation of the benefits of soy protein and isoflavones by an American Heart Association study group in 2006 concluded that “direct cardiovascular health benefits of soy protein or isoflavone supplements is minimal at best”, suggesting that the high content of polyunsaturated fats, fiber, vitamins, minerals, and low content of saturated fat in soy products may account for their observed benefits [Sacks et al., 2006]. Although numerous studies have evaluated the benefits of dietary antioxidants against CHD, there is limited direct evidence linking soy isoflavones with the induction of antioxidant defense genes in the vasculature. In this chapter, we provide an up-to-date review of the molecular mechanisms by which estrogens and dietary isoflavones activate intracellular signal transduction pathways involved in the transcriptional activation of endothelial nitric oxide synthase (eNOS) and antioxidant defense genes in the vasculature. We evaluate the evidence that estrogens and phytoestrogens modulate vascular reactivity *in vitro* and *in vivo* and suggest that these compounds protect against cardiovascular disease by virtue of their ability to activate intracellular signaling pathways, leading to increased bioavailability of the vasodilator nitric oxide (NO) and up-regulation of the activity and/or expression of antioxidant defense genes mediated by the activation of kinase cascades and the key antioxidant transcription factor Nrf2. Dietary polyphenols contained in soy, red wine, green tea, and chocolate influence vascular reactivity by targeting eNOS and redox-sensitive gene expression [Mann et al., 2007]. Increased endothelium-dependent NO generation in response to dietary isoflavones may modulate cellular sensors for oxidative stress and thereby increase NO bioavailability [Liu et al., 2005] in cardiovascular diseases associated with enhanced generation of reactive oxygen species and diminished antioxidant defenses [Stocker and Kearney, 2004].

VASCULAR ACTIONS OF DIETARY ISOFLAVONES IN VIVO

Plasma concentrations of the isoflavones genistein and daidzein range between 50 and 800 ng mL⁻¹ in adults consuming soy-rich foods and can achieve levels found in Japanese consuming their traditional soy-based diet [Adlercreutz et al., 1993; Setchell and Cassidy, 1999; Clarkson, 2002]. The protection against CHD in Asian populations consuming a soy-enriched diet may be due to increased eNOS expression and enhanced bioavailability of NO [Lissin and Cooke, 2000; Hwang et al., 2003; Joy et al., 2006]. Clinical trials evaluating the benefits of soy isoflavones report improvements in systemic arterial compliance in men and postmenopausal women [Teede et al., 2003], increased plasma nitrite/nitrate and decreased endothelin-1 levels, and increased brachial artery flow-mediated dilatation [Squadrito et al., 2003]. Dietary isoflavones have been shown to acutely modulate vascular reactivity in healthy postmenopausal women and male subjects in vivo. Infusion of genistein or dihydroequol directly into brachial arteries, at concentrations achieved in populations consuming an isoflavone-rich diet [Adlercreutz et al., 1993], evoked concentration- and endothelium-dependent increases in forearm blood flow [Walker et al., 2001; Chin-Dusting et al., 2004], while consuming test meals supplemented with 80 mg of soybean isoflavones resulted in significantly greater brachial artery flow-mediated dilatation and plasma levels of NO metabolites after 5–7 h compared to values in subjects consuming control meals [Hall et al., 2008].

As a significant component of the genistein-mediated dilation was shown to be insensitive to the inhibition of eNOS by *N*^G-monomethyl-L-arginine [Walker et al., 2001], however, it is possible that isoflavones can also modulate vascular tone by inhibiting Ca²⁺ influx via L-type Ca²⁺ channels in vascular smooth muscle cells [Ruehlmann et al., 1998; Figtree et al., 2000; Mishra et al., 2000]. Several randomized, double-blind, placebo-controlled trials report cardiovascular benefits of longer-term (2–12 months) supplementation with genistein, tetrahydrodaidzein, or soy isoflavones [Nestel et al., 1997, 2006; Squadrito et al., 2002, 2003; Hallund et al., 2006; Teede et al., 2001]. The consensus of such studies in healthy postmenopausal women is that isoflavone supplementation increases brachial artery flow-mediated dilation and improves systemic arterial compliance. Despite numerous clinical studies, there is still controversy whether isoflavone supplementation lowers arterial blood pressure in vivo [Nestel et al., 1997, 2006; Teede et al., 2001; Kreijkamp-Kaspers et al., 2004, 2005]. It is possible that vascular responses to isoflavone metabolites may be limited to individuals capable of metabolizing ingested daidzein to equol [Cassidy et al., 2006; Setchell et al., 2005; Vergne et al., 2006]. In summary, the clear benefits of soy isoflavone supplementation on endothelial function have largely been observed in humans and animal models with mild to moderate hypertension [Teede et al., 2003; Rivas et al., 2002; Vera et al., 2007; Xu et al., 2004].

Randomized clinical studies in healthy human volunteers, smokers, and patients with coronary artery disease have shown that consumption of black and green tea polyphenols or flavanol-rich chocolate/cocoa enhances

flow-mediated brachial artery dilation within 1–24 h [Duffy et al., 2001; Heiss et al., 2005, 2006; Schroeter et al. 2006; Vlachopoulos et al., 2005]. Clinical studies with healthy volunteers report that ingestion of flavanol-rich chocolate/cocoa results in NO-mediated peripheral vasodilation [Fisher et al., 2003], increased insulin sensitivity, and reduced blood pressure [Grassi et al., 2005a]. Moreover, patients with essential hypertension consuming flavanol-rich dark chocolate exhibit increased brachial artery flow-mediated dilation and a significant reduction in systolic blood pressure [Grassi et al., 2005b]. Although flavanol-rich chocolate/cocoa increases plasma epicatechin concentrations and endothelium-dependent dilation and pure epicatechin mimics these effects [Schroeter et al., 2006; Engler et al., 2004], other bioactive components in chocolate could contribute to vascular relaxation *in vivo*. Apart from having direct antioxidant effects, flavanols and green tea polyphenols can modulate redox signaling in vascular cells providing additional beneficial mechanisms for increasing NO bioavailability and reducing smooth muscle proliferation [Locher et al., 2002; Fraga, 2005; Mackenzie et al., 2004].

NITRIC OXIDE SYNTHESIS AS A VASCULAR TARGET FOR DIETARY ISOFLAVONES

The vasodilator NO is synthesized by eNOS from the cationic amino acid L-arginine in the presence of molecular oxygen and other cofactors [Palmer et al., 1987]. As a Ca^{2+} /calmodulin (CaM)-dependent enzyme, eNOS is regulated by its association with the plasmalemmal scaffolding protein caveolin-1 [Shaul et al., 1996], posttranslational modification via phosphorylation by protein kinases, and an interaction with the molecular chaperone heat shock protein 90 (Hsp90) [Garcia-Cardena et al., 1998; Boo & Jo 2003; Takahashi and Mendelsohn, 2003]. Tethering of eNOS to caveolin-1 maintains the enzyme in an inactive state, and an elevation in intracellular Ca^{2+} leads to vasoactive agonists promoting association of CaM with eNOS and dissociation of the enzyme from caveolin-1 [Ghosh et al., 1998]. In addition to Ca^{2+} -dependent activation of eNOS, laminar shear stress [Boo et al., 2003], 17β -estradiol [Russell et al., 2000], and isoflavones [Joy et al., 2006] can stimulate NO production via phosphorylation of eNOS at cytosolic Ca^{2+} levels, with some studies reporting rapid dissociation of eNOS from caveolin-1 and association with heat shock protein Hsp90 (Fig. 12.1). The major eNOS phosphorylation sites include Ser¹¹⁷⁷ in the reductase domain and Thr⁴⁹⁵ and Thr⁴⁹⁷ in the CaM binding domain. Protein kinase (Akt) [Dimmeler et al., 1999], protein kinase A [Boo et al., 2003], mitogen-activated protein kinases ERK1/2 [Cai et al., 2003], and p38^{MAPK} [Anter et al., 2005] have been reported to phosphorylate Ser¹¹⁷⁷. Phosphorylation at Thr⁴⁹⁵ antagonizes CaM binding to eNOS [Fleming et al., 2001], and thus concerted phosphorylation at Ser¹¹⁷⁷ and dephosphorylation of Thr⁴⁹⁵ occurs in response to different stimuli to modulate eNOS activity.

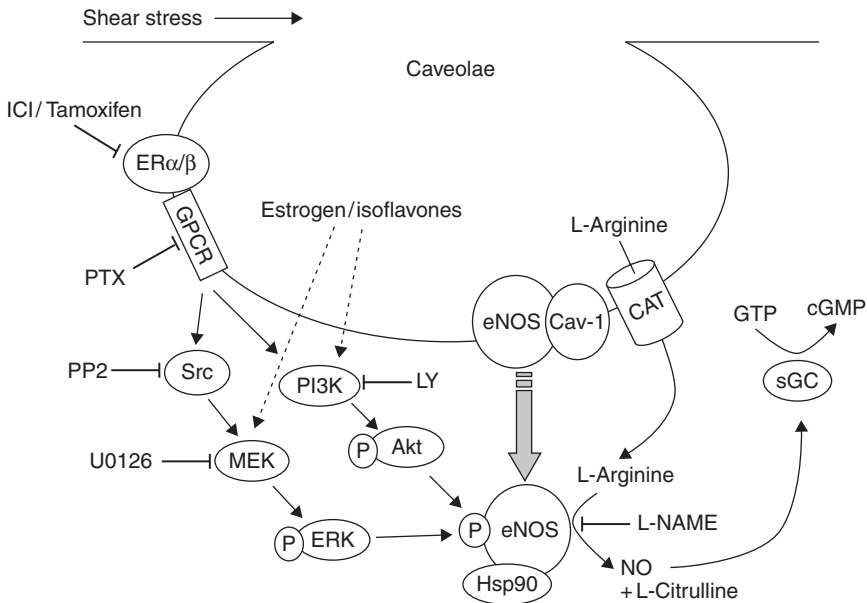


Figure 12.1 Ca^{2+} -independent stimuli such as fluid shear stress, adenosine, isoprenaline, estrogen, and soy isoflavones acutely stimulate eNOS phosphorylation at resting cytosolic Ca^{2+} levels, involving activation of ERK1/2, PI(3)-kinase/Akt and/or PKA (not shown) signaling pathways. Activation of eNOS involves rapid dissociation of the enzyme from membrane-bound caveolin-1 (Cav-1) and association with Hsp90 and metabolism of the cationic amino acid L-arginine to NO and L-citrulline. NO binds to the heme moiety of soluble guanylyl cyclase in target smooth muscle cells to increase intracellular cGMP levels, leading to vascular relaxation. Although ER α and ER β (and truncated ER receptor) are expressed in HUVEC, rapid actions (2 min) of isoflavones appear not to involve coupling of ER receptors to G α i in membrane caveolae in endothelial cells. Inhibitors for specific kinase pathways are indicated, e.g., PP2, U0126, LY294,002, and L-NAME. (Adapted from Siow et al. [2007] and Mann et al. [2007].)

The signaling pathways underlying eNOS activation by estrogens have been reviewed previously [Chambliss and Shaul, 2002; Mendelsohn, 2002], and colocalization of estrogen receptors (ER α and ER β) with eNOS in membrane caveolae in endothelial cells provides a functional signaling unit for enzyme activation [Haynes et al., 2000]. Moreover, Hsp90 can also interact directly with ERs, enabling 17 β -estradiol to rapidly activate eNOS [Russell et al., 2000]. Although a subpopulation of estrogen-like receptors in the plasma membrane of endothelial cells may also mediate rapid activation of intracellular signaling pathways [Joy et al., 2005; Figtree et al., 2003], there is no direct evidence that isoflavones interact with plasma membrane “estrogen receptors”. Isoflavones elicit both endothelium-dependent and -independent relaxation of precontracted arterial rings in vitro, mimicking their dilator actions in the human forearm vasculature [Walker et al., 2001; Ching-Dusting et al., 2004; Hall et al.,

2008]. We previously reported that the daidzein metabolite equol causes acute relaxation of precontracted rat aortic rings [Joy et al., 2006]. Equol-mediated ring relaxation was inhibited by the eNOS inhibitor L-NAME, whereas the environmental estrogenic pollutant 4-octylphenol and ICI 182,780 reduced coronary perfusion pressure in isolated hearts via an inhibition of L-type Ca^{2+} channels in vascular smooth muscle [Ruehlmann et al., 1998]. Low nanomolar concentrations of isoflavones rapidly stimulate NO release from cultured endothelial cells [Liu et al., 2004; Joy et al., 2006]. As summarized in Figure 12.1, studies in human endothelial cells established that genistein, daidzein, and equol (100 nM) rapidly (30 s–2 min) stimulate ERK1/2 and Akt-dependent eNOS phosphorylation at basal cytosolic Ca^{2+} levels. Isoflavone-stimulated NO release was unaffected by the ER antagonists ICI 182,780 (Faslodex) and tamoxifen or uncoupling of G-protein receptors. It was further established that equol induces a rapid dissociation of eNOS from caveolin-1 and association with the chaperone protein Hsp90 [Joy et al., 2006].

ACTIVATION OF CELLULAR SIGNALING PATHWAYS AND ANTIOXIDANT DEFENSE GENES BY ISOFLAVONES

Extensive clinical and experimental evidence links hypertension and atherosclerotic vascular disease with the accumulation of oxidized low-density lipoproteins and enhanced generation of reactive oxygen species within the vessel wall [Stocker and Keaney, 2004]. ROS are short-lived molecules generated as by-products of metabolism and rapidly react with cellular components, causing damage to membrane lipids, proteins, and DNA [Dröge, 2002]. It is now apparent that numerous cellular targets for isoflavones exist that lead to modulation of signaling pathways, including those regulating protective antioxidant and anti-inflammatory transcription factor activity and gene expression [Siow et al., 2007; Rimbach et al., 2008]. Although estrogens and phytoestrogens can act as direct free-radical scavengers [Williams et al., 2004], recent evidence suggests that soy isoflavones [Mahn et al., 2005], red wine, tea and dark chocolate polyphenols [Wallerath et al., 2002, 2005; Leikert et al., 2002] can modulate pathways leading to increased messenger ribonucleic acid (mRNA) and protein levels for eNOS in endothelial cells. Moreover, polyphenols have been implicated in antioxidant response element (ARE)-mediated gene transcription [Ansell et al., 2004; Bianco et al., 2005] and up-regulation of manganese superoxide dismutase (MnSOD) expression in vascular cells [Strehlow et al., 2003].

Induction of antioxidant genes is regulated through a cis-acting ARE element within the regulatory region of target genes [Nguyen et al., 2003]. The redox-sensitive basic leucine zipper protein transcription factor Nrf2 is involved in the regulation of many detoxification and antioxidant genes. Nrf2 belongs to the Cap-N-Collar family of transcription factors, forming heterodimers with small Maf proteins, with subsequent binding to ARE leading to gene transcription

[Ishii et al., 2000]. Since the expression of a wide array of protective antioxidant genes are positively regulated by the ARE sequence, Nrf2 may serve as a regulator of ARE-driven cellular defense systems against oxidative stress induced by dietary isoflavones [Mann et al., 2007; Siow et al., 2007].

Exposure of endothelial cells to donors of NO and/or peroxynitrite leads to adaptive increases in synthesis of the major intracellular antioxidant glutathione (GSH) and Nrf2/ARE-regulated expression of antioxidant genes including heme oxygenase-1 (HO-1) [Foresti et al., 2003]. The microsomal enzyme HO-1 metabolizes heme to generate biliverdin/bilirubin and carbon monoxide, which like NO can inhibit platelet aggregation and act as a vasodilator when the bioavailability of NO is limited [Siow et al., 1999; Ryter et al., 2006]. Biliverdin is subsequently converted by biliverdin reductase to bilirubin, a chain-breaking antioxidant that scavenges lipid peroxy radicals [Baranno et al., 2002]. Accumulating evidence suggests that Nrf2 constitutes a sensor of oxidative stress involved in triggering ARE-mediated gene expression to restore cellular redox status [Siow et al., 2007].

Although protective actions of dietary antioxidants and isoflavones against CHD have been described, few reports have adequately addressed the molecular and cellular targets involved in the induction of antioxidant defense genes in vascular cells. There is limited evidence in vascular endothelial and smooth muscle cells that estrogens, isoflavones (genistein, daidzein, equol), and polyphenols modulate antioxidant gene expression via the transcription factors Nrf2 and nuclear factor- κ B (NF- κ B), however several recent studies have used nonphysiological concentrations of isoflavones ($>20 \mu\text{M}$) that are well recognized to inhibit tyrosine kinase activity [Akiyama et al., 1987]. Thus, it is important to critically evaluate both concentration- and time-dependent actions of estrogenic-like compounds on intracellular signaling cascades and gene expression. It is conceivable that acute activation of NO generation elicited by isoflavones in endothelial cells may lead to nuclear translocation of Nrf2 [Buckley et al., 2003]. As summarized in Figure 12.2, modulation of the Nrf2/Keap1 complex by NO, peroxynitrite, or other reactive oxygen and nitrogen species will lead to induction of ARE-gene transcription [Kang et al., 2002]. In a similar manner, CO has been shown to enhance nuclear translocation of Nrf2 and HO-1 induction in primary human hepatocytes through activation of MAPK pathways [Lee et al., 2006]. It is therefore likely that isoflavone-stimulated NO and CO production in endothelial and smooth muscle cells may sensitize/modulate antioxidant gene expression through Nrf2-mediated activation of the ARE in target defense genes.

The promoter sequences of MnSOD and GPx contain putative NF- κ B-binding motifs, and in MCF-7 cells inhibition of ERK1/2 and NF- κ B signaling pathways prevents up-regulation of antioxidant and longevity-related gene expression induced by both estrogen and genistein [Borrás et al., 2005, 2006]. Although it is well known that NF- κ B coordinates the induction of numerous pro-inflammatory genes, recent evidence establishes that activation of NF- κ B modulates the expression of antioxidant genes, such as MnSOD and HO-1, and

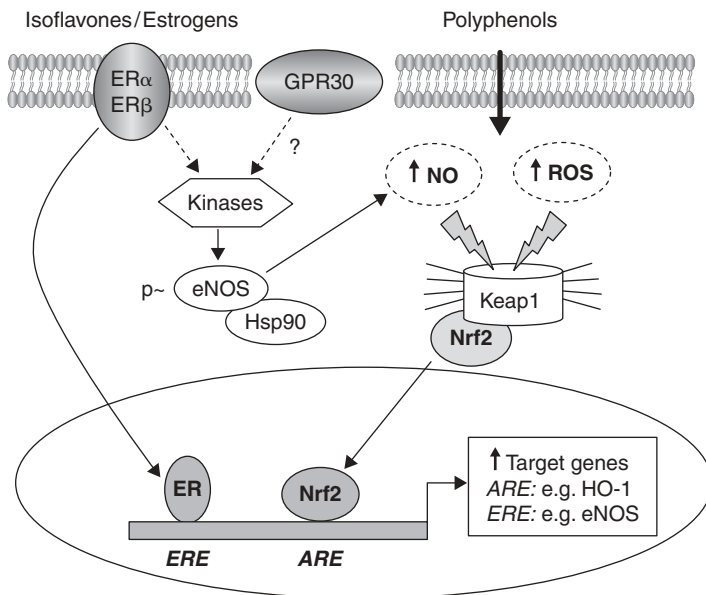


Figure 12.2 Nitric oxide as a mediator of polyphenol-induced transcriptional activation of antioxidant genes. Isoflavones, estrogens, and other polyphenols activate intracellular kinase cascades, leading to acute activation of eNOS and NO and/or ROS, generation. Increased NO, ROS, or peroxynitrite levels will modify cysteine residues on Keap-1 leading to nuclear accumulation of the redox-sensitive transcription factor Nrf2. Nrf2 binds to the antioxidant response element (ARE) or electrophile response element (EpRE) in the promoter region of target genes (e.g., phase II and antioxidant enzymes NQO1, HO-1) while estrogen receptors bind to estrogen response element (ERE) to enhance eNOS expression. Induction of other antioxidant genes such as MnSOD may involve rapid phosphorylation of ERK1/2 and I- κ B and translocation of the p50 subunit of NF- κ B to the nucleus and transactivation of MnSOD expression. (Adapted from Mann et al. [2007].)

confers protection against apoptosis by up-regulating antiapoptotic proteins [Collins and Cybulsky, 2001]. In this context, induction of HO-1 by the dietary polyphenol resveratrol is abrogated by inhibitors of NF- κ B activation or I κ B phosphorylation [Baur et al., 2006] and deletion of NF- κ B binding sites in the HO-1 promoter reduces transcriptional activity [Juan et al., 2005]. Modulation of NF- κ B and Nrf2 signaling pathways by polyphenols via mitogen-activated protein kinases can lead to transcriptional activation of antioxidant defense genes [Chen et al., 2005; Andreadi et al., 2006].

CONCLUSIONS AND FUTURE PERSPECTIVES

The molecular mechanisms by which estrogens and the isoflavones genistein, daidzein, and equol up-regulate antioxidant gene expression in different

vascular cell types merit further investigation. Ongoing studies of the non-genomic and genomic actions of soy-derived isoflavones on vascular reactivity and antioxidant gene expression in human endothelial cells and rodent blood vessels [Mahn et al., 2005; Knock et al., 2006; Joy et al., 2006] have provided an insight into the molecular mechanisms underlying the increased risk of coronary heart disease in postmenopausal women and men consuming a Western diet. These findings have important implications for the design of alternative estrogen receptor modulators in the treatment of postmenopausal women, as studies in rodents have established that improved antioxidant and eNOS gene expression in response to soy isoflavones is associated with decreased ROS production, improved endothelial function, and lower blood pressure in vivo. These findings suggest that patients at risk of coronary heart disease may potentially benefit from an increased intake of dietary soy isoflavones leading to an increased expression and/or activity antioxidant enzymes.

In summary, dietary polyphenols may counteract oxidative stress in vascular and inflammatory diseases [Rahman et al., 2006] by modulating key redox-sensitive gene transcription via NF- κ B and Nrf2/ARE [Siow et al., 2007] signaling pathways. In view of the inherent genetic variability and the potential for noncompliance in human supplementation trials, further studies in genetically modified mice should provide important insights into the mechanisms by which dietary soy isoflavones and other polyphenols regulate eNOS and antioxidant gene expression in endothelial and other vascular cell types, including smooth muscle cells, monocytes, and platelets.

ACKNOWLEDGMENTS

We gratefully acknowledge research funding from the British Heart Foundation (FS/9075, FS/05/005), Biotechnology and Biological Sciences Research Council (BBS/S/K/204/11207), Medical Research Council (G9820929), Heart Research UK (RG2489/04/08), EU COST Action B35, and Wing Yip & Brothers Charitable Foundation. We are indebted to our collaborators whose names appear in the cited publications.

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13 Bioavailability and Metabolism of Resveratrol

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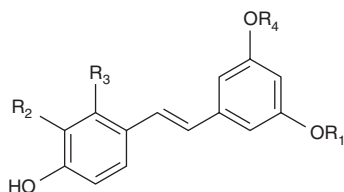
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INTRODUCTION

The essential chemical structure of stilbenes is the *trans*-1,2-diphenylethylene. The parent molecule of this group is the resveratrol (3,4',5- trihydroxystilbene) that exists as two geometric isomers: *cis*- (*Z*) and *trans*- (*E*). The *trans*-form can undergo isomerization to the *cis*-form when exposed to ultraviolet irradiation. Piceid (resveratrol glucoside) is the major resveratrol derivative in plants. Other stilbenes in the vegetal kingdom are pterostilbene, piceatannol, astringin, and viniferins (Fig. 13.1).

Resveratrol and piceid are mainly present in grape and grape products, and its composition is affected by grape variety, maturity degree at harvest, fungal

trans-isomers**Aglycones**

trans-Resveratrol: R₁=H, R₂=H, R₃=H, R₄=H
(C₁₄H₁₂O₃; MW: 228)

Piceatannol: R₁=H, R₂=OH, R₃=H, R₄=H
(C₁₄H₁₂O₄; MW: 244)

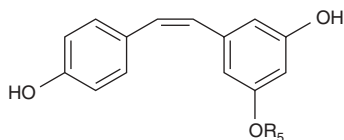
Oxyresveratrol: R₁=H, R₂=H, R₃=OH, R₄=H
(C₁₄H₁₂O₄; MW: 244)

Pterostilbene: R₁=CH₃, R₂=H, R₃=H, R₄=CH₃
(C₁₆H₁₆O₃; MW: 256)

Glucosides

trans-Piceid: R₁=glucose, R₂=H, R₃=H, R₄=H
(C₂₀H₂₂O₈; MW: 390)

Astringin: R₁=glucose, R₂=OH, R₃=H, R₄=H
(C₂₀H₂₂O₉; MW: 406)

cis-isomers**Aglycones**

cis-Resveratrol: R₅=H
(C₁₄H₁₂O₃; MW: 228)

Glucosides

cis-Piceid: R₅=glucose
(C₂₀H₂₂O₈; MW: 390)

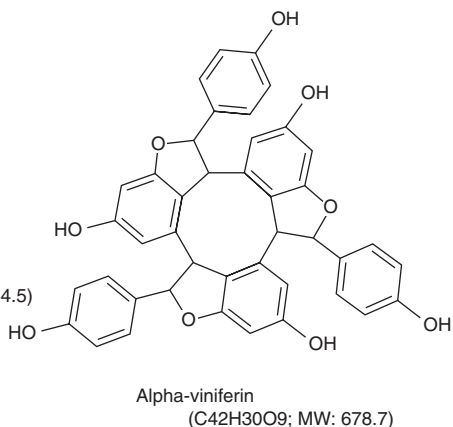
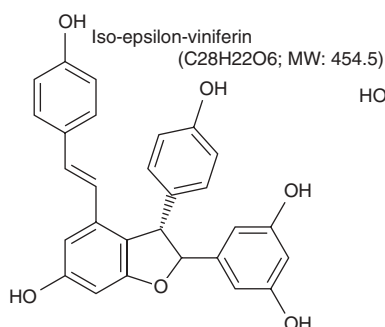
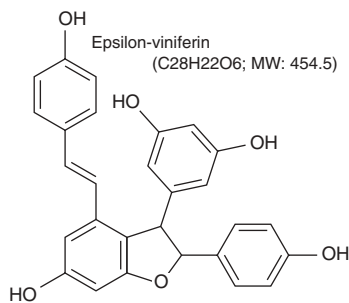


Figure 13.1 Chemical structure of stilbenes present in foods.

stress, climate, soil characteristics (*terroir*), and wine-making process as well as technology [de Andrés-de Prado et al., 2007; González-Barrio et al., 2006; Romero-Perez et al., 2001]. Other slight food sources of stilbenes are peanuts, pistachios, and berries such as bilberry, blueberry, and cranberry [Burns et al.,

2002; Rimando et al., 2004; Sobolev and Cole, 1999; Tokusoglu et al., 2005]. In an adult Spanish cohort resveratrol and piceid, *trans* and *cis*-forms, were evaluated. Estimated median and mean of resveratrol and piceid were 100 and 933 µg/day, respectively, of which 98.4, 1.6, and less than 0.1% come from wines, grape and grape juice, and peanuts, pistachios, and berries, respectively [Zamora-Ros et al., 2008].

IN VITRO AND EX VIVO STUDIES

Several studies have investigated the absorption, transport, and metabolism of resveratrol in vitro and ex vivo. They are summarized in Table 13.1.

Caco-2 cells and isolated small intestine are models of basic nutrition that contributed to the understanding of resveratrol absorption and bioavailability. While the Caco-2 absorption model is a well-defined cellular in vitro system based on a human colonic adenocarcinoma cell line, the isolated small intestine model is nearer to in vivo conditions and is also simpler to handle. It also avoids the methodological problems of in vivo perfusion models [Barthe et al., 1998, 1999].

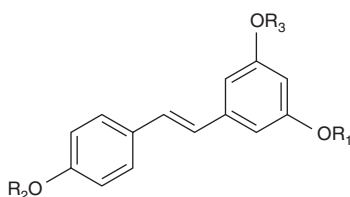
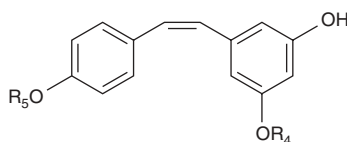
The Caco-2 cells incubated in vitro with *trans*-resveratrol (5–40 µM) showed a concentration-dependent transcellular absorption up to 3 h, with a linear rate for the first hour [Kaldas et al., 2003]. At 3 h of incubation, the concentration of resveratrol reached a plateau [Kaldas et al., 2003; Maier-Salamon et al., 2006]. However, incubations with higher amounts of this polyphenol (40 µM) increased their concentration in the Caco-2 cells, so there was no saturation of the transport systems [Kaldas et al., 2003]. The cellular uptake of *trans*-piceid was also investigated in Caco-2 cells and its transport was slower and about 20% of the resveratrol aglycone [Henry et al., 2005]. *trans*-Resveratrol crosses the apical membrane of the Caco-2 cells using a passive transport, whereas *trans*-piceid seems to use both the active transporter sodium-dependent glucose transporter 1 (SGLT1) and the multidrug resistance protein 2 (MRP2) [Henry et al., 2005]. After piceid absorption, it can be hydrolyzed to resveratrol by the cytosolic-β-glucosidase [Henry-Vitrac et al., 2006]. Another possible pathway to absorb piceid is through its deglycosilation by membrane-bound lactase phlorizin hydrolase, since it then goes across the apical membrane as resveratrol [Henry-Vitrac et al., 2006]. The basolateral to apical efflux also occurs at similar concentrations to apical and basolateral efflux [Henry-Vitrac et al., 2006; Kaldas et al., 2003]. After resveratrol absorption, this is conjugated rapidly in intestinal cells. At 10 µM concentration, *trans*-3-*O*-sulfate was the main metabolite of resveratrol, however, its formation drastically decreased at higher resveratrol concentrations (200 µM), possibly due to saturation or inhibition of metabolism at higher stilbene concentrations [Maier-Salamon et al., 2006]. Glucuronidate forms such as *trans*-resveratrol-4'-*O*-glucuronide and *trans*-resveratrol-3-*O*-glucuronide were also released at less levels than sulfate forms (Fig.13.2) [Maier-Salamon et al., 2006].

Table 13.1 Metabolism of Resveratrol in Vitro and Ex Vivo Models^a

Tissue	Dose, Source (time)	Metabolites (C found)	Reference
Human erythrocytes (1.6×10^9)	21.9 nmol <i>t</i> -Resv (0.25 h)	* <i>t</i> -Resv 10.0 \pm 1.7 nmol/10 ⁹	Blache et al., 1997
Rat erythrocytes (1.6×10^9)		* <i>t</i> -Resv 10.8 \pm 2.2 nmol/10 ⁹	
Rat platelets (10 ⁹)		* <i>t</i> -Resv 2.2 \pm 1.2 nmol/10 ⁹	
Human LDL (0.5 mg/mL)	17.5 μ M <i>t</i> -Resv (0.5 h)	* <i>t</i> -Resv 3.8 \pm 0.9 nmol/mg protein	
Jejunum and ileum of Sprague-Dawley male rats	200 μ M Resv (1.5 h)	Resv (0.03 nmol/cm jejunum) Gluc (1.19 nmol/cm jejunum)	Kuhnle et al., 2000
Small intestine of male Sprague-Dawley rats	28, 34, 57 μ M Resv (1 h)	Vascular effluent: Gluc (16.8%), Resv (3.4%), Sulf (0.3%) Luminal effluent: Gluc (11.2%), Resv (39.7%), Sulf (3.0%) Intestinal tissue: Gluc (0.1%), Resv (1.5%), Sulf (0.3%) <i>c</i> -3-Gluc (+), <i>t</i> -3-Gluc (+), <i>c</i> -4'-Gluc (-), <i>t</i> -4'-Gluc (-)	Andlauer et al., 2000
Human liver microsomes	1 mM <i>cis</i> and <i>t</i> -Resv		Aumont et al., 2001
Rat hepatocytes	20 μ M <i>t</i> -Resv (1 h)		A sensi et al., 2002
Human liver microsomes	5 mM Resv (1 h)		Yu et al., 2002
Human hepatocytes	0.1 mL of 0.1 mM <i>t</i> -resveratrol (4 h)	Free Resv <i>t</i> -3-Gluc, <i>t</i> -4'-Gluc, <i>c</i> -3-Gluc, <i>t</i> -3-Sulf	
Caco-2 cells	5–40 μ M Resv (6 h)	Resv (200–4000 pmol)	Kaldas et al., 2003
Caco-2 cells	150–300 μ M <i>t</i> -Resv and <i>t</i> -piceid (0.03–0.5 h)	<i>t</i> -Resv > <i>t</i> -piceid	Henry et al., 2005
Caco-2 cells	10–200 μ M Resv	<i>t</i> -4'-Gluc, <i>t</i> -3-Gluc, <i>t</i> -3-Sulf	Maier-Salamon et al., 2006
Human liver microsomes	500 μ M <i>t</i> -Resv (5 h)	3-Gluc > 4'-Gluc	Brill et al., 2006
Human intestinal microsomes		3-Gluc < 4'-Gluc	

^aResv: resveratrol; Gluc: glucuronide; Sulf: sulfate; *t*-3-Gluc: *trans*-resveratrol-3-*O*-glucuronide; *t*-4'-Gluc: *trans*-resveratrol-4'-*O*-glucuronide; *c*-4'-Gluc: *cis*-resveratrol-4'-*O*-glucuronide; *c*-3-Gluc: *cis*-resveratrol-3-*O*-glucuronide, *t*-3-Sulf: *trans*-resveratrol-3-sulfate.

*Normalized values.

INTESTINAL METABOLISM*trans*-Isomers*cis*-Isomers*trans*-Isomers

trans-Resveratrol-3-O-glucuronide: R₁=glucuronic acid, R₂=H, R₃=H (C₂₀H₂₀O₉; MW: 404)

trans-Resveratrol-4'-O-glucuronide: R₁=H, R₂=glucuronic acid, R₃=H, (C₂₀H₂₀O₉; MW: 404)

trans-Resveratrol-3,4'-diglucuronide: R₁=glucuronic acid, R₂=glucuronic acid, R₃=H (C₂₆H₂₈O₁₅; MW: 580)

trans-Resveratrol-3-sulfate: R₁=SO₃H, R₂=H (C₁₄H₁₂O₆S; MW: 308)

trans-Resveratrol-4'-sulfate: R₁=H, R₂=SO₃H, R₃=H (C₁₄H₁₂O₆S; MW: 308)

trans-Resveratrol-3,4'-sulfate: R₁=SO₃H, R₂=SO₃H, R₃=H (C₁₄H₁₂O₉S₂; MW: 388)

trans-Resveratrol-3,5'-disulfate: R₁=SO₃H, R₂=H, R₃=SO₃H (C₁₄H₁₂O₉S₂; MW: 388)

trans-Resveratrol-3,5,4'-trisulfate: R₁=SO₃H, R₂=SO₃H, R₃=SO₃H (C₁₄H₁₂O₁₂S₃; MW: 468)

cis-Isomers

cis-Resveratrol-3-O-glucuronide: R₄=glucuronic acid, R₅=H (C₂₀H₂₀O₉; MW: 404)

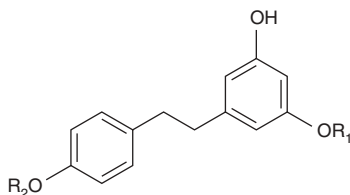
cis-Resveratrol-4'-O-glucuronide: R₄=H, R₅=glucuronic acid (C₂₀H₂₀O₉; MW: 404)

cis-Resveratrol-3,4'-diglucuronide: R₄=glucuronic acid, R₅=glucuronic acid (C₂₆H₂₈O₁₅; MW: 580)

cis-Resveratrol-3-sulfate: R₄=SO₃H, R₅=H (C₁₄H₁₂O₆S; MW: 308)

cis-Resveratrol-4'-sulfate: R₄=H, R₅=SO₃H (C₁₄H₁₂O₆S; MW: 308)

cis-Resveratrol-3,4'-disulfate: R₄=SO₃H, R₅=SO₃H (C₁₄H₁₂O₉S₂; MW: 388)

MICROBIAL METABOLISM

Dihydroresveratrol: R₁=H, R₂=H, (C₁₄H₁₄O₃; MW: 230)

Dihydroresveratrol-glucuronide: R₁=H or glucuronic acid, R₂=glucuronic acid or H (C₂₀H₂₂O₉; MW: 406)

Dihydroresveratrol-sulfate: R₁=H or SO₃H, R₂=SO₃H or H (C₁₄H₁₄O₆S; MW: 310)

Figure 13.2 Chemical structures of resveratrol metabolites.

Maier-Salomon et al. [2006] showed the high influence of metabolized resveratrol on the transepithelial transport of resveratrol and its intracellular accumulation. At 10 μ M concentration in the Caco-2 cells, resveratrol was 84, 8, and 12% conjugated, transported, and accumulated, respectively. Whereas at higher doses (200 μ M) resveratrol was 8, 26, and 61% conjugated, transported, and accumulated, respectively. Moreover, Kaldas et al. [2003] also found a resveratrol accumulation higher than 35-fold when transported through the Caco-2 cells, which suggests enterocytes as a major target site for this polyphenol.

Perfusion of 200 μM *trans*-resveratrol in isolated jejunum and ileum only transferred 6 and 2% of the total amount of resveratrol available, respectively. Resveratrol passed across jejunum as a glucuronide form (1.1 nmol/cm) and in minor amounts as free resveratrol (0.03 nmol/cm) [Kuhnle et al., 2000]. In a single-pass perfusion at low concentrations (28, 34, or 57 μM of *trans*-resveratrol) in the vascular and the luminal side, tissue and blood vessels of rat small intestine, 54, 21, 2, and 0.1% of the doses were recovered, respectively. In isolated luminal small intestine, the stilbene compounds found were free resveratrol (74%), 2-glucuronides (21%), and a sulfate (6%). Whereas in isolated vascular small intestine, the main metabolites were the glucuronidate forms (82%), free resveratrol (17%), and the sulfate form (1.5%). No differences were found in the recoveries using several different doses of resveratrol [Andlauer et al., 2000]. *trans*-Resveratrol was able to bind to human and rat erythrocytes, rat platelets, and low-density lipoprotein (LDL) as free resveratrol after in vitro incubations, confirming that resveratrol can diffuse throughout the body by means of its incorporation into blood cells and lipoproteins [Blache et al., 1997].

Conjugation forms of resveratrol can occur in both enterocytes and hepatocytes. After intestinal microsome incubation with 500 μM *trans*-resveratrol, only glucuronides were formed, in which *trans*-resveratrol-4'-*O*-glucuronide was more abundant than *trans*-resveratrol-3-*O*-glucuronide. In comparison with liver ability to metabolize, glucuronides were formed at higher levels (up to 10-fold) by the intestinal microsomes than the liver microsomes [Brill et al., 2006]. Likewise in liver microsomes, only glucuronidate forms and aglycones were observed after incubation with *trans*- and *cis*-resveratrol. Glucuronidation in liver was stereoselective (*cis*-isomer was 5 to 10-fold faster than *trans*-isomer) at both positions and regioselective (3-position was greater than 4'-position) for both isomers [Aumont et al., 2001]. Moreover Aumont et al. [2001] and Brill et al. [2006] found that resveratrol was only glucuronidized by the UDP-glucuronosyltransferase family 1A (UGT1A). In particular, UGT1A1 and UGT1A9 were mainly involved in the formation of *trans*-resveratrol-4'-*O*-glucuronide and *trans*-resveratrol-3-*O*-glucuronide, respectively. Likewise, in biopsies of human liver it was found that resveratrol is a better substrate for glucuronosyl transferase (K_m 0.15 mM) [de Santi et al., 2000a] than sulfotransferases (K_m 0.60 microM) [de Santi et al., 2000b].

trans-Resveratrol was rapidly metabolized in a dose-dependent manner in rat hepatocytes, approximately 80 and 100% of the resveratrol (20 μM) incubated were conjugated at 20 min and at 1 h, respectively [Asensi et al., 2002]. In rat hepatocytes the main metabolite formed was *trans*-resveratrol-3-*O*-sulfate followed by *trans*-resveratrol-3-*O*-glucuronide. In contrast, in human hepatocytes glucuronides, that is, *trans*-resveratrol-4'-*O*-glucuronide, *trans*-resveratrol-3-*O*-glucuronide, and *cis*-resveratrol-3-*O*-glucuronide, were more abundant than sulfates (*trans*-resveratrol-3-*O*-sulfate) [Yu et al., 2002]. Based on these results, sulfate forms seem to be a minor human hepatic metabolite.

In summary, resveratrol absorption is higher as aglycon than piceid, although piceid can be hydrolyzed by β -glucosidases in the enterocytes [Henry-Vitrac

et al., 2006]. Enterocytes metabolize resveratrol up to a certain extent. At low concentrations it seems that there is mainly a sulfate pathway, but at higher amounts glucuronide forms become more abundant [Maier-Salamon et al., 2006]. Finally, the accumulation of resveratrol in Caco-2 cells suggests that enterocytes is an important target site [Kaldas et al., 2003]. Resveratrol is transported into the bloodstream bounded to blood cells and lipoproteins [Blache et al., 1997]. Hepatocytes also metabolize resveratrol to facilitate its excretion, mainly to glucuronides and, in fewer amounts, to sulfates [Asensi et al., 2002; Yu et al., 2002].

METABOLISM OF RESVERATROL IN VIVO IN ANIMAL MODELS

There is an extensive amount of literature on the in vitro activities of resveratrol. Bertelli et al. [1996] were the first to study the bioavailability of resveratrol in rats. They assessed analysis of plasma and tissues from rats that were administered red wine in a single dose or a regular dose for 15 day. Results indicated that resveratrol is quickly absorbed with a maximum peak at 1 h in plasma as well as in liver and kidney, although in the heart it peak at 2 h. Values obtained after regular consumption of red wine were higher than without the regular consumption in the different organs studies, in particular in the liver. The kidney seemed to be the main route of excretion (Table 13.2) [Bertelli et al., 1996].

Soleas et al. [2001a] performed experiments using *trans*-resveratrol radiolabeled with [³H] in a fixed position in the first benzene ring. Male Wistar rats were administered by gavage 120 nCi as part of three different matrices: 10% (v/v) ethanol, a homogenized vegetable cocktail, or white grape juice. Short-term experiments at 2 h and longer-term experiments at 24 h were carried out. Over a 24-h period only trace amounts of resveratrol (<1%) were detected in tissues such as liver, kidney, heart, or spleen. However, it appeared that 77–80% of *trans*-resveratrol could be absorbed in the rat intestine, with no differences among the three food matrices when absorption was measured as the difference between the dose of radioactivity given and the recovered radioactivity in the stool (24-h feces plus colonic contents and colon). Nevertheless, values ranging from 49 to 61% were present in the urine, regardless the matrix. This 25% difference could be accounted for by excretion via sweat and the respiratory system, metabolism to CO₂, and accumulation in fat-rich tissues such as the brain and nervous system [Soleas et al., 2001a]. Short-term experiments (2 h) showed that over the first 30 min after administration, a significant amount of radioactivity accumulated blood and serum. The radioactivity remained at similar levels during the following 90 min. These observations included the parent compound as well as the metabolites (Table 13.3).

Experiments with unlabeled resveratrol were also conducted in rats after administration of 5 mg of resveratrol. *trans*-Resveratrol concentrations appeared in serum at 15 min, peaked at 30 min, and declined abruptly over the next 30 min. Soleas et al. [2001a] also measured the competition of several polyphenols

Table 13.2 (Continued)

Species	Source and Dose	Administration	Mean (SD) nmol/g											Reference						
			Brain	Lung	Liver	Kidney	Heart	Spleen	Gastrointestinal tract	Small intestine	Stomach	Tooth	Colon		Mucosa	Bile	Plasma (nmol/l)	Feces (%)	Urine (%)	Time
3 Mice per time point	240 mg/kg s-Barv	Intragastric	1.2 (0.1)	50 (25)	51 (35)	36 (10)	75 (27)	-	560 (100)	-	-	-	30 (5)	-	32 (14)	-	-	-	30 min	Sale et al. 2004
10 Male Wistar rats	240 mg/kg s-3,4,5,4'-tetramethoxyflavone	Intragastric	5 (1)	11 (0)	8 (5)	11 (4)	10 (5)	-	7000 (6500)	-	-	130 (500)	20 min	5 (2)	-	-	-	10 min		
10 Male Wistar rats	200 mg/kg day s-Barv during 8 weeks	Oral	-	-	s-Barv n.d. d-Barv n.d. 3-SubE 1.92 (0.20) 4'-SubE 5.75 (2.08) 3-Gluc 1.58 (0.25) Barv: 1.20 (0.01)	n-Barv n.d. d-Barv 5.09 (1.73) 3-SubE 1.19 (0.50) 4'-SubE n.d. 3-Gluc 6.71 (1.46) Barv: n.d.	-	-	-	-	-	-	-	TriSubE 7.0 (2.6) 3,4'-d-Barv 19.25 (6.0) 3,5-d-Barv 3.30 (0.8) 2-SubE 1.28 (0.3) 3-Gluc 1.79 (2.1) Barv: n.d.	TriSubE n.d. 3,4'-d-Barv 3.42% 3,5-d-Barv 0.80% 2-SubE 3.95% 4'-SubE n.d. 3-Gluc 28.1% Barv: 3.99%	TriSubE n.d. 3,4'-d-Barv 8.39% 3,5-d-Barv n.d. 2-SubE 1.29% 3-SubE 1.75% 4'-SubE n.d. 3-Gluc n.d. Barv: 5.13%	24h	Wang et al. 2005		
10 Male Wistar rats	50 mg/kg day s-Barv during 8 weeks	Oral	-	-	n.d.	n.d.	-	-	-	-	-	-	-	n.d.	-	-	-	10 min	Li et al. 2006	
18 Male Wistar rats	50 mg/kg Flavil	Oral	15.56 (7.3)	28.72 (6.9)	11.46 (6.4)	6.62 (3.1)	1.28 (0.7)	71.87 (35.4)	270.60 (76.4)	452.78 (188.5)	15.60 (6.2)	-	-	-	-	-	-	10 min	Li et al. 2006	

Table 13.2 (Continued)

Species	Source and Dose	Administration	Mean (SD) nmol/g										Plasma (μ mol/l)	Feces (%)	Urine (%)	Time	Reference
			Brain	Lung	Liver	Kidney	Heart	Spleen	Gastrointestinal tract	Small Intestine	Stomach	Testis					
6 Male Sprague- Dawley rats	50 mg/kg resveratrol + 1.85 MBq [3H]resveratrol	Gavage	<0.1% dpm	<0.1% dpm	0.98% dpm	0.59% dpm	<0.1% dpm	76.2% dpm	-	-	-	-	1.7% dpm	-	-	2 h	El-Mehsen et al. 2006
			Gluc: 0.2 (0.0) Resv: 0.1 (0.0)	Gluc: 0.5 (0.2) Resv: 0.2 (0.2)	Gluc: 1.2 (0.3)	Gluc: 4.0 (0.6)	Gluc: 0.4 (0.0)	n.d	-	-	-	-	-	Gluc: 7.0 (1.0) Resv	2 Gluc Resv		
6 Male Sprague- Dawley rats	50 mg/kg resveratrol + 1.85 MBq [3H]resveratrol	Gavage	0.35% dpm										0.48% dpm	-	3.3% dpm	18 h	El-Mehsen et al. 2006
			Gluc: 0.13 (0.05) Resv: 0.07(0.05)	Gluc: 0.1 (0.05) Resv: 0.2 (0.05)	Gluc: 0.1 (0.05) Resv: 0.15 (0.05)	n.d	Resv: 0.09 (0.02)	n.d	-	-	-	-	-	-	1.55% dpm		

Table 13.2 (Continued)

Species	Source and Dose	Administration	Mean (SD) nmol/kg													Reference			
			Brain	Lung	Liver	Kidney	Heart	Spleen	Contraceptual tract	Small intestine	Stomach	Testis	Colon	Mile	Plasma (pmol/L)		Feces (%)	Urine (%)	Time
3 Balb/c male mice			n.c.	n.c.	441 (50) dpm/300 mg	342 (165) dpm/300 mg	n.c.	n.c.	n.c.	2208 (1458) dpm/300 mg	-	-	n.c.	106 (80) dpm/100 mg	460 (70) dpm/100 mg	0.5 (0.2) dpm/100 mg	-	180 (26.7) dpm/100 mg	1.5h
3 Balb/c male mice	7.4 kBq ¹⁴ C- <i>sRav</i> (5 mg/kg)	Intragastric	196 (47) dpm/300 mg	380 (144) dpm/300 mg	374 (46) dpm/300 mg	535 (13) dpm/300 mg	280 (132) dpm/300 mg	322 (62) dpm/300 mg	n.c.	1641 (183) dpm/300 mg	-	-	106 (9)	300 (85) dpm/100 mg	1170 (500) dpm/100 mg	0.6 (0.6) dpm/100 mg	-	286 (16.7) dpm/100 mg	3h
3 Balb/c male mice			n.c.	n.c.	186 (20) dpm/300 mg	262 (123) dpm/300 mg	n.c.	n.c.	n.c.	935 (201) dpm/300 mg	-	-	n.c.	88 (26) dpm/100 mg	346 (280) dpm/100 mg	1.29 (0.6) dpm/100 mg	-	239 (23.5) dpm/100 mg	6h
3 Balb/c male mice			-	-	0.05 (0.03) cpm/100 mg	0.07 (0.02) cpm/100 mg	-	-	-	n.c.	-	-	1.89 (0.72) cpm/100 mg	-	-	-	-	-	1.5h
3 Balb/c male mice	74 kBq ¹⁴ C- <i>sRav</i> (50 mg/kg)	Intragastric	-	-	0.1 (0.01) cpm/100 mg	0.07 (0.02) cpm/100 mg	-	-	-	1.7 (0.16) cpm/100 mg	-	-	0.05 cpm/100 mg	-	-	-	-	-	3h
3 Balb/c male mice			-	-	0.05 (0.01) cpm/100 mg	0.03 (0.01) cpm/100 mg	-	-	-	0.2 (0.04) cpm/100 mg	-	-	0.4 (0.04) cpm/100 mg	-	-	-	-	-	6h
3 Balb/c male mice	92.5 kBq ¹⁴ C- <i>sRav</i> (66 mg/kg)	Intragastric	-	-	¹⁴ C- <i>sRav</i> : 25 pmol/L	¹⁴ C- <i>sRav</i> : 30 pmol/L	-	-	-	-	-	-	-	-	-	-	-	-	3h

^aTriStoff: resveratrol-3,4'-5-trisulfate; dStoff: resveratrol-6-sulfate; sStoff: resveratrol-sulfate; Gluc: resveratrol-glucuronide; *sRav*: trans-resveratrol; Radioactivity was measured by dpm or cpm. dpm: disintegrations per minute and cpm: counts per minute; MBq: megabecquerel; kBq: kilobecquerel; n.c.: not detected; n.e.: not collected.

Table 13.3 Metabolism of Resveratrol in Vivo in Animal Models^a

Animals	Source	Administration	Dose mg/kg	Blood or Serum or Plasma	Urinary excretion		Time (h)	Reference
					%	Metabolites		
8 male Wistar rats	<i>trans</i> -Resveratrol	Intragastric	2 μ L of	—	—	—	24	Soleas et al., 2001
2 male Wistar rats	tritiated in 4-position with 10%EtOH or V- 8 homogenized vegetable cocktail or white grape juice		120 nCi/mL	Serum: 690 dpm/mL Blood: 600 dpm/ ml	49–61%	—	0.5	
Male Wistar rats	<i>t</i> -Resv	Intragastric	1.43 mg/kg	<i>t</i> -Resv: Serum: 0.01 μ M	—	—	1	
			4.29 mg/kg	Blood: 0.01 μ M <i>t</i> -Resv: Serum: 0.02 μ M	—	—	1	
			7.14 mg/kg	Blood: 0.01 μ M <i>t</i> -Resv: Serum: 0.03 μ M	—	—	1	
2 male Wistar rats	<i>t</i> -Resv	Intragastric	14.28 mg/kg	Blood: 0.02 μ M <i>t</i> -Resv Serum: 1.44 μ M	—	—	0.5	
3 Sprague–Dawley female rats	Resv	Intraperitoneal	20 mg/kg	Blood: 1.00 μ M	—	—	2 h	Yu et al., 2002
12 Balb/c female mice	Resv	Intraperitoneal	20 mg/kg	<i>t</i> -3-Gluc (3 μ M), <i>t</i> -3- Sulf (13 μ M)	—	—	0.25	
12 Balb/c female mice		Gavage	20 mg/kg	<i>t</i> -3-Gluc (1 μ M), <i>t</i> -3- Sulf (5 μ M)	—	—	0.25	
12 Balb/c female mice		Gavage	60 mg/kg	<i>t</i> -3-Gluc (175 μ M), <i>t</i> -3-Sulf (300 μ M)	—	—	0.25, 0.5	

(Continued)

Table 13.3 (Continued)

Animals	Source	Administration	Dose mg/kg	Blood or Serum or Plasma	Urinary excretion		Time (h)	Reference
					%	Metabolites		
5 male Sprague-Dawley rats	<i>t</i> -Resv	Oral	20 mg/kg	—	—	Gluc, Sulf, DHR, DHR-Sulf	—	Wang et al., 2005
Female CF-1 mice	Grape juice	Oral	~0.7 mg/kg Resv	n.d.	n.d.	—	—	Meng et al., 2004
			~1.4 mg/kg Resv	n.d.	1-2%	<i>t</i> -Resv *	24	
			~2.7 mg/kg Resv	n.d.	0.9-2.3%	<i>t</i> -Resv *	24	
2 female Wistar rats	<i>t</i> -Resv	Intragastric	2 mg/kg	Resv: 0.09 µM	—	—	4	Chen et al., 2007
			5 mg/kg	Total: 1.2 µM	—	—	4	
			5 mg/kg	Resv: 0.11 µM	—	—	1.5	
5 Sprague-Dawley rats	<i>t</i> -Resv	Intravenous	5.13 mg/kg	Total: 1.5 µM	—	—	4	Juan et al., 1999
			4.87 mg/kg	<i>t</i> -Resv (~21.9 µM)	—	—	0.08	
Male Sprague-Dawley rats	<i>c</i> -Resv	Oral	2 mg/kg	<i>c</i> -Resv (~17.5 µM)	—	—	0.08	Juan et al., 1999
			2 mg/kg	<i>t</i> -Resv (0.77 µM)	—	—	0.25	

^a*t*-Resv: *trans*-resveratrol; *t*-3-Gluc: *trans*-resveratrol-3-*O*-glucuronide; *t*-3-Sulf: *trans*-resveratrol-3-sulfate; Gluc: resveratrol glucuronide; Sulf: resveratrol-sulfate; DHR: 7,8-dihydroresveratrol; DHR-Sulf: 7,8-dihydroresveratrol sulfate; radioactivity was measured by dpm: desintegrations per minute. * Quantified after hydrolysis.

when catechin, quercetin, and resveratrol (1–10 nM) were co-administered in rats. They found no competition between the three polyphenols and the absorption of *trans*-resveratrol was not saturable in the used concentrations [Soleas et al., 2001a].

In 2006, El-Mohsen et al. investigated the time-dependent appearance and disappearance in various organs of metabolic products of [³H] *trans*-resveratrol (2 and 18 h following gastric administration of 50 mg/kg + 1.85 MBq) to Sprague–Dawley rats. At 2 h postgavage, most of the recovered radioactivity was still present in the gastrointestinal tract. The total dose administered reached only 1.7% in plasma. The only tissues with high concentrations were the liver and the kidney while the amount detected in other tissues was <0.1%. In contrast, at 2 and 18 h postadministration, approximately 11% of total dose was accounted for in all of the studied tissues (Table 13.2). They found that around 90% of the administered dose was absorbed, however, only 3.3% of absorbed resveratrol was detected in urine. The undetected radioactivity is expected to be lost via respiration and/or accumulation in other tissues, such as skeletal muscle and adipose tissue [El-Mohsen et al., 2006; Soleas et al., 2001a].

The metabolites of [³H] *trans*-resveratrol detected in tissues and plasma were also investigated. In kidney, liver, heart, lungs, brain, and plasma (2-h samples), the only metabolite found was resveratrol–glucuronide. Glucuronides in plasma and kidney disappeared completely at 18 h. In lungs, liver, heart, and brain, the main detected metabolite at 18 h was the *trans*-resveratrol (Table 13.2). This study provided data on the metabolic fate of resveratrol. While glucuronides were predominant in plasma and tissues at the earlier times, the aglycone represented the main form at later times [El-Mohsen et al., 2006].

The kinetics of absorption, tissue distribution, and excretion was assessed after a single oral dose of ¹⁴C-*trans*-resveratrol to male Balb/c mice. Blood and tissue samples were collected at 1.5, 3, and 6 h postadministration [Vitrac et al., 2003]. The autoradiographic examination of mice tissue sections and the radioactivity quantification revealed a higher fixation of ¹⁴C-*trans*-resveratrol in the stomach, liver, kidney, intestine, bile, and urine and other organs of absorption and elimination. The concentration of radioactivity in blood was low and regular during the experimental period. During the entire experimental period, nearly complete absorption occurred in the small intestine as suggested by the higher concentration found in the proximal section compared to the distal section. After 6 h of oral administration the high concentration in stomach and duodenum was perhaps located in the mucosa, although this was also probably due to residual stomach content. The low concentrations found in the colon suggests that it was a minor way of elimination. The major concentrations found in urine and the decreasing concentrations in kidney showed that renal excretion was a major way of elimination. The kidney and the liver were the organs with highest deposition of ¹⁴C-*trans*-resveratrol. In contrast to the kidney in which the parent drug was the major radioactive product, liver extracts 3 h after administration showed the presence of ¹⁴C-*trans*-resveratrol with a high concentration of radioactive glucuronide or sulfated conjugated [Vitrac et al., 2003].

Contrasting with other studies that showed the accumulation of labeled resveratrol in tissues, the following studies addressed the search for the formed metabolites in biological fluids and tissues. Yu et al. [2002] synthesized and identified for the first time, the monosulfate isomers of resveratrol, resveratrol-3 and 4'-sulfate. These studies were performed in female Sprage-Dawley rats after intraperitoneal administration of 20 mg/kg of resveratrol with urine collection at 2 h and in female Balb/c mice after intraperitoneal (20 mg/kg) and oral administration (20 and 60 mg/kg) with collection of serum samples up to 4 h. The mass spectrometry analysis of rat urine samples only detected *trans*-resveratrol-3-glucuronide. In the mouse serum samples, after administration of 20 mg/kg via intraperitoneal or oral, maximum concentrations of resveratrol-3-glucuronide and resveratrol-3-sulfate were observed at 15 min. The sulfate was almost three-fold greater than the glucuronide (Table 13.3). Only traces of free resveratrol were observed. Furthermore, no resveratrol or metabolites were detected after 1 h. When higher doses were orally administered to mouse (60 mg/kg), the same metabolites as before were observed, but the maximum value for sulfate metabolite were reached after 30 min instead of 15 min, probably because more time was required to absorb the large volume that was administered. This was not the case for the minor dosage both glucuronide and sulfate metabolite were still detected after 3 h, suggesting that resveratrol was distributed to tissues and cleared slowly.

Wenzel et al. [2005] synthesized the same resveratrol-3 and 4'-sulfates as Yu et al [2002] but also the 3 and 4'-glucuronide, 3,4'-disulfate, 3,5-disulfate, and 3,4',5-trisulfate metabolites of resveratrol. To search for these compounds in vivo conditions, two experiments were carried out. Resveratrol aglycone was administered to male Wistar rats in a dosage of 50 or 300 mg/kg/day during 8 weeks, and urine, feces, and tissue samples were collected. As shown in Table 13.2, the administration of 50 mg/kg of resveratrol resulted in the formation of *trans*-resveratrol-3-sulfate, *trans*-resveratrol-disulfate, *trans*-resveratrol-3-glucuronide, and resveratrol in urine. Furthermore, an increase of the dosage (sixfold) showed the additional formation of *trans*-resveratrol-trisulfate. In both experiments, the 3-glucuronide was the main metabolite, and sulfate (3-sulfate and 3,5-disulfate) derivatives were 100- and 50-fold less, in relation to the dosage, respectively. The total recovery in urine of rats on 50 and 300 mg/kg was 15 and 54%, respectively. In feces samples of rats of the 50-mg/kg group, only 3-sulfate and resveratrol were determined, and 300 mg/kg administration resulted in the formation of all possible sulfates except trisulfate metabolite. The total recovery in feces samples was 15 and 31%, respectively, for both dosages [Wenzel et al., 2005]. They also studied the different distribution of these metabolites in plasma, kidney, and liver tissues and only after feeding 300 mg/kg were metabolites observed in 50% of the animals. The main metabolite in plasma samples was 3,4'-disulfate followed by 3,4',5-trisulfate and 3-glucuronide metabolites (Fig. 13.2). In liver samples only 3 and 4'-monosulfates and 3-monoglucuronide were identified. The main metabolite in kidneys was the 3-glucuronide metabolite, followed by disulfates and minor 3-sulfate. In contrast to plasma and kidney, free resveratrol was only observed in liver samples.

Similarly in 2005, Wang et al. identified the microbial metabolites of resveratrol in rats (Table 13.3). Urine samples were obtained after oral administration of 20 mg/kg to Sprague–Dawley rats. They identified resveratrol–glucuronide, resveratrol–sulfate, 7,8-dihydroresveratrol, and 7,8-dihydroresveratrol–sulfate as the main 12-h urinary metabolite in rats by mass spectrometry after are SPE treatment [Wang et al., 2005].

In 2004, Meng et al. investigated the urinary and plasma levels of resveratrol and quercetin after their administration as constituents of grape juice or as pure aglycones. The first study was carried out during 4 days with female CF-1 mice receiving solutions containing 18.4 and 36.8% of grape preparation. The urinary excretion of resveratrol increased gradually during the study period, excreting a cumulative amount of approximately 1–2% of the ingested dose when receiving 18.4% grape juice and 0.9–2.3% when the dose was 36.8%. The second study was done after the oral dose of 2 and 5 mg/kg resveratrol to female Wistar rats. In plasma for both doses, resveratrol was mainly present as conjugates and the resveratrol aglycone constituted around 10–11% of total resveratrol at the beginning and declined to 5–7% at 4 h (Table 13.3) [Meng et al., 2004].

PHARMACOKINETICS OF RESVERATROL AND DERIVATIVES

The evaluation of pharmacokinetic analysis of resveratrol was carried out in different animal models such as rats, mice, and rabbits [Asensi et al., 2002; Chen et al., 2007; Juan et al., 2002; Marier et al., 2002; Sale et al., 2004]; furthermore, pharmacokinetic analysis was also evaluated with other resveratrol derivatives such as piceid [Lv et al., 2006; Zhou et al., 2007], a *Smilax china* root extract [Huang et al., 2008], 3,4,5,4'-tetramethoxystilbene [Sale et al., 2004], piceatanol, pinosylin, and rhapontigenin [Roupe et al., 2006] (Table 13.4).

In the first kinetic study, Juan et al. [2002] focused on the determination of the time course of *trans*-resveratrol level in plasma after the 2-mg/kg orally administrated dose to rats. Resveratrol had already reached the bloodstream at 5 min, presented its maximum level at around 10 min, and was still detected after 60 min [Juan et al., 2002].

Another pharmacokinetic study was carried out after intravenous administration of 4.87 mg/kg of *cis*-resveratrol and 5.13 mg/kg of *trans*-resveratrol to Sprague–Dawley rats. The study showed that both isomers showed a rapid eliminate disposition in 90 min [Chen et al., 2007].

There is a further pharmacokinetic study in which *trans*-resveratrol in the aglycone form and the glucuronide forms were examined following intravenous (15 mg/kg) and oral (50 mg/kg) administration of *trans*-resveratrol to rats [Marier et al., 2002]. After intravenous administration, the plasmatic resveratrol concentrations declined rapidly over the first 2 h. Then, concentration profiles of resveratrol and resveratrol–glucuronide from intravenous or oral administration increased abruptly due to enterohepatic recirculation over the 4- to 8-h time period that resulted in a significant maintenance in the terminal elimination

Table 13.4 Pharmacokinetic Studies of Resveratrol in Animal Models and Humans^a

Species	Source (dose)	Administration	C _{max} (μmol/L)	T _{max} (h)	T _{1/2} (h)	AUC _{0-∞} (μmol · h/L)	Urinary Excretion (%)	References
6 male Wistar rats	Piceid (50 mg/kg)	Oral	0.93 (0.39)	0.35 (0.14)	1.68 (0.3)	2.23 (0.69)	—	Ly et al., 2006
C57BL/6J male mice	<i>l</i> -Resv (20 mg/kg)	Intragastric	2.6 (1.0)	2.5	—	—	—	Asensi et al., 2002
Wistar male rats		Intragastric	1.2 (0.4)	5	—	—	2	
6 ESD NZW male rabbits		Intragastric	1.1 (0.8)	2.5	—	—	—	
3 mice	<i>l</i> -Resv (240 mg/kg)	IV	—	—	0.24	—	—	Sale et al., 2004
6 male Sprague-Dawley rats	<i>l</i> -Resv (15 mg/kg)	Intravenous	—	—	Resv: 0.13 (0.02) Gluc: n.a.	Resv: 5.64 (0.5) Gluc: 38.7 (5.5)	—	Marier et al., 2002
6 male Sprague-Dawley rats	<i>l</i> -Resv (50 mg/kg)	Oral	Resv: 6.57 (1.55) Gluc:105.2 (32.4)	Resv: 0.29 (0.1) Gluc: 0.42 (0.3)	Resv: 1.48 (0.4) Gluc:1.55 (0.4)	Resv: 7.1 (2.0) Gluc: 324.7 (57.6)	—	
5 female Sprague-Dawley rats	1 g/kg <i>Smilax china</i> root extract equivalent to 180 mg/kg <i>O</i> -Resv and 80 mg/kg Resv	Oral	<i>O</i> -Resv: 21.93 (3.1) Resv: 9.61 (1.5)	0.25 0.25	— —	91.78 (13.7) 17.81 (0.6)	—	Huang et al., 2008
Male Sprague-Dawley rats	<i>l</i> -Resv (2 mg/kg)	Intragastric	Resv: 2.57	<i>l</i> -Resv 0.16	0.25	—	—	Juan et al., 2002
8 Wistar rats	<i>l</i> -Piceid (150 mg/kg)	Oral	<i>l</i> -Gluc: 64.85 (18.5) <i>l</i> -Resv: 3.55 (0.7) <i>l</i> -Piceid: 4.35 (1.3)	2 1 0.5	4 2 1	— — —	—	Zhou et al., 2007
5 male Sprague-Dawley rats	Piceatannol: (10 mg/kg) Pinosylvin: (10 mg/kg)	Intravenous	—	—	4.23 (1.25)	34.75 (10.2)	32.8	Roupe et al., 2006
			—	—	0.82 (0.05)	24.67 (5.7)	9.46	

(Continued)

Table 13.4 (Continued)

Species	Source (dose)	Administration	C _{max} (µmol/L)	T _{max} (h)	T _{1/2} (h)	AUC _{0-∞} (µmol · h/L)	Urinary Excretion (%)	References
5 male Sprague-Dawley rats	Rhapontigenin: (10 mg/kg)	Oral	—	—	3.0 (1.35)	32.52 (0.4)	1.25	
5 male Sprague-Dawley rats	<i>t</i> -Resv (7.7 mg/kg)		<i>t</i> -Resv: 0.32 (0.16) Gluc 1: 1.00 (0.35) Gluc 2: 0.91 (0.36) 3-Sulf: 3.69 (0.95)	<i>t</i> -Resv: 0.83 (0.5-1.5) Gluc 1: 2.00 (1.0-6.0) Gluc 2: 1.50 (1.0-5.0) 3-Sulf: 1.50 (1.0-5.0)	<i>t</i> -Resv: 2.85 Gluc 1: 2.85 Gluc 2: 3.09 3-Sulf: 3.21	<i>t</i> -Resv: 0.98 Gluc 1: 8.4 (0.1) Gluc 2: 5.6 (0.1) 3-Sulf: 17.8(0.1)	<i>t</i> -Resv: 0.04 (0.05) Gluc 1: 2.0 (0.4) Gluc 2: 8.9 (2.6) 3-Sulf: 11.4 (2.3)	Boocock et al 2007
10 humans (45% males)	<i>t</i> -Resv (15.4 mg/kg)		<i>t</i> -Resv: 0.51 (0.38) Gluc 1: 1.17 (0.90) Gluc 2: 1.66 (1.35) 3-Sulf: 6.82(21.39)	<i>t</i> -Resv: 0.759 (0.5-4.0) Gluc 1: 2.25 (1.0-6.0) Gluc 2: 1.75 (1.0-5.1) 3-Sulf: 2.00 (1.0-5.0)	<i>t</i> -Resv: 8.87 Gluc 1: 7.27 Gluc 2: 6.64 3-Sulf: 4.51	<i>t</i> -Resv: 2.4 (0.3) Gluc 1: 13.4(0.3) Gluc 2: 11.4(0.3) 3-Sulf: 44.1(0.3)	<i>t</i> -Resv: 0.1 (0.1) Gluc 1: 2.1 (1.1) Gluc 2: 3.2 (1.7) 3-Sulf: 7.3 (3.1)	
10 humans (45% males)	<i>t</i> -Resv (38.5 mg/kg)		<i>t</i> -Resv: 1.18 (0.65) Gluc 1: 2.16 (0.81) Gluc 2: 4.02 (2.88) 3-Sulf: 9.05 (2.46)	<i>t</i> -Resv: 1.38 (0.5-4.0) Gluc 1: 2.375 (1.0-8.0) Gluc 2: 2.00	<i>t</i> -Resv: 4.22 Gluc 1: 10.6 Gluc 2: 8.42 3-Sulf: 11.5	<i>t</i> -Resv: 3.4 (0.2) Gluc 1: 24.8(1.2) Gluc 2: 18.9(0.1) 3-Sulf: 74.5(0.2)	<i>t</i> -Resv: 0.1 (0.1) Gluc 1: 1.7 (1.7) Gluc 2: 3.1 (1.4)	

(Continued)

Table 13.4 (Continued)

Species	Source (dose)	Administration	C_{max} ($\mu\text{mol/L}$)	T_{max} (h)	$T_{1/2}$ (h)	$AUC_{0-\infty}$ ($\mu\text{mol}\cdot\text{h/L}$)	Urinary Excretion (%)	References
10 Humans (45% males)	<i>t</i> -Resv (76.9 mg/kg)		<i>t</i> -Resv: 2.36 (1.71) Gluc 1: 3.18 (1.47) Gluc 2: 4.29 (2.85) 3-Sulf: 13.94(6.69)	(1.0-6.0)	<i>t</i> -Resv: 8.52 Gluc 1: 7.90 Gluc 2: 5.83 3-Sulf: 7.71	<i>t</i> -Resv: 5.8(0.3) Gluc 1: 43.5(0.2) Gluc 2: 37.5(0.3) 3-Sulf: 135.5(0.2)	3-Sulf: 5.2 (2.6)	
				3-Sulf: 2.00				
				(1.0-5.2)				
				<i>t</i> -Resv: 0.83				
				(0.5-1.5)				
				Gluc 1: 2.00				
				(1.0-6.0)				
				Gluc 2: 1.50				
				(1.0-5.0)				
				3-Sulf: 1.50				
(1.0-5.0)								

^a *t*-Resv: *trans*-resveratrol; *O*-Resv: oxyresveratrol; Gluc: resveratrol-glucuronide; 3-Sulf: resveratrol-3-sulfate.

half-life of resveratrol aglycone. The clearance of resveratrol after oral or intravenous administration was higher than that of resveratrol-glucuronide, which resulted in a systemic exposure of approximately 46- or 7-fold, respectively, lower than that of glucuronide.

Asensi et al. [2002] studied tissue levels and pharmacokinetics of resveratrol after intravenous (20 mg/kg) and oral (20 mg/kg) administration to rabbits, rats, and mice. The highest concentration levels in plasma of *trans*-resveratrol were reached within the first 5 min in all animals studied but showed a short half-life and a rapid clearance. They found extravascular levels of resveratrol after its oral administration to rabbits, rats, and mice with the highest levels occurring within the first 10 min in liver, lung, brain, and kidney; therefore, it appears that resveratrol does not accumulate extravascularly and its presence in the tissues is parallel in time to its bioavailability in blood [Asensi et al., 2002]. They suggested that most or all circulating resveratrol may be removed by liver metabolism and if high doses are administered, high rates of hepatic metabolism could be occurring [Asensi et al., 2002].

Sale et al. [2004] studied the pharmacokinetic properties of 3,4,5,4'-tetramethoxystilbene compared with those of resveratrol in the plasma and mice tissues. This analog compound was a novel congener of pharmacological interest, and it was under preclinical evaluation as a potential antitumor prodrug. This tetramethoxystilbene was capable of preferentially interfering with the proliferation and survival of transformed human lung-derived cells, with much lower growth inhibitory and apoptotic properties in its untransformed counterparts than resveratrol, which does not possess this discriminatory potential. Therefore, a kinetic evaluation and a tissue distribution for both were applied after a single dose (240 mg/kg) oral administration to mice. The results suggested that the introduction of four methoxy groups into the stilbene structure, three of which replaced the hydroxyl moieties in resveratrol, did not increase the systemic availability of the molecule in comparison to resveratrol [Sale et al., 2004].

They also evaluated the pharmacokinetic properties of resveratrol compared to the synthetic analog in different mice tissues in which resveratrol might prevent malignancy or delay its onset. The availability of the synthetic analog was inferior in plasma, liver, kidney, lung, and heart than resveratrol; meanwhile, it was more available in intestinal and colonic mucosa and in brain [Sale et al., 2004]. These results provided a good argument to assess 3,4,5,4'-tetramethoxystilbene as a colorectal cancer chemo preventive agent. Furthermore, in the search for the main conjugated forms, resveratrol showed its glucuronidated and sulfated conjugates, while, the 3,4,5,4'-tetramethoxystilbene underwent metabolic hydroxylation or single and double *O*-demethylation [Sale et al., 2004].

The pharmacokinetic dispositions of other stilbenes that are structurally similar to resveratrol and have pharmacological activity across many anticancer, anti-inflammatory, and antioxidant assays have been studied. The pharmacokinetics was characterized in male Sprague-Dawley rats after single intravenous

doses of 10 mg/kg of piceatannol, pinosylvin, or rhanpontigenin. The detectable plasma half-lives of these compounds appear to be relatively short. The estimates of oral bioavailability characterize these stilbenes as poorly bioavailable compounds. All three stilbenes undergo extensive glucuronidation upon intravenous administration, as was determined by plasma and urine concentrations. The total amount excreted shows that the three stilbenes excreted in urine—32.8, 9.5, and 1.3%, respectively—are very small compared with the overall dose given of each one (3.5 mg). This indicates that the three stilbenes in contrast to resveratrol are eliminated predominantly via nonrenal excretion [Roupe et al., 2006].

Recently, the pharmacokinetics of resveratrol from *Smilax china*, a rhizome extensively used in traditional Chinese medicine was evaluated [Huang et al., 2008]. Forty-five female rats were orally administered with 1 g/kg *S. china* extract equivalent to 180 mg/kg of oxyresveratrol and 80 mg/kg of resveratrol. The pharmacokinetic parameters showed that the two stilbenes were rapidly absorbed into the body fluid from the gastrointestinal tract and could still be detected in the plasma at least 6 h after the administration [Huang et al., 2008], probably due to the high dose administered.

PICEID, THE GLUCOSIDE OF RESVERATROL

Various studies have focused on the metabolism of piceid, the glucoside of resveratrol. These studies are of great interest due to the higher amount of piceid compared to resveratrol in food. Therefore, bioavailability studies of this compound are required. In vitro studies have already observed the absorption of piceid in the enterocytes, but in vivo studies in animal models are still scarce.

The bioavailability and tissue distribution of *trans*-piceid was studied in Wistar rats after its oral administration [Lv et al., 2006; Zhou et al., 2007]. At present, the studies of the pharmacokinetics and distribution of piceid have been poorly documented. The first study with piceid administration to rats, measured its pharmacokinetics and its tissue distribution after a single oral administration of 50 mg/kg to 6 male Wistar rats. This was the first in vivo study that demonstrated the absorption of piceid with maximum plasma concentrations of 0.93 (0.4) μM at 21 min (Table 13.2) [Lv et al., 2006]. Another relevant result of this study was the diffusion of piceid to tissues. The highest concentrations were found in the stomach, then, in the small intestine, followed by spleen, lung, brain, testis, liver, kidney, and heart at 10 min. At 30 min, high concentrations were still detected in stomach and relatively high concentrations were present at 120 min. The absorption, distribution, and elimination of piceid were quick after the oral administration. The major distribution organs in rats were stomach, small intestine, and spleen; furthermore, it was able to cross the blood–brain and blood–testis barriers. Nevertheless, no long-term accumulation of piceid in tissues took place [Lv et al., 2006].

A recent study showed the bioavailability of piceid after oral administration of 150 mg/kg of piceid to rats. *trans*-Piceid was absorbed, with maximum plasma levels at 30 min, and metabolized to *trans*-resveratrol, with a maximum plasma concentration at 60 min, and this to *trans*-resveratrol–glucuronide, with maximum concentration at 120 min [Zhou et al., 2007]. The resveratrol–glucoside was absorbed by transepithelial transport across the intestine with maximum concentration occurring at 30 min after administration. This glycosylated derivative is deglycosylated in *trans*-resveratrol in the intestine with a cleavage by the CBG after passing the brush–border membrane by SGLT1 or by the membrane-bound enzyme LPH followed by passive diffusion of the released *trans*-resveratrol, which is further metabolized inside the cells into glucuronconjugates [Henry-Vitrac et al., 2006]. The constant absorption of piceid from the first minutes of ingestion is reflected in the *trans*-resveratrol–glucuronide with the highest concentrations (30-fold higher) taking place in plasma and having a relatively long elimination half-life. Furthermore, the parent drug and the metabolites, *trans*-resveratrol and *trans*-resveratrol–glucuronide were detected at 8, 12, and 24 h after the oral dose [Zhou et al., 2007].

In conclusion, resveratrol is absorbed and already shows plasmatic and serum levels between 5 min and 4 h, depending on the dose and the animal species. Furthermore, plasmatic levels increase between 4 and 8 h due to the enterohepatic recirculation [Marier et al., 2002]. When absorbed, resveratrol is metabolized and the major conjugated forms in plasma consisted of sulfate conjugates, in which minor concentrations of the 3-glucuronide were observed. Further studies are required to obtain more standards of metabolites and more data about the major sulfate metabolite since Wenzel et al. [2005] and Yu et al. [2002] found major amounts for 3,4'-disulfate and 3-sulfate conjugates, respectively. Resveratrol is also distributed to different tissues such as liver and kidney, the major organs of deposition, and also in the lung, spleen, and heart. It crosses the blood–brain and blood–testis barriers showing major concentration levels in the intestinal tract. Maximum concentrations were found at early hours and trace amounts at later hours, showing no accumulation extravascularly [Asensi et al., 2002]. The main metabolite found in tissues at early hours was the glucuronide form, and the free form of resveratrol predominated at later hours [El-Mohsen et al., 2006].

Renal excretion was the major way of elimination compared to the colonic one. Urinary excretion varied between 3 and 61%, depending on the study, animal species, and dose. Some studies had also shown a possible excretion via sweat and respiratory system and metabolism to CO₂ [El-Mohsen et al., 2006; Soleas et al., 2001a]. The major conjugated form present in urine is the 3-glucuronide metabolite [Wenzel et al., 2005; Yu et al., 2002] although mono-, di-, and tri-sulfated metabolites and free resveratrol were also determined [Wang et al., 2005; Wenzel et al., 2005]. Furthermore, microbial metabolites such as dihydroresveratrol and its sulfate conjugate were also identified in 12 h rat urine [Wang et al., 2005].

HUMAN STUDIES

Studies that investigate the bioavailability of resveratrol in humans are scarce. Moreover, the research in this area is quite recent. It has been summarized in Table 13.5. The experimental approaches have been improved with the use of new analytical techniques such as mass spectrometry to identify and quantify metabolites present in very low concentrations. Resveratrol and its metabolites have been measured in several biofluids: plasma or serum, urine, LDL, and feces.

In 2001, the group of Soleas, Yang, and Goldberg [Soleas et al., 2001b] was the first to investigate the oral administration of resveratrol: 25 mg of *trans*-resveratrol standard dissolved in 120 mL of white wine were consumed by 10 healthy volunteers. The analyses were performed by gas chromatography–mass spectrometry (GC-MS) after treatment with β -glucuronidases and sulfatases. After stilbene intake, free resveratrol and its conjugates were found in all subjects and at all times, even after an abstinence of at least 24 h from food sources of this polyphenol. In plasma samples, they found that the highest resveratrol concentration (345.1 $\mu\text{g/L}$) occurred at 30 min. Moreover, resveratrol conjugates were 20- to 50-fold more abundant than free resveratrol. After resveratrol intake, the recovery in urine of 24 h was 24.6% as free and conjugated forms. Likewise, the urine concentrations of resveratrol conjugates were 30- to 50-fold higher than aglycone. At 2 h the highest concentration of resveratrol was observed, it was nearly 8 mg/L.

Three years later the same group [Goldberg et al., 2003] tested the absorptive efficiency of *trans*-resveratrol standard (25 mg) dissolved in three different matrices: white wine, grape juice, and vegetable juice. The conditions of study were the same as in the previous work. The results were also similar and serum showed the highest level at 30 min. Furthermore, the total absorption curves were similar regardless the matrices. In this study slight amounts of resveratrol at basal time were detected too. Urinary 24-h resveratrol excretions were 17.0, 16.8, and 16.0% after oral administration of vegetable juice, wine, and grape juice, respectively. The results in plasma and urine supported that there were no differences in resveratrol absorption by using the different matrices.

In 2004, Meng et al. published the first study that investigated the bioavailability of grape juice (ranged from 200 to 1200 mL) after oral ingestion, whose composition was 1.6 mg/L of stilbene, mainly as piceid [Meng et al., 2004]. Oral consumption of *trans*-resveratrol standard at several concentrations (0.03, 0.5, and 1 mg/kg) were also studied. In this case, the analyses were performed by liquid chromatography–tandem mass spectrometry (LC-MS/MS) after enzymatic hydrolysis. Resveratrol was only found in plasma when high doses (1 mg/kg) were ingested. At lower concentrations of standard or grape juice were ingested, no peaks were reached. However, urinary recoveries were 52, 34, and 26% after 0.03, 0.5, and 1 mg/kg, respectively. These results could suggest an inversely dose-dependent manner. Furthermore with a dose of 0.03 mg/kg, resveratrol was mainly excreted in the first 2–3 h; however, with 1 mg/kg, 7–10 h were necessary to excrete most of the resveratrol. Resveratrol was mainly found in the conjugated form as

Table 13.5 Human Bioavailability Studies^a

Participants	Gender (%)	Age (y ^c)	Resveratrol Source	Dose (mg/kg body weight)	Concentration (µmol/L)	Time (h)	Urinary Excretion (%) (Time, h)	Reference
10	Male (45%)	19-61	RESV Standard in 120 mL of white wine	0.357 mg/kg (25 mg total)	Resv 0.031 Conjugated ^b 1.48	0.5-1	Total 24.6% (24 h)	Soleas et al., 2001
4	Males (100%)	25-45	RESV Standard dissolved in 100 mL vegetable juice	0.357 mg/kg (25 mg total)	Resv 0.037 Conjugated ^b 2.03	0.5	17.0 (24 h)	Goldberg et al., 2003
4			RESV Standard dissolved in 100 mL white wine	0.357 mg/kg (25 mg total)	Resv 0.031 Conjugated ^b 1.80	0.5	16.8 (24 h)	
4			RESV Standard dissolved in 100 mL grape juice	0.357 mg/kg (25 mg total)	Resv 0.035 Conjugated ^b 1.82	0.5	16.0 (24 h)	
1	Male	30-50	RESV Standard	0.03 mg/kg	n.d.		Gluc: 52 (24 h)	Meng et al., 2004
1				0.5 mg/kg	n.d.		Gluc: 34 (24 h)	
1				1 mg/kg	Gluc 1.86	1.5	Gluc: 26 (24 h)	
1			200 mL grape juice	0.005 mg/kg ^c	n.d.		n.d. (24 h)	
1				(0.32 mg total)				
1			400 mL grape juice	0.009 mg/kg ^c	n.d.		n.d. (24 h)	
1				(0.64 mg total)				
1			600 mL grape juice	0.014 mg/kg ^c	n.d.		Gluc: (24 h)	
1				(0.96 mg total)				
1			1200 mL grape juice	0.027 mg/kg ^c	n.d.		Gluc: 5.0 (24 h)	
1				(1.92 mg total)				
6	3 Males (50%)	23-34	¹⁴ C- RESV standard Oral	0.385 mg/kg ^c (25 mg total)			53.4-84.9% (72 h)	Walle et al., 2004
5			¹⁴ C- RESV standard Intravenous	0.023 mg/kg ^c (1.5 mg total)			42.3-83.2% (72 h)	
1			RESV Standard ORAL	1.538 mg/kg ^c (100 mg total)	Tr.		Gluc: 13 (1) Sulf: 24 (3) Total 37 (12 h)	Vitaglione et al., 2005
10	Males (100%)	30 (25-40)	300 mL red wine	0.0034 g/kg	Gluc 0.096	1		
5	1 Male (20%)	29 (24-38)	Lambrusco + meal	0.0329 µg/kg	Gluc 0.687	0.5-2		
10	3 Males (30%)	31 (24-54)	Cabernet Franc	0.0075 µg/kg	Resv 0.004 Gluc 0.150	0.5		
10	Male (100%)	28.2 (25-41)	600 mL red wine Agljanico + meal	0.005 mg/kg/d ^c	n.d.	1-2		
			300 mL/d sparkling wine (28 d)	(0.357 mg/d) ^c			<i>t</i> -3-Gluc: 4.8 (2.5) <i>c</i> -3-Gluc: 2.4 (1.3) Total 7.2 (2.7) (morning urine)	Zamora-Ros et al., 2006 (Continued)

Table 13.5 (Continued)

Participants	Gender (%)	Age (y ^c)	Resveratrol Source	Dose (mg/kg body weight)	Concentration (µmol/L)	Time (h)	Urinary Excretion (%) (Time, h)	Reference
10	Women (100%)	38.1 (25–50)	200 mL/d white wine (28 d)	0.007 mg/kg/d (0.398 mg/d) ^c	n.d.		<i>t</i> -3-Gluc: 11.7 (2.8) <i>c</i> -3-Gluc: 3.3 (3.6) Total 15.0 (4.3) (morning urine) <i>t</i> -3-Gluc: 4.2 (3.2) <i>c</i> -3-Gluc: 1.2 (1.2) Total 5.4 (3.9) (morning urine)	Urpi-Sarda et al., 2007
10	Women (100%)	38.1 (25–50)	200 mL/d red wine (28 d)	0.043 mg/kg/d (2.56 mg/d) ^c	n.d.		<i>t</i> -4 ['] Gluc: 0.13 (0.19) <i>t</i> -3 Gluc: 0.38 (0.59) <i>c</i> -4 ['] Gluc: 0.75 (1.2) <i>c</i> -3 Gluc: 1.9 (1.9) <i>t</i> -4 ['] Sulf: 0.01 (0.03) <i>t</i> -3 Sulf: 0.16 (0.67) <i>c</i> -4 ['] Sulf: 19.6 (17.4) <i>c</i> -3 Sulf: 0.47 (2.2) Total 23.4 (4 h)	
5	Male (100%)	25–28	250 mL red wine	0.077 mg/kg ^c (5.4 mg total)			<i>t</i> -3-Sulf: 4.53 <i>t</i> -3,4'-Disulf: 1.71 <i>t</i> -3,5'-Disulf: 7.18 3-Gluc: 2.99 4'-Gluc: 0.69 (2) <i>t</i> -Digluc: 2.65 Total 13.6-35.7 (48 h)	Burkon and Somoza 2008
9	Males (100%)	23–41	PICEID Standard dissolved in 100 mL ethanol (15%) + 400 mL milk (1.5% fat)	1.22 mg/kg (85.5 mg/70 kg)	<i>t</i> -3-Sulf: 0.95 (0.16) <i>t</i> -3,4'-Disulf: 0.33 (0.07) <i>t</i> -3,5'-Disulf: 0.94 (0.17) 3-Gluc: 0.16 (0.04) 4-Gluc: 0.19 (0.05) (2) <i>t</i> -Digluc: 0.35 (0.09)	<i>t</i> -3-Sulf: 1 <i>t</i> -3,4'-Disulf: 6 3,5'-Disulf: 8 3-Gluc: 6-8 4'-Gluc: 6 (2) <i>t</i> -Digluc: 6		

^aResv: resveratrol; Gluc: glucuronide; Sulf: sulfate; *t*-4 Gluc: *trans*-resveratrol-4-*O*-glucuronide; *t*-3 Gluc: *trans*-resveratrol-3-*O*-glucuronide; *c*-4 Gluc: *cis*-resveratrol-4-*O*-glucuronide; *c*-3 Gluc: *cis*-resveratrol-3-*O*-glucuronide; *t*-4 Sulf: *trans*-resveratrol-4'-sulfate; *t*-3 Sulf: *trans*-resveratrol-3-sulfate; *c*-4 Sulf: *cis*-resveratrol-4'-sulfate; *c*-3 Sulf: *cis*-resveratrol-3-sulfate; *t*-3,4'-Disulf: *trans*-resveratrol-3,4'-disulfates; *t*-3,5'-Disulf: *trans*-resveratrol-3,5-disulfates; *t*-digluc:*trans*-resveratrol-*C*/*O*-diglucuronides.

^bQuantified after hydrolysis of resveratrol conjugates.

^cCalculated as weight estimation 70 and 60 kg for males and females, respectively. n.d. non detected.

glucuronide. After grape juice consumption, at low doses (200 and 400 mL) peaks of resveratrol in urine were not detected. Although at high doses (600 and 1200 mL) only conjugated forms were found. Moreover, after 1200 mL of grape juice, the recovery was only about 5% of the dose administered. This study showed that the glycoside forms are absorbed less than aglycones.

In the same year, Walle et al. [2004] were the first to administer intravenous and oral labeled resveratrol in humans. After 25 mg of an oral ^{14}C -resveratrol dose (6 healthy subjects), total radioactivity in plasma was maximum (491 ng/mL) at approximately 1 h after the intake, and then it kept falling during the following 72 h over the study. After 1.5 mg intravenous ^{14}C -resveratrol (5 healthy subjects) total radioactivity fell rapidly, but plasma radioactivity remained for the following 72 h. Moreover, both half-lives ranged from 7 to 14 h after any dose. This data is important because a single high dose of resveratrol can be active in plasma at least half a day. After oral dosage, 53–85 and 0.3–38 radioactivity were recovered in urine and feces, respectively. Similar results were observed after intravenous doses: 42–83 and 0.6–23 of total radioactivity were found in urine and feces, respectively. High variability was observed in the urinary and fecal recoveries. Elimination half-lives in urine ranged from 6.5 to 18.8 h after oral or intravenous doses. The authors also tested the metabolites formed after a large unlabeled oral dose of 100 mg of resveratrol. The analyses were performed by LC-MS-UV. This was the first study of human urine that analyzed resveratrol metabolite profile, showing the presence of two monoglucuronides, a monosulfate, a dihydroresveratrol monoglucuronide, and a dihydroresveratrol monosulfate. Dihydroresveratrol metabolites could be formed by the intestinal microbiota as occurs with other polyphenols [Gonthier et al., 2003]. The sulfate and glucuronide conjugates excreted in the urine accounted for 24 and 13% of the dose, respectively. However, in plasma resveratrol or its metabolites were not detected at any time. Only trace amounts (less than 5 ng/mL) could be found in plasma after an oral dose of the 100 mg.

Vitaglione et al. [2005] evaluated the bioavailability of red wine resveratrol consumed with several meals: standard, fat, or lean meal. Identification and quantification of resveratrol and its metabolites in serums were done by LC-MS/MS. In the first experiment, 10 healthy males were involved in the assessment of the bioavailability of Lambrusco red wine (0.82 mg *trans*-resveratrol/L) consumed with a standard meal (Milanese beef cutlet and chips). Only in 4 of the volunteers at 1 h were some amount of resveratrol glucuronides that ranged from 15 to 168 ng/mL found. In the second experiment, 5 healthy volunteers were recruited to intake 600 mL of Cabernet Franc red wine (3.2 mg *trans*-resveratrol/L) over night while fasting. Only 3 of the 5 subjects showed resveratrol free or metabolites in serum. In 2 volunteers resveratrol aglycone was detected but not in quantifiable amounts. Resveratrol glucuronides (isomers 3 and 4) were reached at different times (0.5–2 h) and different concentrations (77–900 ng/mL). In the third experiment, 10 healthy subjects consumed 600 mL of aglianico red wine (0.8 mg *trans*-resveratrol/L) with either a lean meal or with a fat meal. Free resveratrol was detected in 2 of the subjects

at concentrations ranging from 1 to 6 ng/mL at 30 min after wine consumption. Resveratrol–glucuronides were only detected in one subject of each intervention at 1–2 h after intake. This study clearly showed a high interindividual variation in the absorption and bioavailability of resveratrol.

Zamora-Ros et al [2006] carried out the first work that assessed the bioavailability of resveratrol (provided by different wines) in a regular intervention during 28 day. The analyses were performed by LC-MS/MS. In the first study, 10 healthy males were recruited to consume 300 mL/day of sparkling wine (1.19 mg resveratrol/l). After 28 day of supplementation, urinary *trans*- and *cis*-resveratrol-3-*O*-glucuronides were 75 and 38 nmol/g creatinine, respectively. In the second study, 10 healthy females were selected to consume 200 mL of white wine (1.99 mg resveratrol/L) or 200 mL of red wine (12.8 mg resveratrol/L) in a crossover clinical trial. Likewise after 28 days only resveratrol metabolites were detected in morning urine. *trans*- (205 and 473 nmol/g creatinine) and *cis*-resveratrol-3-*O*-glucuronides (58 and 140 nmol/g creatinine) were found after white and red wine intake, respectively. Those studies showed that urinary excretion was dose dependent. Furthermore, slight amounts of resveratrol metabolites were also detected at baseline periods. No free resveratrol or piceid were detected in any of the studies.

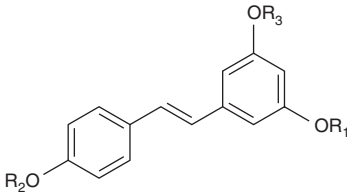
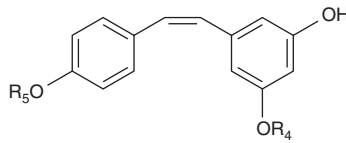
Urpi-Sarda et al. [2005, 2007] published the first works that investigated the presence of resveratrol in LDL. The analyses were performed by LC-MS/MS. Eleven healthy males were recruited to consume 250 mL of merlot wine (10.2 mg resveratrol/L). Free resveratrol, glycoside, glucuronidate, and sulfate forms were found in 24-h LDL. The detected metabolites were *cis*- and *trans*-, 3- and 4'-position, glucuronides, and sulfates. The more abundant metabolites were 88% glucuronides (*trans*-resveratrol-3-*O*-glucuronide, 112 pmol/mg LDL protein), 10.4% sulfates, and 2.0% *trans*-aglycone. Piceid was also found in LDL 24 h in lower concentrations (1.1–28.5 pmol/mg LDL protein). In the second experiment the metabolic profile was assessed at low resveratrol doses. Five healthy males were recruited to consume 250 mL of merlot wine (10.2 mg/L). Only conjugated forms were detected in urine 4 h after wine consumption. The more abundant metabolites were *cis*-resveratrol-4'-*O*-sulfate (9.3 μ mol/g creatinine) and *cis*-resveratrol-3-*O*-glucuronide (0.9 μ mol/g creatinine). Sulfation and glucuronidation represented 86.6 and 13.4% of total urinary resveratrol excretion, respectively.

In 2007, Boocock et al. [2007] were the first to publish a complete phase I dose pharmacokinetic study in humans. Ten healthy volunteers were recruited to consume single doses of oral resveratrol (0.5, 1, 2.5, or 5 g). Consumption of resveratrol did not cause serious adverse events. Analyses of resveratrol and its metabolites were performed by LC-MS/MS. In plasma in all intake doses resveratrol-3-sulfate (56%) was the highest metabolite, the second and third metabolites were monoglucuronides (17 and 23%, respectively), and, finally, the lowest was free resveratrol (5%). Resveratrol was rapidly absorbed, the T_{\max} for all metabolites ranged between 0.8 and 2.4 h, although the half-lives of free resveratrol and the conjugated forms remained for a long time in plasma, between 2.9 and 11.5 h.

Urinary excretion mainly took place in the first 4 h after consumption (77% of total excretion), although resveratrol metabolites remained in urine between 12 and 24 h after intake. Free resveratrol, 2 glucuronides, and the 3-sulfate excreted in the urine 24 h after intake were below 0.04, 2, 9, and 11% of the 0.5 mg provided, respectively. At higher dose (5 mg) resveratrol, glucuronides and sulfate recoveries in the urine at 24 h were 0.1, 0.5, 3, and 5% of the dose, respectively. In urinary excretion, the sulfate forms were also higher than the glucuronide and free forms.

The piceid absorption was recently investigated for the first time. Nine healthy males participated in this controlled trial, which consisted of the administration of a single oral dose of 85.5 mg piceid standard per 70 kg. Resveratrol metabolites in plasma and urine were identified by LC-MS/MS, although these were quantified by HPLC-DAD. The same number of resveratrol metabolites were detected in both urine and plasma: *trans*-resveratrol-3-sulfate, *trans*-resveratrol-3,4'-disulfate, *trans*-resveratrol-3,5-disulfate, *trans*-3-*O*-glucuronide, *trans*-4'-*O*-glucuronide, and two resveratrol diglucuronides (*trans*-resveratrol-2-*C*- β -/4'- β -*O*-diglucuronide and *trans*-resveratrol-2-*C*- β -/5- β -*O*-diglucuronide). The two disulfates, previously identified in animals, and the two diglucuronides have been found in humans for the first time, thereby increasing the classical metabolic profile (monosulfates and monoglucuronides). The authors did not detect piceid nor resveratrol aglycone in any sample. Piceid was absorbed rapidly (1 h) in the form of *trans*-resveratrol-3-sulfate, whereas the other resveratrol metabolites reached their maximum concentration between 6 and 8 h after piceid administration. Sulfation pathway was more efficient than glucuronide. These authors also observed that 34, 44, and 46% of sulfates, disulfates, and diglucuronides, respectively, were non-covalently bound to plasma proteins; the rest of the percentage of conjugates were transported freely in plasma. After 24 h of piceid intake, no resveratrol metabolites were detected. The total urinary recovery ranged between 14 and 36%. The metabolic profile was approximately 15 and 8% as sulfate and glucuronide conjugates, respectively. Urinary excretion was completed within 48 h of oral piceid administration (Fig. 13.3).

In conclusion, resveratrol seems to have a greater absorption than piceid at nutritional doses [Meng et al., 2004], although pharmacological doses of piceid standard is also recovered at similar percentages than resveratrol standard [Burkon and Somoza, 2008]. Moreover, resveratrol and piceid are absorbed and metabolized quickly. In blood samples, the highest resveratrol peak is detected at around 30–60 min [Boocock et al., 2007; Goldberg et al., 2003; Soleas et al., 2001b; Vitaglione et al., 2005] and 6 h [Burkon and Somoza, 2008] after consumption of resveratrol or piceid, respectively. Nevertheless traces of resveratrol could remain in plasma for at least 72 h after ingestion [Walle et al., 2004]. Resveratrol conjugates are more abundant than the free form. It seems that sulfation is a more efficient metabolic pathway than glucuronidation (56 vs. 39%) [Boocock et al., 2007; Burkon and Somoza, 2008]. Part of resveratrol is transported through the body bound to LDL mainly as glucuronides (88%)

INTESTINAL METABOLISMtrans-isomerscis-isomerstrans-Isomers

trans-Resveratrol-3-O-glucuronide: R₁=glucuronid acid, R₂=H, R₃=H (C₂₀H₂₀O₉; MW: 404)

trans-Resveratrol-4'-O-glucuronide: R₁=H, R₂=glucuronid acid, R₃=H, (C₂₀H₂₀O₉; MW: 404)

trans-Resveratrol-3,4'-diglucuronide: R₁=glucuronid acid, R₂=glucuronid acid, R₃=H (C₂₆H₂₈O₁₅; MW: 580)

trans-Resveratrol-3-sulfate: R₁=SO₃H, R₂=H (C₁₄H₁₂O₆S; MW: 308)

trans-Resveratrol-4'-sulfate: R₁=H, R₂=SO₃H, R₃=H (C₁₄H₁₂O₆S; MW: 308)

trans-Resveratrol-3,4'-sulfate: R₁=SO₃H, R₂=SO₃H, R₃=H (C₁₄H₁₂O₉S₂; MW: 388)

trans-Resveratrol-3,5'-disulfate: R₁=SO₃H, R₂=H, R₃=SO₃H (C₁₄H₁₂O₉S₂; MW: 388)

trans-Resveratrol-3,5,4'-trisulfate: R₁=SO₃H, R₂=SO₃H, R₃=SO₃H (C₁₄H₁₂O₁₂S₃; MW: 468)

cis-Isomers

cis-Resveratrol-3-O-glucuronide: R₄=glucuronid acid, R₅=H (C₂₀H₂₀O₉; MW: 404)

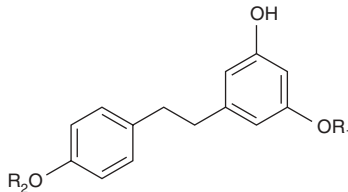
cis-Resveratrol-4'-O-glucuronide: R₄=H, R₅=glucuronid acid (C₂₀H₂₀O₉; MW: 404)

cis-Resveratrol-3,4'-diglucuronide: R₄=glucuronid acid, R₅=glucuronid acid (C₂₆H₂₈O₁₅; MW: 580)

cis-Resveratrol-3-sulfate: R₄=SO₃H, R₅=H (C₁₄H₁₂O₆S; MW: 308)

cis-Resveratrol-4'-sulfate: R₄=H, R₅=SO₃H (C₁₄H₁₂O₆S; MW: 308)

cis-Resveratrol-3,4'-disulfate: R₄=SO₃H, R₅=SO₃H (C₁₄H₁₂O₉S₂; MW: 388)

MICROBIAL METABOLISM

Dihydroresveratrol: R₁=H, R₂=H, (C₁₄H₁₄O₃; MW: 230)

Dihydroresveratrol-glucuronide: R₁=H or glucuronid acid, R₂=glucuronid acid or H (C₂₀H₂₂O₉; MW: 406)

Dihydroresveratrol-sulfate: R₁=H or SO₃H, R₂=SO₃H or H (C₁₄H₁₄O₆S; MW: 310)

Figure 13.3 Pathways of resveratrol absorption, distribution, metabolism, and excretion.

and sulfates (11%) [Urpi-Sarda et al., 2005, 2007]. In a recent study, it was shown that more than 50% of resveratrol conjugates (sulfates, disulfates, and C/O-diglucuronides) were bound to proteins in plasma [Burkon and Somoza, 2008]. Urine (53–85%) and fecal (0.3–38%) were the most important ways of excretion of resveratrol measured by total radioactivity [Walle et al., 2004]. However, urinary recoveries by mass spectrometry ranged from 5 to 37%, depending on dose and the kind of resveratrol source [Boocock et al., 2007; Burkon and Somoza, 2008; Goldberg et al., 2003; Meng et al., 2004; Soleas et al., 2001b; Urpi-Sarda et al., 2007; Walle et al., 2004; Zamora-Ros et al., 2006]. Metabolites identified in urine are four monoglucuronides, four monosulfates, two

disulfates, two C/O-diglucuronides, free aglycone, dihydroresveratrol monoglucuronide, and monosulfate. Likewise in urinary excretion the sulfate forms seem to be higher than the glucuronide and free forms [Boocock et al., 2007; Burkon and Somoza, 2008; Urpi-Sarda et al., 2007; Walle et al., 2004]. The most important limitation of the bioavailability is the great individual variability; for this reason, further investigation with a higher number of volunteers is necessary in order to assess the percentage of absorption and excretion, and the metabolite profile of this polyphenol.

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14 Resveratrol: Biochemistry and Functions

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INTRODUCTION

Interest in the potential health benefits associated with dietary consumption of plant polyphenols has increased significantly in the past decade. Moreover, the role of these phytochemicals to combat oxidative stress, which plays a major role in the pathophysiology associated with various diseases, is enormous. Resveratrol (3,4',5-trihydroxy stilbene) is one of the numerous polyphenolic compounds which is found in nearly 72 vegetal sources [Dercks and Creasy, 1989]. After the French paradox study in 1992 [Renaud and de Lorgeril, 1992], resveratrol got recognized proving best among all the natural polyphenolic compounds. Resveratrol is a member of a family of polyphenols called viniferins. A mild-to-moderate wine-drinking habit attenuates cardiovascular, cerebrovascular, and peripheral vascular risk due to reduced platelet and monocyte adhesion and attenuates the risk of prostate as well as a variety of cancers including pancreatic, gastric, and thyroid cancer. Resveratrol, a polyphenol phytoalexin, possesses diverse biochemical and physiological properties including estrogenic, antiplatelet, and anti-inflammatory actions. Several recent studies have revealed that resveratrol mediates protection from a wide variety of degenerative diseases and hence increases the life span. Resveratrol inhibits apoptotic cell death at a lower concentration, thereby providing protection from various diseases including myocardial ischemic reperfusion injury, atherosclerosis, and ventricular arrhythmias. Both in acute and in chronic models, resveratrol-mediated cardioprotection is achieved through the preconditioning effect, rather than direct effect as found in conventional medicine. Used in higher doses resveratrol facilitates apoptotic cell death, behaving in contrast, as a chemopreventive agent. Resveratrol likely fulfills the definition of a pharmacological preconditioning compound and gives hope for its therapeutic promise from alternative medicine. The purpose of this review is to provide evidence on how the biochemical properties of resveratrol is helping it to use as a preventive medicine for the maintenance of health.

CHEMICAL OVERVIEW OF RESVERATROL

Resveratrol is a member of the stilbene family, a group of compounds which consist of two aromatic rings joined by a methylene bridge. 3,4',5-trihydroxystilbene is the IUPAC (International Union of Pure and Applied Chemistry) nomenclature for resveratrol but is also known as 3,4',5-stilbenetriol, and it has

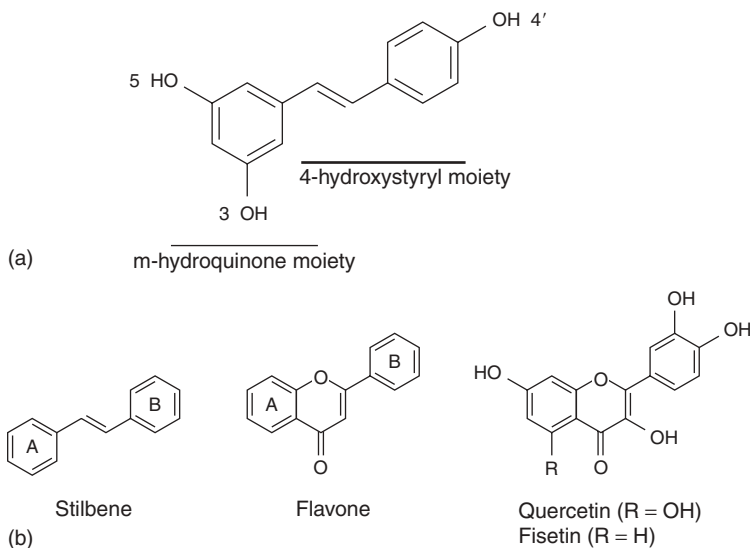


Figure 14.1 (a) Chemical structure of resveratrol. (b) Chemical structure of stilbene and the structurally similar polyphenols (quercetin and fisetin). The common rings are lettered.

the molecular formula $C_{14}H_{12}O_3$ with a molecular weight of 228.25 Da (Fig. 14.1).

Resveratrol exists in two structural isomeric forms, *cis* and *trans* (Fig. 14.2). Although both *cis*- and *trans*-resveratrol (with their glucosides) occur naturally and seem to exert similar biological effects, but the actions of the *trans*-isoform are more widely investigated and are better known [Orallo, 2006]. It has been identified that the greater biological activity of the *trans*-isomer is due to the 4'-hydroxystyryl group [Stivala et al., 2001]. *Trans*-resveratrol in powder form is found to be stable under "accelerated stability" conditions of 75% humidity and 40°C in the presence of air [Baur et al., 2006]. The nuclear magnetic resonance (NMR)-derived solution structure of 3,4',5-trihydrostilbene is an accurate representation of the line segment 1- α - α' -1', the angles 1- α - α' and 1'- α' - α , and the dihedral angle 2-1-1'-2', all of which are related to the *trans*-stereochemistry of the phenolic rings, which are free to rotate about the C1-C α and C1'-C α' bonds [Commodari et al., 2005].

Resveratrol-3-*O*- β -D-glucoside is called piceid. Resveratrol is a naturally occurring phytoalexin ("defender of the plant") which is produced in response to an injury, such as mechanical trauma, ultraviolet light, and infection by pathogenic microorganisms, especially fungi, providing means for defense [Bertelli et al., 1995; Baolin et al., 2004; Bak et al., 2006; Baur et al., 2006]. It is formed via a condensation reaction between three molecules of malonyl CoA and one molecule of 4-coumaroyl CoA [Soleas et al., 1997]. Resveratrol synthase facilitates this condensation reaction, which also produces four

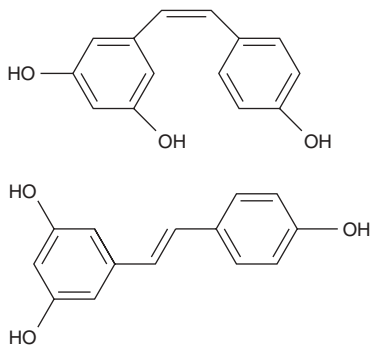


Figure 14.2 *Cis* (top) and *trans* (bottom) isomers of resveratrol.

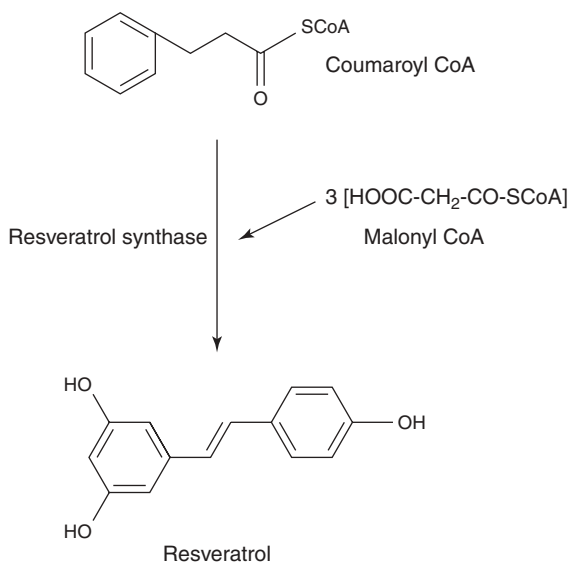


Figure 14.3 Synthesis of resveratrol.

molecules of CO₂ (Fig. 14.3). The biosynthesis of resveratrol is similar to that of the chalcone, which is the precursor of ubiquitous flavonoids and anthocyanins, except for the formation of the final product, which is due to the ring folding after the formation of a tetraketide.

SOURCES OF RESVERATROL

Polygonum cuspidatum, a weed used in Chinese and Japanese medicine, is one of the first plants identified to extract resveratrol and is one of the richest

sources of resveratrol. In certain higher order plants, such as eucalyptus, spruce, lily, mulberry and peanut, stilbene synthase (STS) genes produce resveratrol from the reaction between one molecule of *p*-coumaroyl CoA and three molecules of malonyl CoA [Cellotti et al., 1996]. External stimuli such as fungal attack and ultraviolet (UV) radiation activate the stilbene synthase genes in grapes to produce resveratrol in order to adequately protect the grapes from those stimuli [Soleas et al., 1997; Pervaiz, 2003]. This STS gene is also found in peanut root, strawberry, blueberry, mulberry, grapes, and other plants such as eucalyptus, spruce, and lily. *Vitis vinifera*, *V. labrusca*, and *V. muscadine* are three different types of grapes, that contain a very high concentration of resveratrol. The skin and seeds of these types of grapes contain 50–100 µg/g of resveratrol [Koop, 1998]. These varieties of grapes are particularly suitable to make red wine. Thus, grapes and red wines are considered as the major sources of resveratrol. In addition to grapes, a large variety of fruits including mulberry, bilberry, lingo berry, sparkle-berry, deer berry, partridgeberry, cranberry, blueberry, jackfruit, peanut a wide variety of flowers and leaves including gnetum, white hellebore, corn lily, butterfly orchid tree, eucalyptus, spruce, poaceae, and rheum also contain resveratrol [Burns et al., 2002]. In contrast to the constitutive isoform of stilbene synthase occurring in the *Rheum rhaponticum* (rhubarb), an inducible enzyme is expressed in the Vitaceae family [Hain et al., 1990]. Since fungal infections are more common in cooler climates, grapes grown in cooler climates have a higher concentration of resveratrol [Koop, 1998]. However, grapes cultured in the zone of the equator also contain resveratrol in high concentration because of higher ultraviolet irradiation [Schubert et al., 1997].

EPIDEMIOLOGIC OBSERVATIONS OF RESVERATROL

There are several lines of epidemiologic data suggesting the beneficial effects of resveratrol. There are some circumscribed areas around the globe where average age of people is remarkably high and there is an unusual presence of centenarians.

The well-known French paradox was first noted by Irish physician Samuel Black in 1819. Back in the nineteenth century, he was the first to observe the fact that people in France suffer relatively low incidence of coronary heart disease, despite their diet being rich in saturated fats. It was proposed that France's profound red wine consumption is a primary factor contributing to the protective effect. The first scientific evidence, however, for the cardiovascular benefits of red wine was put forward by Renaud and his associates in 1992 [Renaud and Lorgeril, 1992]. In this study, popularly known as the French paradox, the researchers found that there had been a low mortality rate from, and incidence of, coronary heart disease among French men above the age of 40 years compared to men in the United Kingdom and the United States, despite their high consumption of saturated fats and the prevalence of other

risk factors such as smoking. This was attributed to their so-called Mediterranean diet, which includes a moderate intake of wine. It has been proposed that one of the active ingredients potentially related to this effect in red wine is resveratrol [Corder et al., 2001].

METABOLISM OF RESVERATROL

The potential health benefits of resveratrol depend, in part, upon its absorption, bioavailability, and metabolism. Several *in vitro* and *in vivo* models have been utilized to characterize the absorption and bioavailability of resveratrol. Using the Caco-2 human intestinal cell model, it was demonstrated that resveratrol uptake remained linear, for an hour, and transportation was nondirectional [Kaldas et al., 2003]. Metabolites identified in the Caco-2 cells were resveratrol sulfate and resveratrol glucuronide, with resveratrol sulfate being predominant. The ease of absorption and accumulation of resveratrol suggests gastrointestinal cells as a possible biological target *in vivo*. Henry and co-workers [2005] also observed passive diffusion of resveratrol in Caco-2 cells; however, the transport of *trans*-piceid required the sodium-dependent glucose co-transporter SGLT1. Similar to Caco-2 cell uptake, normal and tumor human hepatic cell lines utilize both passive diffusion and active transport for resveratrol uptake [Lancon et al., 2004]. In the rat small intestine model, resveratrol was absorbed on the serosal side of the jejunum, with the majority being metabolized to resveratrol glucuronide [Kuhnle et al., 2000]. Recently, several studies have examined resveratrol absorption *in vivo*. A detailed study on the metabolism of resveratrol in humans have demonstrated increased absorption after oral administration. Extensive metabolism of resveratrol in the gut and liver leads to its trace amount in the plasma (5 ng/mL). Rapid metabolism is one of the main reasons for short initial half-life of the primary molecule (8–14 min) [Asensi et al., 2002; Marier et al., 2002]. The bulk of an intravenous dosing of resveratrol was converted to sulfate conjugates within ~30 min in humans. However, glucuronide conjugates were also detected in the plasma [Walle et al., 2004]. The food matrix in which resveratrol is consumed may have an effect on absorption and bioavailability. Following oral administration of pure resveratrol to human subjects, resveratrol glucuronide was the major metabolite detected in the plasma and urine. High oral doses of grape juice resulted in the detection of the glucuronide and sulfate conjugates in the subjects plasma and urine [Meng et al., 2004]. Grape juice consists of mostly resveratrol glucosides, *cis*- and *trans*-piceid, with low amounts of the free resveratrol, suggesting a lower bioavailability of the glucosides compared to the pure compound.

More recently, the sulfation of resveratrol in human liver cytosol has been examined [Miksits et al., 2005]. In the presence of 30-phosphoadenosine-50-phosphosulfate, three metabolites occurred whose structures were identified by mass spectrometry and NMR as *trans*-resveratrol-3-*O*-4'-*O*-disulfate (S1),

trans-resveratrol-4'-*O*-sulfate (S2), and *trans*-resveratrol-3-*O*-sulfate (S3), respectively. Incubation in the presence of human recombinant sulfotransferases (SULTs) demonstrated that S1 is almost exclusively catalyzed by SULT1A1 and only to a minor extent by SULT 1A2, 1A3, and 1E1, whereas S2 is selectively formed by SULT1E1. S3 is catalyzed by SULT1A1, SULT1E1, SULT1A2, and 1A3 (depending on the resveratrol concentration) [Miksits et al., 2005]. The metabolic pathway of resveratrol in human liver cytosol *in vitro* is shown in Figure 14.4.

In addition, the dose-dependent effect of sulfation and glucuronidation on intestinal absorption of resveratrol was investigated [Maier-Salamon et al., 2006]. The intestinal epithelial membrane transport kinetics and metabolism of resveratrol (10–200 mM) was studied using Caco-2 monolayers cultured in transwells.

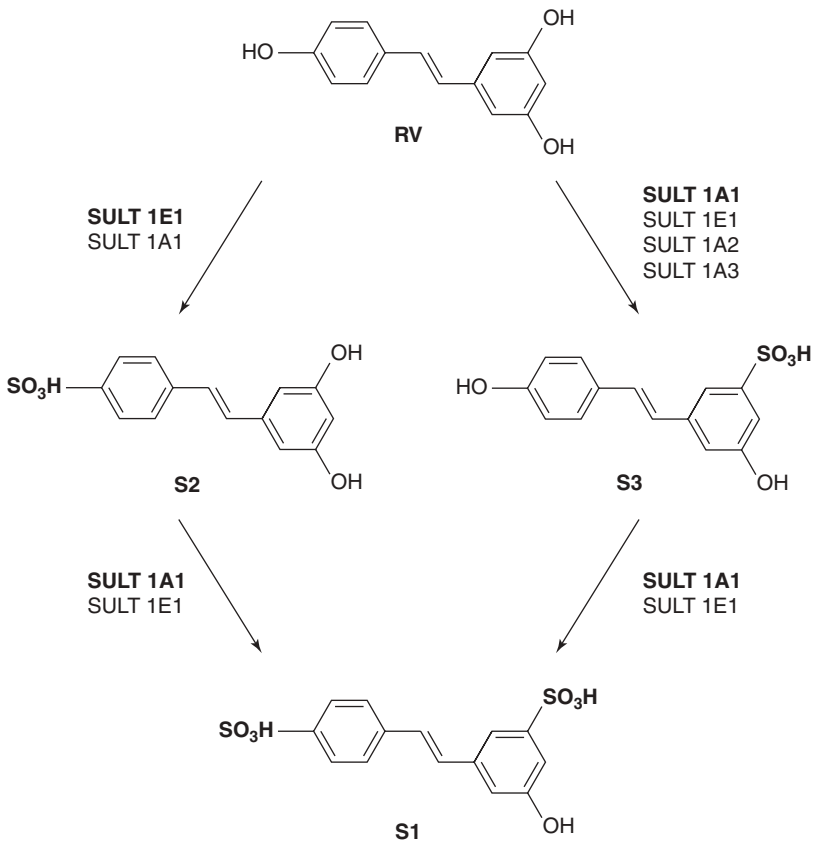


Figure 14.4 Resveratrol (RV) metabolic pathway proposed in human liver cytosol. SULT enzymes shown in bold represent the predominant contribution to sulfate formation.

Along with resveratrol, it was possible to identify three metabolites, namely *trans*-resveratrol-4'-*O*-glucuronide (G1), *trans*-resveratrol-3-*O*-glucuronide (G2), and *trans*-resveratrol-3-*O*-sulfate (S3) by liquid chromatography/mass spectrometry (LC/MS) and NMR. Efflux of the glucuronides G1 and G2 significantly followed Michaelis–Menten kinetics favoring basolateral efflux. The predominant metabolite was the monosulfate S3, however, its formation was strongly inhibited at higher resveratrol concentrations. As metabolism was either inhibited or saturated, the total amount of resveratrol transported across the Caco-2 monolayers increased as much as 3.5-fold at 200 mM resveratrol, demonstrating a concentration-dependent biotransformation of resveratrol in Caco-2 cells, which may also apply to human enterocytes, thereby affecting oral bioavailability [Maier-Salamon et al., 2006]. The intestinal metabolic pathway of resveratrol in humans is depicted in Figure 14.5. Given that in vivo concentrations of individual metabolites can be much higher than those of the native compound, further studies are needed to determine whether the metabolites represent inactivated forms of the drug, act as a pool from which free resveratrol can be released into various tissues, or are themselves active in promoting many of the health benefits attributed to resveratrol. [Saiko et al. 2008].

INTERACTION OF RESVERATROL WITH DIETARY CONSTITUENTS

The diet consists of varied ingredients that impart their potential benefits to human health. Potential interaction of resveratrol with other constituents of the diet is worth considering. Resveratrol has been shown to synergize with both quercetin and ellagic acid present in most of our natural products, in the induction of apoptosis in human leukemia cells [Mertens-Talcott and Percival 2005], with ethanol in the inhibition of inducible nitric oxide synthase (iNOS) expression [Chan et al., 2000], with vitamin E in the prevention of lipid peroxidation [Fang et al., 2002], with catechin in the protection of PC12 cells from β -amyloid toxicity [Conte et al., 2003], and with nucleoside analogs in the inhibition of HIV1 replication in cultured T lymphocytes [Heredia et al., 2000]. These effects could help to explain how a relatively low dose of resveratrol obtained from red wine or other dietary sources could produce a measurable health benefit. However, no adverse action of resveratrol with other chemical constituents in the body has been reported so far, but instead it detoxifies the chemical carcinogens and proves to be chemopreventive [Baur and Sinclair, 2006].

TARGET ENZYMES OF RESVERATROL ACTION

Resveratrol is commonly referred to as a “dirty” molecule in the pharmaceutical industry, meaning that it seems to interact with many different proteins,

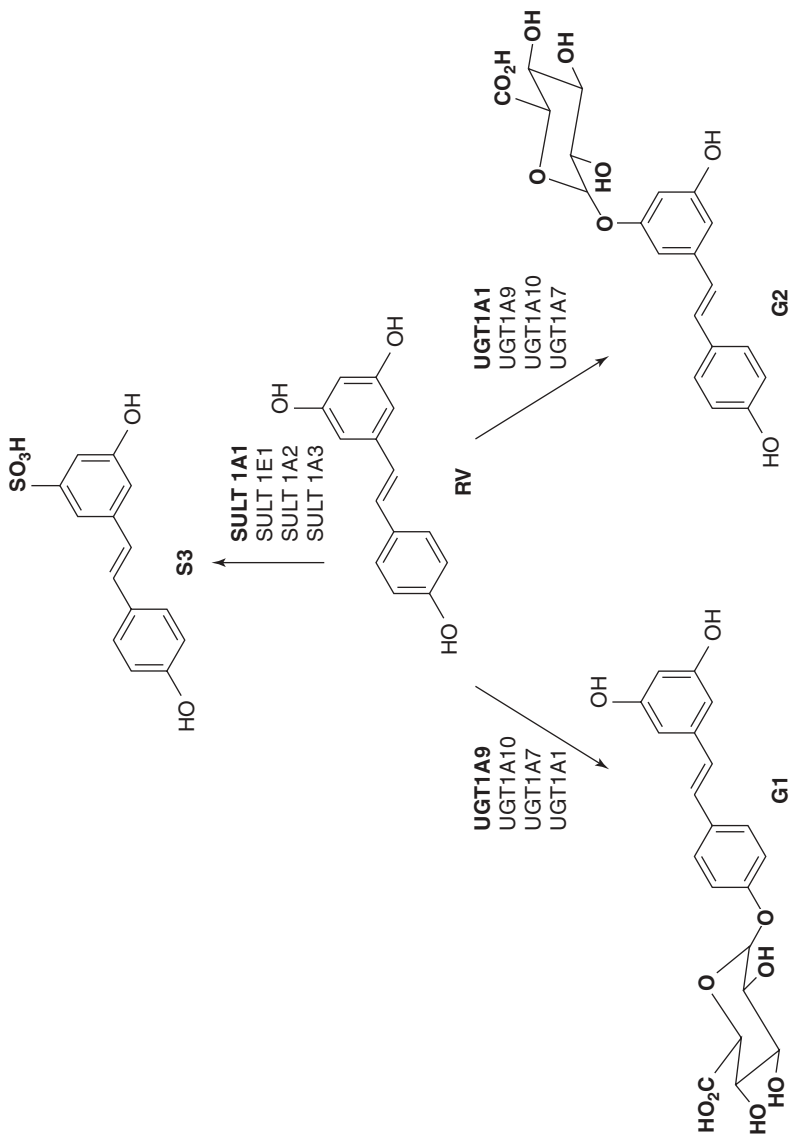


Figure 14.5 Intestinal resveratrol metabolic pathway proposed after oral administration using Caco-2 monolayers. SULT and UGT enzymes shown in bold represent the predominant contribution to sulfate and glucuronide formation.

including cyclooxygenases, ribonucleotide reductase, and DNA polymerases [Saiko et al., 2008]. Thus, its activity cannot be resumed in a unique mode of action but likely results from many complementary actions of different biochemical pathways. Resveratrol has been shown to inhibit a plethora of enzymes belonging to different classes, including (but not limited to) kinases, lipo- and cyclooxygenases, sirtuins, and other proteins [Pirola and Frojdo, 2008]. From a mechanistic point of view, both the *m*-hydroxyquinone and 4-hydroxystyryl moieties (Fig. 14.1) of the molecule have been shown to be important for the determination of resveratrol's inhibitory properties toward various enzymes such as STAT3, JNK1, PKCs, ERK1, Src, Cyclo and lipoxygenases, aromatases, and DNA polymerases [Pirola and Frojdo, 2008]. The current evidence about the various resveratrol targets, which provide a framework of possible pathways mediating some of the endpoint responses elicited by resveratrol treatment, is overwhelming, which gives an idea that the effects of resveratrol may reflect its simultaneous action on several targets by both activating and inhibiting.

STRUCTURE–ACTIVITY RELATIONS OF RESVERATROL

Quantitative structure–activity relationships (QSAR) are powerful tools in predicting the action of chemicals in biological systems [Karcher et al., 1990; Bradbury, 1994]. The chemicals may be synthetic or a derivative of a natural product, which exhibit a wide array of biological activity exhibiting potential health benefits. As evidenced by many reports, resveratrol and its analogs are a therapeutic promise of alternative medicine [Das and Maulik, 2006]. Activity of resveratrol cannot be resumed in a unique mechanism of action, but it likely results but it results from various complementary actions of different biochemical pathways. PAGE analysis (parametric analysis of gene set enrichment) indicated that resveratrol caused a significant alteration in 127 pathways, including the TCA cycle, glycolysis, the classic and alternative complement pathways, butanoate and propanoate metabolism, sterol biosynthesis, Stat3 signaling, insulin signaling, IGF-1 and mTOR signaling, oxidative phosphorylation, and electron transport [Baur et al., 2006]. Such a diverse range of effects may depend on the interplay between resveratrol and a very specific cellular target that must be an upstream controller of many cellular events.

Resveratrol is one of the many naturally occurring hydroxystilbenes consisting of two benzene rings which are connected with an olefin. The structural features of hydroxystilbenes (C6–C2–C6) are similar to those of flavonoids (C6–C3–C6), which have various biological activities including the inhibition of mast cell degranulation [Cheong et al., 1998]. Resveratrol exerts an inhibitory effect on the nitric oxide production in macrophage cells not through estrogen-mediated pathway but through direct non-receptor-mediated pathway, and the hydroxystilbene moiety is the main constituent involved in its activity [Cho et al., 2002].

PHARMACOLOGICAL PRECONDITIONING EFFECTS OF RESVERATROL

A state-of-the-art technique, preconditioning, was initially reported by Murry et al. in 1986, where several brief periods of ischemia followed by short interval of reperfusion for a few cycles caused cardioprotection against ischemic heart injury [Das et al., 2005]. There are numerous attempts to mimic the protective effects of preconditioning by exogenous agents, and thereby to produce pharmacological preconditioning. Resveratrol has also, cardioprotective effect which can be related to its antioxidant activity. Therefore, Bradamante et al. [2000] and De Jonge et al. [2002] have investigated how resveratrol affects high-energy phosphate metabolism, using ^{31}P -NMR, and contractility of isolated Langendorff perfused rat hearts subjected to 20 min no-flow ischemia and 30 min reperfusion. It is well established from various studies that adenosine (A) receptors play a crucial role in ischemic preconditioning [Das et al., 2005]. In this study beside the resveratrol pretreatment, all the adenosine receptor blockers were used with the resveratrol, and then the heart was subjected to 30 min global ischemia followed by 120 min reperfusion. In addition to this, Akt, p-Akt, Bcl-2, p-Bcl-2, Bad, p-Bad, CREB, p-CREB were determined. The results of this study are parallel with many others reports indicating the role of A_1 and A_3 , but not A_{2a} receptors, in the resveratrol-mediated preconditioning [De Jonge et al., 2002]. The main finding of this study and another follow-up study by the same group [Das et al., 2005b] is that resveratrol-mediated preconditioning is related to the activation of A_1 and A_3 receptors, which triggers a survival pathway through the phosphatidylinositol (PI) 3-kinase-Akt-Bad/Bcl-2 and by activating adenosine A_3 -CREB-Bcl-2 (antiapoptotic) signaling.

Hattori and co-workers [2002] also proved the preconditioning effects of resveratrol which is to be mediated by nitric oxide (NO) or NOS. To confirm this hypothesis, a NO inhibitor, N^G -nitro-L-arginine methyl ester (L-NAME), as well as an iNOS blocker, aminoguanine (AG), were used in their studies. The L-NAME and AG pretreatment abolished the resveratrol-mediated cardioprotection, suggesting the role of NO in resveratrol-induced cardioprotection. To gather further evidence, Imamura and collaborators [2002] used isolated iNOS knockout mouse hearts. Both resveratrol treated and nontreated iNOS knockout mice hearts displayed relatively poor recovery in cardiac function as compared to the wild-type mice. Obviously, resveratrol induced an increased expression of iNOS in the wild-type mice but not in the iNOS knockout hearts, indicating an essential role of iNOS in resveratrol-mediated preconditioning. In an additional study, the expression of the molecular targets of NO [e.g., vascular endothelial growth factor (VEGF), KDR, iNOS, eNOS] were examined by western blot and immunohistochemistry [Das et al., 2005c]. Recent studies have also demonstrated that NO can induce the expression of heme-oxygenase (HO-1). Das and co-workers showed that protoporphyrin (SnPP), an HO-1 inhibitor treatment, was able to abolish the cardioprotective effects of resveratrol (i.e., increased cardiac function parameters, reduced myocardial infarct size, decreased

cardiomyocytes apoptosis) [Das et al., 2006]. The HO-1, mediated mechanisms were related to the p38MAP kinase and Akt survival signaling, but independent of NF- κ B activation using p38MAPK and Akt inhibitor. The cardioprotective mechanisms of resveratrol using sour cherry seed kernel extract, against ischemia-reperfusion-induced damage through the reduced caspase-3 activity was confirmed by Bak et al. [2006]. Similarly HO-1 up-regulation via the antioxidant response element (ARE)-mediated transcriptional activation of NF-E2-related factor-2 (Nrf2) was demonstrated [Chen et al., 2005].

ANTIOXIDANT POWER OF RESVERATROL

Many compounds with aromatic groups are able to function as antioxidants by forming stable radicals via resonance structures, thereby preventing continued oxidation. Resveratrol contains two aromatic groups and has been shown to have a higher 2,2'-azinobis (3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), 1,1-diphenyl-2-picrylhydrazyl (DPPH), and hydroxyl radical scavenging capacity than propyl gallate, vitamin C, and vitamin E [Soares et al., 2003]. A positive correlation has been established between the antioxidant power of wine and resveratrol content [Alonso et al., 2002]. Molecules bearing ortho-dihydroxyl or 4-hydroxy-3-methoxyl functionality are appreciably more active than those bearing no such functionalities. It has been proven that the ortho-methoxyl group can form an intramolecular hydrogen bond with the phenolic hydrogen, making the H-atom abstraction from the ortho-methoxyphenols surprisingly easy [de Heer et al., 2000]. It is also known that the ortho-hydroxyl substitution on phenol would make the oxidation intermediate, ortho-hydroxyphenoxy radical, more stable due to the intramolecular hydrogen-bonding interaction as reported recently from both experiments by spectrophotometric measurements [Foti and Ruberto; 2001] and theoretical calculations. The theoretical calculations show that the intramolecular H bond in ortho-hydroxyphenoxy radical is ca. 4 kcal/mol stronger than that in the parent molecule catechol, and the bond dissociation energy (BDE) of catechol is 9.1 kcal/mol lower than that of phenol [Wright et al., 2001]. In addition, ortho-hydroxyphenoxy radical and/or ortho-semiquinone radical anion will be more easily further oxidized to form the final product ortho-quinone as exemplified in Figure 14.6. As an antioxidant, resveratrol may delay and/or prevent oxidative stress-induced cellular damage and disease. Resveratrol is thus a promising source to combat most of the human ailments and to increase longevity of life.

ANTI-INFLAMMATION WITH RESVERATROL

Recently, numerous possible ways have been identified by which resveratrol may attenuate inflammation in various organs. The anti-inflammatory response of resveratrol was realized from its ability to down-regulate pro-inflammatory

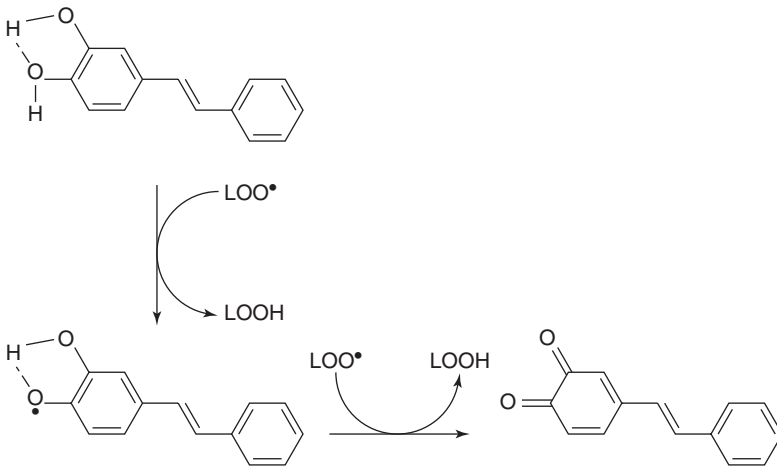


Figure 14.6 Mechanism of 3,4-DHS-inhibited peroxidation.

cytokines [Pervaiz, S 2003]. Tissue injury is a multistep process and such processes last till the time the region is healed. The first step of inflammation includes the activation and migration of leukocytes, including neutrophils, monocytes, and eosinophils, to the injured tissue site from the various parts of the body. Resveratrol is found to reduce inflammatory responses induced by formyl methionyl leucyl phenylalanine (fMLP), component fragment C5a, or calcium ionophore A23187 [Rotondo et al., 1998]. The next step, the macrophages, takes over the process of inflammation. NO production can have some beneficiary effects on the activation of macrophages. Inducible NO synthase (iNOS) plays an important role in this process. As mentioned earlier, resveratrol has been found to induce iNOS [Sharma et al., 2007; and Chander et al., 2005]. Resveratrol also interferes with the pro-inflammatory signaling of thrombin, resulting in the inhibition of adenosine nucleotide secretion from activated platelets and decreased neutrophils functions via inhibition of PAP and P2-receptor signaling through MAPK and cJun and JNK [Kaneider et al., 2004]. A recent study showed that in mouse epidermal cells, resveratrol activated extracellular signal-regulated kinases (ERK), c-Jun NH₂-terminal kinases (JNK), and p38 MAPK, leading to the serine 15 phosphorylation of p53 [She et al., 2001].

Recent studies revealed that resveratrol protects from inflammation by acting at different phases of inflammation. Protection at the pro-inflammatory phase appears to be very important for reducing inflammation effectively and promptly. A recent study [Ge et al., 2006] showed that resveratrol inhibits macrophage expression of EMMPRIN by activating PPAR- γ . In another similar study, Ma et al., [2006] showed a similar observation, but additionally found a role of nuclear transcription factor κ B (NF- κ B) in macrophage inhibition. Numerous studies confirmed that resveratrol suppresses the TNF- α

activation [Marier et al., 2005; Moon et al., 2006]. Some preclinical as well as clinical studies have shown significant suppression of interleukin-1 (IL-1) and IL-6 with resveratrol [Baggiolini et al., 1995; Marier et al., 2005]. Similarly, IL-8 plays an important role in inflammation as it recruits leucocytes [Olas et al., 2001]. Donnelly et al. [2004] showed that resveratrol could inhibit IL-8. In another study, resveratrol also inhibited the TNF- α and histamine release by immunoglobulin E (IgE) in mouse mast cells [Baolin et al., 2004]. There are three different soluble adhesive molecules present in the leukocytes and endothelium; integrins (α - and β -integrins), selectins (L-, P-, and E-selectin), and immunoglobulin subfamily of cell surface proteins (vascular cell adhesion molecule-1, VCAM-1 and intracellular adhesion molecule-1, ICAM-1). In an acute in vivo study, Das et al. [2006a] successfully showed that resveratrol significantly inhibited the generation of adhesion molecules.

There are two different enzyme systems that are involved in the synthesis of pro-inflammatory mediators, such as cyclooxygenase (COX) and lipoxygenase, which finally release inflammatory substances, prostanoids and leukotrienes, respectively. Resveratrol inhibited the induction of LTB₄ and attenuated PAF in rats [Shigematsu et al., 2003]. Similarly, it has been found that resveratrol has significant effect on the production of the peptide leukotriene LTC₄ [Kimura et al., 1995]. The anti-inflammatory response of resveratrol was showed by Jang et al. [1997] who found inhibition of prostaglandin synthesis by the inhibitory effect of COX-1 with resveratrol. Subsequently, the same group found that resveratrol could selectively inhibit COX activity by inhibiting COX-1 pathway, but not through COX-2 pathway. Szewczuk et al. [2004] confirmed this finding. In contrast, another study found that resveratrol suppressed the synthesis PGE₂ by the inhibition of COX-2 but not altering the COX-1 [Subbaramaiah et al., 1998].

In the process of evaluating certain derivatives of resveratrol, inhibition assays for COX-1 and COX-2 were done on hydroxylated and methoxylated resveratrol analogs and compared to celecoxib, a known COX inhibitor. Quantitative structure-activity relationship (QSAR) analysis exhibited a high correlation with the topological surface area TPSA ($r = 0.93$) and the percentage of inhibition. Docking studies on both COX-1 and COX-2 protein structures also revealed that hydroxylated but not methoxylated resveratrol analogs are able to bind to the previously identified binding sites of the enzymes [Murias et al., 2004]. Hydroxylated resveratrol analogs, therefore, represent a novel class of highly selective COX-2 inhibitors and promising candidates for in vivo studies. In another study, resveratrol was found to be a potent inhibitor of both the cyclooxygenase and peroxidase activities of COX-1, but the drug acted only as a reducing co-substrate for COX-2 [Szewczuk et al., 2004]. The observation that resveratrol acted as a noncompetitive inhibitor of the cyclooxygenase activity of COX-1 suggests that arachidonic acid and resveratrol bind at different sites that correspond to the cyclooxygenase and peroxidase active sites, respectively. The observation that resveratrol acted as an uncompetitive inhibitor of the peroxidase activity of COX-1 suggests that

resveratrol requires a peroxide substrate to exert its inhibitory effects via the formation of an E-S-I complex and confirms a novel mode of inhibition for resveratrol. It has been confirmed that the *m*-hydroquinone moiety (3,5-di-OH group) of resveratrol is required for mechanism-based inactivation of COX-1. The *m*-hydroquinone is unique because oxidation of one hydroxy group results in a semiquinone radical that cannot be stabilized through the ring structure to the remaining hydroxy group, as is the case for *o*- and *p*-hydroquinones. However, with COX-2, all of the hydroxy groups on resveratrol can serve as reducing co-substrates.

In a related study, resveratrol significantly reduced colonic injury, neutrophil infiltration, and drastically reduced the PGD₂ concentration by inhibiting COX-2, but not affecting COX-1 [Martin et al., 2004]. It appears that the anti-inflammatory activity of resveratrol may be realized through the inhibition of both COX-1 and COX-2-mediated pro-inflammatory signaling, suppression of pro-inflammatory mediator production, as well as from its potent antioxidative effects.

DIABETES CURE WITH RESVERATROL

Diabetes is a disease when islets of Langerhans cells in the pancreas do not produce, or poorly produce, insulin or the body does not properly use the insulin present in the system. Insulin is a hormone which mobilizes sugar and starches to get the bloodstream to get converted into energy which is needed for the daily activity of the body. The cause of diabetes is still a mystery to the research world. Although both genetics and environmental factors such as obesity, food habit, or lack of exercise appears to play an important role, still the underlying mechanism remains unclear.

According to the latest report of the American Diabetes Association in 2006, there are at least 20.8 million children and adults in the United States, or 7% of the population, who have diabetes. While an estimated 14.6 million have been diagnosed with diabetes, unfortunately, 6.2 million people (or nearly one-third) are unaware that they have the disease. That is why diabetes is also known as the “silent killer.” The rapid increase in the number of silent killers has caught the attention of the research world and recently almost double the number of scientists are working in this area compared to the last decade.

Recently, resveratrol was found to reverse fat-induced insulin resistance [McCarty, 2005]. This observation provides more enthusiasm for researchers to use resveratrol as an antidiabetic agent. Su and associates [2006] showed that resveratrol significantly reduced the plasma glucose concentration as well as the dramatic reduction of triglyceride concentration in streptozotocin (STZ)-induced diabetic mellitus rats in 14 days treatment. They concluded from this observation that resveratrol possesses hypoglycemic and hypolipidemic properties [Su et al., 2006]. Baur et al., [2006] added more value to this conclusion by showing that resveratrol increases insulin sensitivity by lowering the blood

glucose level in a group of high-calorie diet mice. They have pointed out that reduced insulin-like growth factor-1 (IGF-I) levels and increased AMP-activated protein kinase (AMPK) probably play a major role.

Some other related studies established that resveratrol can attenuate diabetic nephropathy in rats [Sharma et al., 2006a] and reduce thermal hyperalgesia and cold allodynia in streptozotocin-induced diabetic rats [Sharma et al., 2006b].

CANCER CURE WITH RESVERATROL

Resveratrol plays critical roles in signaling mechanisms of different tumors. Currently, it is well documented that many factors play a role in the pathomechanisms of cancers. However, the exact mechanisms are not precisely known. If resveratrol could provoke an influence in only one pathological factor, then the effects of anticancer drugs (i.e., in combination therapy) might beneficially modulate the signal transduction pathways. This is the basic reason to investigate the precise mechanisms and effects of resveratrol and its derivatives on various cancers.

The inhibition of COX-2 (inducible form of COX) could be an important strategy for preventing the development of cancers. Subbaramaiah and his team treated human mammary and oral epithelial cells with a phorbol ester, PMA, which induced the COX-2 mRNA, COX-2 protein, protein-kinase C, c-Jun (promoter of COX-2), and prostaglandin synthesis. Phorbol ester-mediated inductions of these agents were inhibited by resveratrol [Subbaramaiah et al., 1999]. Nakagawa et al. [2001] examined the effects of resveratrol on the growth of estrogen receptor (ER)-positive (KPL-1 and MCF-7) and negative (MKL-F) human breast cancer cell lines. Synthetic resveratrol at high concentration ($\geq 44 \mu\text{M}$) suppressed the cell growth in all cell lines. The chemical structure of resveratrol is similar to the 4,4'-dihydroxy-*trans*-diethylstilbene that belongs to the type I class of estrogens and acts as an ER agonist [Levenson et al., 2003]. The effect of resveratrol was related to the apoptosis cascade (up-regulated Bax and Bak proteins, down-regulated Bcl-xL proteins, and activated caspase-3). Jazirehi and Bonavida, [2004] have also shown that resveratrol selectively down-regulated the expression of antiapoptotic proteins Bcl-xL and myeloid cell differentiation factor-1 (Mcl-1) and up-regulated the expression of proapoptotic proteins (Bax) and apoptosis protease activating factor-1 (Apaf-1). Scarlatti et al. [2003] found that resveratrol could provoke growth inhibition and apoptosis in metastatic breast cancer cells (MDA-MB-231) by activating the ceramide synthesis pathway. Furthermore, Dorrie et al. [2001] showed that resveratrol induced extensive apoptotic cell death by depolarizing mitochondrial membranes in CD95-sensitive leukemia cell lines as well as B-lineage leukemic cells, which are resistant to CD95-signaling. In addition, resveratrol induced the activation of caspase-9 in all lines. However, the benzyloxycarbonyl-Val-Ala-Asp-fluoromethylketone (wide-spectrum caspase-inhibitor) failed to inhibit the depolarization of mitochondrial membranes elicited by resveratrol,

suggesting that resveratrol activation is independent of upstream caspase-8 activation via receptor ligation.

Resveratrol is a sensitizer of tumor necrosis factor-related apoptosis through p53-independent induction of p21 and p21-mediated cell cycle (G_1) arrest associated with down-regulation of surviving cells [Fulda et al., 2004]. Kuwajerwala et al. [2002] reported that resveratrol-induced increase in DNA synthesis was associated with enrichment of LNCaP cells in S phase, and a concurrent decrease in nuclear p21Cipl and p27Kip1 levels. In addition, Cao et al. [2004] have shown that resveratrol inhibited hypoxia-inducible-factor 1α (HIF- 1α) and VEGF expression in human ovarian cancer through multiple mechanisms: (i) inhibition of Akt and mitogen-activated protein kinase activation, (ii) inhibition of protein translational regulators, and (iii) proteasome pathway [Kim et al., 1993]. Resveratrol also reduced the antiapoptotic kinase Akt in various uterine cancer cell lines [Sexton et al., 2006]. Similar effects occurred in human tongue squamous cell carcinoma and hepatoma cells, [Zhang et al., 2005]. It was reported that resveratrol down-regulated the expression of NF- κ B, TNF- α , interleukin 1β , interleukin-6, Bcl-2, Bcl-xL, XIAP, c-IAP, VEGF, and matrix metalloproteinase-9 (MMP-9) in human multiple myeloma (MM) cells or ex vivo studies [Millauer et al., 1994]. In a further study, it was investigated whether resveratrol-Cu (II) system is capable of causing DNA degradation in lymphocytes isolated from human peripheral blood [Azmi et al., 2005]. This study partially supports the hypothesis that anticancer properties of resveratrol may involve mobilization of endogenous copper and the consequent pro-oxidant action. Kotha et al. [2006] was among the initial group to identify Src-Stat3 signaling as a target of resveratrol in tumors. Beside the effects of resveratrol and its derivatives alone, it is important to emphasize the combined effects of resveratrol with other anticancer drugs. Therefore, resveratrol combined with cisplatin or doxorubicin produced an additive growth-inhibitory and anticancer effects and protection against doxorubicin-induced cardiac toxicity both in human gynecologic cancer cell lines and *in vivo* [Rezk et al., 2006]. Resveratrol analogs with hydroxyl groups in positions 3',4, and 5' showed an even higher cytotoxicity in HL-60 cells than resveratrol, indicating an increased antitumor activity [Murias et al., 2004]. Their data were consistent with another group who also found that 3,4-dihydroxyl groups are important for enhanced antioxidant and anticancer activities of *trans*-resveratrol analogs [Cai et al., 2004].

ANTIAGING EFFECTS OF RESVERATROL

In many eukaryotic cells such as rodents, flies, and nematode worms, and even single-celled organisms such as baker's yeast, only SIR2 among many longevity regulatory genes has received significant attention from researchers [Hall, 2003]. In human cells, the analog gene of SIR2 is SIRT1, which can extend life span [Howitz et al., 2003].

In a recent study, Howitz et al. [2003] showed red-wine-derived resveratrol could increase the SIRT1 activity 13-fold by inhibiting apoptotic cell death through the deacetylation of p53. In the same study they also showed that resveratrol extended the life span by 70% by mimicking calorie restriction by stimulating SIR2 in the yeast cells and, thus, increased DNA stability. In another very recent study on calorie restriction experiments on monkey and other mammalian species, the concept of wine as “fountain of youth” was reconfirmed [Kujoth et al., 2005].

ANTIULCER EFFECTS OF RESVERATROL

In 1982, the bacterium *Helicobacter pylori* was discovered by Marshall and Warren which was identified as the major cause of peptic ulcer rather than only stress and lifestyle factors which was thought before. This bacterium ruptures the mucus membrane of the stomach. In an in vitro study, it was shown that wine could effectively reduce the growth of *H. pylori* propagation [Marimon et al., 1998]. A few other studies showed that red wine is more effective over white wine to inhibit the growth of *H. pylori* [Mahady and Pendland, 2000; Daroch et al., 2001]. Mahady and associates [2003] showed in their study that resveratrol is the active component that causes the inhibitory effect of 15 different stained *H. pylori* propagations [Mahady et al., 2003]. This observation was also confirmed by another in vitro study [Mahady et al., 2003] by the same group of researchers.

ANTIOBESE EFFECTS OF RESVERATROL

Adult-onset obesity is a serious health problem because it is implicated in various diseases including type II diabetes, hypertension, coronary heart disease, and cancer [Kopelman, 2000]. Obesity is characterized by an increase in adipose tissue mass which results both from increase fat cell numbers and increased fat cell size [Couillard et al., 2000]. Picard et al. [2004] showed that resveratrol activated the expression of Sirt1, and this, in turn, resulted in decreased lipid accumulation by repression of PPAR- γ in differentiated adipocytes. Chronic low-grade inflammation characterized by adipose tissue macrophage accumulation and abnormal cytokine production is a key feature of obesity and type II diabetes. Adipose-tissue-derived monocyte chemoattractant protein (MCP)-1, induced by cytokines, has been shown to play an essential role in the early events during macrophage infiltration into adipose tissue. In a recent study, resveratrol was found to inhibit TNF- α -induced MCP-1 secretion and gene transcription, as well as promoter activity, which is based on down-regulation of TNF- α induced MCP-1 transcription [Zhu et al., 2008]. One of the latest studies from our laboratory reveals that resveratrol induced cardiac protection in Zucker obese rats. It was confirmed by the increased GLUT-4

expression and reduced endothelin expression and cardiac apoptosis in ischemic-reperfused hearts in the presence or absence of glucose intake [Lekli et al., 2008]. Parametric analysis of gene set enrichment revealed that resveratrol opposed the effects of the high-calorie diet in 144 out of 153 significantly altered pathways such as increased insulin sensitivity, reduced insulin-like growth factor-1 (IGF-I) levels, increased AMP-activated protein kinase (AMPK), and peroxisome proliferator-activated receptor-c coactivator 1 α (PGC-1 α) activity, increased mitochondrial number, and improved motor function [Baur et al., 2006]. These data show that improving general health in mammals using small molecules such as resveratrol is an attainable goal, and point to new approaches for treating obesity-related disorders.

OTHER HEALTH BENEFITS OF RESVERATROL

Resveratrol has been recognized as a phytoestrogen since it possesses structural similarities with estrogenic compounds and may exert some biological activities through estrogen receptors [Cheng et al., 1996; Mgbonyebi et al., 1998; Gehm et al., 1997]. In some studies, resveratrol has been shown to bind to estrogen receptors as an agonist [Lu and Serrero, 1999; Henry and Witt, 2002; Klinge et al., 2003].

The resveratrol-induced protection against ischemia/reperfusion has been documented in various organs (e.g., kidney, brain, heart, liver, etc.). In a study of spinal cord ischemia model (SCI), resveratrol-induced neuroprotection was found to be mediated by decreased oxidative stress, and increased NO release. Organotypic hippocampal slice cultures were exposed to oxygen–glucose deprivation (OGD) using LY294002 and PD98059 treatment to confirm the exact mechanism. Neuroprotection was arrested by LY294002 but not by PD98059. Thus, these findings suggest that PI3-k/Akt pathway but not mitogen-activated protein kinase (MAPK) are involved in neuroprotection [Zamin et al., 2006]. Ischemic preconditioning was mimicked by resveratrol in brain via the SIRT1 pathway, which was confirmed by sirtinol [Raval et al., 2006]. Recent studies have suggested that resveratrol may act as not only an antioxidant agent but as a signaling molecule also [Dore, 2005] within tissues and cells resveratrol acts not only as an antioxidant agent but also as a signaling molecule within cells and tissues to modulate the expression of genes and proteins (i.e., HO-1, COX-2, eNOS, iNOS, endothelin-1, TNF-, insulin-like growth factor binding protein). HO-1 protein has been documented with different functions in the brain. Since HO-1 is a heat-shock protein, which is induced in several cells and following different stimuli (e.g., hypothermia, global ischemia, subarachnoid hemorrhage, Parkinson disease, Alzheimer disease, etc.), the modulation of the different genes may explain the cytoprotective actions afforded by resveratrol, as well as the influence of resveratrol on blood flow, cell death, and inflammatory cascades [Sener et al., 2006].

Protection against ischemia/reperfusion-induced oxidative injury occurred in rat kidney as well. Resveratrol caused a significant increase in tissue

glutathione (GSH), and decreased the renal luminal, lucigenin CL, MDA levels, MPO activity, and collagen content [Sener et al., 2006]. Acute renal failure (ARF) can be induced by glycerol, and glycerol provokes a marked decrease in tissue and urine nitric oxide levels, causes renal oxidative stress, deterioration of renal morphology, and renal function. Resveratrol could reverse the aforementioned effects. However, the renoprotective effect was abolished using N^G -nitro-L-arginine methyl ester, a nonspecific NO-synthase-inhibitor (L-NAME) co-treatment, suggesting that resveratrol exerts the protective effects through the NO release [Chander et al., 2005, 2006]. Leikert et al., [2002] also reported that renoprotective effects of resveratrol were attributed to the release of endothelial nitric oxide. It is well known that reactive oxygen species (ROS) are harmful for glomeruli and tubular epithelial cells. The up-regulation of NF- κ B activates the cytokines, chemokines, and adhesion molecules. These are very harmful mediators of inflammation, leading to fibrosis, glomerular damage, and tubulointerstitial damage. Resveratrol reinforces the endogenous antioxidant systems that deperates ROS and thereby contributes to cytoprotective effects [Rodrigo et al., 2006]. The deterioration of lipid peroxidation caused by resveratrol is also related to lung, liver, and kidney protection [Bertelli et al., 2002]. Angiotensin II (Ang II) also plays a crucial role in the progression of renal diseases by activating membrane-bound nicotina-mide adenine dinucleotide phosphate (NADPH) oxidase and superoxide anion leading to hypertrophy of renal tubular cells. Since Ang II regulates the overexpression of TGF- β and TNF- α , this “side” mechanism also contributes to the obstructive nephropathy. This pathomechanism pathway (Ang II) is inhibited by resveratrol and plays a part in nephroprotection [Klahr, 1998].

The oxidative stress also plays a key role in the pathogenesis of various liver diseases and their progression. The use of resveratrol has been proposed as a therapeutic agent as well as coadjuvant, to prevent liver damage [Vitaglione et al., 2004]. The antioxidant activity was evaluated by measuring the inhibition of citronellal thermo oxidation or the reduction of 2,2-diphenil-1-picrylhydrazy radical [Vitaglione et al., 2004]. Furthermore, resveratrol can directly interact with DNA polymerases alpha and delta beyond the antioxidant activity [Stivala et al., 2001]. In a further study, hepatotoxicity was induced by acetaminophen. Alanine aminotransferase (ALT), aspartate aminotransferase (AST), MDA, TNF- α levels, and MPO activity were significantly increased, and GSH level was significantly decreased after the acetaminophen treatment [Sener et al., 2006]. Co-treatment with resveratrol reversed these effects. Acetaminophen is not the only medicine that can provoke liver damage. Therefore, these results suggest that resveratrol and natural antioxidant nutrients can be used as therapeutic agents in order to prevent hepatic oxidative injury due to hepatotoxic drugs.

It is also well documented that an antioxidant-rich diet protects against age-related macular degeneration (AMD), the leading cause of vision loss among the elderly. Development of AMD in the retinal pigment epithelium (RPE) is associated with oxidative stress. King and co-workers [2005] reported that resveratrol treatment (100 μ mol/L) inhibited basal and H_2O_2 -induced

intracellular oxidation, and protected RPE cells from cell death via the MAPK/ERK and extracellular signal-regulated kinase (ERK 1/2) pathways. Moreover, Sparrow and colleagues showed that resveratrol reduced A2E-epoxide formation in RPE [Sparrow et al., 2003]. Doganay et al. [2006] demonstrated that resveratrol suppressed selenite-induced oxidative stress and cataract formation in the rat eye. The protective effect was associated with higher GSH and lower MDA in lens and erythrocytes. The main point of this study is that resveratrol-rich diet could prevent human senile cataract. The protection of resveratrol against the ischemia/reperfusion injury also occurs in the eye (e.g., in retina). Retinal ischemia/reperfusion resulted in a significant reduction in HO-1-protein expression, and HO-1-related endogenous CO production which affects the ion levels in retina. Cellular Na⁺ and Ca²⁺ levels were increased, and K⁺ content was decreased. In rats treated with resveratrol-rich extract, tissue Na⁺ and Ca²⁺ accumulation and K⁺ loss were prevented through the HO-1-related endogenous CO production [Szabo 2004].

Huang et al. [2005] reported that resveratrol induced HO-1 protein up-regulation in rat aortic smooth muscle cells via the NF- κ B pathway. Pendurthi and co-workers [1999] showed that resveratrol inhibited the tissue factor (TF) expression, LPS-induced expression of TNF- α , and IL-1 β in vascular cells. In contrast, Di Santo and associates [2003] demonstrated that resveratrol significantly reduced TF activity, which originated from a reduction in nuclear binding activity of the transacting factor c-Rel/p65 in human endothelial and mononuclear cells. Antiplatelet activity of resveratrol is beneficial in many diseases. Olas et al. [2001] showed that resveratrol inhibited chemiluminescence and generation of O₂ in blood platelets caused by LPS or thrombin. This antiplatelet effect is in agreement with the results obtained by another study [Bertelli et al., 1995]. Moreover, resveratrol significantly inhibited ICAM-1 and VCAM-1 expression on TNF- α -stimulated human umbilical vein endothelial cells and LPS-stimulated human saphenous vein endothelial cells [Ferrero et al., 1998]. This group showed that resveratrol induced a significant inhibition in the adhesion of U937 monocytoid cells and neutrophils to TNF- α -stimulated NIH/3T3 ICAM-1-transfected cells. These results suggest an independent pathway of its antioxidant function [Ferrero et al., 1998].

ACKNOWLEDGMENT

The study was supported by the following grants: NIH HL 22559, HL33889, and HL69910 to DKD.

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15 Resveratrol: The Biochemistry Behind Its Anticancer Effects

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INTRODUCTION

Cancer is a group of heterogeneous diseases characterized by uncontrolled growth and spread of transformed cells. Although numerous anticancer therapies are currently under clinical use, the mortality from cancer as well as new cancer cases are still alarmingly high. According to a report published by American Cancer Society, 7.6 million people around the world have died of cancer in 2007, and this figure is expected to rise to 17.5 million by the year 2050. In this context, the fight against cancer has now been shifted to a new front, that is, the prevention of cancer. With the progress in our understanding of the molecular biology of cancer, it is now evident that the multistage carcinogenesis involves alterations in biochemical processes, which disrupt cellular homeostasis. Physiologically, the cellular biochemistry is under strict control of a divergent network of intracellular signaling pathways, which often functions inappropriately during tumorigenesis. Many of these altered cell signaling pathways can reversibly be restored to a normal state by chemopreventive agents, which can block the onset and the progression of cancer [Bode and Dong, 2004; Chen and Kong, 2005; Kundu and Surh, 2005]. Therefore, the prevention of cancer at early stages through restoration of altered biochemical processes might be the most practical strategy to fight against cancer. Population-based and laboratory studies suggest that regular consumption of fruits and vegetables can reduce the risk of certain malignancies [Chen and Kong, 2005; Surh, 2003]. In fact, the search for plant-originated anticancer principles has led to the identification of diverse classes of chemopreventive agents.

Resveratrol (trans-3,5,4'-trihydroxystilbene), a polyphenolic phytoalexin present in grapes, red wine, peanuts, mulberries, and in many other medicinal plants is an extensively investigated phytochemical with chemopreventive and chemotherapeutic potential [Kundu and Surh, 2004; Kundu and Surh, 2008a]. Since its first isolation in 1940 from the roots of white hellebore (*Veratrum glandiflorum* O. Loes), resveratrol has received the attention of the scientific community in 1990s, when the compound has been shown to be responsible for the cardioprotective effects of red wine [Wu et al., 2001]. Resveratrol emerged as nature's gift with a wide spectrum of health beneficial effects including antibacterial, antifungal, antioxidant, anti-inflammatory, and cardioprotective functions [Baur and Sinclair, 2006]. Momentum in the research on the anticancer activity of resveratrol has flared up by John M. Pezzuto and colleagues [Jang et al., 1997], who have reported that the compound interferes with multiple biochemical events associated with the initiation, promotion, and progression stages of carcinogenesis. Since this pioneering study, there has been rapid progress in understanding how resveratrol modulates the altered cellular biochemistry associated with tumorigenesis [Aggarwal et al., 2004]. The transformation of cells and their subsequent journey to progressive cancer involve improper cell-signaling pathways. Resveratrol modulates various components of abnormal signal transduction cascades implicated in the tumorigenesis [Aggarwal et al., 2004; Kundu and Surh, 2004].

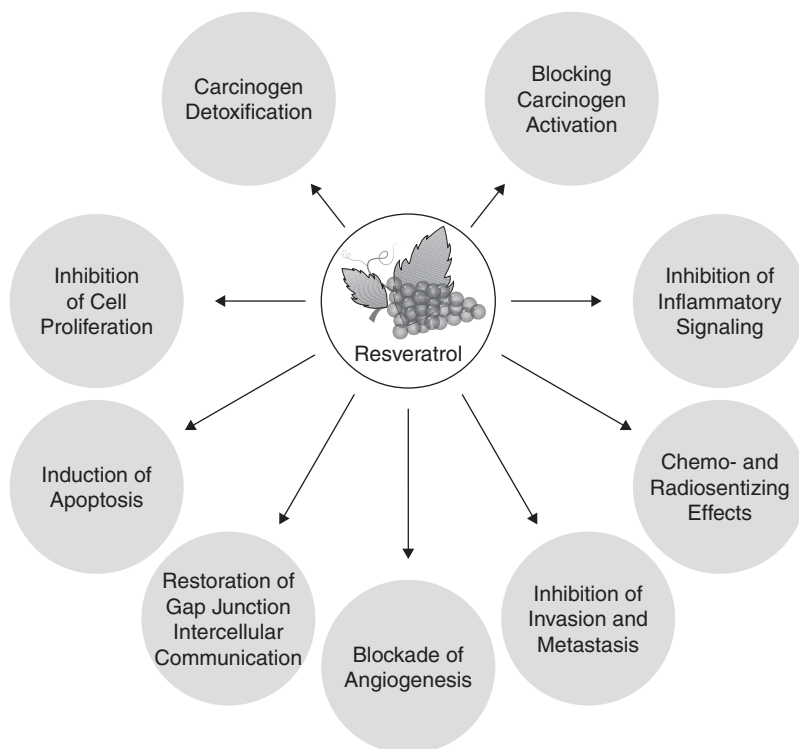


Figure 15.1 Biochemical mechanisms of anticancer effects of resveratrol.

Over the last 10 years, multidirectional studies with resveratrol have resulted in several key findings, which can explain the biochemistry behind its anticancer effects (Fig. 15.1). Resveratrol prevents oxidative damage of cellular macromolecules, blocks the activation of carcinogens, stimulates carcinogen detoxification, reduces inflammatory responses, diminishes proliferation, induces apoptosis in cancer cells, inhibits angiogenesis and metastasis, and sensitizes cancer cells to chemotherapy and radiotherapy [Aggarwal et al., 2004; Kundu and Surh, 2004; Shankar et al., 2007]. This chapter focuses on the biochemical basis of anticancer effects of resveratrol with particular emphasis on the components of cell-signaling pathways as major targets.

RESVERATROL IN CANCER PREVENTION AND THERAPY

The chemopreventive and chemotherapeutic potential of resveratrol has been extensively investigated in different *in vivo* models of tumorigenesis and *in vitro* cell culture systems [Aggarwal et al., 2004; Kundu and Surh, 2004]. Repeated topical application of resveratrol significantly reduced the incidence and the

multiplicity of chemically induced skin papillomas in female CD-1 mice [Jang et al., 1997]. Subsequently, several other studies have also revealed the ability of resveratrol to reduce experimental carcinogenesis in different rodent models [Aziz et al., 2005; Banerjee et al., 2002; Harper et al., 2007; Sengottuvelan and Nalini, 2006]. Resveratrol given with diet significantly reduced the incidence of poorly differentiated prostatic adenocarcinomas by 7.7-fold in the TRansgenic Adenocarcinoma Mouse Prostate (TRAMP) model [Harper et al., 2007]. In contrast, dietary administration of resveratrol failed to inhibit intestinal tumorigenesis in adenomatous polyposis coli (*Apc*)^{Min/+} mice [Ziegler et al., 2004]. Similarly, resveratrol given with diet was ineffective in reducing pulmonary tumorigenesis in female A/J mice treated with benzo[*a*]pyrene (B[*a*]P) or 4-(methyl-nitrosamino)-1-(3-pyridyl)-1-butanone [Hecht et al., 1999]. Several factors, such as the dosage of resveratrol, the route of administration of the compound, the tumor origin, and the presence of other dietary components, may be attributed to such discrepancies in the efficacy of dietary administered resveratrol.

Recent studies reported that resveratrol suppressed the growth of transplanted tumors in vivo [Garvin et al., 2006; Zhou et al., 2005]. Intratumoral, peritumoral or intraperitoneal administration of resveratrol significantly arrested the growth and induced apoptosis in xenografted tumors in athymic nude mice [Garvin et al., 2006; Zhou et al., 2005]. In contrast, intraperitoneal administration of resveratrol did not inhibit the growth of human melanoma xenograft [Niles et al., 2006]. Resveratrol was found to inhibit proliferation of various cancer cells in culture. The transformation of mouse epidermal JB6 C141 cells stimulated with epidermal growth factor (EGF) or a tumor promoter 12-*O*-tetradececanoylphorbol-13-acetate (TPA) was blunted by resveratrol [Huang et al., 1999; She et al., 2003]. Although, resveratrol attenuated the growth of mouse breast cancer (4T1) cells in culture [Bove et al., 2002], intraperitoneal administration of the compound failed to affect the growth and metastasis of these cells xenografted in Balb/c mice [Bove et al., 2002]. Resveratrol also induced apoptosis in various cancerous or transformed cells, sensitized cancer cells to chemotherapy- or radiotherapy-induced growth arrest and apoptosis, and suppressed tumor-associated angiogenic and metastatic processes [Aggarwal et al., 2004; Garg et al., 2005; Kundu and Surh, 2004]. Based on the promising anticancer effects of resveratrol in numerous preclinical models, the compound has been subjected to the first phase of clinical trials [Boocock et al., 2007].

BIOCHEMICAL BASIS OF CHEMOPREVENTION AND CHEMOTHERAPY WITH RESVERATROL

Inhibition of Metabolic Activation of Carcinogens and DNA Adduct Formation

Many exogenous and endogenous carcinogens undergo oxidative metabolism by phase I enzymes, especially by the members of the cytochrome P450 (CYP)

superfamily. Some chemical carcinogens are naturally inactive but are converted to reactive species through phase I metabolism. The phase I metabolic end products are usually eliminated through a second phase of metabolic reactions, commonly known as detoxification. Inadequate detoxification leads to the accumulation of metabolically activated carcinogens, which can directly attack the target cell DNA, thereby contributing to tumor initiation [Perwez Hussain and Harris, 2007].

Genes encoding CYP enzymes are transcriptionally regulated by arylhydrocarbon receptor (AhR), a member of the nuclear receptor transcription factor superfamily. For example, the transactivation of *CYP1A1*, which encodes an enzyme frequently involved in metabolic activation of a wide spectrum of polycyclic aromatic hydrocarbons (PAHs), requires the binding of activated AhR to the promoter segment of the gene. Resveratrol, by acting as an AhR antagonist, inhibits expression and/or activities of different isoforms of CYP enzymes (Fig. 15.2). Resveratrol inhibits the activation of AhR by blocking the conversion of ligand-bound cytosolic AhR into its nuclear DNA-binding form [Ciolino et al., 1998] and by suppressing the interaction between the AhR and the transcription initiation complex at the *CYP1A1* gene promoter [Ciolino and Yeh, 1999]. Resveratrol inhibited the induction of *CYP1A1* expression in rat primary hepatocytes, suggesting that the compound acts as an AhR antagonist [Andrieux et al., 2004]. A study from our laboratory also revealed that resveratrol strongly inhibited 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD)-induced AhR DNA-binding activity in human mammary epithelial (MCF-10A) cells [Chen et al., 2004]. In contrast, Lee and Safe [2001] demonstrated that resveratrol enhanced the degradation of *CYP1A1* (messenger ribonucleic acid), and diminished the expression and the activity of *CYP1A1* in TCDD-stimulated human breast cancer (T47D and MCF-7) cells in an AhR-independent manner. Resveratrol suppressed the expression and/or the activity of *CYP1A1*, *CYP1B1*, and *CYP1A2* in murine hepatoma (Hepa1c1c7) cells [Gerhauser et al., 2003], TCDD-stimulated mammary epithelial (MCF-10A) cells [Chen et al., 2004], 7,12-dimethylbenz[*a*]anthracene (DMBA)-treated MCF-7 cells [Ciolino and Yeh, 1999], and B[*a*]P-treated human hepatoma (HepG2) cells [Ciolino and Yeh, 1999]. Chang et al. [2001] demonstrated that resveratrol exerted direct inhibitory effects on the activities of *CYP1A1* and *CYP1B1* but it inactivated *CYP1A2* indirectly. In contrast, treatment of normal human esophageal (HET-1A) cells with resveratrol failed to inhibit B[*a*]P-induced expression of *CYP1B1* mRNA and protein [Wen and Walle, 2007].

Resveratrol also inhibits the activity of *CYP19*, alternatively known as aromatase, which is a rate-limiting enzyme in the biosynthesis of estrogens. A recent molecular modeling and docking study revealed that resveratrol binds to the active site of aromatase [Neves et al., 2007]. Since estrogens function as a risk factor for breast cancer, the inhibitory effect of resveratrol on the aromatase/*CYP19* activity in MCF-7 cells [Wang et al., 2006] suggests that the compound exerts chemopreventive effects on mammary carcinogenesis partly due to its antiestrogenic property. Resveratrol protects MCF-10A cells from

carcinogenic estrogen metabolites as evidenced by the reduced formation of DNA adducts from 4-hydroxyestradiol or estradiol-3,4-quinone [Zahid et al., 2008]. However, a weak estrogenic effect of resveratrol has also been reported [Bhat et al., 2001].

As a consequence of its inhibitory effects on the expression and/or activity of CYP enzymes, resveratrol suppressed carcinogen-DNA adduct formation. Resveratrol abrogated the B[a]P-diol epoxide-DNA adduct formation in mouse lung tissue by down-regulating the expression of CYP1A1 [Revel et al., 2003]. Although, resveratrol diminished DMBA-DNA adduct formation and B[a]P-induced arylhydrocarbon hydrolase activity, it did not inhibit B[a]P-diol epoxide-DNA adduct formation in mouse epidermis [Szaefer et al., 2004]. The compound attenuated the genotoxicity induced by *N*-hydroxy-2-amino-1-methyl-6-phenylimidazo-[4,5-*b*]pyridine (*N*-hydroxy-PhIP) in human CYP1A2 overexpressing Chinese hamster lung fibroblast V79 cells, possibly by blocking the activity of CYP1A2 [Boyce et al., 2004]. Since the AhR and various CYP enzymes are involved in the detoxification of many xenobiotics, the inactivation of AhR and the inhibition of CYP enzymes by resveratrol should be carefully considered in achieving chemoprevention.

Induction of Phase II Detoxification or Antioxidant Enzymes

The biochemical basis of anticancer effects of resveratrol is partly ascribed to its antioxidant potential. It is generally accepted that the ROS-induced DNA damage plays a critical role in oncogenesis. Resveratrol functions as a natural antioxidant by inducing antioxidant enzymes, restoring cellular reduced glutathione (GSH) levels and scavenging ROS [de la Lastra and Villegas, 2007; Kode et al., 2007; Kundu and Surh, 2004]. The activation of signaling pathways involved in the induction of phase II detoxification or antioxidant enzymes is one of the well-defined mechanisms underlying chemoprevention with resveratrol (Fig. 15.2).

Several studies have demonstrated that resveratrol enhances the expression and/or the activity of phase II antioxidant or detoxification enzymes, such as glutathione-*S*-transferase (GST) [Hebbar et al., 2005], glutathione peroxidase (GPx) [Kluth et al., 2007], UDP glucuronosyl transferase (UGT)-1A [Hebbar et al., 2005], NAD(P)H:quinone oxidoreductase (NQO) [Gerhauser et al., 2003; Hebbar et al., 2005; Hsieh et al., 2006; Jang et al., 1997], heme oxygenase-1 (HO-1) [Chen et al., 2005; Juan et al., 2005], and glutamate cysteine ligase (GCL) [Kode et al., 2007]. Resveratrol induces aforementioned cytoprotective enzymes largely by activating nuclear factor erythroid E2-related factor-2 (Nrf2) [Chen et al., 2005; Hsieh et al., 2006; Kode et al., 2007], which is a basic-region leucine zipper (bZIP) transcription factor.

Resveratrol induced the activity as well as the expression of NQO-1 at both protein and mRNA levels in human K562 cells by promoting nuclear translocation and subsequent binding of Nrf2 to antioxidant response element (ARE) [Hsieh et al., 2006]. The compound induced the protein and mRNA expression

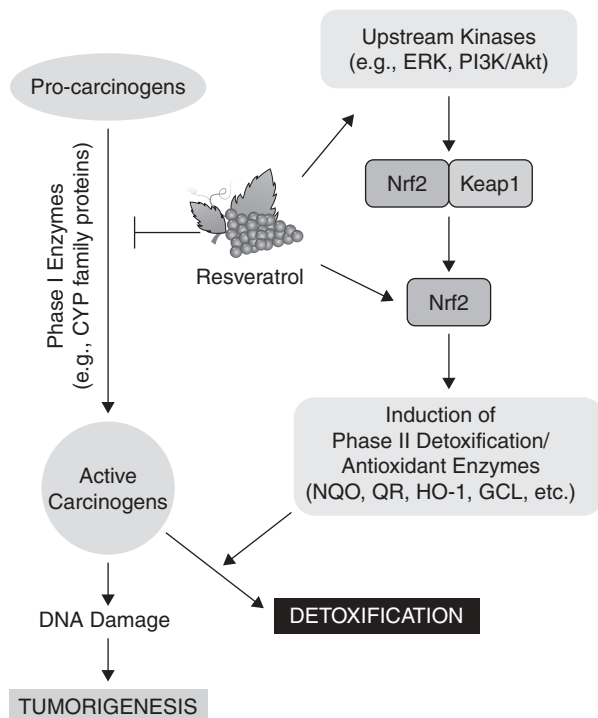


Figure 15.2 Inhibition of carcinogen activation and induction of phase II detoxification enzymes by resveratrol.

of HO-1 in human aortic smooth muscle [Juan et al., 2005] and rat pheochromocytoma (PC12) cells [Chen et al., 2005] by activating nuclear factor-kappaB (NF- κ B) and Nrf2, respectively. According to the former study, resveratrol (1–10 μ M) activated NF- κ B and increased the expression and the promoter activity of HO-1, while the compound at a concentration higher than 20 μ M suppressed NF- κ B activation, accounting for its anti-inflammatory effect [Juan et al., 2005]. Chen et al. [2005] demonstrated that resveratrol induced HO-1 expression in PC12 cells via Akt-mediated activation of Nrf2. Resveratrol restored cigarette smoke extract (CSE)-induced depletion of cellular GSH level by inducing Nrf2-driven GCL expression and subsequent GSH biosynthesis in human primary small airway epithelial cells (SAEC) and human alveolar epithelial cells (A549) [Kode et al., 2007]. Since Nrf2 inhibitory protein Keap1 is a zinc metalloprotein [Dinkova-Kostova et al., 2005], the resorcin moiety of resveratrol may form a zinc ion chelate, thereby leading to inactivation of Keap1 and subsequent activation of Nrf2.

Suppression of Pro-inflammatory Signaling Pathways

Pro-inflammatory mediators, such as prostaglandins (PGs), nitric oxide (NO), and cytokines are involved in carcinogenesis [Kundu and Surh, 2005; Perwez

Hussain and Harris, 2007]. PGs are produced through the breakdown of arachidonic acid by the enzyme cyclooxygenase (COX), while NO is generated from arginine metabolism by inducible nitric oxide synthase (iNOS). The elevated expression and/or activity of COX-2 and iNOS, and the enhanced production of various pro-inflammatory mediators have been implicated in the initiation, promotion, and progression stages of tumorigenesis [Kundu and Surh, 2008b]. The intracellular signaling pathways involved in regulating the expression of COX-2, iNOS and various pro-inflammatory mediators are composed of cell surface receptors (e.g., epidermal growth factor receptor, cytokine receptors), a distinct set of serine/threonine kinases and tyrosine kinases, and transcription factors. These include members of the mitogen-activated protein (MAP) kinase family, PI3K/Akt, PKC, glycogen synthase kinase (GSK), janus-activated kinase (JAK), and DNA-binding proteins, such as NF- κ B, activator protein-1 (AP-1), cyclic adenosine monophosphate response element binding protein (CREB), CCAAT/enhancer binding protein (C/EBP), and signal transducer and activator of transcription (STAT). Resveratrol has been reported to interfere with multiple components of pro-inflammatory signaling pathways (Fig. 15.3).

Pro-inflammatory Mediators Resveratrol attenuated the expression and/or the activity of various components of pro-inflammatory signaling pathways. The compound significantly inhibited the expression of COX-2 in lipopolysaccharide (LPS)-, TPA-, or H₂O₂-stimulated mouse peritoneal macrophages (Martinez and Moreno, 2000), LPS plus interferon (IFN)- γ -treated RAW 264.7 macrophages [Murakami et al., 2003], and TPA-stimulated mouse skin [Kundu et al., 2006a] and down-regulated the expression of COX-2 mRNA transcript in *N*-nitrosomethylbenzylamine (NMBA)-induced esophageal tumors in F344 rats [Li et al., 2002]. The inhibition of COX-2 promoter activity in both unstimulated and transforming growth factor- α -stimulated colon cancer (DLD-1) cells by resveratrol was partly attributed to the resorcin moiety present in the molecule [Mutoh et al., 2000]. Resveratrol also diminished the COX-2 activity and reduced the production of PGE₂ in peripheral blood leukocytes stimulated with LPS plus IFN- γ [Richard et al., 2005] and human mammary epithelial cells treated with TPA [Subbaramaiah et al., 1998]. A recent study by Zykova et al. [2008] demonstrated that resveratrol inhibited anchorage-independent growth of human colon cancer (HT-29) cells by directly binding to COX-2 and decreasing the production of PGE₂. The study also revealed that resveratrol reduced the growth of COX-2^{+/+} cells in culture, but did not affect the growth of cells deficient in COX-2.

The expression of iNOS and the generation of NO in LPS-activated RAW 264.7 cells were inhibited by resveratrol [Murakami et al., 2003; Tsai et al., 1999]. The compound significantly diminished the expression of tumor necrosis factor (TNF)- α mRNA in LPS-activated J774.2 macrophage cells [Kowalski et al., 2005] and peripheral blood leukocytes [Richard et al., 2005]. The expression of interleukin (IL)-8 protein and/or its mRNA in human monocytic leukemia (U937) cells [Shen et al., 2003] and human peripheral blood

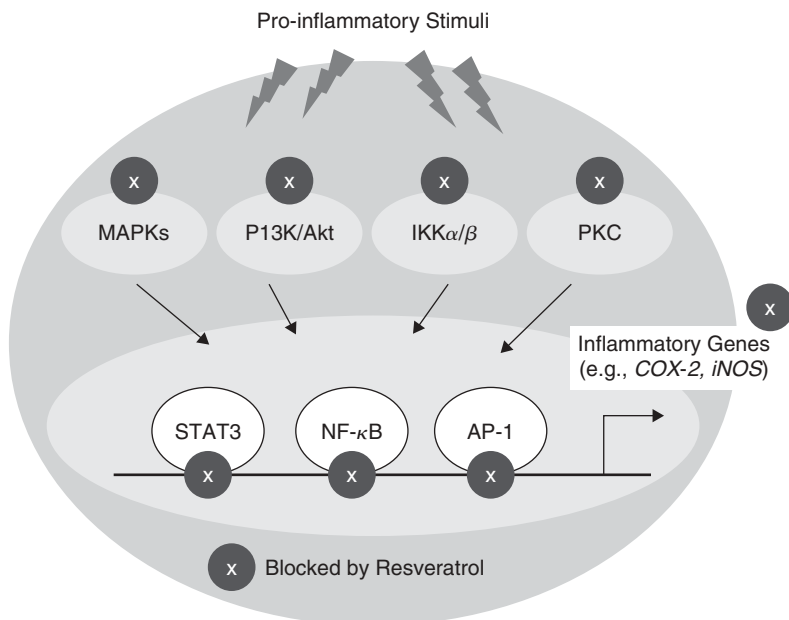


Figure 15.3 Resveratrol modulation of pro-inflammatory signaling pathways. Resveratrol represses transcriptional activation of various pro-inflammatory genes by inhibiting pro-inflammatory stimuli-induced activation of upstream kinases, such as MAP kinases, PI3K/Akt, IKK, PKC, etc., and blocking the DNA binding of eukaryotic transcription factors, such as NF- κ B, AP-1, and STAT3.

leukocytes [Richard et al., 2005] was also attenuated by resveratrol. Li et al. [2007] demonstrated that resveratrol reduced the serum IL-6 level in mice transplanted with lymphocytic leukemia L1210 cells.

Upstream Kinases Resveratrol exerts antiinflammatory and antitumor promoting effects partly by suppressing the phosphorylation of MAP kinases [Kundu et al., 2006a, 2006b; Reagan-Shaw et al., 2004; Tang et al., 2008; Yu et al., 2001]. The TPA-induced phosphorylation of all three representative MAP kinases such as ERK1/2, p38 MAP kinase, and JNK was diminished by resveratrol in HeLa cells [Yu et al., 2001] and mouse skin in vivo [Kundu et al., 2006a, 2006b]. Likewise, resveratrol inhibited the phosphorylation of ERK1/2 in human epidermoid carcinoma (A431) cells [Kim et al., 2006] and in heregulin- β 1-stimulated human breast cancer cells [Tang et al., 2008]. Resveratrol attenuated ultraviolet B (UVB)-induced expression of MAP kinase kinase (MEK) in SKH-1 hairless mouse skin [Reagan-Shaw et al., 2004]. Subbaramaiah et al. [1998] demonstrated that resveratrol down-regulated the expression of PKC in human mammary and oral epithelial cells stimulated with TPA. The compound attenuated the proliferation of human gastric adenoma cells by blocking the PKC

activity, without influencing the phosphorylation of ERK1/2 [Atten et al., 2001]. Moreover, the inhibition of TPA-induced growth of human prostate cancer (PC3) cells by resveratrol was partly associated with the translocation of cytosolic PKC α to the plasma membrane as well as autophosphorylation of both cytosolic and membrane-bound PKC α [Stewart and O'Brian, 2004]. The elevated expression of PKC δ in TPA-treated human cervical cancer (Caski) cells was blunted by resveratrol, resulting in reduced metastasis of these cells [Woo et al., 2004]. Resveratrol suppressed the phosphorylation of another upstream kinase Akt in ovarian [Kueck et al., 2007], breast [Li et al., 2006], uterine [Sexton et al., 2006], and prostate [Aziz et al., 2006; Hudson et al., 2007] cancer cells and multiple myeloma cells [Bhardwaj et al., 2007], resulting in apoptosis of these cells. In addition, resveratrol induced apoptosis in human T cell acute lymphoblastic leukemia cells by inhibiting phosphorylation of Akt and subsequent activation of GSK3 β [Cecchinato et al., 2007].

Transcription Factors Several DNA-binding proteins, such as NF- κ B, AP-1, CREB, and C/EBP are well-known transcriptional regulators of various pro-inflammatory genes including *cox-2* [Kim and Fischer, 1998; Surh and Kundu, 2005]. Upon stimulation of cells/tissues with inflammatory stimuli, a distinct set of intracellular signaling pathways comprising cell surface receptors and protein kinases are turned on and activate these transcription factors to bind to target gene promoter. Detailed molecular mechanisms of activation of these transcription factors have been discussed elsewhere [Chun and Surh, 2004]. Resveratrol exerted its anti-inflammatory effects by targeting some of these transcription factors. Manna et al. [2000] demonstrated that resveratrol inhibited the activation of NF- κ B in Jurkat-T, HeLa, and glioma cells treated with different stimuli such as TPA, LPS, H₂O₂, okadaic acid, and ceramide. Resveratrol also suppressed the activation of NF- κ B in IL-1 β - and Cr (VI)-stimulated acute myeloid leukemia (OCIM2) cells [Estrov et al., 2003] and mouse epidermal (JB6) cells [Leonard et al., 2003], respectively. We have reported that resveratrol diminished TPA-induced NF- κ B activation in mouse skin in vivo by blocking the activation of IKK, phosphorylation of I κ B α and p65, nuclear translocation of p65 and interaction of p65 with a transcriptional co-activator CREB-binding protein (CBP) [Kundu et al., 2006a]. Likewise, the compound inhibited UVB-induced activation of NF- κ B in normal human epidermal keratinocytes by blocking the activation of upstream IKK α as well as phosphorylation and degradation of I κ B α [Adhami et al., 2003]. Resveratrol also suppressed proliferation and induced apoptosis in human multiple myeloma cells by inhibiting the constitutive activation of NF- κ B via blockade of IKK activity and subsequent phosphorylation of I κ B α and p65 [Bhardwaj et al., 2007]. The compound also attenuated the nuclear translocation and the DNA binding of NF- κ B in LPS-stimulated RAW 264.7 cells by blocking phosphorylation and degradation of I κ B α [Cho et al., 2002; Tsai et al., 1999]. Although resveratrol negated TNF- α -induced activation of NF- κ B in U937 cells by suppressing phosphorylation and nuclear translocation of p65, the compound did not affect

the phosphorylation and degradation of I κ B α [Manna et al., 2000]. Pendurthi et al. [2002] reported that resveratrol suppressed LPS-induced activation of NF- κ B by inhibiting phosphorylation and transactivation potential of p65, but it failed to inhibit nuclear translocation of NF- κ B/Rel proteins.

Alternatively, resveratrol exerted epigenetic control on NF- κ B activation via SIRT1 activation [Yang et al., 2007; Yeung et al., 2004]. It was reported that SIRT1, a nicotinamide adenosine dinucleotide-dependent histone deacetylase, interacted physically with the RelA/p65 and negated NF- κ B-driven gene transcription by deacetylating RelA/p65 at lysine 310 [Yeung et al., 2004]. Resveratrol inhibited CSE-induced NF- κ B activation and NF- κ B-regulated pro-inflammatory gene expression by activating SIRT1 in monocyte-macrophage (MonoMac6) cells, bronchoalveolar lavage fluid, and rat lungs [Yang et al., 2007].

AP-1 is another molecular target of resveratrol in its suppression of inflammatory responses. Resveratrol abrogated TPA-induced activation of AP-1 in human mammary epithelial cells [Subbaramaiah et al., 1998, 1999], U937 human leukemia cells (Li et al., 2003), and mouse skin in vivo [Kundu et al., 2006b] and inhibited TNF- α -induced AP-1 DNA binding in U937 cells [Manna et al., 2000]. Resveratrol diminished UVC- or TPA-induced AP-1 reporter gene activity in HeLa cells by blocking the activation of MAP kinases and PKC (Yu et al., 2001). In contrast, resveratrol failed to suppress AP-1-driven transcriptional activity in LPS-stimulated human monocytic (THP-1) cells [Pendurthi et al., 2002].

Restoration of Gap–Junction Intercellular Communication (GJIC)

The dysfunction of GJIC is a characteristic feature of premalignant and malignant cells [Upham et al., 2007]. Many tumor promoters and growth factors have been shown to inhibit GJIC [Upham et al., 2007]. Several studies suggest that the anticancer activity of resveratrol is, partly, ascribed to its ability to restore GJIC [Kim et al., 2008; Nielsen et al., 2000; Upham et al., 2007]. Resveratrol has been reported to restore the decreased level of GJIC in WB-F344 rat liver epithelial cells treated with TPA (Nielsen et al., 2000), dicumyl peroxide [Upham et al., 2007], or gallic acid [Kim et al., 2008].

Inhibition of Cell Proliferation

Resveratrol exerts antitumor effects partly by arresting the growth of various cancer cells in culture [Kundu and Surh, 2004]. The inhibition of ornithine decarboxylase (ODC), a biochemical hallmark of tumor promotion, has been shown to account for the antiproliferative and antitumor effects of resveratrol [Schneider et al., 2000; Ulrich et al., 2007]. Aberrant changes in cell-cycle machinery are considered as the biochemical basis of abnormal proliferation of transformed cells. Major cell-cycle regulatory proteins include various cyclins, cyclin-dependent kinases (Cdk), Cdk inhibitors, and check point kinases (Chk1

and Chk2), which maintain the homeostatic control of cell growth and differentiation [Collins and Garrett, 2005; Gali-Muhtasib and Bakkar, 2002]. Resveratrol blocks inappropriate signaling through modulation of these cell-cycle regulatory proteins and suppresses the growth of various cancer cells in culture [Kundu and Surh, 2004] (Table 15.1). Moreover, the antiproliferative and growth inhibitory effects of resveratrol have been attributed to its ability to inhibit DNA synthesis [Fontecave et al., 1998] and telomerase activity [Fuggetta et al., 2006].

Resveratrol inhibited the expression and/or activities of various cyclins (D1, D2, and E) and Cdks (-2, -4, and -6), and induced the expression of the Cdk

Table 15.1 Molecular Targets of Resveratrol as an Antiproliferative Agent

Cells/Tissues/ Stimuli	Effects	References
A431 cells	G1 phase arrest, \uparrow p21 ^{WAF1/CIP1} expression, \downarrow cyclin D1/D2-cdk6, \downarrow cyclin D1/D2-cdk4 and cyclin E-cdk2 complex formation	Ahmad et al., 2001
	Block G1 \rightarrow S phase transition, \downarrow cyclin E-Cdk2 complex formation \downarrow hyperphosphorylated Rb, \uparrow hypophosphorylated Rb, \downarrow expression of E2F and DP, \downarrow free E2F level	Adhami et al., 2001
	G1 phase arrest, \downarrow expression of cyclin A, D1, and cdk-6, \uparrow accumulation of hypophosphorylated Rb, \uparrow expression of p21 ^{WAF1/CIP1} (independent of p53), \uparrow p27 ^{KIP1} \downarrow c-Jun expression, \downarrow AP-1 DNA binding, \downarrow MEK1, \downarrow ERK1/2	Kim et al., 2006
A549 cells	S phase arrest, \downarrow phosphorylation of Rb, \uparrow p21 ^{WAF1/CIP1} (p53-dependent)	Kim et al., 2003a
DU-145 cells	\downarrow Expression of cyclin D1, and cdk-4, \downarrow activity of cyclin E and cdk-2, \uparrow expression of p21 ^{WAF1/CIP1} and p53	Kim et al., 2003b
SW480 cells	S phase arrest, \downarrow expression of cyclin B1, D1, A1, \downarrow β -catenin expression, No inhibitory effect on cyclin D1 promoter activity, \downarrow cyclin D1 mRNA expression only at 300 μ M	Joe et al., 2002
OVCAR-3 cells	S phase arrest, \uparrow phosphorylation of Cdc25c at tyrosine 15 residue, \uparrow phosphorylation of H2A.X at serine 139 residue, \uparrow chk1/2 expression, \uparrow ATM/ATR kinase activity	Tyagi et al., 2005
Caco2 and HCT-116 cells	Blocks S \rightarrow G2 transition, \downarrow expression of cyclin D1 and Cdk4, \uparrow cyclin E and A expression, \downarrow hyperphosphorylated Rb, \uparrow hypophosphorylated Rb	Wolter et al., 2001
UVB-irradiated SKH-1 hairless mouse skin	\downarrow Phosphorylation of ERK, \downarrow expression of cyclin D1/D2 and cdk-2,-4,-6, \uparrow expression of p21 and p53	Reagan-Shaw et al., 2004

inhibitor p21^{WAF1/CIP1} in human epidermoid carcinoma (A431) cells, thereby blocking growth of these cells [Ahmad et al., 2001]. The antiproliferative effect of resveratrol in A431 cells was also associated with a decrease in the expression of E2F transcription factor as well as the reduced level of the hyperphosphorylated form of retinoblastoma (Rb) protein [Adhami et al., 2001]. Likewise, resveratrol suppressed UV-induced expression of Cdks (-2, -4, -6) and cyclins (D1 and D2), and up-regulated the expression of p21^{WAF1/CIP1} and p53 in SKH-1 hairless mouse skin [Reagan-Shaw et al., 2004]. Moreover, the compound diminished the expression and activities of cyclin D1 and Cdk4 in association with the induction of p53 and p21^{WAF1/CIP1} in human prostate (DU-145) [Kim et al., 2003b] and breast (MCF-7) [Kim et al., 2004] cancer cells. Although resveratrol attenuated the expression of cyclin D1 in SW480 cells, it failed to inhibit the cyclin D1 promoter activity [Joe et al., 2002]. Resveratrol inhibited the formation of a complex between cyclin E-Cdk-2 in human prostate cancer (DU-145) cells without altering the levels of interacting proteins [Kim et al., 2003b]. By inactivating AP-1, resveratrol suppressed proliferation of human epidermoid carcinoma (A431) cells [Kim et al., 2006]. The inhibition of Rb phosphorylation and induction of p21^{WAF1/CIP1} and p53 proteins by resveratrol led to S-phase arrest in human lung cancer (A549) cells in culture [Kim et al., 2003a]. Treatment of a series of human cancer cells (MCF-7, SW480, HCE7, Seg-1, Bic-1, and HL60) with resveratrol reduced cell proliferation via down-regulation of cyclin B1 [Joe et al., 2002]. Resveratrol exerted antiproliferative effects in human multiple myeloma cells by suppressing NF- κ B activation by inhibiting upstream kinases IKK and Akt, and blocking the phosphorylation of I κ B α and p65 [Bhardwaj et al., 2007]. This study also demonstrated that resveratrol repressed phosphorylation and DNA binding of STAT3 and down-regulated STAT3-regulated cyclin D1, Bcl-xl, and Mcl-1 genes in various human multiple myeloma cells [Bhardwaj et al., 2007].

Resveratrol activated ataxia telangiectasia mutated (ATM)/ataxia telangiectasia-Rad3-related (ATR)-Chk1/2, phosphorylated cell division cycle (Cdc)-25C, Cdc-2 and H2A.X, and induced S phase arrest in human ovarian cancer (OVCAR-3) cells, while it caused only marginal S phase arrest in normal human foreskin fibroblasts [Tyagi et al., 2005], suggesting that the compound selectively inhibited proliferation of cancer cells. Besides modulating the expression and/or activities of various cell-cycle regulatory proteins, resveratrol attenuated tumor growth by targeting several components of protein translation machinery. For example, resveratrol inhibited insulin-like growth factor-1-induced phosphorylation of protein translation regulators, such as 4E-BP1, eIF4E, and 70S6K1, and expression of S6 ribosomal kinase in ovarian cancer (A2780/CP70 and OVCAR-3) cells (Cao et al., 2004).

Induction of Apoptosis

The biochemistry behind the anticancer effects of resveratrol has been corroborated by its ability to induce apoptotic death in various cancer cells in

culture, xenografted tumors, and chemically induced mouse skin tumors *in vivo* [Garvin et al., 2006; Kalra et al., 2007; Kundu and Surh, 2004]. Resveratrol activates both extrinsic (death receptor-mediated) and intrinsic (mitochondria-dependent) pathways of cell death machinery (Fig. 15.4).

Extrinsic Pathway The induction of apoptosis in human promyelocytic leukemia (HL-60) and human breast cancer (T47D) cells by resveratrol was mediated via activation of the CD95-CD95L signaling, while it did not affect the survival of normal peripheral blood lymphocytes [Clement et al., 1998]. Delmas and colleagues [2003, 2004] demonstrated that resveratrol did not cause any change in the expression level of FAS or FAS-L in human colon cancer (SW480) cells, but rather it redistributed cell surface receptors such as CD95, and death receptor-4 and -5 in membrane lipid rafts and induced apoptosis in a

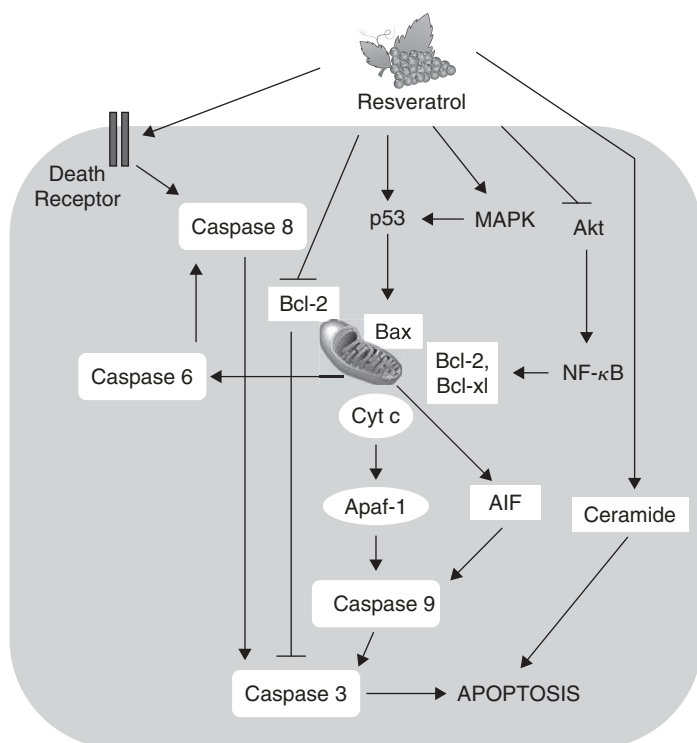


Figure 15.4 Mechanisms of apoptosis induction by resveratrol. Resveratrol selectively induces apoptosis in various cancer cells in culture by several mechanisms including activation of death receptor-mediated signaling, mitochondria-dependent cytochrome *c* release and caspase activation, induction of *p53* and *p53*-regulated proapoptotic genes, activation of MAP kinase-mediated *p53* phosphorylation, blockade of Akt-mediated cell survival pathways, and accumulation of intracellular ceramide level.

caspace-dependent and Bcl-2-independent manner. Co-treatment of these cancer cells with nystatin, a cholesterol sequestering agent, abrogated resveratrol-induced redistribution of death receptors into membrane lipid rafts and death-receptor-mediated cell death [Delmas et al., 2004]. Pretreatment of human prostate cancer (PC-3 and DU-145) cells with resveratrol resulted in TNF-related apoptosis inducing ligand (TRAIL)-, Fas-, or TNF- α -mediated cell death by multiple mechanisms involving down-regulation of inhibitor of apoptotic protein (IAPs), suppression of Akt phosphorylation, and subsequent activation of caspases (Gill et al., 2007).

Intrinsic Pathway Resveratrol induced apoptosis by targeting the mitochondria-dependent pathway. The activation of intrinsic pathway of cell death by resveratrol is supported by its inhibitory effect on the mitochondrial F1F0-ATPase, which is an enzyme involved in mitochondrial ATP synthesis [Gledhill et al., 2007]. Resveratrol activated p53, up-regulated proapoptotic Bax, down-regulated antiapoptotic Bcl-2, reduced the mitochondrial membrane potential, stimulated cytochrome *c* release and induced various caspases, thereby inducing apoptosis [Gusman et al., 2001; Kim et al., 2004; Zhou et al., 2005]. The induction of apoptosis by resveratrol has been shown to be cell type specific, being p53-dependent in certain cancer cells [Heiss et al., 2007; Huang et al., 1999], while p53-independent in others [Mahyar-Roemer et al., 2001, 2002]. Resveratrol increased the MAP kinase-mediated phosphorylation of p53 at serine 15 residue, thereby inducing apoptosis in JB6 Cl41 cells [She et al., 2001, 2002]. Moreover, resveratrol induced apoptosis in HepG2 cells by a mechanism involving p53-dependent increases in Bax and p21 [Kuo et al., 2002]. Likewise, the induction of p53-responsive genes, such as *p21^{WAF1/CIP1}*, *p300/CBP*, and *Apaf1*, by resveratrol was attributed to apoptosis of prostate cancer (LNCaP) cells [Narayanan et al., 2003]. Besides inducing apoptosis in cancer cells, resveratrol also induced apoptosis in chemically induced mouse skin papillomas *in vivo* via the induction of p53, release of cytochrome *c*, activation of Bax, inhibition of Bcl-2, and proteolytic cleavage of various caspases, such as caspase 9 and caspase 3 as well as poly-(ADP)ribosylpolymerase (PARP) [Kalra et al., 2007].

Other Mechanisms Resveratrol activated caspase-2 and -8, resulting in the activation of downstream caspases, and induced cell death in a death receptor- or mitochondria-independent manner [Mohan et al., 2006]. The induction of apoptosis in HCT-116 (*Bax^{+/-}*) cells by resveratrol was mediated via activation of caspase 6 and subsequent degradation of nuclear coat protein lamin A [Lee et al., 2006]. Resveratrol induced a senescence-like growth arrest in HCT-116 cells via ROS-dependent activation of p38 MAP kinase and ATM kinase, and subsequent phosphorylation of p53 and induction of *p21^{WAF1/CIP1}* [Heiss et al., 2007]. In contrast, a p53-independent mechanism for resveratrol-induced apoptosis of HCT-116 cells was reported [Mahyar-Roemer et al., 2001, 2002].

Lin et al. [2006] demonstrated that resveratrol induced apoptosis in MCF-7 cells by interacting with the $\beta 3$ domain of a cell surface receptor integrin- $\alpha V\beta 3$,

thereby transducing the activating signals to ERK and p53. Another interesting mechanism involved in p53-dependent apoptosis was observed in MCF-7 and MDA-MB-231 cells treated with resveratrol [Tang et al., 2006]. According to this study, resveratrol induced apoptosis through enhanced co-localization of COX-2, phosphorylated p53 (at serine 15 residue), and transcriptional co-activator p300. Blocking the COX-2 function with a pharmacologic inhibitor or small interfering RNA (COX-2 siRNA) reduced resveratrol-induced phosphorylation of p53 and induction of apoptosis in MCF-7 cells [Tang et al., 2006]. The inhibition of Akt, activation of GSK-3 β , and attenuation of Notch-mediated survival signals partly accounted for resveratrol-induced apoptosis in T-cell acute lymphoblastic leukemia cells [Cecchinato et al., 2007].

Resveratrol inhibited proliferation and/or induced apoptosis of different cancer cells by accumulating intracellular ceramide, which is a key component of sphingolipids and a mediator of many cellular processes including proliferation, differentiation, and senescence [Scarlatti et al., 2003, 2007]. Resveratrol induced apoptosis in MDA-MB-231 cells by inducing de novo synthesis of ceramide and hydrolysis of sphingomyelin, thereby increasing ceramide level [Scarlatti et al., 2003]. In another study, resveratrol-induced accumulation of ceramide sensitized DU-145 cells to apoptosis upon exposure to ionizing radiation [Scarlatti et al., 2007].

Inhibition of Tumor Angiogenesis

Angiogenesis, the formation of new blood vessels, is an important feature of rapidly proliferating tumors to meet the requirement of adequate oxygen and nutrient supply for their survival. Increased metabolic activities and oxygen consumption by rapidly proliferating cells in a solid tumor create an intratumoral hypoxic environment [Liao and Johnson, 2007; Lopez-Lazaro, 2006], which leads tumor cells to induce hypoxia-responsive genes [Hickey and Simon, 2006; North et al., 2005]. One of the master regulators of cellular oxygen homeostasis is hypoxia inducible factor (HIF), which regulates the expression of various hypoxia-responsive genes [Semenza, 2004] including vascular endothelial growth factor (VEGF), basic fibroblast growth factor (bFGF), VEGF receptor (VEGFR), IL-8, iNOS, and angiopoietins [Hickey and Simon, 2006; Pollard, 2004]. Several studies have reported that resveratrol exerts anticancer effects by blocking various angiogenic switches. Treatment of OVCAR-3 cells with resveratrol resulted in the down-regulation of HIF-1 α and VEGF through multiple mechanisms involving inhibition of Akt and MAP kinases, inhibition of protein translational regulators, and enhancement of proteasomal degradation of HIF-1 α protein [Cao et al., 2004]. Likewise, resveratrol reduced the accumulation of HIF-1 α protein and the expression of VEGF in human tongue squamous cell carcinomas (SCC-9) and HepG2 cells, partly by inhibiting the activation of ERK and Akt, and enhancing the proteasomal degradation of HIF-1 [Zhang et al., 2005]. Resveratrol reduced the extracellular levels of VEGF

in vitro and suppressed the growth of MDA-MB-231 cells xenografted in nude mice by blocking angiogenesis [Garvin et al., 2006].

Suppression of Invasion and Metastasis

The shedding of cells from primary tumors, invasion of tumor cells through the tumor-associated stroma and subsequent colonization in distant sites in the body are major events in tumor progression. Genes encoding extracellular matrix processing proteases, adhesion proteins, and motility factors are the main mediators of invasion and metastasis. One of the mediators of tumor invasion and metastasis is lysophosphatidic acid (LPA), which enhances the migration of cancer cells [Park et al., 2007]. Resveratrol significantly attenuated LPA-induced expression of HIF-1 α and VEGF, and subsequent migration of human ovarian cancer cells via blockade of the activation of upstream ERK1/2 and p70S6 kinase [Park et al., 2007]. Intraperitoneal administration of resveratrol conferred 40% protection against lung metastasis in mice intramuscularly transplanted with Lewis lung carcinoma cells [Busquets et al., 2007]. Matrix metalloproteinase (MMP), urokinase-plasminogen activator (uPA), and uPA receptor (uPAR) are primarily involved in the metastatic process. The expression of MMP-9 mRNA, but not of uPA or uPAR, was diminished in murine bladder cancer (MB 49) cells cultured in the presence of resveratrol [Garcia Mediero et al., 2005]. Likewise, resveratrol blocked the invasiveness of various cancer cells by reducing the expression and/or the activity of MMP-2 and -9 [Sun et al., 2006; Tang et al., 2008; Yu et al., 2007]. Resveratrol attenuated the invasion of TNF- α -stimulated HepG2 cells by down-regulating the expression of MMP-9 via blockade of NF- κ B activation [Yu et al., 2007]. The compound suppressed TNF- α -induced MMP-9 expression in vascular smooth muscle cells by blocking the activation of NF- κ B and AP-1 [Lee and Moon, 2005]. Similarly, TPA-induced expression of MMP-9 protein and its mRNA transcript in Caski cells was attenuated by resveratrol through inhibition of NF- κ B, AP-1, and upstream kinases JNK and PKC α [Woo et al., 2004]. According to Tang et al. [2008], resveratrol inhibited heregulin-1-induced MMP-9 expression and invasion of MCF-7 cells by blocking phosphorylation of ERK. Resveratrol decreased the chemotactic response of metastatic MDA-MB-231 cells by reducing focal adhesion kinase activity [Azios and Dharmawardhane, 2005]. Alternatively, incubation with resveratrol or resveratrol-treated rat sera diminished the peroxide levels and the expression of hepatocyte growth factor in H₂O₂-stimulated rat ascites hepatoma (AH109A) cells, and reduced the invasive capacity of these cells, suggesting that the antioxidant property of resveratrol accounts for its anti-invasive effects [Miura et al., 2004].

Augmentation of Chemotherapy, Radiotherapy, and Cancer Gene Therapy

Recently, the combined use of chemopreventive phytochemicals with conventional anticancer therapy or radiotherapy has been shown to sensitize

many chemoresistant and/or radioresistant cancer cells to apoptosis [Garg et al., 2005]. Products of multidrug resistant (*MDR*)-1 gene, for example P-glycoprotein, have been involved in acquiring chemoresistance by cancer cells. P-glycoprotein reduces intratumoral concentrations of chemotherapeutic drugs by actively effluxing drugs from cells and reduces their efficacy. Treatment of P-glycoprotein overexpressing multidrug-resistant human carcinoma KB-C2 cells with resveratrol and daunorubicin sensitized the cells to daunorubicin-induced apoptosis as a consequence of decreased P-glycoprotein functions and increased accumulation of daunorubicin in these cells [Nabekura et al., 2005]. Moreover, resveratrol enhanced the apoptotic effects of bortezomib and thalidomide in multiple myeloma cells [Bhardwaj et al., 2007]. A combination therapy with resveratrol plus etoposide induced apoptosis of HT-29 cells via a ROS-dependent activation of adenosine monophosphate-activated protein kinase [Hwang et al., 2007]. Resveratrol potentiated the growth inhibitory effects of cisplatin or doxorubicin in OVCAR-3 and human uterine cancer (Ishikawa) cells, and reduced doxorubicin toxicity in mice [Rezk et al., 2006], suggesting that the compound simultaneously enhances chemosensitivity of cancer cells and alleviates chemotherapy-associated adverse effects.

Irradiation with ionizing radiation (IR) is an important modality for the treatment of cancer. While resveratrol protects normal cells from radiation damage, the compound enhances the sensitivity of many radioresistant cancer cells to IR-induced apoptosis [Reagan-Shaw et al., 2008]. Pretreatment of DU-145 cells with resveratrol enhanced IR-induced apoptosis via increased accumulation of ceramide in these cells [Scarlatti et al., 2007]. In combination with γ radiation, resveratrol reactivated the apoptotic pathway in TRAIL-resistant human melanoma cells [Ivanov et al., 2008]. According to this study, an initial increase in the γ -radiation-induced expression of death receptor-5 followed by down-regulation of antiapoptotic cFLIP and Bcl-xL via inactivation of STAT3 and NF- κ B by resveratrol led to melanoma cell death [Ivanov et al., 2008]. Combination therapy with γ -radiation and resveratrol may cause either apoptosis or necrosis of melanoma cells depending on the ability of resveratrol to induce surface expression of TRAIL. Melanoma cells exhibiting a suppressed translocation of TRAIL to cell surface undergo necrosis upon receiving γ -radiation, while cells responsive to resveratrol-induced TRAIL surface expression follow γ -radiation-induced apoptosis [Johnson et al., 2008].

In addition to its sensitizing effects in chemo- or radioresistant cells, resveratrol also enhances the antitumor effects of cancer gene therapy. Treatment of xenografted (human pancreatic carcinomas or rat colorectal carcinomas) tumors with replication-deficient adenoviral gene therapy vector Ad.Egr.TNF, resveratrol or their combination showed that combined administration of Ad.Egr.TNF and resveratrol caused more growth inhibition of tumor xenografts *in vivo* via activation of early growth response-1 gene and elevation of an intratumoral TNF- α level in comparison to treatment with either agent alone (Bickenbach et al., 2008). The same study also demonstrates that the

combination of resveratrol with Ad.Egr.TNF does not produce any adverse effects in tumor bearing animals [Bickenbach et al., 2008].

CONCLUSION

With millions of cancer-afflicted people around the world, scientists are making all efforts to find an effective strategy to reduce the incidence and the mortality of cancer. Research projected toward searching for effective chemopreventive/chemotherapeutic agents has been expedited over the last few decades. Although multidirectional approaches, such as synthesizing novel anticancer lead compounds, developing cancer gene therapy and immunotherapy, etc have been adopted to find a successful cure for cancer, the search for chemopreventive and chemotherapeutic phytochemicals from edible plants has received special attention. The complex heterogeneity of cancer cells imposes a major hurdle in finding a molecular target-based prevention or treatment modality for cancer. Therefore, fighting cancer with dietary phytochemicals, which can simultaneously modulate diverse biochemical events, appears as a timely approach to prevent or cure cancer.

Among the nature's bounty of anticancer agents, resveratrol has been studied extensively to elucidate its underlying biochemical basis of chemopreventive and chemotherapeutic effects. Recently, a few clinical trials with resveratrol have been launched. According to a recent phase I clinical trial, the consumption of resveratrol does not cause any serious adverse effects in healthy volunteers, but the peak plasma level remains below the minimum effective concentration of the compound required to exhibit chemopreventive effects in cultured cells [Boocock et al., 2007]. Another phase I clinical trial has recently been undertaken to evaluate the safety and the pharmacokinetic profile of resveratrol given in a multiple-dosage regimen [Baur and Sinclair, 2006]. A phase I colon cancer prevention trial with resveratrol was conducted at the University of California, Irvine, [Baur and Sinclair, 2006]. Despite favorable preclinical and clinical findings, and a significant progress in clarifying the biochemistry behind anticancer properties of resveratrol, pharmacokinetic studies in rodent models suggest a poor bioavailability of the compound *in vivo*. Thus, one of the critical issues of future resveratrol research would be to improve its bioavailability by developing an appropriate formulation.

ACKNOWLEDGMENTS

This work was supported by the National Research Laboratory Fund and the Biofood Research Program from the Ministry of Science and Technology, Republic of Korea.

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INTERNET RESOURCES

http://www.cancer.org/docroot/STT/content/STT_1x_Cancer_Facts_and_Figures_2008.asp?from=fast (Cancer Facts and Figures, 2008. pdf; page 57).

16 Curcumin: The Biochemistry Behind Its Anticancer Effects

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INTRODUCTION

Curcumin is a hydrophobic polyphenol derived from turmeric: the rhizome of the herb *Curcuma longa*. Traditionally, turmeric and other curcuminoids have been used in therapeutic preparations for various ailments in different parts of the world. Numerous therapeutic effects of curcumin/turmeric have been confirmed by modern scientific research. It is a highly pleiotropic molecule that modulates numerous targets, including the activation of transcription factors (e.g., NF- κ B, STAT-3, AP-1, NRF-2, PPR- γ , HIF-1), receptors (e.g., HER-2, IL-8, CXCR-4), kinases (e.g., EGFR, ERK, JAK, AAKP), cytokines (e.g., TNF, IL, MIP, MCP), enzymes (e.g., MMP, iNOS, GST, ATPase), and

growth factors (e.g., EGF, NGF, HGF, PDGF). Because of its ability to interact with a diverse range of molecular targets, curcumin can affect numerous molecular and biochemical cascades. One of our recently published reviews presents a more detailed description of the molecular targets of curcumin [Goel et al., 2007].

Extensive research conducted during the past century has established the complexity and involvement of multiple signaling pathways in the cancer growth and progression, which in turn suggests that a drug, which can interact with multiple target molecules, will be more efficacious than the current monotargeted anticancer drugs. Curcumin's multitargeting ability may be the key to its therapeutic potential against cancer. Furthermore no dose-limiting toxicity is reported for this molecule yet, and doses as high as 12 g/day is proved to be well tolerated and safe in humans [Cheng et al., 2001]. This chapter describes the preclinical and clinical data on the use of curcumin for the treatment of cancer.

CHEMISTRY OF CURCUMIN AND ITS ANALOGS

Chemically, it is a bis- α , β -unsaturated β -diketone (commonly called diferuloylmethane) that exhibits keto-enol tautomerism, having a predominant keto form in acidic and neutral solutions and a stable enol form in alkaline media. It is a member of the linear diarylheptanoid class of natural products in which two oxy-substituted aryl moieties are linked together through a seven-carbon chain. The C7 chain of linear diarylheptanoids is known to have unsaturation, oxo functions, enone moiety, and 1,3-diketone group. Except for the oxo and hydroxy functions, the C7 chain is generally unsubstituted. This unsaturation in the linker unit has an E-configuration (trans C=C bonds). Besides curcumin, other analogous molecules such as demethoxycurcumin (DMC), bisdemethoxycurcumin (BDMC), and cyclocurcumin are also present in turmeric (Fig. 16.1). Commercially available curcumin contains 77% curcumin, 17% DMC, and 3% BDMC. DMC and BDMC are structurally very similar to curcumin except they lack one and two methoxy groups, respectively.

Although curcumin, DMC, and BDMC differ in their chemical structure only with regards to methoxy substitution, they showed significantly different antioxidant, antitumor, and anti-inflammatory activities. Up to now there is no systematic study that clearly correlates the physicochemical and molecular properties of the three curcuminoids with their biological activities. However, the existing literature provides some clues to understand which group is actually responsible for a given biological activity of the curcuminoids.

Since many reports favor better radical scavenging and antioxidant ability of curcumin when compared with the other two, followed by DMC, the *o*-methoxy substitutions are certainly involved in this activity. The hydrogen-bonding interaction between the phenolic OH and the *o*-methoxy groups in curcumin markedly influences the O-H bond energy and H-atom abstraction

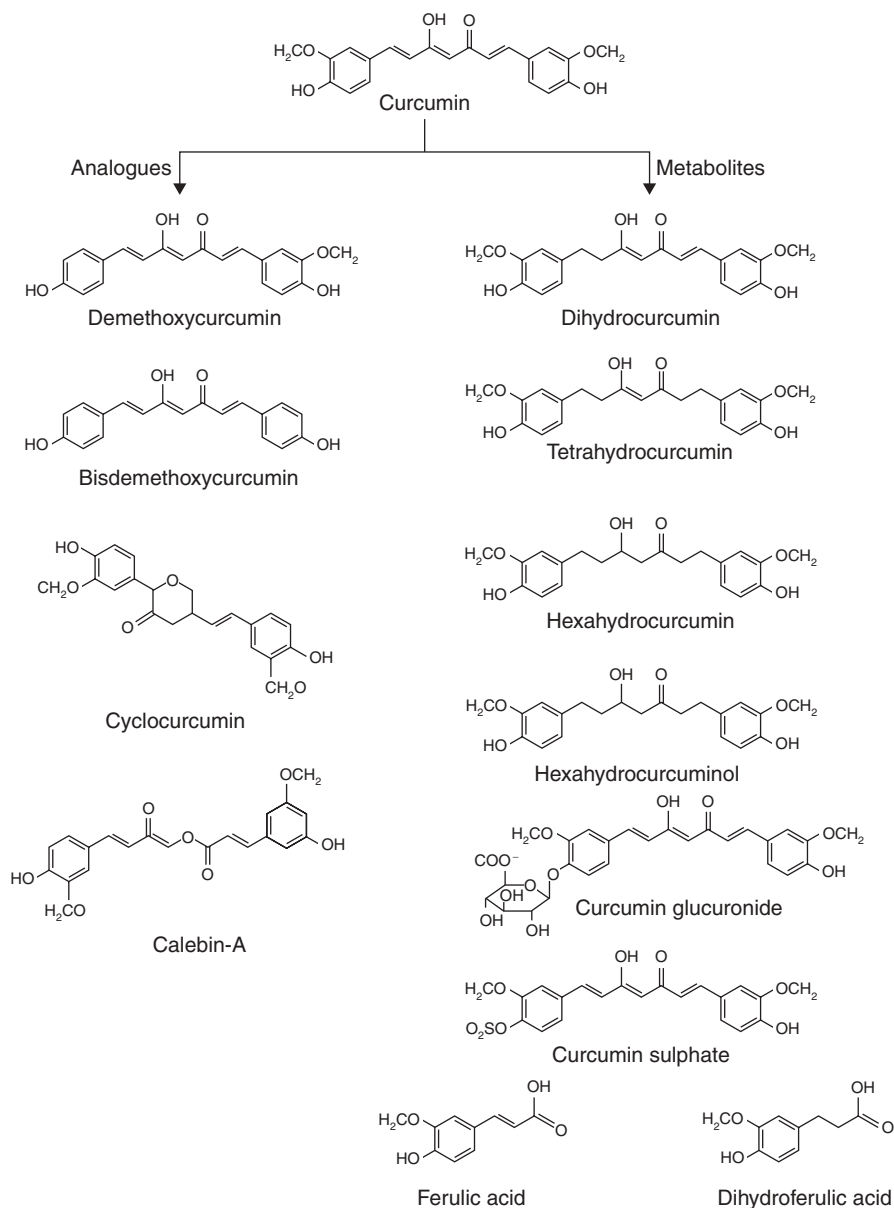


Figure 16.1 Curcumin and its Analogs.

by free radicals, thus making it a better free-radical scavenger than BDMC [Somparn et al., 2007].

The α , β -unsaturated diketone moiety in the curcuminoids is a Michael reaction acceptor, which belongs to the major class of phase II enzyme inducers

[Jeong et al., 2006]. Therefore, this property may be responsible for the induction of HO-1 and NF- κ B suppression in cells by curcuminoids. Methoxy substitution on the aromatic ring can significantly influence their interaction with nucleophiles in Michael reaction. The reasons and the actual mechanism of the antitumor activities of the curcuminoids are still far from understood. It is still not known how the *o*-methoxy-deficient BDMC is a more potent ROS inducer and the *o*-methoxy-substituted curcumin is a more potent suppressor of NF- κ B activation [Sandur et al., 2007]. The effect of change in the lipophilicity of the curcuminoids with methoxy substitution in influencing some of these activities also cannot be ignored.

Further studies are required to unravel this mystery of how the methoxy substitutions and the α , β -unsaturated β -diketone moiety actually influence conformational changes, lipophilicity, electron density distribution, and redox properties of curcuminoids. Correlating these physicochemical properties with the unique pleiotropic effects of curcuminoids is a rewarding exercise. Such studies would definitely provide proper reasoning in understanding these markedly different antioxidant, antitumor, and anti-inflammatory activities of natural curcuminoids from turmeric.

Cyclocurcumin differs from curcumin in the β -diketone link. In this molecule, the α , β -unsaturated β -diketone moiety of curcumin is replaced by α , β -unsaturated dihydropyranone moiety. Up to now, not many biological studies are reported with cyclocurcumin except for one study on inhibition of MCF-7 tumor cell proliferation by Simon et al. [1998] where it has been found to be ineffective in inhibiting cell proliferation and arrest of cell-cycle progression.

ANTICANCER EFFECTS OF CURCUMIN

Studies during the past century have shown the anticancer effect of curcumin against cancers of various anatomical sites. The preclinical anticancer potential of curcumin has been established both *in vitro* and *in vivo*, which lead to the clinical trials with this promising molecule. Below is a description of the studies, that have evaluated the preclinical and clinical anticancer activity of curcumin.

Anticancer Effects *in Vitro*

Several reports have described the anticancer activity of curcumin in a variety of cancer cell lines. *In vitro* studies have established the activity for curcumin against breast, gastric, hepatic, pancreatic, colorectal, urinary bladder, kidney, prostate, cervical, ovarian, uterine, lung, oral, thymic, and skin cancers. Besides these cancer types, curcumin has shown *in vitro* therapeutic efficacy against hematological cancers including leukemia, lymphoma, and multiple myeloma. One of our early studies established that the antiproliferative effect of curcumin in human breast cancer cell lines, including hormone-dependent, hormone-independent,

and multidrug-resistant cells, was time and dose dependent and correlated with curcumin's inhibition of ornithine decarboxylase activity [Anand et al., 2008]. Several mechanisms have been proposed to account for the action of curcumin in breast cancer cells. For example, curcumin was found to inhibit the aryl hydrocarbon receptor and cytochrome P450 1A1 [Anand et al., 2008]; the tyrosine kinase activity of p185neu; the expression of Ki67, PCNA, and p53 mRNAs; and COX-1 and COX-2 enzymes. Curcumin also induced p53-dependent Bax expression, inhibited angiogenesis factors VEGF (vascular endothelial growth factor), b-FGF (basic fibroblast growth factor) [Schindler, 2006; Shao et al., 2002], and disrupted mitotic spindle structure and induced micronucleation [Holy, 2002]. It has been shown that curcumin inhibits telomerase activity through human telomerase reverse transcriptase [Ramachandran et al., 2002], down-regulates the expression of MMP-2 (matrix metalloproteinase-2), up-regulates TIMP-1 (tissue inhibitor of metalloproteinase-1) [Di et al., 2003], and blocks NF- κ B and AP-1 activation [Aggarwal et al., 2005; Bachmeier et al., 2007; Bobrovnikova-Marjon et al., 2004; Yoon and Liu, 2007]. Studies have also shown curcumin to inhibit LOX pathways [Hammamieh et al., 2007], induce the degradation of cyclin E expression through a ubiquitin-dependent pathway, up-regulate cyclin-dependent kinase inhibitors p21 and p27 [Aggarwal et al., 2007], and down-regulate the insulin-like growth factor-1 (IGF-1) [Xia et al., 2007] in breast cancer cell lines.

The cytotoxic effect of curcumin on gastric carcinoma cell lines has been established. In a study curcumin and 5-fluorouracil (5-FU) synergistically inhibited the growth of gastric carcinoma cells. In another study, curcumin reversed the MDR of a human gastric carcinoma cell line in correlation with a decrease in P-gp function and a promotion of caspase-3 activation [Anand et al., 2008].

Several studies have examined the anticarcinogenic activity of curcumin in hepatic cancer cells *in vitro*. In one of these studies, conducted in curcumin-treated human hepatoblastoma cells, several hallmarks of apoptosis, including DNA laddering, chromatin condensation, fragmentation, and apoptosis-specific cleavage of 28S and 18S ribosomal RNA were observed. Curcumin has also exhibited significant anti-invasion activity in human HCC SK-Hep-1 cells, an effect that is associated with curcumin's inhibitory action on MMP-9 secretion. Curcumin undergoes metabolic conjugation and reduction in sub-cellular fractions of human and rat hepatic tissues [Anand et al., 2008]. It has also been established that the elevation of GSH levels mediates the effect of curcumin in hepatocytes [White et al., 1998b].

Curcumin has also been found to interrupt the cell cycle, to have cytotoxic effects, and to have a role in antiproliferation and the induction of apoptosis in a hepatocarcinoma cell line. Curcumin is a potent inhibitor of phenol sulfotransferase (SULT1A1) in human liver and extrahepatic tissues [Vietri et al., 2003]. Curcumin inhibited the interleukin-6 (IL-6) production, histone acetyltransferase (HAT) activity, and AP1 activation [Chen et al., 2003a] and prevented cell death and apoptotic biochemical changes, such as the

mitochondrial release of cytochrome c, the activation of caspase-3, and the cleavage of PARP in human hepatoma cells [Anand et al., 2008; Labbozzetta et al., 2006]. Another proposed mechanism for curcumin's inhibition of tumor growth in HCC is through the inhibition of hypoxia-inducible factor-1 by degrading the aryl hydrocarbon receptor nuclear translocator [Bae et al., 2006; Cao et al., 2007; Choi et al., 2006]. Further, it has been shown that mitochondrial hyperpolarization is a prerequisite for curcumin-induced apoptosis and that mtDNA damage is the initial event in a chain leading to apoptosis in HepG2 cells [Cao et al., 2007]. In an *in vitro* study using hepatic cancer cells, a combination of curcumin and cisplatin had synergistic antitumor effects, and that with doxorubicin in additivity or sub-additivity [Anand et al., 2008].

Research over the past decade has indicated that curcumin has an anticarcinogenic effect in various pancreatic cell lines, with numerous mechanisms having been proposed to account for this effect. In human pancreatic cancer MIA PaCa-2 cells, curcumin was found to inhibit the farnesyl protein transferase [Anand et al., 2008]. Also, NF- κ B was found to be overexpressed in human pancreatic tumor tissues and cell lines; investigators suggested that this overexpression could be inhibited by curcumin because it has the ability to suppress the NF- κ B expression [Khanbolooki et al., 2006; Li et al., 2004; Wang et al., 1999]. Likewise, curcumin reduces numerous IL-8 bioactivities that contribute to tumor growth and the cell viability of pancreatic carcinoma cells [Anand et al., 2008; Kamohara et al., 2007]. Other mechanisms have been proposed to account for the growth inhibitory effect of curcumin alone [Starr et al., 2005] or in combination with celecoxib [Lev-Ari et al., 2005] including the down-regulation of COX-2, EGFR, ERK1/2 [Lev-Ari et al., 2006b], and Notch-1 [Wang et al., 2006c]. When coupled with gemcitabine, curcumin has been observed to have synergistic antiproliferative effects in pancreatic cancer cell lines [Holcomb et al., 2007; Lev-Ari et al., 2007]. Liposomes containing curcumin down-regulated NF- κ B machinery, suppressed growth, and induced apoptosis of human pancreatic cells *in vitro* [Goel et al., 2007]. A polymeric nanocurcumin formulation also demonstrated a therapeutic efficacy comparable to that of free curcumin in a panel of human pancreatic cancer cell lines *in vitro*, and the mechanisms of action of nanocurcumin in pancreatic cancer cells mirrored those of free curcumin [Anand et al., 2007].

Studies using various colorectal cell lines have proven curcumin's use as a therapeutic agent and its ability to act through numerous target molecules. For example, curcumin has been shown to disrupt Lovo cells in the S, G2/M phase and interrupt Wnt signaling and adhesion pathways causing G2/M phase arrest and apoptosis in HCT-116 cells, regardless of prostaglandin synthesis. Curcumin-induced apoptosis is a result of PARP cleavage, caspase 3, reduction in Bcl-XL level, and increased activity of capsase-8, which encourages Fas signaling of apoptosis. Curcumin reduces NAT1 mRNA expression and AF-DNA adducts formation in human colon tumor cells. Curcumin was found to inhibit the proliferation of and induce apoptosis in colorectal cell lines

[Anand et al., 2008; Wei et al., 2004]. Heat shock aids colon cancer cells by inhibiting the discharge of apoptosis-inducing factors, an event that is enhanced by curcumin [Rashmi et al., 2003]. Curcumin causes cell shrinkage, chromatin condensation, and DNA fragmentation by enhancing DNA damage in HT-29 cells and HCT-116 colonocytes; it also increases GADD153 mRNA and protein expression [Anand et al., 2008; Scott and Loo, 2004]. Curcumin up-regulates TRAIL-induced apoptosis via ROS-mediated DR5 activation in human renal cancer cells [Anand et al., 2008]. Likewise, curcumin enhanced the silencing of hsp70 expression and may therefore prove to be a valuable therapeutic agent for cancers whose resistance is due to hsp70 expression [Rashmi et al., 2004b]. EF24, a synthetic curcumin analog, induces apoptosis in HT29 cells through a redox-dependent mechanism [Anand et al., 2008]. Similarly, the curcumin derivative HBC disrupts cell-cycle progression in HCT15 cells by antagonizing Ca^{2+} /CaM function [Shim et al., 2004].

The fact that curcumin-induced apoptosis is regulated by Bax suggests that the targeting of Bcl-XL or Smac can be used to treat Bax-deficient, chemotherapy-resistant cancers [Anand et al., 2008; Rashmi et al., 2004a, 2005]. Together, curcumin and either 5-FU or celecoxib downmodulate COX-2 expression via the inhibition of prostaglandin formation by curcumin and curcuminoids [Du et al., 2006]. Curcumin can also induce apoptosis via a parallel ceramide-associated pathway and ROS-associated mechanism that converges at JNK activation [Moussavi et al., 2006]. In vitro, curcumin activates JNK, p38 MAPK, and AP-1 transcriptional activity. Similarly, it inhibits neurotensin-mediated activator protein-1, NF- κ B activation, Ca^{2+} mobilization, PGE-2, and EGFR and down-regulates COX-1 and -2, MMP-2 and -9, IL-8 gene induction, and colon cancer cell migration [Chen et al., 2006; Collett and Campbell, 2004; Jeong et al., 2004; Lev-Ari et al., 2006a; Moussavi et al., 2006; Wang et al., 2006a]. Curcumin has also proven effective at the mRNA level [Su et al., 2006]. Curcumin down-regulates sulfoconjugation and weakly inhibits the glucuronosyl conjugation of 1-naphthol in Caco-2 cells [Naganuma et al., 2006]. Curcumin coupled with ERRP significantly regulates downstream effectors, including NF- κ B, Akt, BAD activation, and procaspase-3, in HCT-116 and HT-29 cells [Reddy et al., 2006]. Curcumin in conjugation with FOLFOX inhibits colon cancer cells by inhibiting the EGFR and IGF-1R signaling pathways [Patel et al., 2008]. Treatment with curcumin and epigallocatechin gallate reduced the amount of viable Apc mutant cells by 220–430%, more than each agent alone did [Telang et al., 2007].

Curcuminoids obstruct cell proliferation and programmed cell death in primary colon cancer cells [Hsu et al., 2007]. Liposomal curcumin attenuates colorectal cancer by reducing CD31, VEGF, and IL-8 expression. This inhibition may be enhanced by the addition of oxaliplatin for the treatment of p53wt and p53 mutant colorectal tumors, as shown in HCEC, HT29, and HCT116 cell lines [Howells et al., 2007; Li et al., 2007a]. Some curcumin derivatives were also found to be effective against colon cancer cells. Dimethoxycurcumin, for example, is more potent than curcumin in inhibiting

proliferation and inducing apoptosis in HCT116 cells [Tamvakopoulos et al., 2007].

Curcumin has been shown to suppress the proliferation of bladder cancer cells in culture either through the suppression of NF- κ B [Kamat et al., 2007; Sun et al., 2004b] or through the down-regulation of cyclin A and up-regulation of p21 [Park et al., 2006]. Certain synthetic analogs of curcumin have been shown to exhibit activity against bladder cancer cell lines [Lu et al., 2005; Tong et al., 2006].

In human kidney cancer cells, curcumin up-regulates apoptotic events such as cell shrinkage, chromatin condensation, and DNA fragmentation [Jiang et al., 1996] and inhibits FPTase [Chen et al., 1997]. Curcumin serves as a COX-1 and COX-2 inhibitor [Ramsewak et al., 2000]; inhibits microsomal lipid peroxidation and DNA damage [Iqbal et al., 2003]; deactivates the Akt pathway; down-regulates Bcl-2, Bcl-XL, and IAP proteins [Woo et al., 2003]; and increases TRAIL-induced apoptosis by augmenting DR5 expression at the mRNA and protein levels by producing reactive oxygen species (ROS) [Jung et al., 2005]. In HCC cells, curcumin reduces tumor growth and the side effects when activated via the hydrolysis of prodrugs [Lu et al., 2005].

Curcumin has shown activity against various prostate cancer cells, such as LNCaP, DU145, C4-2B, and PC3. Curcumin can induce programmed cell death in androgen-dependent and androgen-independent prostate cancer cells. It can inhibit capillary tube formation and cell migration and exert significant effects on actin cytoskeletons in prostate cancer cells [Guo et al., 2006; Shankar et al., 2007; Shenouda et al., 2004]. Several mechanisms have been proposed to explain curcumin's anticancer effects in prostate cancer cells. For example, curcumin up-regulates the expression of the maspin gene and downmodulates the expression of androgen receptor (AR), AP-1, cyclin D1, NF- κ B, and camp response element binding (CREB) protein and EGFR tyrosine kinase activity [Anand et al., 2008; Shi et al., 2006b]. By inducing p21 and C/EBP β expression and suppressing NF- κ B activation, curcumin augments the cytotoxicity of chemotherapeutic agents in prostate cancer cells and induces the degradation of cyclin E expression [Anand et al., 2008].

In prostate cancer cells curcumin was found to act as an inhibitor of arachidonate 5-lipoxygenase [Ghosh, 2003]. Likewise, curcumin and TRAIL together cause apoptosis via both receptor-mediated and chemical-induced pathways, owing to an enhanced sensitivity of tumor cells to NF- κ B [Deeb et al., 2003, 2004, 2005]. Curcumin interferes with osteoblastic and osteoclastic cell components, inhibiting growth factor collaboration between prostate cancer cells [Dorai et al., 2004]. Due to its organic structure as a Michael acceptor, curcumin serves as a HAT inhibitor [Marcu et al., 2006]. Curcumin down-regulates the expression of NKX3.1 via AR expression-induced p38-dependent proinflammatory changes in normal epithelial cells [Nonn et al., 2007]. Curcumin inhibits VIP-induced COX-2 expression and VIP-stimulated VEGF mRNA expression via the inhibition of AP-1 binding [Collado et al., 2005; Fernandez-Martinez et al., 2007; Park et al., 2003].

In PC3 cells, curcumin down-regulates MDM2 proteins and mRNA. enhances the expression of the tumor suppressor p21 and inhibits I κ B α [Guo et al., 2006; Li et al., 2007b]. Curcumin can also inhibit prostate cancer via the Akt pathway or the induction of apoptosis by Bcl-2 family members and mitochondrial p53 [Chaudhary and Hruska, 2003; Deeb et al., 2007; Shankar et al., 2007].

The *in vitro* antitumor activity of curcumin in HPV-associated cells has been established [Roy et al., 2002]. Curcumin modulates the *in vitro* expression and function of Pgp in multidrug-resistant human KB-V1 cells [Anand et al., 2008; Chearwae et al., 2004] and sensitizes cisplatin-resistant SiHa cells to cisplatin-induced apoptosis [Venkatraman et al., 2005], indicating its ability to reverse MDR in cervical cancer cells. The effect of curcumin in HPV-associated cells was found to involve the down-regulation of viral oncogenes, NF- κ B and AP-1 [Anand et al., 2008; Divya and Pillai, 2006].

Some *in vitro* studies over the past decade have shown that curcumin [Anand et al., 2008; Guo and Xu, 2005; Syu et al., 1998] and a curcumin–paclitaxel conjugate [Nakagawa-Goto et al., 2007] had therapeutic effects in ovarian cancer cell lines. Curcumin was found to act through the down-regulation of NF- κ B [Zheng et al., 2002, 2006] and allied gene products [Shi et al., 2006a; Weir et al., 2007; Zheng et al., 2004]. Furthermore, curcumin was found to increase the sensitivity of chemotherapy-resistant ovarian cancer cell lines to standard chemotherapeutic agents by activating both the cells' extrinsic and intrinsic pathways of apoptosis [Wahl et al., 2007]. A recent study of ours also showed that curcumin had therapeutic and chemosensitization effects and reversed multidrug resistance *in vitro*. In one of the studies, curcumin displayed *in vitro* apoptosis-inducing activity against an endometrial cancer cell line [Wei et al., 2004] by the down-regulation of Ets-1 and Bcl-2 expression [Yu and Shah, 2007].

Curcumin exhibits anticancer effects in various lung cancer cells through a variety of molecular targets. At the cellular level, curcumin derivatives inhibit FPTase in A549 cells. Curcumin inhibits AP-1 transcription and mediastinal lymph node metastasis in Lewis lung carcinoma cells and ornithine decarboxylase activity in rat tracheal epithelial cells [Ichiki et al., 2000; White et al., 1998a]. Curcumin eradicated the DNA-binding of NF- κ B, I κ B α kinase activation, I κ B α deterioration and phosphorylation, and p65 nuclear translocation, and it down-regulated COX-2 [Anand et al., 2008; Chen et al., 2003b]. Likewise, treatment with curcumin induces apoptosis and inhibits growth in A549 and H1299 cells [Pillai et al., 2004]. In A549 cells, curcumin interferes with cell growth and down-regulates NAT activity and STAT1 activation [Lee et al., 2005, 2006; Zhang et al., 2004]. Curcumin regulates the invasive activity of CL1-5 cells and demonstrates antiproliferative properties in NCI-H460 and H520 cells, suggesting its suitability as an adjunct chemotherapeutic agent [Pescic et al., 2006; Sen et al., 2005].

Curcumin inhibited the growth of oral cancer cell lines *in vitro* [Atsumi et al., 2005a, 2006] by blocking the S/G2M phase. It acted synergistically with a G1 phase blocker, epigallocatechin-3-gallate [Anand et al., 2008]. Curcumin

inhibited the growth of and DNA synthesis in SCC-25 oral cancer cells [D'Ambrosio et al., 2000]. Curcumin increased both the expression and function of cytochrome P450 (CYP) 1A1 and/or CYP1B1 in oral cancer cells, indicating that it has chemopreventive properties mediated by the inhibition of carcinogen bioactivation [Rinaldi et al., 2002]. Further, curcumin exhibited radiotherapy-sensitizing effects on SCC cells in vitro [Khafif et al., 2005]. Moreover, the ability of curcumin to induce apoptosis in oral cancer cells was associated with the inhibition of COX-2 [Atsumi et al., 2005b]. A recent study of ours also revealed that curcumin down-regulates smokeless-tobacco-induced NF- κ B activation and COX-2 expression in human oral premalignant and malignant cells [Sharma et al., 2006].

The anticancer effect of curcumin in murine thymoma cells was found to be due to the blocking of IL-1 signaling by the inhibition of the recruitment of the IL-1 receptor-associated kinase (IRAK) [Jurrmann et al., 2005]. A recent study showed that curcumin could prevent tumor-induced thymic atrophy in thymic T cells, leading to the neutralization of tumor-induced oxidative stress and the restoration of NF- κ B activity and the re-education of the TNF- α signaling pathway, resulting in thymic protection [Bhattacharyya et al., 2007].

In vitro, curcumin has been shown to have synergistic and remedial properties in leukemia. In HL-60 cells, a regimen of 10 μ M curcumin for 48 h has been the most effective in decreasing cell proliferation and increasing differentiation. These effects were exacerbated when curcumin was given in conjunction with RA, vitamin D₃, and vitamin D₃ analogs [Liu et al., 1997; Pan et al., 2001; Roy et al., 2002; Sokoloski et al., 1997]. Curcumin alone causes a significant reduction in NF- κ B expression, bcl-2 activity, and TPA-induced DNA binding. It also induces ER stress and caspases 3 and 8; and degrades PARP [Bielak-Mijewska et al., 2004; Mukherjee Nee Chakraborty et al., 2007; Pae et al., 2007; Sokoloski et al., 1997]. The proposed mechanism involves the interruption of G₀/G₁ phases associated with the up-regulation of P27kip1, P21waf1, and pRbp expression and the down-regulation of cyclin D₃ [Anand et al., 2008; Chen et al., 2002].

Within HL-60 cells, curcumin induced ROS levels and up-regulated Ca²⁺ production and the release of cytochrome c and lowered MMP levels [Atsumi et al., 2005b; Chen et al., 2005; Tan et al., 2006]. In Raji cells, curcumin selectively blocks tumor cells in the G₀/G₁ and G₂/M phases; dose dependently up-regulates Ac-histone H4 expression; inhibits the proliferation and degradation of I κ B α and Notch 1; and inhibits the translocation of the NF- κ B/p-65 subunit via the downmodulation of HDAC1 and p300/Notch 1 signal molecules [Chen et al., 2007; Liu et al., 2005; Sun et al., 2004a; Wu et al., 2006]. Similarly, in the presence of curcumin, TERT is translocated, causing a loss of telomerase activity, and the expression of STAT3, -5a, and -5b are reduced without altering STAT1 or the phosphorylation states of STAT1, -3, or -5 in the K562 cell line via the release of cytochrome c from mitochondria [Blasius et al., 2006; Chakraborty et al., 2006]. Curcumin also affects GST-modulated lipid peroxidation, AP-1 and NF- κ B binding to GSTP1-1 promoters, ADP

ribose polymerase cleavage, and pro-caspases 8 and 9 induction in K562 cells [Duvoix et al., 2003; Singhal et al., 1999].

Curcumin dose dependently down-regulates JAK and STAT phosphorylation, causing growth inhibition and apoptosis in T-cell leukemia, HTLV-I-transformed T-cell leukemia, MT-2, HuT-102, and SLB-1 cell lines. It does so by inhibiting cyclin D1, cdk1 Cdc25C, and XIAP and Survin expression [Rajasingh et al., 2006; Tomita et al., 2006]. Curcumin suppresses the proliferation of WEHI-3B cells and blocks STAT5 mRNA expression and STAT5 activation in CML cells [Chen et al., 2004; Jiang et al., 2000]. In TK-10, MCF-7, and UACC-62 cell lines, curcumin initiates apoptosis via telomerase II poisoning, resulting in DNA damage [Martin-Cordero et al., 2003]. Acute leukemia cells exposed to curcumin for 4 h have increased nitric oxide (NO) levels [Kellner and Zunino, 2004]. This increased NO production by macrophages and the inhibition of Th1 cytokines in NK cells in the presence of curcumin lead to significant tumoricidal results [Bhaumik et al., 2000]. Likewise, MDR1 mRNA levels were reduced more significantly in leukemia cells from patients with higher MDR1 gene groups [Anuchapreeda et al., 2006a]. The proliferation of Jurkat cells was reduced with curcumin treatment, resulting in chromatin condensation and caspase-3 induction via the prevention of a decrease in glutathione levels [Piwocka et al., 2001; Sikora et al., 2006]. In Bcr-Abl-transfected mouse progenitor 32D cells, curcumin inhibits proliferation by arresting cells in the G(2)-M phase of the cell cycle, resulting in irregular chromatin organization, multipolar chromosome segregation, aberrant cytokinesis, and multinucleated cells with morphologic changes [Wolanin et al., 2006]. Like curcumin, curcumin analogs in KBM-5 cells blocked TNF-induced NF- κ B activation and proliferation, and curcuminoids inhibited COX-1 and COX-2 enzymes [Zambre et al., 2006].

Curcumin was found to inhibit cellular proliferation and enhance apoptosis in a variety of lymphoma cell lines in vitro [Skommer et al., 2006; Thompson et al., 2004; Wu et al., 2002]. The proposed mechanism of curcumin's action in the majority of these studies involves the suppression of the expression of NF- κ B-regulated gene products. One study suggested a novel function for curcumin as a suppressor of JAK-1 and STAT3 activation in primary effusion lymphoma cells, a function that would lead to the inhibition of proliferation and the induction of caspase-dependent apoptosis [Uddin et al., 2005].

Numerous reports suggest that curcumin exhibits antiproliferative effects against MM cells. The mechanisms of the antiproliferative effects of curcumin in MM cells have been studied and described extensively. The role of the NF- κ B and STAT3 pathway as a target for curcumin in MM cells has been demonstrated [Liu et al., 2007a; Thomas et al., 2005]. Curcumin is known to suppress both the production and signaling of IL-6, a critical growth factor for MM cells [Labbozzetta et al., 2006]. Curcumin also interrupts the interaction between MM cells and endothelial cells by reducing TrkB expression in endothelial cells and inhibiting brain-derived neurotrophic factor (BDNF)

production in MM cells, eventually resulting in the inhibition of angiogenesis [Wang et al., 2006b].

Several reports describe the antitumor activity of curcumin and of a formulation of the synthetic curcumin analog, EF-24 [Sun et al., 2006] in various melanoma cell lines. The effects of curcumin were found to be mediated through the inhibition of glutathione-*S*-transferase activity [Iersel et al., 1996], the inhibition of COX-1 and COX-2 enzymes, the induction of apoptosis through the Fas receptor/caspase-8 pathway, and the down-regulation of the NF- κ B pathway [Marin et al., 2007; Siwak et al., 2005]. The modulation of integrin receptors and collagenase activity, the expression of Nm23 and E-cadherin [Ray et al., 2003], the down-regulation of FAK, and the reduction of MMP-2 activity [Banerji et al., 2004] were found to be responsible for the antimetastatic effect of curcumin in melanoma cells. Curcumin was found to reverse the resistance of melanoma cells to multiple drugs by inhibiting glutathione-*S*-transferases [Depeille et al., 2004, 2005].

Curcumin and its analogs were found to have antitumor effects in bone cancer cells. Numerous mechanisms have been proposed for the activity of curcumin against fibrosarcoma cells in particular. Curcumin induced apoptosis by inhibiting NF- κ B [Anto et al., 2000] and the expression of IL-6 and IL-11 [Kondo et al., 2001] and by abolishing the inhibitory effect of TGF- β on GR-mediated gene expression [Kwak et al., 2006; Periyasamy and Sanchez, 2002] in fibrosarcoma cells. Curcumin suppressed MMP-13 expression in chondrosarcoma cells. Synthetic curcumin analogs were also found to be potent against bone cancer cells. In fibrosarcoma cells, synthetic curcumin analogs inhibit activator protein-1 transcription and tumor-induced angiogenesis by down-regulating the expression of angiogenesis-associated genes, VEGF, and MMP-9. Further, in human osteosarcoma cells curcumin was found to inhibit the ERK expression. Curcumin was found to induce apoptosis in a variety of osteosarcoma cells by down-regulating the BCL-2 expression [Walters et al., 2007].

Numerous other mechanisms, like the induction of heat shock proteins [Anand et al., 2008], the inhibition of MMP transcriptions [Kim et al., 2005; Woo et al., 2005], TRAIL-induced apoptosis [Gao et al., 2005], the inhibition of G6PT gene expression [Belkaid et al., 2006], the activation of both receptor-mediated and mitochondria-mediated proteolytic pathways [Karmakar et al., 2006], the induction of histone hypoacetylation leading to apoptosis in a (PARP)- and caspase-3-mediated manner [Kang et al., 2006], the inhibition of the ING4 signaling pathway [Liu et al., 2007b], and the induction of nonapoptotic autophagic cell death [Aoki et al., 2007; Shinjima, 2007] have also been established. Furthermore, curcumin was found to sensitize glioma cells to several chemotherapeutic agents and to radiation therapy [Dhandapani et al., 2007].

Anticancer Effects in Vivo

Several *in vivo* studies have established the chemopreventive as well as anticancer effect of curcumin against a variety of cancers, as summarized in

Table 16.1. Perhaps the first *in vivo* study to report the anticancer activity of curcumin was by Kuttan et al. in 1985. In this study the authors demonstrated, using an ascites mice model of Dalton's lymphoma, that both curcumin and turmeric extract could reduce the development of animal tumors [Kuttan et al., 1985]. Several reports have been published supporting the efficacy of curcumin treatment against cancer.

In 1998 a group studied curcumin's capacity to inhibit 7,12-dimethylbenzanthracene (DMBA)-induced mammary tumor and the *in vivo* formation of mammary DMBA-DNA adducts in the female rat. Administration (ip) of curcumin at 100- and 200-mg/kg doses prevented the development of the number of palpable mammary tumors and mammary adenocarcinomas significantly. The *in vivo* formation of mammary DMBA-DNA adducts also was depressed in animals administered with curcumin, and there was no significant enhancement of liver GST activity following curcumin administration. However, one group showed that animals fed with diets containing 1% curcumin had no effect on DMBA-induced mammary tumor. In 1996, Pereira et al. showed that curcumin (8 and 16 g/kg in diet) was only weakly effective in DMBA-induced mammary carcinogenesis. Another study evaluated the modulating effects of turmeric (T), ethanolic turmeric extract (ETE), and curcumin-free aqueous turmeric extract (CFATE) on the initiation or postinitiation phases of DMBA-induced mammary tumorigenesis in female Sprague-Dawley rats. Dietary administration of 1% turmeric/0.05% and ethanolic turmeric extract 2 weeks before, on the day of DMBA treatment (day 55) and 2 weeks after the single dose (15 mg/animal) of DMBA (during the initiation period) resulted in significant suppression of DMBA-induced mammary tumorigenesis as seen by a reduction in tumor multiplicity, tumor burden, and tumor incidence. The chemopreventive effect of curcumin on diethylstilbestrol (DES)-induced tumor promotion of rat mammary glands initiated with radiation was also evaluated in a study. The administration of dietary curcumin significantly reduced the incidence (28%) of mammary tumors. Multiplicity and Iball's index of mammary tumors were also decreased by curcumin. Rats fed the curcumin diet showed a reduced incidence of the development of both mammary adenocarcinoma and ER(+)PgR(+) tumors in comparison with the control group. The effect of curcumin on γ -radiation-induced mammary tumors was also demonstrated in rats [Goel et al., 2007].

In addition to the chemopreventive effects, antimetastatic effect of curcumin was also established by the *in vivo* model studies. In a xenograft model study (nude mice) conducted in our laboratory, the primary tumor was surgically removed after 58–60 days of tumor cell inoculation, and dietary curcumin (2%) was given to the animals starting from the fifth day to 5 weeks of primary tumor removal. We observed that administration of curcumin significantly decreased the incidence of breast cancer metastasis to the lung and suppressed the expression of NF- κ B, COX-2, and MMP-9. Another group also evaluated the effect of curcumin on lung metastasis of breast cancer. In this study, intercardiac inoculation of breast cancer cells was done in the nude mice and

Table 16.1 Curcumin Exhibits Chemopreventive and Anticancer Effects Against Various Cancers

Cancer	Carcinogen or Route	Animal or Model	Dose
Aberrant crypt foci (ACF) ^a	Azoxymethane	Rat	2000 ppm
Colon cancer	Azoxymethane	Mice	0.5–0.2% w/w
	DMH	Mice	0.5%
	Azoxymethane	Rat	2000 ppm or 0.2–2% w/w
Duodenal tumor	PhIP	Apc (min) mice	2000 ppm
	1,2-dimethylhydrazine	Rat	0.6%
Esophageal cancer	MNNG	Mice	0.5–2.0% w/w
FAD ^a	NMBA	Rat	500 ppm
FAP ^a	Azoxymethane	Mice	2%
Stomach cancer	—	Min/ + mice	0.1, 0.2 or 0.5% w/w
	B[a]P	Mice	2% w/w
Liver cancer	MNNG	Rat	0.05% w/w
	Diethylnitrosamine	Rat	200 or 600 mg/kg
Lung cancer	Diethylnitrosamine	Mice	0.2% w/w
	B[a]P & NNK	A/J mice	2000 ppm
Lymphoma/leukemia	DMBA	Sencar mice	2% w/w
Mammary tumor	DMBA	Rat	0.8–1.6% w/w or 50–200 mg/kg
	DMBA	Sencar mice	2% w/w
	Gamma radiation	Rat	
Oral cancer	MNA	Hamster	
	NQO	Rat	500 ppm
Prostate cancer	DMAB & PhIP	Rat	15–500 ppm
Skin tumor	TPA	Mice	
	DMBA	Mice	
	TPA	Mice	10–30 μmol or 1–3000 nmol
Multiorgan cancer	DMBA	Mice	
	B[a]P and DMBA	Mice	
Ascites ^b	DHPN, EHEN	Rat	1% w/w
Breast ^c	IP	Ascites	50 mg/kg
Colon ^b	Diet	Orthotopic	1 or 2% w/w
	IV	Orthotopic	40 mg/kg
Glioblastoma	Oral	Xenograft	50–200 mg/kg
	IT	Orthotopic	10 mg/kg
HCC ^d		Orthotopic	100–200 mg/kg
	Oral	Xenograft	50–200 mg/kg
HNSCC	Sub cute	Xenograft	50–250 mol/L
Leukemia	Oral	Xenograft	50–200 mg/kg

(Continued)

Table 16.1 (Continued)

Cancer	Carcinogen or Route	Animal or Model	Dose
Melanoma	IP	Xenograft	25 mg/kg
Ovarian	IP	Orthotopic	500 mg/kg
Pancreas ^b	IV	Xenograft	40 mg/kg
	Gavage	Orthotopic	1 gm/kg
Prostate	Diet	Xenograft	2% w/w
	Gavage	Xenograft	5 mg/kg

^aNote: FAP: familial adenomatous polyposis; ACF: aberrant crypt foci; FAD: focal areas of dysplasia; B[a]P: benzo[a]pyrene; DMBA: 7,12-dimethylbenz[a]nthrane; TPA: 12-O-tetradecanoylphorbol-13-acetate; NNK: 4-(methyl-nitrosamino)-1-(3-pyridyl)-1-butanone; NQO: 4-nitroquinoline 1-oxidase; DMAB: 3,2'-dimethyl-4-aminobiphenol; PhIP: 2-amino-1-methylimidazo[4,5-b]pyridine; DHPN: 2,2'-dihydroxy-di-*n*-propylnitrosamine; EHEN: *N*-ethyl-*N*-hydroxyethylnitrosamine.

^bLiposomal curcumin.

^cLung metastases.

^dIntrahepatic metastasis; IP, intraperitoneal; IT, intratumoral; IV, intravenous.

the animals were fed with diet containing 1% curcumin. Thirty-five days after tumor implantation the animals were sacrificed and enumerated the lung metastases. It was observed that all the animals in the untreated group had lung metastasis, whereas 21% of animals in the treated group were metastases free [Goel et al., 2007]. In contrast to the above *in vivo* studies, Somasundaram et al. [2002] reported a significant inhibition of tumor regression in a xenograft mouse model of human breast cancer. These contradictory findings could have been caused by the difference in administered doses as well as the time of treatment. For example, the authors studied the effect of curcumin in a breast xenograft model for 3 days, which is not normally suitable for the xenograft model studies. Even though it is the only study reporting the inhibition of tumor regression, further studies are needed to resolve the contradictions about the effectiveness of curcumin against breast cancer *in vivo*.

Two *in vivo* studies have been reported with curcumin in esophageal cancer. In one, dietary curcumin (500 ppm) fed during initiation and postinitiation stages inhibited the incidence of esophageal carcinogenesis by 27 and 33%, respectively, in rats [Goel et al., 2007]. In the other study, the efficacy of curcumin as a chemopreventive agent was assessed by measuring the modulation in the incidence of neoplastic change in rat esophagus [Wax et al., 2005].

Several *in vivo* chemoprevention studies have been reported with curcumin in gastric cancers. In some of the chemoprevention studies, curcumin fed as dietary turmeric (2% or 5%) to mice and Syrian golden hamsters significantly inhibited the benzo[a]pyrene-induced forestomach tumors. Furthermore, the incidence and multiplicity of forestomach tumors induced by benzo[a]pyrene in female Swiss mice were significantly inhibited by pure curcumin given 2 weeks before, during and after the carcinogen treatment. Other studies also revealed the chemopreventive effect of curcumin on benzo[a]pyrene-induced

forestomach cancer. A significant reduction in benzo[a]pyrene-induced forestomach papillomas in mice due to treatment with dietary turmeric extract containing curcumin was also reported. It was also showed that curcumin inhibited MNNG-induced duodenal tumor in mice and gastric cancer in rats [Anand et al., 2008].

In vivo studies using mouse models have proved that curcumin modifies apoptosis resistance, leading to the inhibition of tumor formation and the prevention of adenoma development in the intestinal tract. The chemopreventive effect of curcumin for intestinal tumors in Min/+ mice was investigated. A dietary level of 0.15% curcumin decreased tumor formation in Min-/- mice by 63%. Examination of intestinal tissue from the treated animals showed the tumor prevention by curcumin was associated with increased enterocyte apoptosis and proliferation. Curcumin also decreased expression of the oncoprotein β -catenin in the erythrocytes of the Min/+ mouse, an observation previously associated with an antitumor effect. Curcumin enhanced PhIP-induced apoptosis and inhibited PhIP-induced tumorigenesis in the proximal small intestine of Apc (min) mice. Experiments performed on intestinal tumors in C57BL/6J-Min/+ (Min/+) mice demonstrated that curcumin has a regulatory role in lymphocyte-mediated immune function [Churchill et al., 2000]. Furthermore, levels of COX-2 protein expression have been found to reflect the retardation of adenoma development in mouse intestines after treatment with curcumin [Tunstall et al., 2006].

A considerable number of reports have also described curcumin in HCC in vivo. In one of these studies, curcumin significantly reduced the number of γ -glutamyl transpeptidase-positive foci, a characteristic considered to be the precursor of hepatocellular neoplasm in rats. Curcumin also had anticarcinogenic effects mediated through the induction of glutathione-linked detoxification enzymes in rat livers. In a murine hepatocarcinogenesis model, at the age of 42 weeks, the curcumin group had 81% less multiplicity and 62% fewer hepatocarcinomas than the nontreated group. It also suppressed liver inflammation in rats. In rats, curcumin glucuronide and curcumin sulfate were identified as the major products of curcumin biotransformation, whereas hexahydrocurcumin, hexahydrocurcuminol, and hexahydrocurcumin glucuronide were present only in small amounts. Another in vivo study showed that curcumin mixed into a diet could achieve levels of the drug in the liver sufficient to explain its pharmacological effects. Dietary curcumin increased the activity of hepatic UGT enzymes, which can detoxify carcinogens, in male Wistar rats. In an orthotopic implantation model, curcumin suppressed both intrahepatic metastases and the development of altered hepatic foci (AHF) in rat livers. Inhibition of tumor growth by systemic administration of 20 μ g/kg curcumin for 6 consecutive days to rats bearing the highly cachectic Yoshida AH-130 ascites hepatoma was also reported. In one of the studies, although the growth of tumors at the implanted site was not affected by the curcumin treatment, there was a significant and dose-dependent decrease in the number of intrahepatic metastases [Aggarwal et al., 2003].

Curcumin also prevented the induction of hepatic hyperplastic nodules, body weight loss, increase in the levels of hepatic diagnostic markers, and hypoproteinemia in carcinogen-induced as well as xenograft hepatic cancer models. The antiangiogenic activity of curcumin in hepatic carcinoma cells implanted in nude mice was found to be mediated through the reduction of the angiogenic biomarkers COX-2 and VEGF [Aggarwal et al., 2003].

Two *in vivo* studies were reported showing the antitumor activity as well as chemosensitization effect of curcumin against pancreatic cancer. In a xenograft model study mice received intravenous liposomal curcumin (40 mg/kg, 3 times per week) for 20 days. Treatment with liposomal curcumin resulted in reduced tumor size showing decreased expression of CD31 as well as VEGF and IL-8. These results indicate that curcumin suppressed pancreatic carcinoma growth in murine xenograft models and inhibited tumor angiogenesis [Li et al., 2005]. A recent study conducted in our group investigated the chemosensitization effect of curcumin using an orthotopic pancreatic cancer model. The tumor volume in the combination of curcumin and gemcitabine group was significantly lower than the gemcitabine alone or control group, indicating the chemosensitizing effect of curcumin. Our results showed that curcumin in combination with gemcitabine significantly down-regulated the expression of cell proliferation marker Ki-67 in tumor tissues compared with the control group. Further, curcumin alone significantly suppressed the expression of microvessel density marker CD31, and the presence of gemcitabine further enhanced the down-regulation of CD31 [Goel et al., 2007].

Several *in vivo* studies were reported to show the chemopreventive as well as anticancer activity of curcumin against colorectal cancer. Wargovich and co-workers [1996] showed the chemopreventive activity of curcumin against carcinogen-induced ACF in rats. Sulindac, curcumin, and PEMC administered during promotion and progression have been found to up-regulate apoptosis in rat colonic tumors [Anand et al., 2008]. Dietary curcumin (0.2%) inhibited the formation of carcinogen-induced colorectal tumors in rats [Wijnands et al., 2004]. In rodent models, curcumin hinders tumor suppressor p53 function, but in AOM-induced rat models, apoptosis is induced via a mitochondrial pathway [Goel et al., 2007; Volate et al., 2005]. The modulatory role of dietary curcumin on azoxymethane (AOM)-induced aberrant crypt foci (ACF) formation in the colon of F344 rats was evaluated and showed that AOM-induced colonic ACF were significantly inhibited in the animals fed with the curcumin (2000 ppm/day) diet. The chemopreventive activity of curcumin was also observed when it was administered before, during, and after carcinogen treatment as well as when it was given only during the promotion/progression phase of colon carcinogenesis in rats. Several studies evaluated the effect of curcumin on AOM-induced colon cancer and showed a significant inhibition of colon carcinogenesis after the treatment with curcumin.

Dimethylhydrazine (DMH)-induced rat colon carcinogenesis model was used for evaluation of the synergistic inhibitory effect between curcumin and catechin in light of ACF formation and tumor incidence. The results of this

study indicated that curcumin, catechin, and their co-treatment caused significant inhibition of DMH-induced ACF and colon carcinogenesis as compared with untreated DMH-induced rat models [Xu et al., 2005]. Similarly, in another study it was showed that curcumin and celecoxib additively inhibits the growth of DMH induced growth of colorectal cancer in rats [Goel et al., 2007]. An *in vivo* study by Kwon and Magnuson [2007] suggested that during initiation, AOM inhibits colonic COX-1 expression without affecting COX-2, and dietary curcumin may increase COX-2 expression to compensate AOM-induced reduction of COX-1 expression in rats. In male rats, curcumin and curcumin analog increased celecoxib-mediated growth inhibition [Anand et al., 2008].

The preclinical anticancer activity of a liposomal curcumin formulation in colorectal cancer was also recently evaluated. This study also compared the efficacy of liposomal curcumin (40 mg/kg administered *iv*) with that of oxaliplatin, a standard chemotherapeutic agent for colorectal cancer. Significant tumor growth inhibition was observed in Colo205 and LoVo xenograft models in mice. Tumors from animals treated with liposomal curcumin showed an antiangiogenic effect measured as attenuation of CD31, vascular endothelial growth factor, and IL-8 expression. Thus, this study established the comparable or greater growth-inhibitory and apoptotic effects of liposomal curcumin with oxaliplatin *in vivo* in colorectal cancer [Li et al., 2007a].

In order to investigate the anticancer potential of curcumin against prostate cancer, androgen-dependent LNCaP prostate cancer cells were injected subcutaneously to mice. The experimental group received a synthetic diet containing 2% curcumin for up to 6 weeks. At the endpoint, mice were killed and sections taken from the excised tumors were evaluated for pathology, cell proliferation, apoptosis, and vascularity. Curcumin induced a marked decrease in the extent of cell proliferation as measured by the BrdU incorporation assay and a significant increase in the extent of apoptosis as measured by an *in situ* cell death assay. Moreover, microvessel density as measured by CD31 antigen staining decreased significantly [Aggarwal et al., 2007]. *In vivo*, PEITC and curcumin alone or in combination possess significant cancer-preventive characteristics in PC-3 prostate tumor xenografts in mice [Khor et al., 2006]. In another study [Hong et al., 2006], the mean tumor volumes at 4 weeks after tumor inoculation in the control and experimental animals were determined to be $168.6 \pm 40.7 \text{ mm}^3$ and $99.5 \pm 27.2 \text{ mm}^3$, respectively. Curcumin was shown to induce a marked reduction of MMP-2, and MMP-9 activity in the tumor-bearing site. The metastatic nodules were significantly fewer in the curcumin-treated group than untreated group. Li et al. [2007b] evaluated the antitumor, chemosensitizing, and radiosensitizing effect of curcumin using a xenograft prostate cancer model. Analysis of tumors collected at the end of the experiment showed that curcumin reduced the expression of MDM2 oncogene in xenografts treated with curcumin alone, and in xenografts treated with combinations of curcumin and gemcitabine or irradiation. These results

indicate a novel mechanism of action that may be essential for curcumin's chemotherapeutic effects.

It was demonstrated that curcumin effectively inhibits tumor implantation and growth in a murine bladder tumor model [Anand et al., 2008]. Another study demonstrated that dietary curcumin treatment reduced risk for kidney cancer metastasis in rats [Frank et al., 2003].

A recent study of ours showed that curcumin had therapeutic and chemosensitization effects against ovarian cancer and reversed multidrug resistance both in vitro and in vivo in athymic mice. In the in vivo study, tumors were grown by orthotopic injection of cells and one week after orthotopic implantation animals were treated with curcumin (500 mg/kg/day, gavage) alone or in combination with docetaxel (35–50 µg/animal/week, ip) for 4 weeks. Curcumin alone resulted in 49–55% reductions in mean tumor growth compared with controls, whereas when combined with docetaxel 77% reductions in mean tumor growth compared with controls was obtained for curcumin in normal ovarian tumor models. In these ovarian tumors, curcumin alone and with docetaxel decreased both proliferation and microvessel density and increased tumor cell apoptosis. In mice with multidrug-resistant ovarian tumors, treatment with curcumin alone and combined with docetaxel resulted in significant 47% and 58% reductions in tumor growth, respectively [Lin et al., 2007].

Orthotopic implantation of a metastatic cell line of Lewis lung carcinoma (LLC-MLN), which was isolated by an in vivo selection method, resulted in greater metastatic growth in mediastinal lymph nodes as compared with that of the original LLC cells. Oral administration of curcumin significantly inhibited the mediastinal lymph node metastasis of orthotopically implanted LLC cells in a dose-dependent manner, but did not affect the tumor growth at the implantation site. Combined treatment with curcumin and cis-diamine-dichloroplatinum (CDDP), resulted in a marked inhibition of tumor growth at the implanted site and of lymphatic metastasis, and a significant prolongation of the survival time [Ichiki et al., 2000]. Deshpande and Maru [1995] showed that curcumin can inhibit BP-derived DNA adducts by interfering with the metabolic enzymes, and its physical presence is essential for this effect. In the year 1999 one group [Anand et al., 2008] studied the activity of curcumin as chemopreventive agent against lung tumor induction in A/J mice by the tobacco smoke carcinogens benzopyrene (BaP) and 4-(methyl-nitrosamino)-1-(3-pyridyl)-1-butanone (NNK). The treatment of curcumin (2000 ppm) 1 week after carcinogen treatment until termination had no effect on lung tumor multiplicity. In another study, oral administration of curcumin (200 nmol/kg body weight) was, however, found to inhibit the lung metastasis of melanoma maximally as seen by the reduction in the number of lung tumor nodules (80%). Consequent to the inhibition of the lung tumor nodules, the life span of animals treated with the polyphenol was also found to be increased (143.85%). The results indicate a possible use of these compounds in arresting the metastatic growth of tumor cells. In Wistar rats, however, marker enzymes and plasma lipid levels decreased after treatment with 80 mg/kg of curcumin or

a curcumin analog [Anand et al., 2008]. In a group of 10 male smokers, 10 male nonsmokers, and 10 nonsmoking women between 25 and 45 years of age, curcumin reduced BP-stimulated strand breaks in a sex-dependent manner [Polasa et al., 2004].

Several *in vivo* studies have also revealed the potency of curcumin against oral cancer. Curcumin alone or in combination with other has acted as a chemopreventive agent in oral cancer models in rats and hamsters. It was showed that male F344 rats fed with dietary curcumin (0.5 g/kg) during the initiation and postinitiation stages exhibited 91% reduction in the frequency of 4-nitroquinoline-1-oxide-induced tongue carcinoma with a decrease in incidence of oral preneoplasia [Anand et al., 2008]. Another study showed that curcumin alone or in combination with catechin inhibited methyl-(acetoxy-methyl)-nitrosamine (MNA)-induced oral mucosal tumors in Syrian golden hamsters. In Syrian golden hamsters, 10 mmol curcumin (applied topically 3 times/week) decreased the number of visible oral papillomas and papilloma volume by 39.6 and 61.3%, respectively. Furthermore, curcumin treatment also decreased the incidence of oral squamous cell carcinoma (SCC) and reduced the number of oral SCC lesions by 51.3%. In this study, curcumin treatment resulted in inhibition of tumor angiogenesis in the case of papilloma and SCC. Decrease of tumor proliferation index in hyperplasia, displasia, and papilloma was also observed due to curcumin treatment [Anand et al., 2008].

Studies have also demonstrated curcumin's therapeutic properties *in vivo*. In 6-week-old mice, the administration of a 2% curcumin diet via oral gavage resulted in a 53% reduction in lymphomas and leukemias. When topically applied prior to the administration of TPA in mice, curcumin down-regulated TPA-induced NF- κ B and AP-1. It was also showed that oral administration of curcumin (50–200 mg/kg) inhibits the development of leukemia (HL 60) cell-induced xenografts in nude mice [Anand et al., 2008].

It was shown that oral administration of curcumin (50–200 mg/kg) inhibits the development of lymphoma (SGC7901) cell-induced xenografts in nude mice [Goel et al., 2007]. Curcumin inhibited the growth of both murine and human B lymphoma cells *in vitro* and murine B lymphoma cells *in vivo* by the down-regulation of spleen tyrosine kinase (Syk) activity accompanied by the down-regulation of Akt activation [Gururajan et al., 2007].

The chemopreventive effects of curcumin on several carcinogen-induced skin carcinogenesis models have been investigated. Topical application of curcumin (even lower doses of 20–100 nmol) together with tumor promoter TPA, twice weekly for 20 weeks to female CD-1 mice strongly inhibited TPA-induced papilloma formation. Further, in female Swiss mice dietary administration of 2% turmeric significantly inhibited DMBA plus TPA-induced skin tumor formation. In this benzopyrene-initiated and TPA-promoted two-stage skin tumorigenesis model, curcumin reduced the number of tumors per mouse and decreased the number of tumor-bearing mice. Another study conducted showed that curcumin inhibited ultraviolet (UV)-induced dermatitis in mouse skin [Goel et al., 2007].

The *in vivo* antimetastatic effect of curcumin was also established. In one study, oral administration of curcumin (200 nmol/kg body weight) was found to inhibit the lung metastasis, induced by B16F10 melanoma cells, measured as the reduction in the number of lung tumor nodules (80%), and there was an increase in the life span of mice by 143.85%. The effectiveness of a prophylactic immune preparation of soluble proteins from B16-R cells, or a treatment with curcumin alone or in combination was evaluated using a mouse melanoma model. The combination treatment resulted in substantial inhibition of melanoma growth compared to each treatment by itself. A significant percentage increase in the median survival time was also observed in the combination group (>82.8%) as opposed to the 48.6% increase in the immunization-only group and 45.7% increase in the curcumin-only group [Aggarwal et al., 2003; Anand et al., 2008].

In an *in vivo* study in rats, dietary curcumin with cisplatin modulated tumor marker indices of fibrosarcoma toward normal controls [Navis et al., 1999]. Treatment with radiotherapy and curcumin resulted in enhanced tumor cell killing and reduced radioresistance in mice bearing fibrosarcoma, as indicated by the significant inhibition of radiation-induced ERK and NF- κ B expression [Kumar Mitra and Krishna, 2004].

Curcumin significantly decreased the incidence of radiation-induced pituitary tumors in rats [Anand et al., 2008]. In the subcutaneous xenograft model of glioblastoma cells, curcumin inhibited tumor growth significantly and induced autophagy. An approximate three-fold decrease in mean tumor volume was observed in the curcumin-treated group compared to the controls [Aoki et al., 2007].

Anticancer Effects—Clinical Trials

Several clinical trials are reported with curcumin in cancer patients around the world. Some of our recent review [Anand et al., 2008; Goel et al., 2007; Kunnumakkara et al., 2008] gives a detailed description of the clinical trials with curcumin, which are summarized in Table 16.2. An early clinical trial evaluated the effectiveness of topical application of a curcumin ointment in patients with external cancerous lesions. Patients with cancers of oral cavity (37 patients), breast (7 patients), vulva (4 patients), skin (3 patients), and miscellaneous unspecified sites (11 patients) were enrolled in this study. Remarkable symptomatic relief was observed in this study with the reduction in smell in 90% of the cases, reduction in itching in almost all cases, and reduction in exudates in 70% of cases. Reduction in lesion size and pain was observed in about 10% of the cases and only one melanoma (scalp) patient showed an adverse effect of local itching, which may be due to the allergic reaction to curcumin.

In a phase I clinical trial patients with recently resected urinary bladder cancer, uterine cervical intraepithelial neoplasm (CIN), oral leucoplakia, and intestinal metaplasia of the stomach were enrolled and treated with 0.5–12 g/

Table 16.2 A List of Clinical Trials with Curcumin in Cancer Patients^a

Disease	Dose/Frequency	Patients	Endpoint Modulation
Colorectal cancer	36–180 mg/day × 120 days	15	Lowered GST
Colorectal cancer	450–3600 mg/day × 120 days	15	Lowered inducible serum PGE2 levels
Colorectal cancer	450–3600 mg/day × 7 days	12	Decreased M1G DNA adducts
Crohn's disease	360 mg; × 3/day × 30 days; × 4 for 60 days	5	Improved symptoms
External cancer lesions	–	62	Reduction in lesion size in 10% patients Reduction in smell in 90% patients Reduction in itching in all patients Reduction in exudates in 70% patients
Familial adenomatous polyposis	480 mg; x3/day × 180 days	5	Decrease in the number of polyps was 60.4% Decrease in the size of polyps was 50.9%
<i>Helicobacter pylori</i> infection	300 mg/day × 7 days	25	Significant improvement of dyspeptic symptoms Reduction of gastric inflammation
Idiopathic inflammatory orbital	375 mg; 3x /day × 180–660 days	8	4 pts recovered completely 1 pt showed decrease in swelling No recurrence
Irritable bowel syndrome	72–144 mg/day × 56 days	207	Reduced symptoms
Liver metastasis of CRC	450–3600 mg/day × 7 days	12	Low bioavailability
Multiple myeloma	2–12 g/day	24	Inhibits NF-κB, COX-2, and pSTAT3
Pancreatic cancer	8 g/day	17	70% reduction in tumor in one pt.
Precancerous lesions	8 g/day × 90 days	19	Histological improvement
Tropical pancreatitis	500 mg/day × 42 days	20	Reduction in the erythrocyte MDA levels

(Continued)

Table 16.2 (Continued)

Disease	Dose/Frequency	Patients	Endpoint Modulation
Prostatic intraepithelial neoplasia (PIN)		24	Increased in erythrocyte GSH levels Inhibits NF- κ B, COX-2, and pSTAT3
Ulcerative proctitis	550 mg; \times 2–3/day \times 60 days	5	Improved symptoms
Ulcerative colitis	2000 mg/day \times 180 days	89	Low recurrence; improved symptoms

^aFor details regarding the above-mentioned studies see Goel, et al. [2007] and Kunnumakkara et al. [2008].

day of curcumin for 3 months. It was found that one of four patients with CIN and one of seven patients with oral leucoplakia proceeded to develop frank malignancies in spite of curcumin treatment, whereas histologic improvement of precancerous lesions was seen in one out of two patients with recently resected bladder cancer, two out of seven patients of oral leucoplakia, one out of six patients of intestinal metaplasia of the stomach, and one out of four patients with CIN.

In a pilot trial with 12 patients with hepatic metastases from colorectal cancer, the concentrations of the curcumin in normal and malignant human liver tissue after patients received 450–3600 mg of curcumin daily for 1 week prior to surgery were not sufficient to elicit pharmacological activity, perhaps because of the extensive degree to which curcumin was metabolized in the intestine.

In another clinical trial, researchers evaluated the effect of oral curcumin with piperine on the pain, and the markers of oxidative stress in patients with tropical pancreatitis (TP). Twenty patients with tropical pancreatitis were randomized to receive 500 mg of curcumin with 5 mg of piperine, or placebo, for 6 weeks, and the effects on the pattern of pain, and on red blood cell levels of malonyldialdehyde (MDA) and glutathione (GSH) were assessed. There was a significant reduction in the erythrocyte MDA levels following curcumin therapy compared with placebo; with a significant increase in GSH levels. There was no corresponding improvement in pain.

The studies from our group showed that curcumin inhibited pancreatic cancer in patients. Twenty-five patients were enrolled in this study. Patients received 8 g of curcumin orally daily until disease progression, with restaging every 2 months. Serum cytokine levels for IL-6, IL-8, IL-10, and IL-1 receptor antagonists and peripheral blood mononuclear cell (PBMC) expression of NF- κ B and COX-2 were monitored. Out of 25 patients, 21 were evaluable for

response. Circulating curcumin was detectable as drug in glucuronide and sulfate conjugate forms, albeit at low steady-state levels, suggesting poor oral bioavailability. Two patients demonstrated clinical biologic activity. One had ongoing stable disease for more than 18 months and, interestingly, one additional patient had a brief, but marked, tumor regression (73%), accompanied by significant increases (4- to 35-fold) in serum cytokine levels (IL-6, IL-8, IL-10, and IL-1 receptor antagonists). No toxicities were observed. Curcumin down-regulated expression of NF- κ B, COX-2, and phosphorylated STAT3 in PBMC from patients (most of whom had baseline levels considerably higher than those found in healthy volunteers).

Studies conducted by our group showed that curcumin inhibited constitutive activation of NF- κ B, COX-2, and STAT3 in the PBMC from multiple myeloma patients. Curcumin was given at 2, 4, 8, 12g/day orally, which was well tolerated with no adverse events. Out of 29 patients 12 patients continued treatment for 12 weeks and 5 completed one full year of treatment with stable disease. Clinical studies performed with leukemia patients were also reported. In a study of the 70 childhood leukemia patients samples, curcumin reduced WT1 gene expression in 35 samples [Anuchapreeda et al., 2006b].

The pharmacodynamic and pharmacokinetic effect of oral curcuma extract in patients with colorectal cancer was evaluated. Fifteen patients with advanced colorectal cancer refractory to standard chemotherapies received curcuma extract daily for up to 4 months. The results showed that oral curcuma extract was well tolerated, and dose-limiting toxicity was not observed. Neither curcumin nor its metabolites were detected in blood or urine, but curcumin was recovered from feces. Curcumin sulfate was identified in the feces of one patient. A dose escalation pilot study of a standardized formulation of curcuma extract in 15 patients with advanced colorectal cancer revealed a dose-dependent inhibition of COX-2 activity, measured as basal and LPS-mediated PGE(2) production, in blood revealing the efficacy of curcumin in colorectal cancer. Ingestion of 440 mg of curcuma extract for 29 days was accompanied by a 59% decrease in lymphocytic glutathione-*S*-transferase activity. At higher dose levels, this effect was not observed. Leukocytic M(1)G levels were constant within each patient and unaffected by treatment. Radiologically stable disease was demonstrated in five patients for 2–4 months of treatment. Another study showed that a daily dose of 3.6 g curcumin engendered 62 and 57% decreases in inducible PGE(2) production in blood samples taken 1 h after dose on days 1 and 29, respectively, in advanced colorectal cancer patients. Yet another pilot trial, involving 12 patients with hepatic metastases from colorectal cancer who received 450–3600 mg of curcumin daily, for 1 week prior to surgery, to investigate whether oral administration of curcumin results in concentrations of the agent in normal and malignant human liver tissue, which are sufficient to elicit pharmacological activity. The results of this study suggested that hepatic curcumin levels sufficient to exert pharmacological activity are not achieved in humans with the above-mentioned dose of curcumin and that this may be due to extensive

intestinal metabolism of curcumin leading to lower bioavailability. Curcumin coupled with quercetin significantly decreased the size and number of ileal and rectal adenomas in patients with FAP.

The effect of zyflamend, a herbal preparation containing curcumin against high-grade prostatic intraepithelial neoplasia (HGPIN) was evaluated in patients. A patient with HGPIN was treated with zyflamend three times a day for 18 months. After 6 months the biopsy revealed benign prostatic hyperplasia alone and after 18 months biopsy was negative for cancer and PIN, indicating that the patient was cancer and HGPIN free.

CONCLUSIONS

Almost 3000 studies carried out with curcumin suggest that this natural agent affects numerous pathways linked with tumorigenesis and thus has potential both for prevention and treatment of cancer. Although pharmacologically curcumin is quite safe in humans, its limited bioavailability may be a problem. More clinical trials with curcumin either alone or in combination with existing therapies are needed to fully appreciate its potential. Reformulation of curcumin may also hold promise in the future for the bioavailability problem. Its safety combined with its low cost and multiple targeting potential makes curcumin an ideal agent to be explored for prevention and treatment of various cancers.

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17 Plant Phenolic Compounds: Modulation of Cytoprotective Enzymes and Nrf2/ARE Signaling

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INTRODUCTION: PLANT PHENOLIC COMPOUNDS

Phenolic compounds, mainly polyphenols, are abundant in a wide array of edible plants including various legumes, fruits, vegetables, olive oil, and grains. They are also found in red wine, chocolate, green tea, and coffee. Structurally, phenolic compounds are characterized by the presence of one or more hydroxylated 6-carbon aromatic rings and can be accordingly divided into several main groups: phenolic acids, phenolic alcohols, flavonoids, stilbenes, and lignans. Currently over 8000 phenolic compounds are known, among them flavonoids are the largest and most studied polyphenols and can be subdivided into flavonols, flavones, flavanols (catechins), flavanones, anthocyanidins, and isoflavonoids. There are also many smaller classes of plant phenolic compounds derived from different biosynthetic pathways [Bravo, 1998].

In this chapter, we will discuss the health effects of plant phenolic compounds with special emphasis on their modulation of cytoprotective enzymes and Nrf2/ARE signaling. Curcumin (diferuloylmethane), a hydrophobic polyphenol derived from turmeric (*Curcuma longa*), will be discussed as a typical example of plant phenolic compounds. Chemically, curcumin is characterized by a bis- α,β -unsaturated β -diketone structure that can function as Michael reaction acceptors [Strimpakos and Sharma, 2008]. The commercially available curcumin is a mixture of curcuminoids including curcumin, demethoxycurcumin, and bisdemethoxycurcumin. Upon absorption, curcumin is quickly metabolized and the major metabolites are curcumin-glucuronoside, dihydrocurcumin-glucuronoside, tetrahydrocurcumin-glucuronoside, and tetrahydrocurcumin [Anand et al., 2007]. The structure of some curcuminoids and metabolites are shown in Figure 17.1 together with a synthetic curcumin analog, salicylcurcuminoid.

HEALTH EFFECTS OF PLANT PHENOLIC COMPOUNDS

Despite the wide distribution of phenolic compounds in edible plants and the high dietary intake, the health effects of plant phenolic compounds had not been extensively studied until the mid-1990s due to their diversity of species and chemical structures. Epidemiological studies have revealed that dietary consumption of fruits, vegetables, and other plant-based foods and beverages is inversely correlated with the incidences of many diseases such as cancer, cardiovascular disease, and neurodegenerative diseases [Stevenson and Hurst, 2007]. The evidences from clinical and laboratory studies strongly support

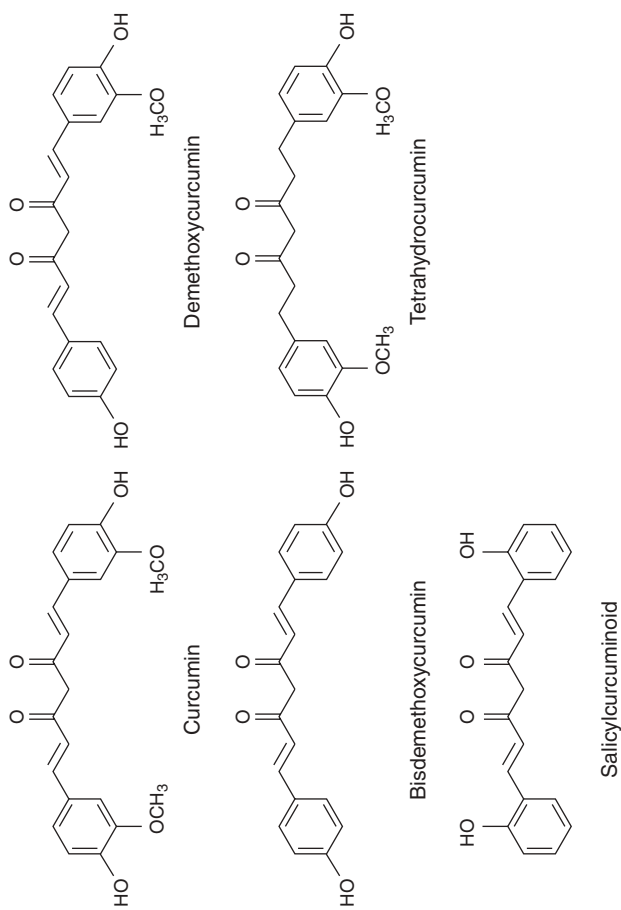


Figure 17.1 The chemical structure of curcumin, demethoxycurcumin, bisdemethoxycurcumin, tetrahydrocurcumin, and salicylcurcuminoid. Curcumin is characterized by two phenolic groups connected by a bis- α,β -unsaturated β -diketone structure. Removal of one or two methoxyl groups, as in demethoxycurcumin or bisdemethoxycurcumin, shows no significant effect on the induction of cytoprotective enzymes but decreases the direct antioxidant activity. On the contrary, tetrahydrocurcumin exhibits higher direct antioxidant activity but lower enzyme induction than curcumin. Salicylcurcuminoid, a synthetic analog of curcumin with *ortho*-hydroxyl groups, is > 30 times potent than curcumin in enzyme induction and is more potent in cytoprotection than curcumin.

plant phenolic compounds as important candidates of the bioactive components in plant-based foods and beverages. Since many plant phenolic compounds have been widely consumed for many years as dietary components without safety problems, they are especially important in prevention of cancers, cardiovascular diseases, and other degenerative diseases. Curcumin has been widely used as a food flavoring and coloring agent and for medical purposes for many years in Asia. Since the publication of the first report on the usage of curcumin to treat human diseases in 1937, curcumin has been one of the most extensively investigated plant phenolic compounds. Curcumin has been shown to exhibit a surprisingly wide range of beneficial biological activities including anti-inflammation, antioxidant, anticarcinogenesis, antidiabetes, myocardial protection, and neuron protection [Strimpakos and Sharma, 2008]. Furthermore, curcumin is extremely safe even at very high doses, as demonstrated in various animal models or human studies [Anand et al., 2007]. These properties make curcumin a promising compound for treatment and prevention of a variety of diseases.

PLANT PHENOLIC COMPOUNDS AS DIRECT ANTIOXIDANTS

As described above, plant phenolic compounds have been shown to be useful in prevention or treatment of many degenerative diseases. The underlying mechanisms have been suggested as inhibition of proliferation, induction of apoptosis, suppression of inflammation, modulation of immune responses, and protection against oxidative stresses, and many signaling pathways have been suggested as the molecular targets of plant phenolic compounds. However, most of the health effects of plant phenolic compounds can be attributed to their cytoprotective activities against environmental and endogenous stresses imposed by electrophiles/oxidants [Stevenson and Hurst, 2007].

Oxidative stress plays important roles in the pathogenesis of many degenerative diseases. Reactive oxygen/nitrogen species (ROS/RNS) potentially can react with all bio-macromolecules including protein, nucleic acids, and lipids and impair their normal functions. Reduced forms of plant phenolic compounds exhibit strong antioxidant capacities *in vitro*, by scavenging a wide array of reactive oxygen, nitrogen, and chlorine species such as superoxide, hydroxyl radical, peroxy radicals, singlet oxygen, hypochlorous acid, and peroxyxynitrous acid. In addition, they can chelate redox-active metal ions, often leading to reduced pro-oxidant activities. Their direct antioxidant activities require one or more free phenolic hydroxyl groups and are generally enhanced by electron repelling or large alkyl groups in the 2- and 6-positions [Stevenson and Hurst, 2007]. As other typical small-molecule antioxidant such as ascorbate and tocopherol, these phenolic compounds can undergo redox reactions and react with ROS/RNS to quench them.

The antioxidant activity of curcumin has been investigated for over 30 years [Sharma, 1976]. Curcumin has been shown to inhibit lipid peroxidation,

ROS- or radiation-mediated DNA strand breakage or adduct formation, and protein oxidative/nitrosative damages. Curcumin can scavenge various electrophiles/antioxidants including singlet oxygen, superoxide, polyunsaturated lipid peroxy radicals, NO radicals, and many others [Menon and Sudheer, 2007]. In addition, curcumin chelates metal ions such as cadmium, copper, and manganese, reducing their pro-oxidant activities [Corona-Rivera et al., 2007; Daniel et al., 2004]. Moreover, it was proposed that the copper or manganese complexes of curcumin mimics superoxide dismutase, further potentiates the antioxidant activity of curcumin [Barik et al., 2005; Dutta et al., 2001; Vajragupta et al., 2003]. The direct antioxidant activity of curcumin has been ascribed to its phenolic hydroxyl and/or β -diketone moieties. A reactive electrophile or oxidant can undergo electron transfer or abstract H atom from either of these two sites.

However, the concentrations required for efficient protection against oxidative stresses are generally tens or even hundreds of micromolar. For example, the concentration required to inhibit 40% of superoxide-mediated ferricytochrome *c* reduction is 80 μ M, and over 20 μ M to scavenge NO radical [Das and Das, 2002; Sumanont et al., 2004]. On the contrary, despite that plant phenolic compounds were considered as the most abundant antioxidants in the diet, the physiologically achievable concentrations of plant phenolic compounds are very low and sometime even negligible. In rat 2% dietary curcumin yielded only low levels of plasma concentration between 0 and 12 nM, even in colon mucosa the concentrations were only 0.2 – 1.8 μ mol/g [Anand et al., 2007]. In addition, the half-lives of plant phenolic compounds in circulation are generally short because of rapid metabolism and elimination. Many metabolizing reactions such as methylation or glucuronidation will decrease their direct antioxidant activity by blocking of phenolic hydroxyl groups. In fact, dimethoxy curcumin is much less active than curcumin in terms of quenching free radicals [Priyadarsini et al., 2003]. Furthermore, during the antioxidant reactions, these compounds are either consumed or chemically modified, and have to be regenerated or replenished for continuing action. In contrast to these exogenous antioxidants, glutathione (GSH), a universal endogenous small-molecule antioxidant, is presented in millimolar ranges in all cells; on the other hand, the total circulating concentrations of ascorbate and urate, two main endogenous small-molecule antioxidants, are over 500 μ M. Thus the plant phenolic compounds in tissues or plasma only represent a transient and small increase of total antioxidant capacity [Stevenson and Hurst, 2007; Dinkova-Kostova and Talalay, 2008].

Moreover, under certain conditions these phenolic compounds could also act as pro-oxidants. In the presence of redox-active metal ions such as Cu or Fe, phenolic compounds react with O₂ to generate phenoxyl radicals. Under normal growth conditions phenoxyl radicals can be rapidly deactivated by polymerization or enzymatic reduction. However, if the phenoxyl radical concentrations are too high and/or the lifetime is increased, they could initiate DNA damage or lipid peroxidation and exhibit cytotoxicities. Curcumin, demethoxycurcumin, and bisdemethoxycurcumin have been reported to induce

DNA damage in the presence of cytochrome P450s (CYPs) and Cu(II) in vitro or in cells [Yoshino et al., 2004; Ahsan et al., 1999]. At higher concentrations curcumin exhibited genotoxicity and cytotoxicity in different systems [Cao et al., 2007]. At last, in vivo intervention trials using typical antioxidants such as ascorbate or carotenes yielded mostly disappointing results in terms of protection against oxidation-related diseases, sometime even increased the incidences of diseases [Stevenson and Hurst, 2007; Dinkova-Kostova and Talalay, 2008]. Obviously, the direct antioxidant capacity of plant phenolic compounds cannot explain their cytoprotective activities.

INDIRECT CYTOPROTECTIVE ACTIVITY OF PLANT PHENOLIC COMPOUNDS AND CYTOPROTECTIVE ENZYMES

For many years, the cytoprotective effects of plant phenolic compounds were attributed to their ability to directly scavenge oxidants and free radicals. However, as discussed in the last section, this concept is oversimplified and misleading. More and more evidence suggests that plant phenolic compounds could interact with cellular components and trigger a series of cellular responses, which are able to modulate the redox status of the cells and protect the cells from potentially toxic electrophiles/oxidants.

All eukaryotic cells are equipped with elaborate cytoprotective machinery to protect cells from those harmful factors, and the activity of this cellular defense system is often up-regulated in response to exogenous or endogenous stresses. This phenomenon was first described as the “hormesis effect,” which is characterized by adaptive beneficial effect induced by exposure to a low dose of a chemical agent or environmental factor that is harmful at higher doses [Mattson, 2008]. In some cases it was also called “adaptation” or “preconditioning,” in which cells and organisms acquire resistance to damaging stresses by exposure to a mild stress [Arumugam et al., 2006]. One typical example is the mechanisms of ischemic preconditioning in the heart and brain, where preexposure to moderate ischemia could enhance the tolerance of cells to severe oxidative stress. Similarly, it was found that weakly carcinogenic hydrocarbons could inhibit the tumorigenicity of potent carcinogens. This inhibition was effective in distal organs/tissues; and even the inhibitor and carcinogen were administered by different route [Holtzclaw et al., 2004]. It was not dependent on local interaction between inhibitor and carcinogen but correlated with increased activity of metabolizing enzymes that collectively deactivate carcinogens. Actually, in the early days most compounds identified as enzyme inducers were carcinogens such as 7,12-dimethylbenz[a]anthracene (DMBA), benzo[a]pyrene (B[a]P), and Sudan III. Further investigations found out that several phenolic compounds such as butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), and *tert*-butylhydroquinone (t-BHQ) potently inhibited the toxicity and carcinogenicity of chemical carcinogens [Frankfurt et al., 1967; Wattenberg, 1972], and this protection was also

associated with increased phase 2 and antioxidant enzyme activities. Unlike the previously studied potential carcinogens, these phenolic antioxidants have been safely consumed by humans as food additives, so this finding was considered as a major breakthrough in the search of safe chemopreventives. These investigations finally led to the concept that induction of phase 2 and antioxidant enzymes could be a plausible strategy for protection against detrimental electrophiles/oxidants and related diseases.

Phase 2 enzymes catalyze the conjugation of reactive electrophiles/oxidants with small endogenous water-soluble molecules such as glutathione, sulfate, UDP-uridine diphosphate-glucuronic acid, or acetyl coenzyme A, which generally leads to detoxification of those electrophiles/oxidants and facilitates their elimination [Yu and Kong, 2007]. Phase 2 enzymes consist of many superfamilies of enzymes including γ -glutamylcysteine synthetase (γ -GCS), glutathione-*S*-transferases (GST), sulfotransferases (SULT), NAD(P)H:quinone oxidoreductase (NQO, or quinone reductase, QR), UDP-glucuronosyl transferases (UGT), epoxide hydrolases (EPH), and *N*-acetyltransferases (NAT). On the other hand, glutathione peroxidase (GPX), glutathione reductase (GSR), catalase, thioredoxin reductase (TrxR), superoxide dismutase (SOD), heme oxygenase (HO), and biliverdin reductase (BLVR) are the most important antioxidant enzymes that catalyze the neutralization of ROS/RNS and free radicals. Beside these enzymes, some protective proteins that may not have enzymatic activities (e.g., ferritin, thioredoxin) are also important members of the cytoprotective machinery. Many cytoprotective enzymes play important roles in both detoxification of electrophiles and elimination of oxidants. For example, certain GSTs exhibit glutathione peroxidase activity in addition to catalyzing the conjugation with glutathione [Hurst et al., 1998]. Another example is γ -GCS, which catalyzes the rate-limiting step in the synthesis of glutathione [Wild and Mulcahy, 2000]. All of these enzymes collectively protect cells from the damages of electrophiles/oxidants, and are designated as cytoprotective enzymes [Dinkova-Kostova and Talalay, 2008]. In many ways, induction of cytoprotective enzymes is much more efficient as an "antioxidant" mechanism than direct antioxidant, because these enzymes catalyze a wide spectrum of reactions that almost invariably lead to inactivation and detoxification of electrophiles/oxidants, and are not consumed during their antioxidant action.

Most of the cytoprotective enzymes are highly inducible in response to enzyme inducers or oxidative stress. As an important class of enzyme inducers, many plant phenolic compounds have been shown to be able to induce cytoprotective enzyme activities. In the search for chemopreventive compounds, tumeric or curcumin has been shown to significantly increase hepatic GST, UGT and EPH activities and glutathione content in carcinogen-treated mice [Goud et al., 1993, Susan and Rao, 1992]. Dietary supplementation of 2% curcumin to male ddY mice for 30 days significantly increased the activities of GPx, GSR, glucose-6-phosphate dehydrogenase, catalase, GST, and NQO1 in liver and kidney [Iqbal et al., 2003]. Curcumin also dose dependently induced UGT, GPx, and GST activities in rat hepatic and intestinal tissues, and the

increased enzyme activities contributed to the anti-inflammatory and anticarcinogenesis activity of curcumin. Pregnant mice fed with tumeric or curcumin could even increase the hepatic levels of GST and acid-soluble sulfhydryl of translactationally exposed F1 pups [Singh et al., 1995]. In a study using curcumin to prevent cataractogenesis in rat lenses, induction of GST activity was suggested as a mechanism of protection against lipid peroxidation [Awasthi et al., 1996]. In cultured cell models, curcumin is a potent inducer of cytoprotective enzymes. Despite its moderate inhibition of UGT activities, curcumin induced the expression of UGT 1A1 and 1A6 in Caco-2 cells [Usta et al., 2007]. Exposure of bovine aortic endothelial cells to curcumin resulted in increased HO-1 messenger ribonucleic acid (mRNA), protein, and activity and protected cells from oxidative stress. It has been reported that curcumin induced HO-1 and GST P1 in normal lung fibroblasts but not in scleroderma lung fibroblasts, and this might contribute to the discriminative induction of apoptosis in scleroderma lung fibroblasts [Tourkina et al., 2004]. Curcumin also induced HO-1, NQO1, and GST in astrocytes and hippocampal neurons and protected cells from oxidative damages [Scapagnini et al., 2006].

MODULATION OF CYTOPROTECTIVE ENZYMES BY PLANT PHENOLIC COMPOUNDS: STRUCTURE–ACTIVITY RELATIONSHIP

To better understand the health effects of plant phenolic compounds and to better utilize them, it is necessary to know the molecular mechanisms by which plant phenolic compounds induce cytoprotective enzymes. In vitro studies indicated that plant phenolic compounds such as curcumin often inhibited the enzymatic activities of GST, UGT, SULT as well as cytochrome P450s [Oetari et al., 1996], suggesting that the induction of cytoprotective enzyme activities could not be explained by direct interaction with plant phenolic compounds. On the other hand, much evidence indicates that the increased activity of cytoprotective enzymes are mainly attributable to enhanced transcriptional activation and enzyme synthesis [Holtzclaw et al., 2004].

Based on the results from experiments using aryl hydrocarbon receptor (AhR)- or CYP1A1-deficient cells and mice, enzyme inducers were designated as monofunctional and bifunctional inducers [Prochaska and Talalay, 1988]. Bifunctional inducers (generally planar aromatics) AhR dependently increase the activities of both phase 1 and phase 2 enzymes, while monofunctional inducers selectively induce phase 2 enzymes without the participation of AhR. Bifunctional inducers directly induce phase 1 enzymes by binding to and activating AhR or are metabolized by phase 1 enzymes such as CYP1A1 to be converted to electrophilic monofunctional inducers. Many plant phenolic compounds belong to the monofunctional inducers. Curcumin has been reported to bind to AhR and induce phase 1 enzymes in cells [Ciolino et al., 1998], but in a recent study curcumin was found to inhibit benzo[a]pyrene-[B[a]P] induced AhR and phase 1 enzyme expression in mice [Garg et al., 2008].

Moreover, the induction of phase 2 enzymes by curcumin is independent on AhR or CYP1A1, thus curcumin is classified as a monofunctional inducer [Dinkova-Kostova and Talalay, 1999].

A wide variety of monofunctional inducers with very different chemical structures has been identified. These compounds could be classified into at least 10 classes, with plant phenolic compounds belonging to oxidizable diphenols or Michael reaction acceptors [Prochaska and Talalay, 1988]. Michael reaction acceptors (olefins or acetylenes conjugated to electron-withdrawing groups) constitute a major class of phase 2 enzyme inducers, and their inducer potency was closely correlated with their reactivity with nucleophiles in the Michael reaction. The induction of cytoprotective enzymes by curcumin could be attributed to the two Michael reaction acceptor functionalities in its molecule. The structure–activity relationship of curcumin and its analogs as NQO1 inducers were studied in Hepa1c1c7 murine hepatoma cells [Dinkova-Kostova and Talalay, 1999]. Removal of methoxyl groups, as in demethoxycurcumin and bisdemethoxycurcumin, only slightly decreased the inducer activity. Removal of phenolic hydroxyl group also showed no significant effect on the inducer activity, however, salicylcurcuminoid with *ortho*-hydroxyl groups is >30 times potent than curcumin in inducer activity. Tetrahydrocurcumin, a metabolite of curcumin, exhibited much lower inducer activity, though it is more potent than curcumin as a direct antioxidant. On the other hand, the β -diketone moiety is also an important functional group for induction of NQO1 due to the dominance of the keto-enol tautomerism. In general, the inducer activity is parallel to the reactivity with nucleophilic groups such as thiols. The structure–activity relationship in induction of NQO1 has also been confirmed in induction of HO-1 and the protection against oxidative damages [Jeong et al., 2006].

Further structure–activity relationship (SAR) analyses of other cytoprotective enzyme inducers revealed the fact that all inducers can react with thiol/disulfide groups by alkylation, oxidoreduction, or thiol-disulfide interchange [Dinkova-Kostova and Talalay, 1999]. In fact, the capability of enzyme inducers to induce cytoprotective enzymes is well correlated with their reactivity with thiols. These results suggested a cellular sensor of inducers with highly reactive sulfhydryl groups, possibly reactive thiols in cysteine residues of a sensor protein. Nevertheless, the initial search for the sensor protein by using radioactively labeled inducers was not successful due to the abundance of thiol groups presented in many proteins in cells [Holtzclaw et al., 2004]. The molecular mechanism by which cytoprotective enzymes are induced remained to be elucidated.

MODULATION OF CYTOPROTECTIVE ENZYMES BY PLANT PHENOLIC COMPOUNDS: FROM ARE TO NRF2

New understanding of the mechanism underlying the induction of cytoprotective enzymes came from analysis of the DNA sequences in the 5'-flanking promoter regions of several phase 2 genes. Two sequences in the upstream

region of rat GST Ya were identified as essential for its induction by reporter assay [Rushmore and Pickett, 1990; Nguyen et al., 1994]. One of them contained an xenobiotic response element (XRE, 5'-TNGCGTG-3'), which is involved in AhR-mediated induction. The other one could be activated independent of AhR and was named antioxidant response element (ARE). The core ARE sequence was further defined as 5'-TGACNNNGC-3' by deletion and mutation analysis [Rushmore et al., 1991]. Another 41-bp region was identified in the 5-flanking region of mouse GST Ya gene, which is responsive to electrophiles and was named electrophile response element (EpRE) [Friling et al., 1992]. One of the functional sequences in this region is the same as ARE. Latter on, the core ARE sequence, which is responsive to enzyme inducers, was identified in the promoter regions of NQO1, HO-1, GCS, ferritin H, and GST P1. Further studies revealed that the ARE sequences in different genes was variable, and some other ARE-like or nonclassic ARE sequences were also identified. After more detailed analysis, the core sequence was extended as 5'-TMAnnRTGAYnnnGCRwww-3', where M = A or C, R = A or G, Y = C or T, W = A or T [Wasserman and Fahl, 1997]. Recently, a 21-base sequence logo of AREs was created based on 57 functional ARE sequences identified in human, rat, and mouse [Wang et al., 2007]. With the help of a systematic computational approach combining transcription factor binding site recognition, comparative genome analysis, gene expression profiling and genotype—expression phenotype association, 2388 genes common in human, rat, and mouse were found to contain AREs in their upstream 5-kb sequences.

There is an embedded 12-O-tetradecanoylphorbol-13-acetate (TPA) response element (TRE, 5'-TGACTCA-3') in the core ARE sequence, though the ARE and TRE are functionally distinct. The TRE is recognized by AP-1, which shares a DNA recognition sequence [5'-TGCTGA(G/C)TCA(C/T)] with another transcription factor, nuclear factor-erythroid 2 (NF-E2). NF-E2 is a basic leucine zipper (b-Zip) protein and belongs to a subfamily of b-Zip cap 'n' collar (CNC) genes, including NF-E2, Nrf2, Nrf2, Nrf3, and Bach1/2. These proteins heterodimerize with other b-Zip proteins such as small Maf proteins through their b-Zip domain, and function as transcription factors. The small Maf proteins, namely MafG, MafK, and MafF, are homologs of the *v-maf* oncogene product Maf. The Maf protein recognizes two similar palindromic consensus sequences, 5'-TGCTGACTCAGCA-3' and 5'-TGCTGACGTCAGCA-3'. These two sequences were called Maf recognition elements (MAREs) [Kataoka et al., 1994]. Interestingly, there are embedded TREs in these MAREs, and one consensus ARE in the first MARE.

The striking resemblance in ARE, TRE, MAREs, and NF-E2 recognition sequences raises the hypothesis that certain members of CNC and/or Maf family transcription factors could bind to ARE and regulate the expression of ARE-driven genes. Indeed, both Nrf1 and Nrf2 were found to bind with ARE in the human NQO1 gene and to potentiate the basal and inducible ARE-mediated transcription [Venugopal and Jaiswal, 1996]. Based on their expression profiles, Nrf2 was selected as the most likely candidate, and *nrf2*-deficient

mice were generated by disruption of the *nrf2* gene in embryonic stem cells [Itoh et al., 1997]. Compared to the wild-type mice, both the basal and the BHA-inducible expression of phase 2 enzymes such as GST and NQO1 were largely diminished in *nrf2*-deficient mice. Furthermore, a heterodimer composed of Nrf2 and a small Maf protein was found to bind to ARE with high affinity. In another study, Nrf2 (-/-) mice exhibited significantly lower expression of catalase, GCS, HO-1, NQO1, SOD1, and UGT1A6 and were much more susceptible to BHT-induced pulmonary injury [Chan and Kan, 1999]. These results clearly demonstrated that Nrf2 is essential for the transcriptional activation of phase 2 enzymes and provided a coordinated transcriptional regulation mechanism for the induction of cytoprotective enzymes.

Consequently, the induction of cytoprotective enzymes such as HO-1, GPx2, and GST by curcumin was found to be Nrf2-dependent [Balogun et al., 2003; Banning et al., 2005; Nishinaka et al., 2007]. The modulation of Nrf2-dependent gene expression profile in mice liver and small intestine by curcumin was examined in our lab [Shen et al., 2006]. Wild-type or Nrf2 (-/-) mice were given a single oral dose of curcumin at 1 g/kg, and then liver and small intestine were harvested after 3 or 12 h. The gene expression profiles were analyzed by mouse genome microarray, and the genes that were modulated > twofold by curcumin in wild-type but not in Nrf2 (-/-) mice were considered as Nrf2 dependent. Total 822 in liver (664 induced and 158 suppressed) and 222 in small intestine (154 induced and 68 suppressed) genes were identified as curcumin-modulated Nrf2-dependent. Many cytoprotective enzyme genes, including NQO1, GSTs, HO-1, γ -GCS, UGT, and thioredoxin, were among the identified genes. Interestingly, some phase 1 CYP genes and phase 3 transporters and many other genes were also Nrf2 dependently regulated by curcumin. This observation is further supported by the finding of AREs in over 2000 genes common in human, rat, and mouse [Wang et al., 2007]. Besides this, substantial evidence accumulated to further support the pivotal role of Nrf2 in induction of cytoprotective enzymes by all kinds of inducers and protection against electrophiles/oxidants-related damages and diseases.

In response to electrophiles, the DNA-binding activity and sometimes the protein level of Nrf2 was markedly increased; however, in most cases the Nrf2 mRNA level was not significantly changed, suggesting the activity of Nrf2 is regulated posttranscriptional. Extensive studies revealed that the Nrf2/ARE signaling is modulated at multiple levels.

MODULATION OF NRF2/ARE SIGNALING: IDENTIFICATION AND MODIFICATION OF KEAP1

Based on the homology of cross-species *orthologs*, six domains were identified in the primary structure of Nrf2, namely Nrf2-ECH-homology 1 (Neh1) to Neh6 [Itoh et al., 1999]. The Neh1 contains the CNC homology region and basic-leucine zipper domain for dimerization with small Mafs and DNA binding.

The amino and carboxyl termini of the proteins were referred to as Neh2 and Neh3, respectively. Neh4 and Neh5 are two conserved acidic domains involved in transactivation. Neh3 has also been implied in transactivation [Nioi et al., 2005]. Additionally there is a serine-rich conserved region (Neh6). The primary structure of Nrf2 is illustrated in Figure 17.2.

It was found that the N-terminal of Nrf2, Neh2 domain, is inhibitory to the transcriptional activity of Nrf2. Co-expression of an Neh2 decoy restored Nrf2 transactivation activity, suggesting the existence of a possible repressor protein interacting with Neh2 [Itoh et al., 1999]. A single protein was identified in yeast two-hybrid experiment using the Gal4-Neh2 as bait, and was named as Keap1 (Kelch-like ECH-associated protein 1). In another study, a protein, INrf2, was isolated by co-purification with Nrf2 from rat hepatoma cells, and was identified as a trans-species homolog of Keap1 [Dhakshinamoorthy and Jaiswal, 2001]. The interaction between Keap1 and Nrf2 was further confirmed in vitro and in mammalian cells, and this interaction could be disrupted by cytoprotective enzyme inducers. Moreover, Nrf2 accumulation in nucleus and high constitutive expression of Nrf2 target genes were observed in Keap1-disrupted mice, and this phenotype could be totally reversed by Nrf2::Keap1 double knockout [Wakabayashi et al., 2003]. These findings proved that Keap1 is the negative regulator of Nrf2.

The Keap1 protein consists of 624 amino acids and is structurally related to *Drosophila* actin-binding protein Kelch. Keap1 contains a high number of cysteine residues (25 for murine and rat, 27 for human), and about nine of these cysteines (C23, C38, C151, C241, C273, C288, C297, C319, and C613) were predicted to be “reactive” since they are flanked by basic residues. This feature makes Keap1 a favorable “sensor” of electrophilic/oxidative signals. Indeed, these reactive cysteines were found to be able to react with enzyme inducers [Dinkova-Kostova et al., 2002]. C151 has been shown to be required for stabilization and activation of Nrf2 by sulforaphane and t-BHQ [Zhang and Hannink, 2003]. By using in vitro labeling and mutation assay, two other reactive cysteines, C273 and C288, were also identified as key residues for activation of Nrf2 [Wakabayashi et al., 2004]. In addition, different electrophiles may modify different sets of reactive cysteines [Dinkova-Kostova et al., 2005]. The NQO1 inducer activities of 30 plant phenylpropenoids and synthetic analogs were linearly correlated with their calculated tendency to release electrons (E_{HOMO}) [Zoete et al., 2004]. A similar correlation was reported for about 20 flavonoids, for which their pro-oxidant activity correlated with EpRE inducer activity [Lee-Hilz et al., 2006]. Furthermore, addition of thiol antioxidants such as GSH or NAC significantly abolished phenolic-induced cytoprotective enzyme expression. Most importantly, phenolic Michael acceptors could react with Keap1 in vitro, and their reactivity with Keap1 was parallel to their inducer potency, and the inducer activity was potentiated by free phenolic hydroxyl groups [Dinkova-Kostova et al., 2002].

Structurally, Keap1 is subdivided into five domains (Fig.17.2b): the amino terminal region (NTR), the BTB/POZ (Bric-a-brac, tramtrack, broad-complex/

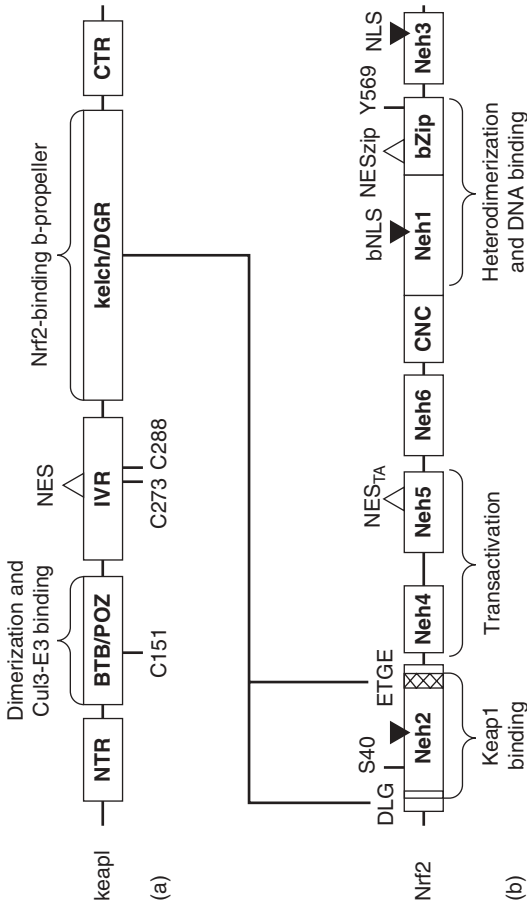


Figure 17.2 Schematic presentation of primary structure of Nrf2 and Keap1 with proposed regulatory domains/motifs. (a) Keap1 is subdivided into five domains. The BTB/POZ domain mediates the homodimerization of Keap1 and bridges Cul3-E3 ligase complex. The Kelch/DGR domain with a 6-blade b-propeller structure binds with the Neh2 domain of Nrf2. The IVR domain contains multiple reactive cysteines and is important for electrophile/oxidant-sensing. In addition, one NES (Δ) was identified in the IVR domain. (b). The six conserved domains were identified in Nrf2, namely Neh1 to Neh6. Neh1 contains the CNC and the basic leucine zipper motifs and is important for heterodimerization with small Mafs and DNA binding. Neh2 binds with Keap1 through the DLG and ETGE motifs. Neh3 at the C-terminal, Neh4 and Neh5 are involved in transactivation, while the function of Neh6 is still unknown. Nrf2 possesses multiple NES and NLS (\blacktriangledown) that control the subcellular distribution of Nrf2. Two identified phosphorylation sites, S40 by PKC and Y568 by Fyn kinase, are also indicated.

poxvirus zinc finger) domain, a cysteine-rich intervening region (IVR), the double-glycine repeat (DGR) or Kelch domain, and the carboxy terminal region (CTR). Keap1 forms homodimer through BTB domain and bridges Nrf2 to a Cul3-dependent E3 ubiquitin ligase complex [Kobayashi et al., 2004]. Two recognition sites, termed the DLG and ETGE motifs, with the Neh2 domain of Nrf2 were showed to bind to the Kelch domain with different affinities. Based on these observations, a “hinge and latch” model was proposed for the Nrf2/Keap1 complex to sense cellular stresses [Tong et al., 2006]. Under basal physiological conditions, Nrf2 is sequestered in cytoplasm by Keap1 through the binding of DLG and ETGE to two Kelch domains, thus the Neh2 is posed to E3-mediated ubiquitination, targeting Nrf2 for degradation by the 26S proteasome. In this way Nrf2/ARE signaling is kept inactivated by Keap1. Upon oxidative or electrophilic challenges, specific reactive cysteines in the IVR and BTB regions are modified [Zhang and Hannink, M, 2003; Wakabayashi et al., 2004]. This modification possibly leads to conformation alteration of the Keap1 dimer, leading to dissociation of the DLG motif and termination of Nrf2 ubiquitination. Furthermore, it has been proposed that Keap1 itself could be targeted for ubiquitination and proteasome-independent degradation upon exposure to electrophiles/oxidants [Zhang et al., 2005]. Collectively, these modifications result in the stabilization and possibly release of Nrf2.

MODULATION OF NRF2/ARE SIGNALING: MODIFICATION OF NRF2

Besides Keap1, Nrf2 itself is targeted for multiple posttranslational modifications. Two cysteine residues, C183 and C506, have been proposed to affect the activation of Nrf2/ARE signaling. Mutation of C506 in the DNA-binding region of Nrf2 to serine decreased its binding affinity to ARE and NQO1 induction in response to t-BHQ treatment, implicating that C506 could be modified [Bloom et al., 2002]. C183, which locates in the Neh5 domain, could be modified upon t-BHQ or H₂O₂ treatment and inhibited the nuclear exporting of Nrf2 [Li et al., 2006].

Nrf2 is also phosphorylated by various kinases including PKC (protein kinase C), MAPKs (mitogen-activated protein kinases), PERK (ER-localized pancreatic endoplasmic reticulum kinase), GSK-3 β (glycogen synthase kinase 3 β), Fyn kinase, and CK2 (casein kinase 2). Phosphorylation of S40 of Nrf2 by a PKC isoform is important for dissociation of Nrf2 from Keap1 and its translocation to nucleus [Huang et al., 2002]. MAPKs, including ERK, JNK, and p38, have been found to phosphorylate Nrf2 and promote its accumulation in nucleus [Kong et al., 2001]. Phosphorylation by MAPKs also stabilizes Nrf2 [Nguyen et al., 2003]. PERK directly phosphorylates Nrf2 and triggers dissociation of Nrf2 from Keap1, and protects cells from ER-stress-mediated death [Cullinan et al., 2003]. GSK-3 β either directly [Rojo et al., 2008] or

indirectly through Fyn kinase [Jain and Jaiswal, 2007] phosphorylates Nrf2, leading to the exportation of Nrf2 from nucleus and negative regulation of Nrf2/ARE signaling. The phosphorylation site of Fyn kinase has been identified as Y568 [Jain and Jaiswal, 2007]. It has been reported that PI3K or Akt was involved in the activation of Nrf2/ARE signaling by curcumin [Pugazhenthil et al., 2007]. Since Gsk-3 β is deactivated by Akt, it is possible that PI3K or Akt indirectly activate Nrf2 through deactivation of Gsk-3 β . Recently, CK2 was found to phosphorylate Nrf2 at the transactivation domains (Neh4 and Neh5), and this phosphorylation promoted the translocation of Nrf2 to nucleus [Apopa et al., 2008]. Except for the phosphorylation sites by PKC and Fyn, the exact phosphorylation sites by other kinases remain elusive.

Many plant phenolic compounds have been shown to modulate protein kinases, and this could be an important mechanism of modulation of Nrf2/ARE signaling. Curcumin has been reported to transiently activate PKC, and PKC activation is required for curcumin-induced expression of HO-1, GST, and GCLM [McNally et al., 2007; Rushworth et al., 2006]. Specifically, PKC δ and PKC ϵ have been implicated in regulation of Nrf2/ARE signaling by curcumin. It has also been reported that p38, ERK, and PI3K/Akt were involved in curcumin-mediated expression of cytoprotective enzymes, and specific pharmacological inhibitors or genetic inhibition of these kinases abrogated curcumin-induced Nrf2 activation and cytoprotective gene expression [McNally et al., 2007; Andreadi et al., 2006]. Another example is genistein, which activates Nrf2/ARE signaling by inhibiting tyrosine kinase Fyn and consequently inhibiting the exporting of Nrf2 [Jain and Jaiswal, 2007].

MODULATION OF NRF2/ARE SIGNALING: NUCLEAR-CYTOPLASMIC TRAFFICKING

Once activated, Nrf2 translocates from cytoplasm into nucleus, dimerizes with small Mafs, binds to ARE, and activates gene transcription. The nuclear translocation of Nrf2 has been viewed as an automatic process after being released from Keap1 or mediated by Keap1 [Itoh et al., 1999]. However, multiple nuclear localization signals (NLS) and nuclear exporting sequence (NES) have been identified in Nrf2 and in Keap1, suggesting the existence of a complicated regulation of nuclear-cytoplasmic trafficking.

A functional NES comprised of hydrophobic leucine and isoleucine residues has been identified in the IVR domain of Keap1 [Velichkova and Hasson, 2005]. Mutation of the hydrophobic residues as well as leptomycin B (LMB) treatment, which inactivates Crm1/exportin, resulted in nuclear accumulation of both Nrf2 and Keap1. It was further demonstrated that the NES in Keap1 is required for termination of Nrf2/ARE signaling, and the Nrf2/Keap1 complex does not bind to the ARE [Sun et al., 2007]. Conversely, in another report the subcellular distribution of endogenous Keap1 was essentially similar before and after LMB treatment [Watai et al., 2007]. This discrepancy could possibly be

explained by the fact that Keap1 does contain any NLS and has to be co-transported into the nucleus with Nrf2, however, under basal condition Nrf2 is quickly degraded, thus few Keap1 protein could be transported into the nucleus.

In contrary, Nrf2 is equipped with multiple NES/NLS. It was almost simultaneously reported that Nrf2 possesses a NES located in the leucine zipper region of Nrf2 (NESzip), and at the same time a bipartite NLS was identified in the basic DNA-binding domain (bNLS) [Li et al., 2005; Jain et al., 2005]. Interestingly, the NESzip overlaps with the dimerization domain with small Mafs, thus the binding of Nrf2 with small Mafs supposedly will disable this NES by depriving the binding of Crm1/exportin, retaining Nrf2 in the nucleus. Another NES was identified in the Neh5 transactivation domain (TAD) of Nrf2 (NES_{T_A}) [Li et al., 2006]. Similarly, the recruitment of cofactors such as CBP to the TAD could also possibly disable the NES_{T_A}. In addition, the NES_{T_A} contains a cysteine residue (C183), and mutation of this cysteine to alanine handicapped the exporting of Nrf2 from the nucleus. Recently two novel NLSs were identified in murine Nrf2, one is located in the Neh2 and the other one near the C-terminal [Theodore et al., 2008]. Once again, the N-terminal NLS is close to the Keap1-binding DLG and ETGE motifs, providing further complexity in the regulation of Nrf2/Keap1 nuclear-cytoplasmic trafficking.

The activity of NES and NLS can be regulated by phosphorylation events. Indeed, most of the kinases that modulate Nrf2/ARE signaling have been shown to regulate the localization of Nrf2. Actually, almost all of the identified phosphorylation sites/domains of Nrf2 by kinases are proximal to a NES or NLS: the PKC phosphorylation site S40 is close to the N-terminal NLS; the Fyn phosphorylation site Y568 is close to the NESzip; CK2 phosphorylates the TAD, which is nearby the NES_{T_A}. Overall, the cellular distribution of Nrf2 is determined by a delicate balance between all these NESs and NLSs. Generally, plant phenolic compounds regulate this balance by modulating the binding with Keap1, small Mafs and cofactors, and the posttranslational modifications such as phosphorylation or sulfhydryl modification of Nrf2.

MODULATION OF NRF2/ARE SIGNALING: TRANSACTIVATION AND TRANSCRIPTIONAL FEEDBACK

After translocation into the nucleus, Nrf2 would need to form a heterodimer with small Maf proteins or other bZIP proteins to bind to the ARE and then recruit necessary co-activators such as the nuclear coactivator CBP (CREB-binding protein) to activate ARE-mediated transcription [Tong et al., 2006]. The role of small Mafs in Nrf2/ARE signaling has been controversial since overexpression of small Maf proteins, MafG or MafK, inhibited ARE-mediated transcriptional activation [Nguyen et al., T 2000; Dhakshinamoorthy and Jaiswal, 2000]. On the other hand, the induction of a wide range of

ARE-dependent genes was abolished in mafG::mafF::mafK triple mutant fibroblasts [Katsuoka et al., 2005]. However the controversy was reconciled by the finding that homodimers of small Mafs could also bind to ARE but lack transactivation domain, and only Nrf2/small Maf heterodimers could activate ARE. Thus overexpressed small Mafs form homodimers to inhibit ARE, while small Mafs are necessary for Nrf2-mediated ARE activation [Motohashi et al., 2000]. Once bound to ARE, the Nrf2/small Maf heterodimer will recruit CBP through Neh4 and Neh5 to activate transcription. Interestingly, CBP could also be phosphorylated by MAPKs and synergistically activate Nrf2/ARE signaling with ERK cascade [Shen et al., 2004]. In addition, some other coactivators or co-repressors including ATF3 [Brown et al., 2008], ATF4 [He et al., 2001], RAC3 [Lin et al., 2006], SMRT [Ki et al., 2005], MOZ [Ohta et al., 2007], and BRG1 [Zhang et al., 2006] have been reported to interact with Nrf2 and modulate Nrf2/ARE signaling. It is intriguing that curcumin is known to activate Nrf2/ARE signaling; however, curcumin has been identified as a specific inhibitor of CBP [Balasubramanyam et al., 2004]. Obviously, this level of regulation of Nrf2/ARE signaling is extremely complicated due to the integration of many upstream signals.

Additionally, Nrf2/ARE signaling is also regulated by several feedback loops. Though Nrf2/ARE signaling is mainly regulated at the posttranscriptional level, the expression of Nrf2 was increased in certain cases. Two ARE-like sequences were identified in the proximal promoter region of Nrf2, and the transcriptional activity of the promoter could be increased by enzyme inducer or by overexpression of Nrf2 (99). Furthermore, Nrf2 could bind to its own promoter. Thus Nrf2 was suggested to autoregulate its own expression through an ARE-like sequence in its promoter. In the same way, a functional ARE was identified in the reverse strand of the proximal promoter of Keap1 [Lee et al., 2007]. Treatment with t-BHQ activated Nrf2/ARE signaling and also increased the expression of Keap1. The increased Keap1 subsequently directs Nrf2 to degradation and terminates Nrf2/ARE signaling. Moreover, tandem AREs were found in the proximal promoter of the PSMB5 subunit of the 26S proteasome [Kwak et al., 2003]. The expression of 26S proteasome could be up-regulated by enzyme inducers and by overexpression of Nrf2, while disruption of Nrf2 diminished this induction. In support of this, the proteasome subunits have been found to be Nrf2-dependently regulated by curcumin in gene expression profiling experiment [Shen et al., 2006]. Besides protection against oxidative stresses, the enhanced expression of proteasome could also affect the degradation of Nrf2.

CONCLUSIONS

Plant phenolic compounds exhibit a plethora of health effects, and protection of cells against electrophilic/oxidative stresses is a major mechanism underlying those health effects. Plant phenolic compounds have been regarded as

direct antioxidants for a long time; however, their capability to induce cytoprotective enzymes is gaining more and more attention. The expression of cytoprotective enzymes is mainly regulated by Nrf2/ARE signaling. In this chapter we discussed the modulation of cytoprotective enzymes and Nrf2/ARE signaling by plant phenolic compounds with curcumin as an example. The modulation of cytoprotective enzymes by plant phenolic compounds occurs at multiple levels, and the overall scenario is summarized in Figure 17.3. Most of the observations were made using t-BHQ or curcumin as prototypical phenolic compounds; however, it is plausible to assume that these mechanisms also apply to many other phenolic compounds.

Nrf2/ARE signaling is mainly regulated posttranslationally. In almost all systems, Keap1 serves as the primary sensor of electrophiles/oxidants or enzyme inducers, and is the most important regulator of Nrf2/ARE signaling. Under basal condition, Keap1 dimer binds Nrf2 and bridges Nrf2 to ubiquitination by a Cul3-E3 ligase complex, thus directing Nrf2 to proteasome-dependent degradation. Keap1 possesses several specific reactive cysteines that

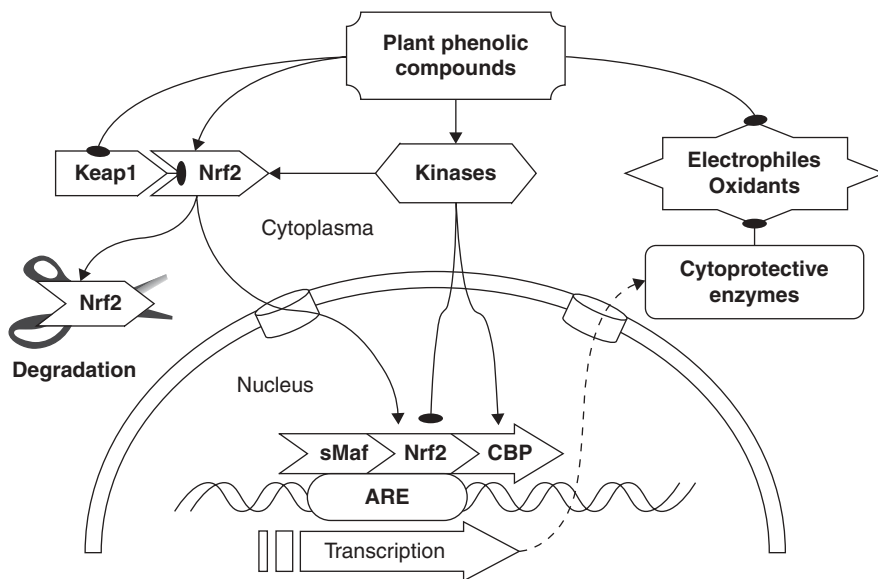


Figure 17.3 Cytoprotective functions of plant phenolic compounds: direct antioxidant activity and modulation of cytoprotective enzymes through Nrf2/ARE signaling. Plant phenolic compounds can directly function as antioxidants to scavenge electrophiles and oxidants. More importantly, plant phenolic compounds regulate the expression of cytoprotective enzymes through modulation of Nrf2/ARE signaling at multiple levels. Plant phenolic compounds can directly modify Keap1 or Nrf2, leading to the stabilization and translocation of Nrf2. A variety of kinases can be modulated by plant phenolic compounds, then phosphorylate Nrf2 or coactivators such as CBP to regulate the stability, localization, and transactivation of Nrf2.

can be modified by electrophiles/oxidants. In agreement with the pivotal role of Keap1, the inducer activity of plant phenolics and synthetic analogs are correlated with their reactivity with sulfhydryl groups and Keap1. The modification of specific cysteines in Keap1 alters the conformation of Keap1, leading to termination of Nrf2 ubiquitination and possibly release of Nrf2. The subcellular localization of Nrf2 is determined by the balance between multiple NES/NLS, and this balance is regulated by the interaction of Nrf2 with its binding partners such as Keap1 and small Mafs and post-translational modification of Nrf2. Once translocated into the nucleus, Nrf2 dimerizes with small Mafs, binds to ARE and recruits coactivators to activate transcription of cytoprotective enzyme genes. Nrf2 itself can be phosphorylated by a variety of kinases including PKC, MAPKs, PERK, GSK-3 β , Fyn kinase, and CK2. In addition, two cysteines in Nrf2 could also be modified. These modifications regulate Nrf2/ARE signaling by disrupting Keap1 binding, changing subcellular distribution, increasing stability, and promoting transactivation of Nrf2. Unlike the ubiquitous regulation by Keap1, these modifications provide compound- and gene-specific and possibly cell type- or tissue-dependent modulation of Nrf2/ARE signaling.

ACKNOWLEDGMENT

The authors thank the members of Kong Lab for insightful discussions. This work was supported by National Institutes of Health Grant R01 CA118947 (to A.-N. T. K.).

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18 Phenolics in Aging and Neurodegenerative Disorders

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PHYTOCHEMICALS AND NEURODEGENERATIVE DISEASES

Phytochemicals are bioactive chemicals derived from plants, including flavonoids, carotenoids, and vitamins, that exert multiple beneficial effects on health. Epidemiological studies strongly indicate that fruits and vegetables are protective against several diseases, particularly cardiovascular disease, cancer, and neurodegeneration. Special interest has been assigned to the therapeutic role of natural antioxidants, such as phytochemicals, present in medicinal and dietary plants, which might help prevent oxidative damage [Halliwell, 1999; Youdim et al., 2002]. In situations of increased reactive oxygen species (ROS) generation, such as the aging process, the supplementation of endogenous antioxidants via intake of dietary antioxidants may be of particular importance in slowing the accumulation of oxidatively damaged molecules.

Numerous *in vitro* studies have implicated ROS in neuronal death [Leonardi and Mytilineou, 1998], and different markers of oxidative stress are found in postmortem examination of brain tissues from patients with neurodegenerative disorders [Sayre et al., 2001]. DNA oxidation, protein oxidation, and lipid peroxidation have been reported in brain regions containing neurofibrillary tangles and senile plaques from Alzheimer's disease (AD) patients [Lovell and Markesbery, 2007; Polidori et al., 2007]. Dopaminergic neurons in the substantia nigra of brains of Parkinson's disease (PD) patients also exhibit hallmarks of oxidative stress [Giasson et al., 2002].

The oxidative stress hypothesis for neurodegeneration postulates that cumulative oxidative damage over time explains the late-life onset and the slowly progressive nature of neurodegenerative disorders [Kregel and Zhang, 2007]. The central nervous system (CNS) is especially vulnerable to free-radical damage as a result of its high oxygen consumption rate, its abundant lipid content, and the low levels of antioxidant enzymes compared with other tissues [Sultana et al., 2006b]. These age-related effects, associated with genetic and environmental risk factors, may provide a merging mechanism for the high incidence of neurodegenerative disorders in the elderly.

In line with these evidences, particular attention has been paid to studying the neuroprotective properties of antioxidants, iron chelating and anti-inflammatory agents with particular regard to polyphenols [Mandel et al., 2006b]. Numerous studies have shown that polyphenols have *in vitro* and *in vivo* activities in preventing and/or reducing the extent of free-radical-induced oxidative damage in different models of neurodegeneration [Mandel and Youdim, 2004; Pan et al., 2003; Scalbert et al., 2005]. The molecular mechanisms for neuroprotection do not merely rely on a direct radical scavenging activity but also polyphenols may function at several cellular levels, including direct interaction and modulation of enzymatic activities and the regulation of signaling pathways with implications for cell survival and death [Ishige et al., 2001; Pan et al., 2000; Dinkova-Kostova and Talalay, 2008]. Epidemiological studies indicated that moderate consumption of wine could be associated with a

lower incidence of AD. Resveratrol (Fig.18.1), a polyphenol that occurs in abundance in red grapes and is present mostly in red wines, exerts antioxidant and neuroprotective properties and therefore contributes to the potential beneficial effect of wine consumption on the neurodegenerative process (Ates et al., 2007).

Curcumin (Fig.18.1), a polyphenol found in the curry spice turmeric, was shown to possess many therapeutic properties including anti-inflammatory [Biswas and Rahman, 2008] and anticancer activities [Choi et al., 2008]. It is currently receiving strong attention due to its antioxidant potential as well as its relatively low toxicity to rodents. In addition to being an exceedingly potent direct antioxidant, curcumin is also an indirect antioxidant, that is, it induces the gene expression of cytoprotective (phase 2) proteins [Dinkova-Kostova and Talalay, 1999; Dinkova-Kostova, 2002]. This indirect antioxidant activity is due to the presence of the electrophilic centers on its molecule that can undergo Michael addition reactions with sulfhydryl groups. Indeed, tetrahydrocurcumin, which lacks these electrophilic centers, is a much weaker inducer [Dinkova-Kostova and Talalay, 1999]. Using model compounds, it was shown that Michael acceptors related to curcumin chemically modify certain highly reactive sulfhydryl groups of the intracellular sensor for inducers, Keap1 [Dinkova-Kostova et al., 2002]. Consequently, Keap1 loses its ability to repress transcription factor Nrf2, which then undergoes nuclear translocation and (as heterodimer with a small Maf protein) binds to the antioxidant response element (ARE) and activates transcription of cytoprotective (phase 2) genes [Dinkova-Kostova et al., 2005].

In light of the antioxidant, anti-inflammatory, and antiamyloid effects, curcumin has become a candidate compound for the prevention or treatment of AD [Calabrese et al., 2007]. Treatment of astrocytes with curcumin induced the cytoprotective proteins HO-1, NAD(P)H:quinone oxidoreductase 1 (NQO1), and glutathione transferase (GST) and provided protection against

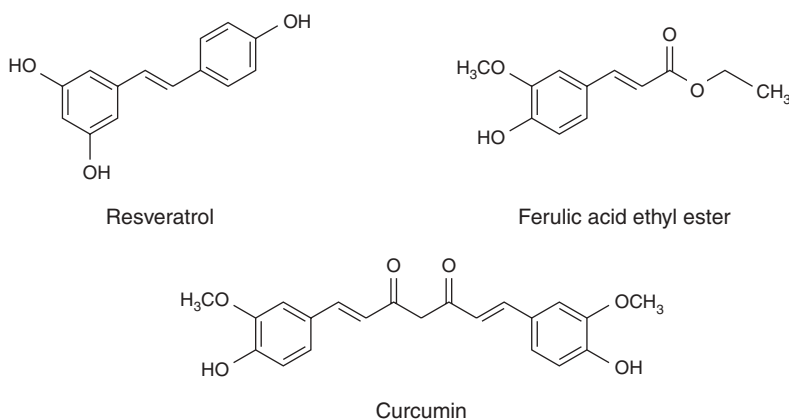


Figure 18.1 Chemical structures of phenolic compounds with neuroprotective activity.

subsequent glucose oxidase-mediated oxidative damage [Scapagnini et al., 2006]. Lim and co-workers [2001] studied the effects of curcumin in transgenic mice, which carry a human mutation in the amyloid precursor protein (APP^{sw}) that causes AD pathology. They found decreased cerebral levels of oxidized proteins, decreased levels of interleukin-1b (IL-1b) and reduced levels of soluble and insoluble A β . Subsequently, it was shown that curcumin crossed the blood–brain barrier, bound to amyloid plaques, and reduced amyloid levels and plaque burden [Yang et al., 2005]. In contrast to curcumin, tetrahydrocurcumin, which lacks the central electrophilic centers required for induction of cytoprotective (phase 2) proteins, did not reduce plaque deposition or protein oxidation, although it decreased neuroinflammation and soluble A β [Begum et al., 2008]. Further studies are needed to test the potential therapeutic use of curcumin in the treatment or prevention of AD in humans.

Green tea, another food high in polyphenols, may also be neuroprotective. The effects of acute and chronic administration of the green tea polyphenol (–)-epigallocatechin-3-gallate (EGCG) in various cellular and animal models of PD and AD revealed various novel molecular targets including the extracellular mitogen-activated protein kinases (MAPK), protein kinase C (PKC), antioxidant enzymes, and survival genes and proteins associated with mitochondrial function, such as Bcl-2 family members [Kalfon et al., 2007; Mandel et al., 2006a]. Recently, Weinreb et al. [2007] showed by a proteomic analysis that EGCG treatment on SHSY5Y, after serum starvation, affected the expression levels of diverse proteins, including proteins related to cytoskeletal components, metabolism, heat shock, and binding proteins [Weinreb et al., 2007].

FERULIC ACID ETHYL ESTER

In search of novel natural antioxidant compounds that might possess a good brain bioavailability, our laboratory has focused attention on the phenolic compound ferulic acid ethyl ester (FAEE) (Fig. 18.1). Ferulic acid is a ubiquitous plant constituent that occurs primarily in seeds and leaves both in its free form and covalently linked to lignin and other biopolymers. Due to its phenolic nucleus and an extended side chain conjugation, it readily forms a resonance stabilized phenoxy radical that accounts for its potent antioxidant potential [Kanski et al., 2002; Kikuzaki et al., 2002]. Ferulic acid has been shown to be protective against oxidative stress *in vitro*; it is absorbed and excreted by humans, and may be a promising candidate for therapeutic intervention in AD [Yan et al., 2001]. Although ferulic acid has been demonstrated to be effective *in vitro*, the low lipophilicity impairs its *in vivo* efficiency, bioavailability, and stability.

In addition to their direct antioxidant activity, ferulic acid and its ester derivatives have also been shown to act as indirect antioxidants, that is, to induce cytoprotective (phase 2) enzymes [Dinkova-Kostova et al., 1998; Dinkova-Kostova, 2002]. Similarly to curcumin, ferulic acid derivatives also

contain Michael acceptor functionalities and have been shown to react with sulfhydryl groups [Dinkova-Kostova et al., 2001]. FAEE, a naturally occurring ester derivative of ferulic acid, is a trace constituent of various plants [Clifford et al., 2007]. Due to its high lipophilicity, FAEE has been shown to present better scavenging properties toward both hydroxyl radicals and superoxide anions in comparison with the corresponding acid form [Scapagnini et al., 2004]. In addition to the radical scavenging activity of an antioxidant, both its polarity and its three-dimensional interaction with lipid bilayers may contribute to strengthen its antioxidant potential. Since synaptic membranes are particularly vulnerable to oxidative stress and are a selective target of A β -mediated neurotoxicity, the affinity of FAEE with lipid substrates (because of its high lipophilicity) may result in higher protective effects. Considering the increased lipophilicity of FAEE, Butterfield et al. showed in *in vitro* or *ex vivo* studies the decreased protein oxidation and lipid peroxidation, decreased free-radical formation, decreased 3-NT formation, improved morphology and elevated mitochondrial function in primary neuronal cultures treated with A β (1-42) [Sultana et al., 2005] and on synaptosomes isolated from FAEE-treated rodents and subsequently treated with A β (1-42) [Perluigi et al., 2006b] or with Fe²⁺/H₂O₂ (hydroxyl radical formation), and AAPH (alkoxyl and peroxy radical formation) [Joshi et al., 2006].

The mechanistic basis of the neuroprotective activity of FAEE appears to rely not only on its general free-radical trapping or antioxidant activity *per se*, but also on its activity in mediating the induction of stress response proteins (HO-1 and HSP72), cytoprotective (phase 2) proteins, and the parallel suppression of genes induced by pro-inflammatory cytokines, such as nitric oxide synthase (iNOS).

In summary, FAEE protects neuronal cells and synaptosomes against oxidative stress and neurotoxicity as shown by a number of oxidative stress markers. We hypothesize a multifaceted mechanism by which FAEE offers neuroprotection on *in vitro* models of AD:

- FAEE is a potent free-radical scavenger that significantly attenuates ROS production, protein oxidation, and lipid peroxidation.
- FAEE is also neuroprotective by leading to elevated levels of stress response proteins, such as HO-1 and HSP72.
- FAEE modulates neuroinflammatory processes mediated by iNOS.

Further studies are required to gain insight into the potential therapeutic use of FAEE in the treatment of AD and other oxidative stress-related disorders. In this effort, Butterfield and co-workers [2006b] have used redox proteomics approach to identify selective targets of oxidative damage in different human and animal models of neurodegenerative diseases. Furthermore, redox proteomics may help to elucidate the potential therapeutic use of phenolics and other phytochemicals for prevention and treatment of neurodegeneration.

REDOX PROTEOMICS

In the postgenome era, proteomics has attracted much more attention due to its potential in understanding biological functions and structures at the protein level. The increased possibility of screening using proteomic techniques provides more comprehensive overview of the interaction of proteins, the interplay among processes, and the context in which a specific molecule or pathway may be operating in the mechanism of action of different antioxidants.

“Proteome” derives from the combination of the terms proteins and genome and defines “the PROTEin complement expressed by a genOME” [Wilkins et al., 1996]. Proteomic analysis (Fig. 18.2) employs: (i) systematic separation of proteins from complex mixture, (ii) protein identification, (iii) protein quantitation, and (iv) structural and functional information of identified proteins. Two-dimensional polyacrylamide gel electrophoresis (2D PAGE) [O’Farrell, 1975] is currently the most powerful protein separation method for the resolution of complex mixtures of proteins, permitting the simultaneous analysis of thousands of gene products. Proteins are separated according to their charge (pI) by isoelectric focusing (IEF) in the first dimension and according to their size (Mr) by SDS-PAGE in the second dimension. The introduction of immobilized pH gradients (IPG) for IEF has overcome the problems of pH gradient instability (caused by prolonged focusing time). IPGs allow the generation of pH gradients of any desired range (broad, narrow, or ultra-narrow) between pH 3 and 12. In addition, the use of pH gradient allowed high reproducibility and large-scale separations. However, some limitations still remain to be solved, including solubilization of membrane proteins, identification of low-abundance proteins, and identification of highly hydrophobic proteins. The protein maps allow comparison of different sets of samples in terms of profiling of isoforms, splice variants, mutants, and posttranslationally modified species, and the definition of protein–protein interactions, and the like, using a computer-assisted program. Each spot on the resulting two-dimensional gel corresponds to a single protein species in the sample [Tilleman et al., 2002]. Thousands of different proteins can thus be separated, and information such as the protein pI, the apparent molecular weight, and the amount of each protein is obtained. 2D-PAGE represents undoubtedly one of the most-used techniques for protein separation, but non-SDS-PAGE methods are also employed. Two-dimensional high-pressure liquid chromatography (2D-HPLC) achieves separation of a protein mixture by eluting the sample through a series of columns with a coupled MS analysis [Wagner et al., 2003]. Alternatively, an expression profiling can also be obtained by labeling at cysteine residues with light and heavy, respectively, tags carrying a biotin moiety. The labeled proteins are then mixed and digested and the resulting isotopic labeling is analyzed by a mass spectrometer. This technique is referred as isotopically coded affinity tags (ICAT) [Smolka et al., 2001]. However, a number of limitations to the ICAT technique has been noted in the literature, including missed identification of proteins with few or no cysteine residue, lost information for posttranslational

modifications, differential reversed-phase elution of identical peptides labeled with the hydrogen/deuterium isotope pairs, and complicated interpretation of tandem mass spectrometry (MS/MS) spectra due to the addition of the biotin group.

The protein posttranslational modifications (PTMs) play a crucial role in modifying the end product of expression and contribute towards biological processes and diseased conditions. Important posttranslational modifications include phosphorylation, acetylation, glycosylation, ubiquitination, and nitration [Mann and Jensen, 2003]. The analysis of posttranslational modifications on a proteome scale is still considered an analytical challenge [Zhou et al., 2001] because of the extremely low abundance of modified proteins among very complex proteome samples.

Among several types of posttranslational protein modifications, phosphorylation and oxidative modifications play essential roles in the regulation of a variety of cell functions. Increasing evidence suggests that changes in protein modifications over time correlate with particular phenotypes and disease states. Reactions of free radicals and ROS and reactive nitrogen species with proteins lead to oxidative modifications such as formation of protein hydroperoxides, hydroxylation of aromatic groups and aliphatic amino acid side chains, nitration of aromatic amino acid residues, oxidation of sulfhydryl groups, oxidation of methionine residues, conversion of some amino acid residues into carbonyl groups, cleavage of the polypeptide chain and formation of cross-linking bonds. If oxidized proteins are not appropriately repaired or removed from cells, they are often toxic and can threaten cell viability [Berlett and Stadtman, 1997]. Numerous studies demonstrated the harmful effects of irreversible oxidative PTM as a result of oxidative stress and increased levels of oxidatively modified proteins have been shown to correlate with aging [Chakravarti and Chakravarti, 2007]. Oxidative modifications of proteins lead to loss of their function, enzymatic activity, accumulation, and inhibition of their degradation. All these metabolic dysfunctions have been observed in several human degenerative diseases such as cancer [Valko et al., 2006] and neurodegeneration [Butterfield et al., 2006a]. Based on these findings, growing interest is currently given to better understand selective protein target of oxidative damage. Recently, redox proteomics approach has been employed to identify posttranslational modification of proteins caused by oxidative damage. Protein oxidation results by the covalent modification induced by ROS or by-products of oxidative stress. Among general types of protein modifications, we focused our attention on protein carbonyls, lipid peroxidation adducts [4-hydroxynonenal (HNE)-adducts], glutathionylation, and nitration of tyrosine residues. Redox proteomics coupled 2D-PAGE with immunochemical detection of protein carbonyl derivatized by 2,4-dinitrophenylhydrazine (DNPH), nitrated proteins indexed by 3-nitrotyrosine (3-NT), glutathionylated proteins (GSH-bound proteins) and HNE-bound proteins followed by MS analysis.

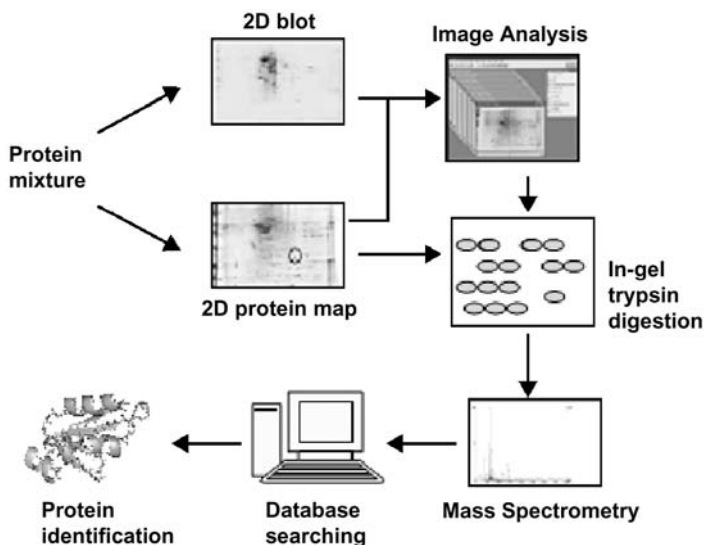


Figure 18.2 Redox proteomics and oxidatively modified proteins in the brain. Redox proteomics has the potential of detecting disease markers and identifying potential targets for drug therapy in neurodegenerative disorders. Redox proteomics involves the separation of brain proteins followed by detection, usually immunochemically, of oxidatively modified proteins, either from a two-dimensional western blot or from column eluents. Subsequent mass spectrometric analysis of tryptic digests and database searching leads to protein identification.

A 2D western blot map is achieved by using specific antibodies, for example, anti-DNP, anti-3-NT, anti-GSH, or anti-HNE, which react with those proteins containing reactive carbonyl groups/3-NT/GSH/HNE. 2D gel images are used to obtain the protein expression profile, and the 2D western blots are analyzed by image software (PD Quest, BioRad). This sophisticated software offers powerful comparative analysis and is specifically designed to analyze many gels or blots at once that were performed under identical experimental conditions. Powerful automatching algorithms quickly and accurately match gels or blots and sophisticated statistical analysis tools identify experimentally significant spots. The principles of measuring intensity values by 2D analysis software are similar to those of densitometric measurements. After completion of spot matching, the normalized intensity of each protein spot from individual gels (or membranes) is compared between groups using statistical analysis [Butterfield et al., 2006b].

Sultana et al. [2006a] employed this experimental approach to investigate the protective effect of the xanthate D609 against amyloid $\beta(1-42)$ -induced oxidative modification of neuronal proteins. Pretreatment of primary neuronal cultures with D609 prior to amyloid $\beta(1-42)$ prevented the oxidation of glyceraldehyde-3-phosphate dehydrogenase, pyruvate kinase, malate dehydrogenase, and 14-3-3 zeta as shown in the cells treated with amyloid $\beta(1-42)$

alone. The information obtained from redox proteomics studies may be helpful in understanding the molecular mechanisms involved in the development and progression of AD disease as well as of other neurodegenerative disorders.

NEURODEGENERATION AND LIPID OXIDATION: ISOPROSTANES

Increasing evidences indicate that ROS-mediated reactions, particularly of neuronal lipids, are extensive in brain areas directly involved in the neurodegenerative process [Andersen, 2004; Christen, 2000]. In recent years, numerous studies investigated the functional importance of oxidative imbalance as a crucial event in mediating the pathogenesis of several neurodegenerative disorders such as AD, PD, amyotrophic lateral sclerosis (ALS), and prion disease [Andersen, 2004; Butterfield et al., 2006b; Moreira et al., 2005]. The availability of specific and sensitive markers to monitor *in vivo* oxidative stress, in combination with studies performed in living patients, are helping to elucidate these issues.

Lipid peroxidation is one of the major sources of free-radical mediated injury that directly damages membranes and generates a number of secondary products. In particular, markers of lipid peroxidation have been found to be elevated in brain tissues and body fluids in several neurodegenerative diseases, and the role of lipid peroxidation has been extensively discussed in the context of their pathogenesis. Peroxidation of membrane lipids can have numerous effects, including increased membrane rigidity, decreased activity of membrane-bound enzymes (e.g., sodium pumps), altered activity of membrane receptors, and altered permeability [Anzai et al., 1999; Yehuda et al., 2002]. In addition to effects on phospholipids, lipid-initiated radicals can also directly attack membrane proteins and induce lipid–lipid, lipid–protein, and protein–protein cross-linking, all of which obviously have effects on membrane function.

Malondialdehyde (MDA), HNE, and acrolein represent the major products of lipid peroxidation [Esterbauer et al., 1991]. In addition, lipid hydroperoxyl radicals undergo endocyclization to produce fatty acid esters; two classes of these cyclized fatty acids are isoprostanes and neuroprostanes. Isoprostanes (IsoPs) are products of arachidonic acid (AA) metabolism of potential relevance to human neurodegenerative diseases [Greco et al., 2000]. They are produced *in vivo* by free-radical-induced peroxidation of esterified AA in membrane phospholipids, independently of cyclooxygenase enzymes. F₂-isoprostanes (F₂-IsoPs) are the stable products of free-radical damage to AA. However, F₂-isoprostane analogs may be formed by peroxidation of other polyunsaturated fatty acid substrates, such as eicosapentaenoic acid, which produces F₃-isoprostanes, and docosahexaenoic acid, which generates F₄-isoprostanes. The latter compounds are also termed neuroprostanes, due to the high levels in the brain (Roberts et al., 1998). In contrast to cyclooxygenase-derived prostaglandins, nonenzymatic generation of isoprostanes favors the

formation of compounds in which the stereochemistry of the side chains is oriented *cis* in relation to the prostane ring. Molecular modeling of isoprostane containing phospholipids shows that they are remarkably distorted, nonflexible molecules. Therefore, the presence of isoprostanes can compromise membrane integrity and fluidity.

After their cleavage, probably by phospholipases, F₂-IsoPs and F₄-IsoPs are released in free form and may participate, due to their biological activity, as mediators of the oxidant injury. Measurement of F₂-IsoPs is one of the most reliable approaches to assess oxidative stress status *in vivo*, providing an important tool to explore the role of oxidative stress in the pathogenesis of human neurodegenerative diseases [Pratico et al., 1998]. Moreover, F₂-IsoPs and other products of the IsoP pathway exert potent biological actions both via receptor-dependent and independent mechanisms and therefore may be pathophysiological mediators of disease. The measurement of IsoP levels in the cerebrospinal fluid (CSF) reflects the metabolic activity of the brain and therefore may provide a unique opportunity to reveal the occurrence of oxidative stress and lipid peroxidation in the living brain.

Isoprostanes have been successfully utilized to investigate the occurrence of oxidative stress in some neurological diseases such as AD [Montine et al., 2007; Pratico et al., 1998], multiple sclerosis [Volpe et al., 2006], and Huntington's disease [Montine et al., 1999].

F₂-IsoP concentration is selectively increased in diseased regions of brain from patients who died from advanced AD, where pathologic changes include amyloid A β -peptide deposition, neurofibrillary tangle formation, and extensive neuron death [Montine et al., 2002]. There is broad agreement that increased CSF levels of F₂-IsoPs also are present in patients with early AD. It has been recently shown that subjects with MCI (mild cognitive impairment) have plasma, urine, and CSF levels of F₂-IsoPs higher than healthy subjects [Pratico et al., 2002]. It has been suggested that measurement of IsoP may identify a subgroup of patients with MCI with elevated lipid peroxidation who are at increased risk to progress to symptomatic AD [Markesbery et al., 2005].

In addition, the contribution of oxidative stress to the pathogenesis of Huntington's disease has been studied by measuring the levels of F₂-IsoPs in the CSF of 20 patients in the early phase of the disease [Montine et al., 1999]. F₂-IsoP concentration was moderately but significantly higher in Huntington's disease patients than in the control group. Current data available on CSF levels of IsoPs in different neurodegenerative disorders proved the usefulness of these markers in the understanding of the role of oxidative damage in neurological diseases.

However, it is unexplored if they might mediate the functional consequences of the lipid peroxidation process, and further studies are needed to investigate their biological impact and to better understand the role of F₂-IsoPs in brain diseases. Growing interest is currently given to the possible exploitation of F₂-IsoP determinations in biological fluids, in particular in the CSF, for clinical purposes. The attraction of urinary IsoPs is that they might serve as

noninvasively acquired biomarkers, which could guide the selection of patients and dosing for trials of antioxidants as well as the timing of dosing. This may prove particularly useful in a disease, such as AD, in which the rate of progression varies markedly between individuals.

GLUTATHIONE AND REDOX HOMEOSTASIS

Glutathione (GSH) is the most abundant nonprotein thiol of the cell that performs various functions ranging from cellular metabolism to transport as well as protection against free radicals and ROS. The antioxidant function of GSH is related to oxidation of the thiol group of its cysteine residue with formation of GSSG, which is catalytically reduced back to the thiol form (GSH) by glutathione reductase. In addition, GSH provides reducing equivalent for enzymes involved in the metabolism of ROS, eliminates potentially toxic oxidation products and reduces oxidized protein thiols. Increased ROS production causes an imbalance between GSH and its corresponding disulfide (GSSG) shifting the GSH/GSSG redox toward the oxidizing state [GSH/GSSG ratio from 100 (normal redox balance) to 10 or even 1] associated with protein mixed disulfide formation [Klatt and Lamas, 2000]. As well as forming disulfides itself, GSH can also form mixed disulfides with cysteines on proteins, a process that is termed *S*-glutathionylation. This covalent modification is a posttranslational modification of proteins that occurs in cells exposed to oxidative stress that can be reversed by enzymatic systems, such as glutaredoxins (Shelton et al., 2005). Indeed, protein thiol groups are highly susceptible to oxidative modifications and they can be reversibly oxidized to sulfenic acid ($-\text{SOH}$) or irreversibly oxidized to sulfinic ($-\text{SO}_2\text{H}$) and sulfonic ($-\text{SO}_3\text{H}$) acid [Chang et al., 2004]. Protein-mixed disulfide formation could potentially serve as protection from irreversible, more dangerous oxidation of cysteine residues [Souza and Radi, 1998]. Accumulating evidence suggests that this mechanism plays a role in regulating protein function in addition to ensure a physiologic reducing microenvironment to the cell. Indeed, protein *S*-glutathionylation is not only a cellular response to oxidative damage but it occurs under normal conditions to regulate protein function at several levels. Growing knowledge in this area now proposes that *S*-glutathionylation may serve to transduce oxidative stimuli into a functional response at various levels of cellular signaling. Increasing evidences suggest that protein *S*-glutathionylation, being characterized by sensitivity, specificity, and reversibility, might be a common mechanism for the global regulation of protein functions in different cellular types [Giustarini et al., 2004; Klatt and Lamas, 2000]. Under conditions of oxidative/nitrosative stress, cysteine residues within proteins are primary targets for oxidation. The presence of millimolar levels of GSH within the cell helps to maintain the equilibrium favorable for the formation of possible glutathionylation precursors. Glutathionylation can be protective, preventing the sequential oxidation of thiol groups to sulfonic acid, a product that leads to inevitable proteosomal degradation controlling cellular

response to changes in redox conditions [Shackelford et al., 2005]. In addition, glutathionylation has been shown to regulate the structure/function of a quite diverse range of cellular proteins. As such, reversibility of glutathionylation provides a viable switch of some importance in controlling cellular response to changes in redox conditions [Chrestensen et al., 2000].

Redox regulation is rapidly evolving as an important metabolic modulator of cellular functions of all living cells and organisms and is being increasingly implicated in many chronic inflammatory and degenerative diseases [Gallogly and Mieczal, 2007]. The cellular redox state is a crucial mediator of multiple metabolic, signaling, and transcriptional processes in cells, and protein thiols in the form of cysteine residues are key players in redox sensing and regulation. Redox alterations of several protein and enzymes have been identified in a wide variety of conditions, and the purpose of such regulation has been speculated in the cellular defense mechanism during oxidative stress. Intracellular redox status has been linked to cellular differentiation, immune response, growth control, tumor progression, and apoptosis. Oxidants and antioxidants can act as signaling molecules that modify the function of enzymes such as phosphatases and kinases and directly or indirectly affect the activity of many transcription factors. Many proteins and enzymes such as *S*-transferases, glyceraldehyde 3-*P*-dehydrogenase, glutathione reductase, thioredoxin/glutaredoxin, and peptidases such as papain, caspase, and calpain in a cell consist of cysteine residues that have a sulfhydryl group in their side chain and the proton is labile, which makes it a chemical hot spot for a wide variety of biochemical interactions. Covalent modifications of proteins at their cysteines may be critical to a particular function of a given protein. Protein sulfhydryls may be oxidatively modified by *S*-thiolation and *S*-nitrosylation, which may significantly modify various cellular processes [Ghezzi et al., 2005]. Both *S*-thiolation and *S*-nitrosation are usually reversible and may be a protective/adaptive strategy of a cell. Exchange between thiols and disulfides are very slow and must be catalyzed by enzymes such as glutaredoxin or other protein disulfide isomerases that have a thioredoxin-like structural motif. Such disulfide exchange is a potential signaling mechanism due to its capacity for modifying cysteine residues in enzymes [Das, 2005].

Dethiolation of *S*-glutathionylated proteins can be achieved by either nonenzymatic reduction or enzymatic cleavage of the disulfide bond involving the action of thioredoxin, glutaredoxin, and/or protein disulfide isomerase [Johansson et al., 2004]. Thus, it is possible to speculate that enzymatically controlled thiolation/dethiolation may confer specificity and regulatory potential on the posttranslational control of protein function by *S*-glutathiolation. Thioredoxins, peroxiredoxins, glutaredoxins, in addition to the general antioxidants of the cells form a powerful combination not only to prevent irreversible damage to crucial proteins but also take part in redox recycling of oxidized thiol molecules [Michelet et al., 2006]. Thus protein function modulation by *S*-glutathiolation and/or *S*-nitrosation spans a wide variety of cellular functions ranging from resistance to oxidative stress, phosphorylation-dependent signal transduction, posttranslational protein modification, and clearance via

proteasomes to transcriptional activation and inhibition [Giustarini et al., 2005]. Many proteins can undergo glutathionylation under oxidative stress [Cotgreave and Gerdes, 1998; Klatt and Lamas, 2000]. Glyceraldehyde-3-phosphate dehydrogenase is the major *S*-glutathionylated protein in endothelial cells exposed to hydrogen peroxide and in monocytes during the endogenous oxidative burst [Ravichandran et al., 1994]. Creatine kinase and glycogen phosphorylase *b* are also targets for *S*-glutathionylation in myocytes and cardiac tissue during cyclic oxidative stress. Carbonic anhydrase III, glutathione *S*-transferase, superoxide dismutase, and hemoglobin become thiolated in cellular models of oxidative stress. Additional proteins, including fatty-acid synthase, 3-hydroxy-3-methylglutaryl-CoA reductase, aldose reductase, human immunodeficiency virus-1 protease, and small HSP25, have been reported as potential targets in vitro for redox-dependent *S*-glutathionylation [Klatt and Lamas, 2000]. Even *c-Jun* DNA binding appears to be redox-regulated by glutathionylation [Klatt et al., 1999] and dopamine biosynthesis is also inhibited by *S*-glutathionylation during oxidative stress [Borges et al., 2002]. In Parkinson's disease, monoamine oxidase-derived H₂O₂ was shown to inhibit mitochondrial respiration by glutathionylation of respiratory chain enzymes [Cohen et al., 1997]. In addition, some of the proteins found to be glutathionylated belong to the class of cytoskeletal proteins, which are particularly abundant in cells. The supramolecular organization of these proteins depends on the presence of exposed sulfhydryl residues; the modification of these groups by glutathionylation could be relevant to their function, by either protecting them against irreversible oxidation or inhibiting polymerization [Dalle-Donne et al., 2000]. Pastore and co-workers [2003] have demonstrated that actin glutathionylation causes an impairment of microfilaments dynamic in Friedreich's ataxia fibroblasts.

In addition, transcription factors such as NF- κ B, *c-jun*, and AP-1, are potential targets for glutathionylation [Dalle-Donne et al., 2007]. Under oxidative stress conditions, glutathionylation of transcription factors regulate their DNA-binding activity resulting in alteration of gene expression. This inhibitory effect has been proposed to be mediated by the oxidation of a conserved cysteine in the DNA-binding domain through unknown biochemical mechanisms [Pineda-Molina et al., 2001].

Although glutathionylation of proteins is seen in certain cells of nonneural origin, it is more pronounced in brain, presumably because extrusion of GSSG, as routinely observed in other tissues such as lung and liver, is not always seen in brain [Sparaco et al., 2006]. Moreover, the aging process is associated with a pro-oxidizing shift in the cellular redox state. The amounts of the redox-sensitive free aminothiols (glutathione, cysteine, Cys-Gly, and methionine) and protein mixed disulfides has been measured at different ages. GSH/GSSG ratios decreased significantly with increasing age. Concentrations of Cys-Gly increased and methionine decreased with age. The amounts of protein-mixed disulfides, measured as protein-cysteinyl, protein-Cys-Gly and protein-glutathionyl mixed disulfides, increased as a function of age [Giustarini et al., 2006]. The pattern of

changes in free aminothiols content, glutathione-redox state, and protein-mixed disulfides is inversely related to the life expectancy of the flies [Rebrin et al., 2004]. Collectively, these results support the idea that the pro-oxidizing shift in the glutathione redox state, the decrease in methionine content and increase in abundance of protein-mixed disulfides are indicative of enhanced oxidative stress during aging and neurodegenerative disorders [Schulz et al., 2000].

Recent studies have shown increased glutathionylation of specific proteins in AD patients compared with control subjects [Newman et al., 2007]. The exact function of this reversible oxidative modification is unknown. Further studies investigating the specific *in vivo* effects of *S*-glutathionylation in oxidative stress are important to determining the role of *S*-glutathionylation in the AD brain and neurodegenerative disorders.

Glutathione levels in human tissues normally range from 0.1 to 10 mM, most concentrated in the liver (up to 10 mM), while plasma concentration is in the micromolar range. Oxidative stressors that can deplete GSH include ultraviolet and other radiations, viral infections, environmental toxins, heavy metals, inflammation, and dietary deficiencies of GSH precursors and enzyme cofactors. The sulfhydryl (-SH) group on the cysteinyl portion confers a strong electron-donating character. As electrons are lost, the molecule becomes oxidized, and two such molecules become dimerized by a disulfide bridge to form glutathione disulfide or oxidized glutathione (GSSG). This linkage is reversible upon re-reduction. GSH is under tight homeostatic control both intracellularly and extracellularly. A dynamic balance is maintained between GSH synthesis, GSH recycling from GSSG, and GSH utilization. GSH synthesis involves two closely linked, enzymatically controlled reactions that utilize ATP. First cysteine and glutamate are combined, by γ -glutamyl cysteinyl synthetase. Second, GSH synthetase combines γ -glutamylcysteine with glycine to generate GSH. As GSH levels rise, they self-limit further GSH synthesis; otherwise, cysteine availability is usually rate limiting. GSH recycling is catalyzed by glutathione disulfide reductase, which uses reducing equivalents from NADPH to reconvert GSSG to 2GSH. The reducing power of ascorbate helps conserve systemic GSH. GSH is used as a cofactor by multiple peroxidase enzymes, to detoxify peroxides generated from oxygen radical attack on biological molecules, to reduce oxidized centers on DNA, proteins, and other biomolecules, and glutathione *S*-transferases (GST) to conjugate GSH with endogenous substances and to exogenous electrophiles and diverse xenobiotics. Direct attack by free radical and other oxidative agents can also deplete GSH. The homeostatic glutathione redox cycle attempts to keep GSH depleted as it is being consumed [Sen, 1998]. The liver is the largest GSH reservoir. GSH equivalents circulate in the blood predominantly as cystine, the oxidized and more stable form of cysteine. Cells import cystine from the blood, reconvert it to cysteine, and from it synthesize GSH. Conversely, inside the cell GSH helps re-reduce oxidized forms of other antioxidants such as ascorbate and α -tocopherol [Meister, 1994]. GSH is an extremely important cell protecting by directly quenching reactive free radicals and GSH/GSSG balance is crucial to

maintain cellular homeostasis and survival. GSH is the essential cofactor for many enzymes that require thiol-reducing equivalents, and helps keep redox-sensitive active sites on enzymes in the necessary reduced state. Other thiol cell systems—the metallothioneins, thioredoxins, and other redox regulator proteins—are ultimately regulated by GSH levels and the GSH/GSSG redox ratio. Glutathione status is a highly sensitive indicator of cell functionality and viability. In humans, GSH depletion is linked to a number of disease states: As intracellular GSH becomes reduced, the cell functionality is progressively reduced [Meister, 1995].

Glutathione is present in the brain in millimolar concentrations [Dringen, 2000]. Although there are some reports favoring the transport of GSH across the blood–brain barrier and their uptake into brain cells, it still needs to be established whether these play a role in GSH homeostasis in the brain [Kannan et al., 1999]. Nevertheless, the constituent amino acids of GSH may cross the blood–brain barrier and be utilized for GSH synthesis in the brain following the same pathway as described above. Several reports employing different techniques have shown the presence of GSH both in neurons and glial cells [Maybodi et al., 1999], but the concentration of GSH appears to be higher in brain astrocytes compared to neurons. Apart from the antioxidant functions of GSH in the brain, extracellular GSH has been hypothesized to have additional functions as a neurotransmitter [Janaky et al., 1999], neurohormone, in the detoxification of glutamate, and in leukotriene metabolism [Dringen, 2000]. It has been observed that there is an age-dependent depletion in intracellular GSH in the CSF during aging in humans [Cudkowicz et al., 1999]. Studies from others have shown that aged mice have a 30% decrease in levels of GSH compared with younger animals. Since the brain requires extensive ROS detoxification, it is evident that a decrease in GSH content could increase oxidative damage, making the brain more susceptible to neurological disorders [Bharath et al., 2002]. Decreased GSH availability in the brain is believed to promote mitochondrial damage by likely increasing the levels of oxidative stress in this organelle. Depletion of brain GSH has been shown to result in decreases in mitochondrial enzyme activities as well as losses in ATP production in the aging murine brain [Martinez et al., 1995].

Based on these notions, one of the ways to counteract oxidative stress-mediated disruption of GSH homeostasis—a central feature of neurodegeneration—is to replenish the GSH pool either by increasing the synthesis of the tripeptide or by slowing its degradation. Schulz and colleagues [2000] have shown that the administration of precursors of GSH metabolism, such as γ -glutamyl cysteine, increase the levels of GSH in rat brains. Similarly, precursors of cysteine synthesis have been administered in various animal models to accelerate cysteine production in the brain, thus increasing GSH levels. GSH replacement can also be achieved by administering thiol reagents such as GSH itself or GSH analogs. GSH cannot easily penetrate the blood–brain barrier due to the presence of the cysteine SH group and is not efficiently absorbed into neuronal cells in the brain [Kannan et al., 1999]. Hence rather

than GSH, modified forms of GSH such as GSH analogs have generally been used in vivo. Recently, Butterfield et al. demonstrated that the xanthate D609—acting as a GSH mimetic—protected against amyloid- β -(1-42)-induced oxidative damage in primary neurons and isolated synaptosomes [Perluigi et al., 2006a; Sultana et al., 2006a]. Further studies are in progress to test the use of GSH or related molecules in GSH metabolism as therapeutics in the treatment of neurodegenerative diseases to elicit an increase in brain GSH levels.

VITAGENE FAMILY: A VITAL PROPOSITION

The term *vitagenes* is used to refer to a group of genes that are strictly involved in preserving cellular homeostasis during stressful conditions. The vitagene family is actually composed of the heat shock proteins (Hsp) Hsp32, Hsp70, and by the thioredoxin system [Calabrese et al., 2006a, 2007a]. Among these genes heme oxygenase-1 (HO-1), also known as Hsp32, is receiving considerable attention because of its major role in counteracting both oxidative and nitrosative stress. In fact, HO-1 induction is one of the earlier events in the cell response to stress. Heme oxygenase-1 exerts α protective role, by degrading the intracellular levels of pro-oxidant heme and by producing biliverdin, the precursor of bilirubin, this latter being an endogenous molecule with powerful antioxidant and antinitrosative features [Calabrese et al., 2007; Mancuso et al., 2008]. Although some beneficial phytochemicals might function solely as antioxidants, it is becoming clear that many of the beneficial chemicals in vegetables and fruits evolved as toxins (to dissuade insects and other predators) that, at subtoxic doses, activate adaptive cellular stress-response pathways, under control of genes defined by us as vitagenes in a variety of cells including neurons. Examples of such “preconditioning” or “neurohormesis” pathways include those involving cell-survival signaling kinases, the transcription factors NRF2, and the histone deacetylases [Calabrese and Baldwin, 1998; Calabrese, 2008a, 2008b; Mattson et al., 2007]. Consistent with this, neurohormetic phytochemicals such as curcumin, resveratrol, and sulforaphanes or other compounds such as acetyl-L-carnitine [Calabrese et al., 2005; Poon et al., 2006] might protect neurons against injury and disease by stimulating, through the vitagene system, the production of antioxidant enzymes, protein chaperones, and other proteins that help cells to withstand stress [Calabrese and Maines, 2006, Calabrese et al., 2006a, 2006b, 2006c, 2006d]. The strong evidence that the vitagene network operates as a defense system in the brain during oxidative and nitrosative stress open new perspectives in the treatment of neurodegenerative disorders. Therefore, the nutritional manipulation of endogenous cellular defense mechanisms represents an innovative approach to therapeutic intervention in neurodegeneration, and proposes potential novel therapeutic strategies relying upon the simultaneous activation of cytoprotective genes of the cell life program and down-regulation of proinflammatory and pro-oxidative genes involved in programmed cell death. Although the term *vitagene*

was first proposed to indicate speculatively the existence of genes as opposed to gerontogenes, the first evidence-based notion identifying vitagenes with stress-responsive genes such as *HO-1* and *Hsps* has been provided by our group [Calabrese et al. 2001].

CONCLUSIONS AND PERSPECTIVES

Modulation of endogenous cellular defense mechanisms via the stress–response signaling represents an innovative approach to therapeutic intervention in diseases causing tissue damage, such as neurodegeneration. Efficient functioning of maintenance and repair processes seems to be crucial for both survival and physical quality of life. This is accomplished by a complex network of the so-called longevity assurance processes, which are composed of several genes that can be termed vitagenes. Consistently, by maintaining or recovering the activity of vitagenes can be possible to delay the aging process and decrease the occurrence of age-related diseases with resulting prolongation of a healthy life span [Calabrese, 2007; Calabrese et al., 2007a, 2007b, 2007c, Mancuso et al., 2007, 2008]. As one of the most important neurodegenerative disorders, AD is a progressive disorder with cognitive and memory decline, speech loss, personality changes, and synapse loss. With the increasingly aging population of the United States, the number of AD patients is predicted to reach 14 million in the mid-twenty-first century in the absence of effective interventions. This will pose an immense economic and personal burden on the people of this country. Similar considerations apply to most regions of the world. There is now strong evidence to suggest that factors such as oxidative stress and disturbed protein metabolism and their interaction in a vicious cycle are central to AD pathogenesis. Brain-accessible antioxidants, potentially, may provide the means of implementing this therapeutic strategy of delaying the onset of AD, and more in general all degenerative diseases associated with oxidative stress.

Emerging evidence strongly supports also the notion that stimulation of various maintenance and repair pathways through exogenous intervention, such as mild stress or compounds targeting the heat shock signal pathway, such as polyphenols, may have biological significance as a novel approach to delay the onset of various age-associated alterations in cells, tissues, and organisms. Hence, by maintaining or recovering the activity of vitagenes, it can be possible to delay the aging process and decrease the occurrence of age-related diseases with resulting prolongation of a healthy life span.

ACKNOWLEDGMENTS

This work was supported by grants from MIUR, FIRB RBRN07BMCT, RCUK, the American Cancer Society (RSG-07-157-01-CNE), Cancer

Research UK, Tenovus, the Royal Society, the Anonymous Trust, and by “Fondi Ateneo” 2007 and 2008.

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19 Natural Phenolics and Metal Metabolism in Neurodegenerative Diseases

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INTRODUCTION

There is a common feature in the two major neurodegenerative diseases: In both Alzheimer's disease (AD) and Parkinson's disease (PD) there is an imbalance of metal metabolism leading to oxidative stress-induced neuronal apoptosis. It is well known that there is no cure or efficient treatment available for these diseases. Is there a way to prevent these diseases? From this review

I propose that by acting as antioxidants, phenolics can prevent and even cure these diseases by modulating the imbalance of metal metabolism.

IMBALANCE OF METAL METABOLISM, OXIDATIVE STRESS, AND NEURODEGENERATIVE DISEASES

The mechanism of AD pathogenesis still remains unclear. However, one mechanism, amyloid β ($A\beta$) accumulation, may be due to the disturbance in metal homeostasis in AD brains [Strausak et al., 2001]. $A\beta$ peptides are the major constituents of the amyloid core of senile plaques, which are derived from the amyloid precursor protein (APP) and are secreted into extracellular spaces. Both APP and $A\beta$ contain a copper-binding domain [Hesse et al., 1994; Atwood et al., 1998]. High concentrations of copper, zinc, and iron have been found within the amyloid deposits in AD brains [Lovell et al., 1998]. $A\beta$ peptides can be rapidly precipitated by copper under mildly acidic conditions and by zinc at low physiological (submicromolar) concentrations [Bush et al., 1994]. An age-dependent binding between $A\beta$ peptides with excess brain metals (copper, iron, and zinc) induces $A\beta$ peptides to precipitate into metal-enriched plaques [Bush, 2002].

When using the APPV717I transgenic mice to measure the metal levels in the brain by using synchrotron radiation X-ray fluorescence, the copper and zinc concentrations in senile plaques and neuropil were higher than those in neuropil of both sucrose- and nicotine-treated groups. Furthermore, the levels of copper and zinc were significantly reduced by about 10–20% in senile plaques and neuropil in nicotine-treated mice relative to sucrose-treated controls. The distribution of copper and zinc in hippocampal CA1 region was also examined. Copper is enriched in the pyramidal neuron layer, whereas the distribution of zinc is relatively spread out. The content of both copper and zinc was significantly decreased after nicotine treatment, particularly in the pyramidal neuron layer. The copper concentrations in both the empty vector (neo) and APPsw mouse cells were measured by synchrotron radiation X-ray fluorescence analysis. In the neo cell line, both of 10 and 100 μM copper treatment increased intracellular copper concentrations. The copper concentration in APPsw cells was higher than in neo cells. Nicotine treatment decreased the copper concentration in both cell types. Incubation in the presence of 10 μM copper increased reactive oxygen species (ROS) generation 28% in APP cells and 59% in APPsw cells compared with neo cells; 100 μM copper increased the ROS generation 35 and 58% in APP and APPsw cells, respectively. Nicotine administration reduced copper-induced ROS accumulation in both cell types at 10 and 100 μM copper. In APPsw cells, the ratio of the expression of copper chaperone for superoxide dismutase (CCS) and SOD-1 (copper/zinc SOD) increased after nicotine treatment. In the hippocampus and cortex of the transgenic mice, the expression of CCS was increased 25 and 67% in the hippocampus and cortex of nicotine-treated mice, respectively, whereas

the concentration of SOD-1 was lowered 28 and 26% in the hippocampus and cortex, respectively. Then, if copper and zinc modulate A β aggregation and deposition, the levels of these metals would be relevant in the pathogenesis of AD. Our group has suggested that nicotine reduces β -amyloidosis in AD transgenic mice, and that effect was also observed in APPsw-overexpressed cells by regulating metal homeostasis. Nicotine may regulate metal homeostasis causing: (i) a decrease of ROS generation and A β aggregation, (ii) a down-regulation of APP expression, and (iii) an increased CCS expression that reduces intracellular free copper.

Reactive oxygen species production is largely catalyzed by transition metals (especially copper and iron), and oxidative stress plays a critical role in AD pathogenesis. In one study, the association of metal levels and A β toxicity was demonstrated by: (i) the effect on cell viability by metal alone and in the combination with APP and A β , (ii) A β -induced neurotoxicity relevant to oxidative stress indicated by ROS production, and (iii) APPsw cells expressed APP and generated A β , so that A β -Cu²⁺ and APP-Cu²⁺ can catalyze more ROS generation than APP cells that only expressed APP.

Nicotine shows protective effects against A β -induced neurotoxicity in vivo and in vitro. Although nicotine acts on nAChRs, it also contains metal chelating abilities. It has been shown that maternal nicotine exposure resulted in a reduction of the copper content in the neonatal lung. In addition, evidence has been accumulated that nicotine might chelate metals. Indeed, nicotine reduces the levels of copper and zinc in senile plaques and neuropil, counteracting the undesirable metal accumulation.

The actions of nicotine on the whole brain and cellular copper concentrations were further supported by the changes of both CCS and SOD-1 levels. CCS directly inserts copper into SOD-1 and prevents the accumulation of free copper ions in cells. In the transgenic mice brain, our data suggest that an increase of CCS expression by nicotine causes a decrease in free intracellular copper levels, since more expression of CCS transfers more copper ions into proteins. Therefore, the copper ions that can be transported to the extracellular space are reduced, which results in an inhibition of free copper-mediated A β aggregation. Although nicotine has been proven to have beneficial effects on neurodegenerative disease, the exact mechanisms of those benefits are still unclear. Our data suggest the novel idea that nicotine may regulate metal homeostasis [Liu et al., 2003; Liu and Zhao, 2004; Xie et al., 2005; Zhang et al., 2006; Zhu et al., 2007]

Magaki et al. [2007] measured the levels of loosely bound, nonheme, and total iron and copper in the frontal cortex and hippocampus of patients with mild-moderate AD ($n = 3$), severe AD ($n = 8$), and dementia with Lewy bodies (DLB, $n = 6$). Additionally, the expression of iron regulatory protein 2 (IRP2) was examined in relation to the pathological hallmarks of AD, that is, 5 amyloid plaques, neurofibrillary tangles (NFT), and Lewy bodies. A significant decrease of loosely bound iron was found in the hippocampal white matter of both mild-moderate and severe AD patients and a trend toward increased

nonheme iron in the hippocampal gray matter of severe AD patients. Furthermore, decreased levels of total copper were seen in severe AD frontal cortex compared to controls, suggesting an imbalance in brain metal levels in AD. The decrease in loosely bound iron in mild–moderate AD patients may be associated with myelin breakdown seen in the beginning stages of AD, and implicates that iron dysregulation is an early event in AD pathogenesis [Magaki et al., 2007].

Copper is essential for some of the enzymes that have a role in brain metabolism. Sophisticated mechanisms balance copper import and export to ensure proper nutrient levels (homeostasis) while minimizing toxic effects. Several neurodegenerative diseases including AD are characterized by modified copper homeostasis. This change seems to contribute either directly or indirectly to increased oxidative stress, an important factor in neuronal toxicity. The association of misfolded proteins and modified copper homeostasis appears to be important in the pathological progression of AD [Donnelly et al., 2007].

Inhibition of neocortical A β accumulation may be essential in an effective therapeutic intervention for AD. A β deposits, which are enriched in copper and zinc, are solubilized with copper and zinc selective chelators in vitro. Cherny et al. [2001] reported a 49% decrease in brain A β deposition (375 μ g/g wet weight, $p < 0.0001$) in APP2576 transgenic mice treated orally for 9 weeks with clioquinol, an antibiotic and chelator of copper and zinc. This was accompanied by a modest increase in soluble A β (1.45% of total cerebral A β); but APP, synaptophysin, and GFAP levels were unaffected. In addition, general health and body weight parameters were significantly more stable in the treated animals. These results support targeting Cu and Zn interactions with A β , as a potential therapy for AD [Cherny et al., 2001].

To explore the effects of copper regulation on AD and A β peptide formation in vivo, toxic-milk (*txJ*) mice with a mutant ATPase7b transporter favoring elevated Cu levels were studied in combination with the transgenic (Tg) CRND8 amyloid precursor protein mice exhibiting robust A β deposition. Unexpectedly, TgCRND8 mice homozygous for the recessive *txJ* mutation examined at 6 months of age exhibited a reduced number of A β plaques and diminished plasma A β levels. In addition, homozygosity for *txJ* increased survival of young TgCRND8 mice and lowered A β before an increase in copper in the central nervous system (CNS) was detectable. These data suggest that the beneficial effect of the *txJ* mutation on CNS A β burden may proceed by alternative mechanisms, for example, by involving increased clearance of peripheral pools of A β [Phinney et al., 2003].

The copper-binding APP and A β have been proposed to play a role in physiological metal regulation. There is accumulating evidence of an unbalanced copper homeostasis with a causative or diagnostic link to AD. Whereas elevated copper levels are observed in APP knockout mice, APP overexpression results in reduced copper in transgenic mouse brain. Moreover, copper induces a decrease in A β levels in APP-transfected cells in vitro. To investigate the

influence of bioavailable copper, transgenic APP23 mice received an oral treatment with copper-supplemented sucrose-sweetened drinking water. Chronic APP overexpression per se reduced SOD-1 activity in transgenic mouse brain, which could be restored to normal levels after copper treatment. A significant increase of brain copper indicated higher bioavailability following copper treatment in APP23 mice, whereas copper levels remained unaffected in littermate controls. Copper treatment lowered endogenous CNS A β before a detectable reduction of amyloid plaques. Thus, APP23 mice reveal APP-induced alterations linked to copper homeostasis, which can be reversed by increasing dietary copper [Bayer et al., 2003].

Evidence is now accumulating to show that reactions involving metals might be the common denominator underlying AD and PD. In these disorders, an abnormal reaction between a protein and a redox-active metal ion (copper or iron) promotes the formation of ROS. It is especially intriguing how the antioxidant Cu/Zn-SOD activity can convert into a pro-oxidant activity, a theme echoed in the recent proposal that A β and PrP, the proteins respectively involved in AD and prion diseases, possess similar redox properties [Bush, 2002].

The main therapeutic approaches attempt to prevent A β production (secretase inhibitors) or to remove A β (vaccine). However, there is now compelling evidence that A β does not spontaneously aggregate, but that there is an age-dependent protein precipitation of metal-enriched (copper, iron, and zinc) plaques. The copper or iron containing A β induces the production of hydrogen peroxide, which may mediate oxidative damage to the brain in AD. Metal-binding compounds have been developed to inhibit the generation of hydrogen peroxide by A β , as well as reverse the aggregation of the peptide as assayed in chemical system and with human brain post-mortem specimens. As indicated, clioquinol is being tested in clinical trials [Bush, 2002].

Additional results on the potential action of clioquinol include treating Chinese hamster ovary cells overexpressing APP with clioquinol and copper or zinc. The treatment resulted in an 85–90% reduction of secreted A β -(1–40) and A β -(1–42) compared with untreated controls. Similar effects were seen in neuroblastoma cells overexpressing APP. The secreted A β was rapidly degraded through up-regulation of matrix metalloproteases 2 and 3 after addition of clioquinol and copper. MMP activity was increased through activation of phosphoinositol 3-kinase and JNK. Clioquinol and copper also promoted phosphorylation of glycogen synthase kinase-3, and this potentiated activation of JNK and loss of A β -(1–40). These findings identify an alternative mechanism of action for clioquinol based on the reduction of A β deposition [White et al., 2006].

There is increasing evidence that iron is involved in several neurodegenerative diseases. Conditions such as neuroferritinopathy and Friedreich ataxia are associated with mutations in genes that encode proteins that are involved in iron metabolism. As the brain ages, iron accumulates in regions that are affected in AD and PD. High concentrations of reactive iron can increase

oxidative stress-induced neuronal vulnerability and the toxicity of environmental or endogenous toxins. Studies on brain iron metabolism, especially the discovery of mutations in the genes associated with iron transport, storage, and regulation, could support the concept that increased brain iron is an initial cause of neuronal death at least in some neurodegenerative diseases. The brain shares with other organs the need for a constant and readily available supply of iron and a number of proteins available for iron transport, storage, and regulation. However, unlike other organs, the brain demands on iron are regional, cellular, and age sensitive. Failure to meet the demands for iron with an adequate supply in a timely manner can result in persistent neurological and cognitive dysfunction. Consequently, the brain has developed mechanisms to maintain a continuous supply of iron. However, in a number of common neurodegenerative disorders, there appears to be an excess accumulation of iron in the brain that suggests a loss of the homeostatic mechanisms responsible for regulating iron in the brain. As a result of a loss in iron homeostasis, the brain becomes vulnerable to iron-induced oxidative stress [Thompson et al., 2001].

OXIDATIVE STRESS AND NEURODEGENERATIVE DISEASES

An imbalance of metal metabolism causes oxidative stress, which can lead to the loss of biological functions. The high oxygen consumption, the low concentration of glutathione and of the antioxidant enzyme catalase, and the high proportion of polyunsaturated fatty acids make the brain particularly susceptible to oxidative stress and consequent damage [Mecocci et al., 1994; Smith et al., 1998]. Accumulated data demonstrated that oxidative damage occurs in AD brain [Markesbery and Carney, 1999; Christen, 2000; Smith et al., 2000]. A β peptide has been proven to produce H₂O₂ through metal ion reduction, with concomitant lipid oxidation [Huang et al., 1999a, 1999b]. The cytotoxicity of A β also seems to be relative to an oxidative mechanism [Behl et al., 1994; Markesbery, 1997; Markesbery and Carney, 1999]. Evidence supporting the notion of oxidative stress in AD brain includes: increased presence of redox-active metal ions in AD brain; increased lipid oxidation detected by decreased levels of polyunsaturated fatty acids and increased levels of lipid, protein, and nucleic acid oxidation, and decreased activity of oxidant-sensitive enzymes, such as glutamine synthetase.

Parkinson's disease is a progressive neurodegenerative disorder, and the hallmark of this disease is the selective loss of dopaminergic neurons in the substantia nigra pars compacta [Xin et al., 1984]. Recently, the death of dopaminergic neurons has been reported to occur by apoptosis [Mochizuki et al., 1996; Anglade et al., 1997; Hirsch et al., 1997]. Oxidative stress has been widely assessed as an important pathogenetic mechanism of neuronal apoptosis in PD [Halliwell, 1992]. Overproduction of ROS can lead to oxidative damage in the brain of PD, as shown by increased lipid oxidation and DNA damage in

the substantia nigra. Increased protein oxidation is also apparent in many areas of the brain, while substantia nigra is particularly vulnerable [Xin et al., 1984]. Under physiological conditions, 6-hydroxydopamine (6-OHDA) is rapidly and nonenzymatically oxidized by molecular oxygen to form the corresponding *p*-quinone and H₂O₂ [Soto-Otero et al., 2000]. The former can undergo an intramolecular cyclization followed by a cascade of oxidative reactions resulting in the formation of an insoluble polymeric pigment related to neuromelanin [Graham et al., 1978; Soto-Otero et al., 2000].

EFFECTS OF PHENOLICS ON METAL-MEDIATED NEURODEGENERATIVE DISEASE

Oxidative stress has been implicated in a variety of neuropathologies, including stroke, trauma, and diseases such as AD and PD. It should be reasonable to use antioxidant strategies to prevent or treat these diseases. In the following sections are discussed the use of several natural phenolics as antioxidants and the potential actions on neurodegenerative diseases.

Tea Phenolics

Tea phenolics, including its major constituent, (–)-epigallocatechin gallate (EGCG), have diverse pharmacological activities. It is considered that these beneficial effects of green tea polyphenols are due to their potent antioxidative properties. In fact, it was demonstrated that *in vitro* green tea polyphenols serve as powerful antioxidants against free radicals such as DPPH radicals [Nanjo et al., 1996], superoxide anion [Zhao et al., 1989; Guo et al., 1996, 1999], lipid free radicals, and hydroxyl radicals [Nie et al., 2001; Zhao et al., 2001]. In the CNS, there is also some evidence showing that oral administration of green tea polyphenols and flavonoid-related compounds has preventive effects on iron-induced lipid peroxide accumulation and age-related accumulation of neurotoxic lipid peroxides in rat brain [Yoneda et al., 1995; Inanami et al., 1998].

Tea phenolics, including catechins are expected to scavenge free radicals but such chemical action is different depending on each compound. When we studied the effect of tea catechins (TC) on the PC12 and SY5Y cells exposed to 6-OHDA, it was demonstrated that TC could protect PC12 cells against apoptosis caused by 6-OHDP. EGCG and (–)-epicatechin gallate (ECG) were more effective than (–)-epigallocatechin (EGC), (–)-epicatechin (EC), and (+)-catechin (C). From 50 to 400 μM, the antiapoptotic effects increased with concentration, and EGCG was the most protective as compared with other TC. The nuclear changes and the DNA ladder characteristic of apoptosis were prevented in both PC12 and SY5Y cells by 200–400 μM of TC [Nie et al., 2002; Guo et al., 2005].

Nitric oxide (NO) and NO-related pathways are thought to play an important role in the pathogenesis of PD. *In vitro* experiments suggested that TC might protect dopamine neurons through inhibition of ROS and NO. The effects of a green tea extract (GTP) on a unilateral 6-OHDA-treated rat model of PD were investigated [Guo et al., 2007]. GTP treatment protected dopaminergic neurons from midbrain and striatal from 6-OHDA-induced increase of: (i) both ROS and NO levels, (ii) lipid oxidation, (iii) nitrite/nitrate content; (iv) inducible NO synthase, and (v) protein 3-nitro-tyrosine. Moreover, GTP treatment preserved, in a dose-dependent manner, the free-radical scavenging capability of both the midbrain and the striatum. These results support the *in vivo* protection of GTP against 6-OHDA-mediated damage and suggest that GTP might provide a treatment for PD [Guo et al., 2007].

Mandel's group [2007] demonstrated the neuroprotective properties of a green tea extract (GTE) and of ECG, in the MPTP mice model of PD. MPTP neurotoxin caused dopamine neuron loss in substantia nigra concomitant with a depletion in striatal dopamine and tyrosine hydroxylase protein levels. Pretreatment with either GTE (0.5 and 1 mg/kg) or ECG (2 and 10 mg/kg) prevented these effects. In addition, the MPTP caused an elevation in striatal SOD (240%) and catalase (165%) activities that was prevented by ECG. The neuroprotective effects are not likely to be caused by inhibition of MPTP conversion to its active metabolite 1-methyl-4-phenylpyridinium by monoamine oxidase-B, as both green tea and ECG were poor inhibitors of this enzyme *in vitro* (770 mg/mL and 660 nM, respectively). Brain penetrating property of polyphenols, as well as their antioxidant and iron-chelating properties, may make such compounds an important class of drugs to be developed for treatment of neurodegenerative diseases where oxidative stress has been implicated [Levites et al., 2001].

The same group showed radical scavenging activities of green tea (GT) and black tea (BT) extracts using brain mitochondrial membrane fraction treated with 2.5 μM iron. Both extracts (0.6–3.0 μM total polyphenols) were shown to attenuate the 6-OHDA-induced neuronal death. 6-OHDA (350 and 50 μM) activated the iron-dependent inflammatory redox-sensitive NF- κB in PC12 rat pheochromocytoma and human neuroblastoma SH-SY5Y cells. Treatment with GT (0.6 and 3 μM total polyphenols) before 6-OHDA inhibited both NF- κB nuclear translocation and binding activity induced by this toxin in SH-SY5Y cells. Cell protection was attributed by the authors to the potent antioxidant and iron-chelating actions of the polyphenolic constituents of tea extracts [Levites et al., 2002b]. It was also demonstrated that EGCG restored the reduced protein kinase C (PKC) and extracellular signal-regulated kinases (ERK1/2) activities caused by 6-OHDA. However, the neuroprotective effect of EGCG on cell survival was abolished by pretreatment with PKC inhibitor GF 109203X. Because EGCG increased phosphorylated PKC, it was suggested that PKC isoenzymes are involved in the neuroprotective action of EGCG against 6-OHDA. In addition, gene expression analysis revealed that EGCG prevented both the 6-OHDA-induced expression of several messenger

riponucler acid (mRNA), such as Bax, Bad, and Mdm2, and the 6-OHDA-induced decrease in Bcl-2, Bcl-w, and Bcl-xL. These results suggest that the protective mechanisms of EGCG against oxidative stress-dependent cell death include the stimulation of PKC and the modulation of cell survival/cell cycle genes [Levites et al., 2002a].

Not all the actions of TC are necessarily beneficial. We demonstrated that high concentrations of green tea polyphenols significantly enhanced sodium nitroprusside (SNP)-induced toxicity. SNP, a NO donor, induced apoptosis in SY5Y cells in a concentration and time-dependent manner, whereas pretreatment with GTP alone had no effect on cell viability. Pretreatment with GTP (50 and 100 μM) had only slightly apoptotic effects in the presence of SNP, while higher doses of GTP (200 and 500 μM) synergistically damage cells. Further research showed that co-incubation of green tea polyphenols and SNP caused loss of mitochondrial membrane potential, depletion of intracellular GSH, accumulation of ROS, and exacerbated NO-induced neuronal apoptosis via a Bcl-2 sensitive pathway [Zhang and Zhao, 2003].

Recent studies suggest that TC may be used for the prevention and treatment of a variety of neurodegenerative diseases. Rezai-Zadeh et al. [2005] report that EGCG reduces A β production in both murine neuron-like cells (N2a) transfected with the human "Swedish" mutant APP (SweAPP N2a cells), and in primary neurons derived from Swedish mutant APP-overexpressing mice (Tg APP^{sw} line 2576). In concert with these observations, we find that EGCG markedly promotes cleavage of the α -COOH-terminal fragment of APP and elevates the N-terminal APP cleavage product, soluble APP- α . These cleavage events are associated with elevated α -secretase activity and enhanced hydrolysis of tumor necrosis factor α -converting enzyme. As a validation of these findings in vivo, we treated Tg APP^{sw} transgenic mice overproducing A β with EGCG and found decreased A β levels and plaques associated with the promotion of the nonamyloidogenic α -secretase proteolytic pathway. These data raise the possibility that EGCG dietary supplementation may provide effective prophylaxis for AD [Rezai-Zadeh et al., 2005].

Obregon et al. [2006] showed that EGCG exerts a beneficial role on reducing brain A β levels, resulting in the mitigation of cerebral amyloidosis in a mouse model of AD, by the increasing α -secretase cleavage activity as indicated above. To gain insight into the molecular mechanism whereby EGCG modulates APP processing, we evaluated the involvement of three potential α -secretase enzymes: (i) disintegrin and metalloprotease (ADAM) 9, 10, or 17, in EGCG-induced nonamyloidogenic APP metabolism. Results show that EGCG treatment of SweAPP N2a cells leads to markedly elevated active (~ 60 kDa mature form) ADAM10 protein. Elevation of active ADAM10 correlates with increased α -COOH-terminal fragment cleavage, and elevated sAPP- α . To specifically test the contribution of ADAM10 to nonamyloidogenic APP metabolism, small interfering RNA knockdown of ADAM9, -10, or -17 mRNA was employed. Results show that ADAM 10 (but not ADAM-9 or -17) is critical for EGCG-mediated α -secretase cleavage activity. In summary,

ADAM10 activation is necessary for EGCG promotion of nonamyloidogenic (α -secretase cleavage) APP processing. Thus, ADAM10 represents an important pharmacotherapeutic target for the treatment of cerebral amyloidosis in AD [Obregon et al., 2006].

Considering the multietiological character of AD, the current pharmacological approaches using drugs oriented toward a single molecular target possess limited ability to modify the course of the disease and thus offer a partial benefit for the patient. In line with this concept, novel strategies include the use of a cocktail of several drugs and/or the development of a single molecule, possessing two or more active neuroprotective-neurorescue moieties that simultaneously manipulate multiple targets involved in AD pathology. A consistent observation in AD is a deregulation of metal homeostasis and the consequent oxidative stress associated with A β aggregation and neurite plaque formation. In particular, iron has been demonstrated to modulate the Alzheimer's APP expression by a pathway similar to that of ferritin L- and H-mRNA translation through iron-responsive elements in their 5'UTRs. Mandel et al. [2007] discussed two separate scenarios concerning multiple therapy targets in AD, sharing in common the implementation of iron-chelation activity: (i) novel multimodal brain-permeable iron-chelating drugs, possessing neuroprotective-neurorescue and APP processing regulatory activities; and (ii) natural plant polyphenols (flavonoids), such as EGCG and curcumin, reported to have access to the brain and to possess multifunctional activities, such as metal chelation–radical scavenging, anti-inflammation, and neuroprotection [Mandel et al., 2007].

Flavonoids

Flavonoids isolated from plants are well investigated as natural antioxidants and widely used to treat patients as effective components of many medical drugs in clinics. To determine the potential protective mechanisms of flavonoids in cell death, the mouse hippocampal cell line HT-22 was used, and it was found that exogenous glutamate inhibits cystine uptake and depletes intracellular glutathione (GSH), leading to the accumulation of ROS and an increase in Ca²⁺ influx, which ultimately causes neuronal death. Many, but not all, flavonoids protect HT-22 cells and rat primary neurons from glutamate toxicity as well as from five other oxidative injuries. Three structural requirements of flavonoids for protection from glutamate are the hydroxylated C3, an unsaturated C-ring, and hydrophobicity. It was also found three distinct mechanisms of protection. These include increasing intracellular GSH, directly lowering levels of ROS, and preventing ROS-mediated influx of Ca²⁺. These data show that the mechanisms of protection from oxidative insults by flavonoids are multiple and depend on the chemical structure and physical properties of each compound [Ishige et al., 2001].

Ginkgo biloba is a plant that contains a high number of flavonoids and terpens and has been reported to protect the brain against hypoxic damage

and inhibit ROS formation in cerebellar neurons. We investigated the protective effects of a *Ginkgo biloba* extract (EGb) on dissociated cortex neurons from damage caused by ROS using spin label and molecular techniques. It was found that the order parameter (S), rotational correlation time (τ), and the ratio of strong immobilized component to weak immobilized component (S/W) of the cell membrane treated with hydroxyl radical were higher than those of control, indicating that ROS diminished membrane fluidity. EGb (5–50 $\mu\text{g/mL}$) produced a dose-dependent increase of membrane fluidity in hydrophobic areas of the membrane. EGb also protected the change of the protein conformation on the membrane caused by ROS. At the same concentration, EGb diminishes ROS-mediated increase of lactate dehydrogenase release and cell apoptosis [Ni et al., 1996]. The protective effect of EGb761 and some of its constituents against apoptosis were also examined. The total flavonoid components of EGb761 and a mixture of flavonoids and terpenes protected cerebellar granule cell from oxidative damage and apoptosis induced by hydroxyl radicals. Total terpenes of EGb761 did not protect against apoptosis, indicating that flavonoids and terpenes act synergistically [Chen et al., 1999; Xin et al., 2000].

$A\beta$ toxicity has been postulated to initiate the synaptic loss and subsequent neuronal degeneration seen in AD. We previously demonstrated that the standardized *Ginkgo biloba* extract EGb 761, commonly used to enhance memory and in AD patients for treating dementia, inhibits $A\beta$ -induced apoptosis in neuroblastoma cells. EGb 761 and its constituents were tested to associate $A\beta$ species with $A\beta$ -induced pathological behaviors in a model organism, *Caenorhabditis elegans*. We observed that EGb 761 and one of its components, ginkgolide A alleviates $A\beta$ -induced pathological behaviors, including paralysis, and reduces chemotaxis behavior and 5-HT hypersensitivity in a transgenic *C. elegans*. We also showed that EGb 761 inhibits $A\beta$ oligomerization and $A\beta$ deposits in the worms. Interestingly, reducing oxidative stress is not the mechanism by which EGb 761 and ginkgolide A suppress $A\beta$ -induced paralysis because L-ascorbate reduced intracellular levels of hydrogen peroxide to the same extent as EGb 761, but was not as effective in suppressing paralysis in the transgenic *C. elegans*. These findings suggest that: (i) EGb 761 suppresses $A\beta$ -related pathological behaviors; (ii) the protection against $A\beta$ toxicity by EGb761 is mediated primarily by modulating $A\beta$ oligomeric species; and (iii) ginkgolide A has therapeutic potential for prevention and treatment of AD [Wu et al., 2006].

Soy Isoflavones

Epidemiological studies have associated estrogen replacement therapy with a lower risk of developing AD, but with a higher risk of developing breast cancer and certain cardiovascular disorders. The neuroprotective effect of estrogen prompted us to determine potential therapeutic impact of soy-derived estrogenic compounds, the isoflavones. Genistein, the most active component of soy

isoflavone, has been investigated because its affinity to bind to estrogen receptors [Kurzer and Xu, 1997], antioxidation activity [Johnson et al., 1996; Chan and Yu, 2000], capacity to increase cellular reduced glutathione [Guo et al., 2002], inhibition of protein tyrosine kinase (PTK) [Ohigashi et al., 2000], and for several other biological actions [Kim et al., 2000]. The existing data strongly suggest that isoflavones have a protective action against several chronic diseases such as atherosclerosis [Clarkson et al., 1998], diseases associated with postmenopausal estrogen deficiency, and hormone-dependent breast and prostate cancers [Lamartiniere et al., 2002]. Recently, it was reported that genistein protected rat brain synaptosome from insult induced by A β ₂₅₋₃₅ [Andersen et al., 2003]. Importantly, genistein is capable of crossing the blood–brain barrier [Chang et al., 2000].

We have studied the neuroprotective effects of genistein against A β ₂₅₋₃₅-induced apoptosis in cultured hippocampal neurons [Zeng et al., 2004]. Exposure to aged A β ₂₅₋₃₅ for 24 h increased the oxidant-dependent dichloro-fluorescein fluorescence two fold relative to controls. The increase in oxidants was reduced by 63% when cells were co-treated with 40 μ M genistein and aged A β ₂₅₋₃₅, while genistein at 0.1 μ M decreased about 18% of the production of ROS induced by A β ₂₅₋₃₅. Treatment with 25 μ g/mL aged A β ₂₅₋₃₅ for 24 h decreased the viability of hippocampal neurons about 43% compared to controls. Genistein at the concentrations of 0.1 and 40 μ M rescued aged A β ₂₅₋₃₅-induced decrease of viability rate by 7 and 14%, respectively. The estrogenic receptor antagonist, ICI182,780, significantly blocked the protective effect of genistein at the concentration of 0.1 μ M while having little effect at 40 μ M genistein. It can be concluded that A β ₂₅₋₃₅-induced apoptosis is reverted by genistein: At submicromolar level, genistein protects mostly via the estrogen-receptor-mediated pathways; at micromolar level, the protective effect of genistein would be mainly mediated by its antioxidant properties.

Transgenic *C. elegans*, which express human A β , were fed genistein, daidzein, and glycitein (100 μ g/mL) and then examined for A β -induced paralysis and ROS levels. Results show that only glycitein alleviated A β -induced paralysis. This activity of glycitein was associated to its capacity to reduce hydrogen peroxide level in the transgenic *C. elegans*. In vitro scavenging effects of glycitein confirmed its antioxidant properties. Furthermore, the transgenic *C. elegans* fed with glycitein exhibited reduced formation of A β . These findings suggest that the soy isoflavone glycitein may suppress A β toxicity through combined antioxidant actions and inhibition of A β deposition and thus may have therapeutic potential for prevention of A β -associated neurodegenerative disorders [Gutierrez-Zepeda et al., 2005].

CONCLUSION

Neurological diseases are difficult to treat after the onset of the pathological condition, so the best way is to protect people from developing neurodegenerative

diseases. This review compiled laboratory information that suggests that some plant phenolics can prevent neurodegeneration by modulating imbalances in metal metabolism, by trapping radicals, and by affecting signaling pathways involved in neuronal dysfunction. As a preventive action, it is easy to increase the intake of natural products, for example, drinking more tea and soybean milk and eating fresh fruits and vegetables. A pharmacological use of active principles still shows potential and depends on further developments.

ACKNOWLEDGMENTS

This work was supported by a grant from the National Natural Science Foundation of China (29935080).

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20 Epidemiology behind Fruit and Vegetable Consumption and Cancer Risk with Focus on Flavonoids

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INTRODUCTION

Several aspects of the Mediterranean diet have been related to a reduced risk not only for cardiovascular disease but also of several cancers. It has been suggested that up to 25% of colorectal, 15% of breast, and 10% of prostate, pancreas, and endometrial cancers could be prevented by shifting to a Mediterranean diet [Trichopoulou et al., 2000]. With specific focus to a network of Italian case-control studies conducted after 1991 (Figs. 20.1 and 20.2), vegetable intake was inversely related to the risk of several common epithelial cancers: the odds ratios (OR) for digestive tract neoplasms ranged between 0.3 and 0.8 for the highest compared with the lowest levels of vegetable intake. Less consistent inverse relations were observed for some hormone-related neoplasms, such as breast and ovary. High fruit intake was associated to reduced ORs of cancers of the upper digestive tract, stomach, colorectum, and

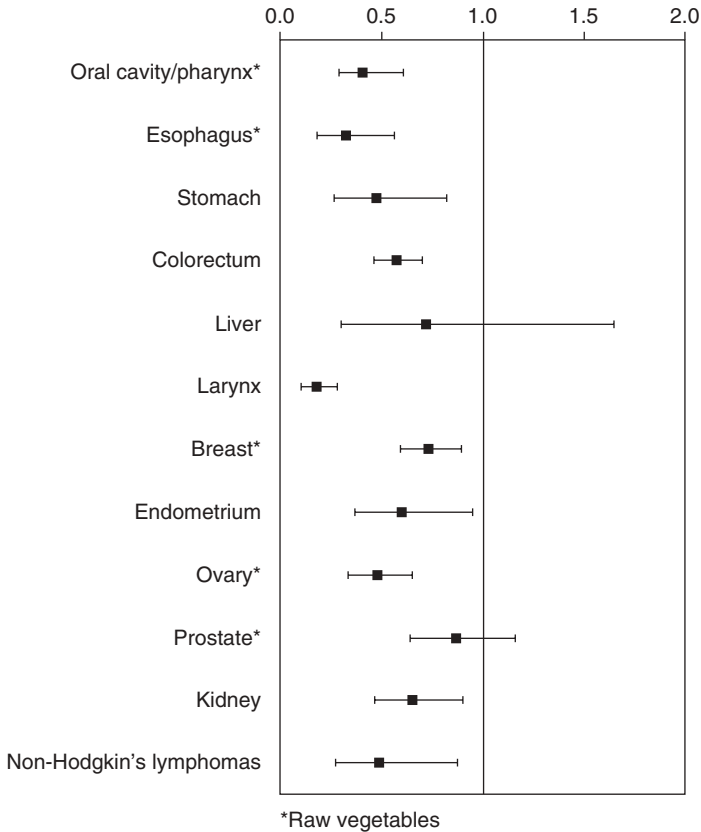


Figure 20.1 Odds ratios and 95% confidence intervals of selected cancers for the highest vs. the lowest levels of vegetable consumption. Italy, 1991–2005.

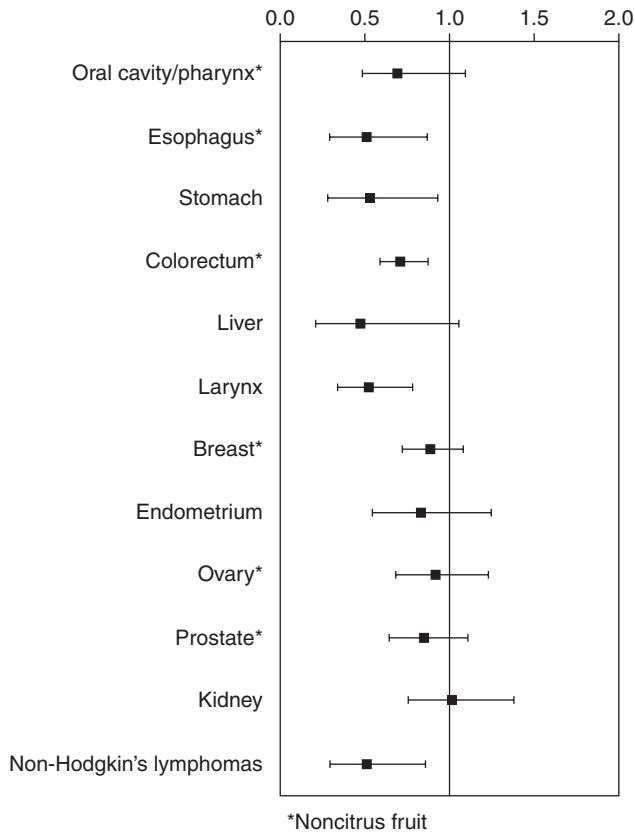


Figure 20.2 Odds ratios and 95% confidence intervals of selected cancers for the highest vs. the lowest levels of fruit consumption. Italy, 1991–2005.

non-Hodgkin's lymphomas. No material effect, however, was observed for fruit intake on neoplasms of the breast, the female genital tract, or the prostate [La Vecchia and Bosetti, 2006]. For digestive tract cancers, population-attributable risks for low intake of vegetables and fruit ranged between 15 and 40% [La Vecchia and Tavani, 1998].

Flavonoids are a group of several thousands of polyphenolic compounds present in fruit, vegetables, and beverages of plant origin [Manach et al., 2004; Ross and Kasum, 2002]. Originally known only for their role in plant pigmentation, flavonoids have been shown to have antioxidant, antimutagenic, and antiproliferative properties in vitro [Nijveldt et al., 2001; Peterson and Dwyer, 1998; Stoner and Mukhtar, 1995]. Flavonoids have been hypothesized to be responsible for the favorable effects of fruits and vegetables against various chronic diseases, including some common neoplasms [Arts and Hollman, 2005; La Vecchia et al., 1998; Neuhouser, 2004; Trichopoulou et al., 2003]. Recently, the availability of detailed and reliable food composition tables

for flavonoids published by the U.S. Department of Agriculture on their six major classes (flavan-3-ols, flavanones, flavonols, anthocyanidins, flavones, and isoflavones) [U.S. Department of Agriculture, 2002, 2003] has allowed epidemiological studies to further investigate the role of flavonoids in cancer etiology. Intake of various flavonoids has been inversely related to the risk of cancers of the upper aerodigestive tract [De Stefani et al., 1999], digestive tract [Lagiou et al., 2004], breast [Fink et al., 2007; Peterson et al., 2003], and urogenital tract [Chang et al., 2007; Kurahashi et al., 2007].

THE ITALIAN DATA SET ON FLAVONOIDS AND CANCER RISK

We investigated flavonoids in relation to the risk of various neoplasms in a series of case-control studies conducted in Italy since the early 1990s [Gallus et al., 2005], which included 805 cancers of the oral cavity and pharynx, 743 of the esophagus, 460 of the larynx, 1953 of the colorectum, 2569 of the breast, 1031 of the ovary, 1294 of the prostate, and 767 of the kidney, and a total of 16,050 controls collected in various regions of northern, central and southern Italy. Cases were individuals admitted to hospitals with incident, histologically confirmed cancer, and controls were patients with no history of cancer admitted to the same hospitals for acute, nonneoplastic conditions. A reproducible [Franceschi et al., 1993] and valid [Decarli et al., 1996] food frequency questionnaire, was used including 78 foods or food groups, to assess the patients' usual diet and to estimate intakes of six major classes of flavonoids. This was performed using food and beverage content of flavonoids obtained from the U.S. Department of Agriculture databases [U.S. Department of Agriculture, 2002, 2003] and other sources [Liggins et al., 2000a, 2000b]. The main flavonoids in each class are the flavan-3-ols, epicatechin and catechin; the flavanones, hesperitin and narigerin; the anthocyanidins, cyanidin and malvidin; the flavonols, quercetin, myricetin, and kaempferol; the flavones, apigenin and luteolin; and the isoflavones, genistein and daidzein.

Using multiple logistic regression models that included the major confounding factors, and total energy intake, the relations between flavonoid intake and the risk of the cancers at the various sites have been examined. This allowed us to investigate the potential effects against cancer of these compounds present in fruit and vegetables on a population characterized by a diet rich in fruits and vegetables and with regular wine consumption [La Vecchia and Bosetti, 2006].

CANCERS OF THE UPPER DIGESTIVE TRACT

The study of oral and pharyngeal cancer (Table 20.1) showed that total flavonoids were inversely related to the risk of this neoplasm [Rossi et al., 2007b]. The ORs for the highest versus the lowest quintile of all classes of flavonoid intake were below unity. The OR was 0.51 (95% confidence interval,

Table 20.1 Odds Ratios^a (OR) and 95% Confidence Intervals (CI) Among 805 Cases of Oral Cavity and Pharyngeal Cancer and 2081 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoid. Italy, 1992–2005.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	23.3	40.3	59.4	99.6	—	
OR	1	1.06	0.85	0.77	0.84	2.05
(95% CI)		(0.76–1.48)	(0.60–1.20)	(0.54–1.09)	(0.60–1.18)	(0.15)
Flavanones (mg)						
Upper cutpoint	10.2	28.6	36.2	67.0	—	
OR	1	0.90	0.70	0.61	0.51	22.03
(95% CI)		(0.68–1.18)	(0.52–0.94)	(0.45–0.83)	(0.37–0.71)	(<0.001)
Anthocyanidins (mg)						
Upper cutpoint	5.3	13.4	20.9	33.2	—	
OR	1	0.89	0.70	0.66	0.86	2.32
(95% CI)		(0.63–1.25)	(0.49–1.01)	(0.47–0.94)	(0.60–1.22)	(0.13)
Flavonols (mg)						
Upper cutpoint	13.9	18.2	23.2	29.9	—	
OR	1	0.92	0.80	0.65	0.62	9.33
(95% CI)		(0.66–1.28)	(0.57–1.12)	(0.46–0.92)	(0.43–0.89)	(0.002)
Flavones (mg)						
Upper cutpoint	0.3	0.4	0.5	0.7	—	
OR	1	1.02	0.74	0.95	0.75	3.22
(95% CI)		(0.76–1.36)	(0.54–1.00)	(0.69–1.29)	(0.55–1.04)	(0.073)
Isoflavones (μg)						
Upper cutpoint	14.7	19.4	24.7	32.5	—	
OR	1	1.05	1.06	0.89	0.90	0.92
(95% CI)		(0.78–1.42)	(0.78–1.44)	(0.65–1.23)	(0.64–1.26)	(0.34)
Total flavonoids (mg)						
Upper cutpoint	83.5	117.9	151.8	204.0	—	
OR	1	0.77	0.64	0.63	0.56	11.92
(95% CI)		(0.56–1.06)	(0.46–0.89)	(0.45–0.87)	(0.40–0.78)	(0.001)

^aEstimates from logistic regression models, conditioned on sex, age, study center, and adjusted for education, alcohol consumption, tobacco smoking, body mass index, and nonalcohol energy intake.

^bReference category.

Source: From Rossi et al. [2007b].

CI, 0.37–0.71) for flavanones, 0.62 (95% CI, 0.43–0.89) for flavonols, and 0.56 (95% CI, 0.40–0.78) for total flavonoids. No significant association emerged for other classes of flavonoids. The ORs were consistent across strata of age, sex, education, body mass index, tobacco, and alcohol. After allowance for vegetable and fruit consumption, the inverse relations with total flavonoids and flavanones remained significant, whereas that with flavonols became nonsignificant. None of the associations was significant after further allowance for

vitamin C, probably on account of the high colinearity between these compounds.

In the study on esophageal cancer (Table 20.2), only flavanones were inversely associated with cancer risk (OR, 0.38, 95% CI, 0.23–0.66) [Rossi et al., 2007a]. The inverse relation tended to be stronger in subjects who drank ≥ 6 drinks of alcoholic beverages per day. After allowance for fruit intake or vitamin C, the association of flavanones with esophageal cancer remained inverse, though nonsignificant, suggesting that flavanone may explain, together with vitamin C, the protective effect of citrus fruits on esophageal cancer, since citrus fruits account for 90% of flavanone intake.

Table 20.2 Odds Ratios^a (OR) and 95% Confidence Intervals (CI) Among 304 Cases of Squamous Cell Cancer of the Esophagus and 743 Controls, According to Daily Intake Quintile of Five Classes of Flavonoids and Total Flavonoids. Italy, 1992–1997.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	32.6	49.4	72.8	109.1	—	
OR	1	1.03	0.72	0.89	1.06	0.08
(95% CI)		(0.55–1.96)	(0.38–1.37)	(0.48–1.64)	(0.58–1.94)	(0.77)
Flavanones (mg)						
Upper cutpoint	6.4	19.7	33.9	58.8	—	
OR	1	0.42	0.59	0.56	0.38	8.47
(95% CI)		(0.26–0.67)	(0.36–0.97)	(0.34–0.92)	(0.23–0.66)	(0.004)
Anthocyanidins (mg)						
Upper cutpoint	8.1	18.2	30.2	41.2	—	
OR	1	0.60	0.56	0.41	0.84	0.45
(95% CI)		(0.29–1.24)	(0.29–1.13)	(0.22–0.79)	(0.46–1.54)	(0.50)
Flavonols (mg)						
Upper cutpoint	15.9	20.4	25.4	31.9	—	
OR	1	1.02	0.76	0.55	0.68	3.54
(95% CI)		(0.59–1.76)	(0.43–1.32)	(0.30–0.98)	(0.38–1.24)	(0.060)
Flavones (mg)						
Upper cutpoint	0.3	0.4	0.5	0.7	—	
OR	1	0.87	1.31	0.78	0.97	0.02
(95% CI)		(0.52–1.44)	(0.81–2.11)	(0.45–1.36)	(0.57–1.67)	(0.88)
Total flavonoids (mg)						
Upper cutpoint	96.5	127.7	166.2	217.4	—	
OR	1	1.29	0.78	0.81	0.99	0.23
(95% CI)		(0.72–2.33)	(0.42–1.42)	(0.45–1.46)	(0.55–1.79)	(0.63)

^aEstimates from multiple logistic regression models adjusted for age, sex, study center, education, alcohol consumption, tobacco smoking, body mass index, and energy intake.

^bReference category.

Source: From Rossi et al. [2007a].

In the study on laryngeal cancer (Table 20.3), significant inverse relations were found for flavan-3-ols (OR,0.64), flavanones (OR,0.60), flavonols (OR,0.32), and total flavonoids (OR,0.60), although the overall trends in risk were significant only for flavanones and flavonols [Garavello et al., 2007]. The estimates persisted after controlling for vegetable, fruit, and vitamin C intake.

The Italian data are in agreement with those of a case-control study conducted in Uruguay that investigated the relation between diet and upper

Table 20.3 Odds Ratios^a (OR) and 95% Confidence Intervals (CI) Among 460 Cases of Laryngeal Cancer and 1088 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoids. Italy, 1992–2000.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	31.2	50.2	72.9	110.4	—	
OR	1	0.63	0.57	0.49	0.64	3.26
(95% CI)		(0.40–1.01)	(0.35–0.91)	(0.31–0.77)	(0.41–0.99)	(0.071)
Flavanones (mg)						
Upper cutpoint	7.7	20.8	33.7	49.2	—	
OR	1	0.55	0.54	0.39	0.60	10.53
(95% CI)		(0.38–0.81)	(0.37–0.80)	(0.26–0.59)	(0.41–0.89)	(0.001)
Anthocyanidins (mg)						
Upper cutpoint	8.6	18.8	30.7	41.1	—	
OR	1	1.21	1.05	0.51	0.77	2.14
(95% CI)		(0.71–2.06)	(0.60–1.83)	(0.30–0.89)	(0.46–1.30)	(0.14)
Flavonols (mg)						
Upper cutpoint	16.8	22.1	26.8	33.7	—	
OR	1	0.53	0.49	0.30	0.32	24.61
(95% CI)		(0.34–0.82)	(0.31–0.75)	(0.19–0.48)	(0.20–0.52)	(<0.001)
Flavones (mg)						
Upper cutpoint	0.3	0.4	0.5	0.7	—	
OR	1	0.76	0.80	0.58	0.76	2.52
(95% CI)		(0.50–1.14)	(0.53–1.20)	(0.38–0.89)	(0.50–1.15)	(0.11)
Isoflavones (µg)						
Upper cutpoint	14.7	19.8	25.1	32.6	—	
OR	1	1.23	0.87	0.67	0.73	6.41
(95% CI)		(0.82–1.85)	(0.57–1.33)	(0.43–1.03)	(0.47–1.14)	(0.011)
Total flavonoids (mg)						
Upper cutpoint	95.5	132.1	168.0	221.8	—	
OR	1	0.62	0.56	0.57	0.60	3.55
(95% CI)		(0.39–0.99)	(0.36–0.88)	(0.36–0.89)	(0.38–0.94)	(0.060)

^aEstimates from multiple logistic regression models adjusted for age, sex, study center, education, alcohol consumption, tobacco smoking, body mass index, occupational physical activity, and nonalcohol energy intake.

^bReference category.

Source: From Garavello et al. [2007].

aerodigestive tract and reported inverse relations between flavonoids and oral (OR, 0.8 for the highest versus the lowest tertile), esophageal (OR, 0.4), and laryngeal cancer risk (OR, 0.6). No specific information on flavonoids are given in that study, and, to our knowledge, no other study investigated the issue. Moreover, flavanones, which were the class of flavonoids most strongly associated to the risk of neoplasms at the upper aerodigestive tract in these Italian studies, have been inversely related to gastric cancer in a Greek case-control study [Lagiou et al., 2004]. This is of particular interest, given the similarities in risk factors between various neoplasms of the upper digestive and respiratory tract (mainly tobacco, alcohol, as well as a diet poor in vegetables and fruit) [Franceschi et al., 1990; La Vecchia et al., 1999], and gastric cancer, too (i.e., tobacco, lower social class, and various indicators of a poor diet) [La Vecchia and Franceschi, 2000]. As also noted for esophageal and laryngeal cancers, the inverse relation between flavanones and stomach cancer was still persistent, although became weaker, after allowance for vitamin C [Garavello et al., 2007; Lagiou et al., 2004; Rossi et al., 2007a].

COLORECTAL CANCER

In the study on colorectal cancer (Table 20.4), a reduced risk was found for increasing intake of anthocyanidins (OR, 0.67 for the highest versus the lowest quintile, p -trend, 0.001), flavonols (OR, 0.64, p -trend < 0.001), flavones (OR, 0.78, p -trend, 0.004), and isoflavones (OR, 0.76, p -trend, 0.001). [Rossi et al., 2006].

The estimates did not substantially differ for colon and rectal cancers. After allowance for fruit and vegetable consumption, for dietary fiber, or for micronutrients previously associated to this tumor including vitamin C, the associations with flavonoids did not change by more than 10%. A recent case-control study of 1456 pairs of cases and controls conducted in Sweden confirmed a significant decrease in risk of colorectal cancer for intake of anthocyanidins and flavonols [Theodoratou et al., 2007], but there was no relation for isoflavones and flavones. However, the results on isoflavones and flavones are questionable due to the unusually and generally low intakes of the populations studied. In the Italian population, anthocyanidins were derived mainly from wine, red fruit, and onions, and flavonols from apples or pears, wine, and mixed salads.

BREAST CANCER

The study on breast cancer (Table 20.5) found a reduced risk of breast cancer for increasing intake of flavones (OR, 0.81, p -trend = 0.02), and flavonols (OR, 0.80, p -trend 0.06) [Bosetti et al., 2005]. These findings are in agreement with those of a case-control study on breast cancer from Greece [Peterson et al., 2003], which found a similar protective effect of flavones. Also a recent

Table 20.4 Odds Ratios^a (OR) and 95% Confidence Intervals (CI) Among 1953 Cases from Colorectal Cancer and 4154 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoids, Italy, 1992–1996.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	25.02	48.79	48.79	78.29	—	
OR	1	0.75	0.75	0.79	0.98	0.11
(95% CI)		(0.63–0.91)	(0.62–0.90)	(0.65–0.95)	(0.82–1.18)	(0.74)
Flavanones (mg)						
Upper cutpoint	12.86	27.94	38.25	62.9	—	
OR	1	0.88	0.89	0.80	0.96	0.62
(95% CI)		(0.74–1.05)	(0.75–1.07)	(0.67–0.96)	(0.81–1.15)	(0.43)
Anthocyanidins (mg)						
Upper cutpoint	9.15	14.88	20.55	29.06	—	
OR	1	0.81	0.78	0.64	0.67	20.02
(95% CI)		(0.68–0.96)	(0.65–0.93)	(0.53–0.77)	(0.54–0.82)	(<0.001)
Flavonols (mg)						
Upper cutpoint	15.3	18.27	21.62	26.9	—	
OR	1	0.80	0.77	0.74	0.64	21.09
(95% CI)		(0.67–0.95)	(0.64–0.91)	(0.62–0.88)	(0.54–0.77)	(<0.001)
Flavones (mg)						
Upper cutpoint	0.30	0.40	0.50	0.65	—	
OR	1	0.82	0.72	0.76	0.78	8.38
(95% CI)		(0.69–0.98)	(0.61–0.86)	(0.64–0.91)	(0.65–0.93)	(0.004)
Isoflavones (μ g)						
Upper cutpoint	16.22	20.88	25.66	32.96	—	
OR	1	0.86	0.79	0.77	0.76	10.81
(95% CI)		(0.72–1.02)	(0.66–0.94)	(0.65–0.92)	(0.63–0.91)	(0.001)
Total flavonoids (mg)						
Upper cutpoint	86.23	112.73	138.93	180.49	—	
OR	1	0.90	0.79	0.81	0.97	0.45
(95% CI)		(0.75–1.08)	(0.66–0.94)	(0.67–0.97)	(0.81–1.16)	(0.50)

^aEstimates from multiple logistic regression models adjusted for age, sex, study center, education, alcohol consumption, body mass index, physical activity, family history of colorectal cancer and energy intake, according to the residual model.

^bReference category.

Source: From Rossi et al. [2006].

case-control study from the United States on 1434 women of Long Island [Fink et al., 2007] confirmed previous results on these Mediterranean populations. Among Italian women, flavonol intake derived mainly from various common vegetables and fruits, and flavone intake from aromatic herbs. Most epidemiological studies also found that dietary phytoestrogens were inversely associated to breast cancer risk [Cotterchio et al., 2008]. The absence of any meaningful association with isoflavone intake in the Italian study may be due to the

Table 20.5 Odds Ratio (OR)^a and 95% Confidence Intervals (CI) Among 2569 Cases of Breast Cancer and 2588 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids. Italy, 1991–1994.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	18.1	30.3	44.1	79.7	—	
OR ^c	1	0.98	0.80	1.01	0.86	1.28
(95% CI)		(0.82–1.18)	(0.66–0.98)	(0.83–1.23)	(0.71–1.05)	(0.26)
Flavanones (mg)						
Upper cutpoint	11.5	29.1	37.7	62.2	—	
OR ^c	1	1.19	1.11	1.15	0.95	0.48
(95% CI)		(1.00–1.43)	(0.92–1.33)	(0.96–1.38)	(0.79–1.15)	(0.49)
Anthocyanidins (mg)						
Upper cutpoint	3.7	7.9	14.3	20.5	—	
OR ^c	1	1.03	1.16	1.11	1.09	0.76
(95% CI)		(0.86–1.25)	(0.95–1.40)	(0.90–1.37)	(0.87–1.36)	(0.38)
Flavonols (mg)						
Upper cutpoint	12.6	16.4	21.5	29.9	—	
OR ^c	1	0.81	1.00	0.82	0.80	3.52
(95% CI)		(0.67–0.98)	(0.83–1.21)	(0.67–1.00)	(0.66–0.98)	(0.06)
Flavones (mg)						
Upper cutpoint	0.2	0.3	0.5	0.6	—	
OR ^c	1	0.94	0.97	0.86	0.81	5.41
(95% CI)		(0.79–1.13)	(0.81–1.17)	(0.71–1.04)	(0.66–0.98)	(0.02)
Isoflavones (μg)						
Upper cutpoint	13.4	19.0	25.2	34.7	—	
OR ^c	1	1.05	1.00	1.02	1.05	0.08
(95% CI)		(0.87–1.27)	(0.83–1.22)	(0.84–1.24)	(0.86–1.29)	(0.78)

^aEstimates from multiple logistic regression models including terms for age, study center, education, parity, alcohol consumption and nonalcohol energy intake.

^bReference category.

Source: From Bosetti et al. [2005].

extremely limited intake of soya or soya products—and consequently of isoflavones—in the Italian population.

OVARIAN CANCER

The study on ovarian cancer (Table 20.6) found an inverse relation with ovarian cancer risk for flavonols (OR, 0.63; 95% CI, 0.47–0.84) and isoflavones (OR, 0.51; 95% CI, 0.37–0.69), with a significant trend in risk [Rossi et al., 2008]. In line with these findings, intake of isoflavones was associated with a lower risk of ovarian cancer in a U.S. cohort study including 280 cancers (relative risk 0.56 for more than 3 mg/day versus less than 1 mg/day of intake)

Table 20.6 Odds Ratios^a (OR) and Corresponding 95% Confidence Intervals (CI) Among 1031 Cases of Ovarian Cancer and 2411 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoids. Italy, 1992–1999.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	16.3	28.3	42.7	77.0	—	
OR	1	0.81	0.73	0.92	0.89	0.23
(95% CI)		(0.62–1.05)	(0.55–0.96)	(0.71–1.19)	(0.67–1.17)	(0.63)
Flavanones (mg)						
Upper cutpoint	12.2	31.3	36.6	67.0	—	
OR	1	1.22	0.99	1.07	1.28	1.44
(95% CI)		(0.93–1.60)	(0.75–1.31)	(0.81–1.41)	(0.98–1.68)	(0.23)
Anthocyanidins (mg)						
Upper cutpoint	3.5	7.4	12.3	19.4	—	
OR	1	0.74	0.90	1.02	0.99	0.68
(95% CI)		(0.56–0.98)	(0.68–1.18)	(0.79–1.34)	(0.76–1.29)	(0.41)
Flavonols (mg)						
Upper cutpoint	11.6	15.4	20.0	28.8	—	
OR	1	0.78	0.65	0.88	0.63	6.89
(95% CI)		(0.60–1.01)	(0.50–0.85)	(0.67–1.14)	(0.47–0.84)	(0.009)
Flavones (mg)						
Upper cutpoint	0.3	0.4	0.5	0.7	—	
OR	1	0.91	0.95	0.87	0.79	2.62
(95% CI)		(0.70–1.19)	(0.73–1.24)	(0.66–1.15)	(0.60–1.04)	(0.11)
Isoflavones (μ g)						
Upper cutpoint	12.8	17.8	23.5	32.5	—	
OR	1	1.12	0.93	0.85	0.51	19.51
(95% CI)		(0.87–1.45)	(0.71–1.21)	(0.64–1.12)	(0.37–0.69)	(<0.001)
Total flavonoids (mg)						
Upper cutpoint	67.3	97.2	127.5	173.6	—	
OR	1	1.03	0.94	0.80	1.07	0.12
(95% CI)		(0.80–1.34)	(0.72–1.24)	(0.61–1.06)	(0.82–1.40)	(0.72)

^aEstimates from multiple logistic regression models including terms for age, study center, year of interview, education, parity, oral contraceptive use, and family history of ovarian and/or breast cancer and energy intake, according to the residual model.

^bReference category.

Source: From Rossi et al. [2008].

[Chang et al., 2007], and in a Chinese case-control study based on 254 cases (OR 0.51 for more than 32.8 mg/day versus less than 11.6 mg/day of intake) [Zhang et al., 2004]. The evidence of an inverse association between isoflavones and ovarian cancer risk is supported by the observation that isoflavones have antiestrogenic effects [Ross and Kasum, 2002] and hence may inhibit the growth and proliferation of ovarian cell lines [Gercel-Taylor et al., 2004; Lukanova and Kaaks, 2005; Spinella et al., 2006].

PROSTATE CANCER

The study on prostate cancer (Table 20.7) found no association between prostate cancer risk with any of the analyzed flavonoids [Bosetti et al., 2006]. Although some flavonoids showed a favorable effect against prostate cancer [Magee and Rowland, 2004], the results from epidemiological studies are inconsistent. A recent prospective study from Japan found that isoflavone

Table 20.7 Odds Ratios^a (OR) and Corresponding 95% Confidence Intervals (CI) Among 1294 Cases of Prostate Cancer and 1451 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoids. Italy, 1991–2002.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	29.9	47.6	67.8	102.1	—	
OR	1	1.33	1.08	0.94	1.30	0.49
(95% CI)		(1.04–1.70)	(0.84–1.40)	(0.72–1.23)	(1.01–1.69)	(0.48)
Flavanones (mg)						
Upper cutpoint	5.2	19.1	33.5	46.9	—	
OR	1	1.10	1.06	1.00	0.96	0.35
(95% CI)		(0.86–1.40)	(0.82–1.36)	(0.78–1.29)	(0.75–1.23)	(0.56)
Anthocyanidins (mg)						
Upper cutpoint	8.3	18.4	29.8	40.3	—	
OR	1	1.13	1.20	1.18	1.18	1.49
(95% CI)		(0.88–1.45)	(0.94–1.54)	(0.91–1.52)	(0.91–1.53)	(0.22)
Flavonols (mg)						
Upper cutpoint	15.1	19.8	24.0	30.7	—	
OR	1	1.31	1.08	1.24	1.23	1.26
(95% CI)		(1.02–1.68)	(0.83–1.40)	(0.95–1.62)	(0.95–1.61)	(0.26)
Flavones (mg)						
Upper cutpoint	0.2	0.3	0.4	0.6	—	
OR	1	1.13	1.09	0.98	1.09	0.02
(95% CI)		(0.88–1.45)	(0.85–1.40)	(0.76–1.26)	(0.85–1.40)	(0.88)
Isoflavones (μ g)						
Upper cutpoint	14.7	19.8	24.8	32.2	—	
OR	1	1.15	0.94	0.92	0.98	0.90
(95% CI)		(0.90–1.47)	(0.73–1.20)	(0.71–1.18)	(0.76–1.26)	(0.34)
Total flavonoids (mg)						
Upper cutpoint	109.4	145.7	184.4	240.8	—	
OR		1.32	0.97	1.13	1.20	0.59
(95% CI)		(1.06–1.64)	(0.76–1.23)	(0.88–1.44)	(0.92–1.58)	(0.44)

^aEstimates from multiple logistic regression models including terms for age, study center, education, body mass index, family history of prostate cancer, and total energy intake.

^bReference category.

Source: From Bosetti et al. [2006].

intake was associated with a decreased risk of localized prostate cancer [Kurahashi et al., 2007], possibly explaining the much lower incidence of prostate cancer in Asian as compared to Western populations characterized by a low consumption of isoflavone-rich foods such as soya. In the Italian study, isoflavones derive mainly from beans, soy, and soy products, whose consumption is limited in Italy, and this may explain the inconsistent relation observed with prostate cancer.

Table 20.8 Odds Ratios^a (OR) and 95% Confidence Intervals (CI) Among 767 Cases of Renal Cell Carcinoma and 1534 Controls, According to Daily Intake Quintile of Six Classes of Flavonoids and Total Flavonoids. Italy, 1992–2004.

	Quintile of Intake					χ^2 Trend (<i>p</i> Value)
	1 ^b	2	3	4	5	
Flavan-3-ols (mg)						
Upper cutpoint	21.3	35.8	54.0	90.6	—	
OR	1	1.15	1.09	0.91	0.77	4.02
(95% CI)		(0.87–1.52)	(0.80–1.47)	(0.66–1.26)	(0.56–1.06)	(0.045)
Flavanones (mg)						
Upper cutpoint	9.6	22.5	33.9	57.8	—	
OR	1	0.94	0.94	0.71	0.90	1.90
(95% CI)		(0.71–1.25)	(0.71–1.24)	(0.53–0.96)	(0.67–1.21)	(0.17)
Anthocyanidins (mg)						
Upper cutpoint	5.5	11.6	19.7	32.4	—	
OR	1	0.96	0.79	1.06	0.94	0.19
(95% CI)		(0.72–1.28)	(0.58–1.09)	(0.74–1.53)	(0.60–1.47)	(0.67)
Flavonols (mg)						
Upper cutpoint	13.3	17.6	22.1	29.9	—	
OR	1	0.89	0.76	0.88	0.69	4.05
(95% CI)		(0.68–1.19)	(0.57–1.03)	(0.65–1.19)	(0.50–0.95)	(0.044)
Flavones (mg)						
Upper cutpoint	0.3	0.4	0.5	0.6	—	
OR	1	1.05	0.87	0.86	0.68	7.37
(95% CI)		(0.80–1.39)	(0.65–1.16)	(0.64–1.15)	(0.50–0.93)	(0.007)
Isoflavones (μ g)						
Upper cutpoint	14.8	19.7	24.8	32.6	—	
OR	1	0.86	0.81	0.77	0.76	3.48
(95% CI)		(0.65–1.14)	(0.61–1.08)	(0.57–1.03)	(0.56–1.03)	(0.062)
Total flavonoids (mg)						
Upper cutpoint	80.6	109.1	139.4	180.9	—	
OR	1	1.01	0.89	0.77	0.80	3.55
(95% CI)		(0.76–1.33)	(0.66–1.19)	(0.56–1.05)	(0.58–1.11)	(0.060)

^aEstimates from conditional logistic regression models, conditioned on sex, age, study center, and adjusted for period of interview, education, alcohol consumption, tobacco smoking, body mass index, occupational physical activity, family history of kidney cancer, and total energy intake.

^bReference category.

Source: From Bosetti et al. [2007].

RENAL CANCER

The study on renal cell carcinoma (Table 20.8) showed that flavonols (OR, 0.69, 95% CI, 0.50–0.95) and flavones (OR, 0.68, 95% CI, 0.50–0.93) were inversely related to the risk of renal cancer [Bosetti et al., 2007]. Allowance for vegetable and fruit consumption only partly explained the inverse relation with flavonoids. No other study systematically investigated the relation between flavonoids and renal cancer risk.

CONCLUSIONS

In conclusion, the findings of this large series of Italian case–control studies provide support for a protective role of flavanones on upper aerodigestive tract, flavonols and anthocyanidins on colorectal, flavonols and flavones on breast, and isoflavones on ovarian cancers. For most investigated neoplasms, adjustment for flavonoids reduced the strength of the inverse association between vegetables or fruit consumption and the risk of cancer, whereas allowance for fruit and vegetable consumption only moderately changed the observed associations with flavonoids. This suggests that, on one side, a diet rich in fruit and vegetables does not alone account for the observed protections on cancer risk, and, on the other side, the relation with fruit and vegetables is not totally explained by flavonoid intake.

ACKNOWLEDGMENTS

This work was conducted with the support of the Italian Association for Cancer Research and the Italian League against Cancer. The work in this chapter was undertaken while CLV was a senior fellow at the International Agency for Research on Cancer. The authors thank Ms. I. Garimoldi for editorial assistance.

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21 Phenylpropanoid Metabolism in Plants: Biochemistry, Functional Biology, and Metabolic Engineering

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INTRODUCTION

Phenylpropanoids constitute a diverse group of phenylalanine-derived secondary metabolites with a multitude of functions in biology and ecophysiology of plants [Taylor and Grotewold, 2005]. Simple phenolics and flavonoids have potent bioactivity, and their presentation at key points in a plant's life cycle can constitute important adaptations, often conferring properties that are integral to plant survival. For example, several plant reproductive processes are mediated by different flavonoids acting to attract pollinators [Mol et al., 1998], contributing to pollen structure and function [Coe et al., 1981; Mo et al., 1992; Taylor and Jorgensen, 1992], and facilitating seed dispersal and protection [Debeaujon et al., 2000; Lepiniec et al., 2006]. Similarly, lignins, which are structural components of plant cell walls, and several flavonoids exert profound effects on plant growth and morphogenesis by modulating structural integrity of the plant body and acting to regulate polar auxin transport, respectively [Jacobs and Rubery, 1988; Mathesius et al., 1998; Murphy et al., 2000; Brown et al., 2001; Buer and Muday, 2004; Peer et al., 2004]. Simple phenolics and flavonoids are often key determinants of the outcome of interactions with other organisms, including serving as allelopathic agents in interspecies plant–plant competition [Bais et al., 2004], acting as insect and herbivore deterrents [Feeny, 1970; Forkner et al., 2004; McAllister et al., 2005], mediating signaling processes with soil-borne symbiotic nitrogen-fixing bacteria [Peters et al., 1986; Redmond et al., 1986; Djordjevic et al., 1987; Harrison, 2005; Wasson et al., 2006] and contributing to defense mechanisms against different pathogens [Treutter, 2005].

Knowledge about most enzymatic steps as well as regulatory mechanisms at the transcriptional and posttranscriptional level has greatly improved over the last 20 years [Grotewold, 2006] in part due to the availability of a wide collection of natural or induced mutants in different model plant systems [Peer et al., 2001]. Several transcription factors of the myeloblastoma (MYB), basic

helix-loop-helix (bHLH), and WD-repeat (WDR) families control expression of different biosynthetic genes during the course of normal plant development [Winkel-Shirley, 2002] or they activate gene expression in response to abiotic and biotic stress elicitors [Lepiniec et al., 2006]. The biosynthetic pathway is thought to be organized as a metabolom on the cytoplasmic side of the endoplasmic reticulum (ER), with colocalization greatly enhancing biosynthetic efficiency [Winkel-Shirley, 2002; Winkel, 2004]. Several excellent reviews have summarized our current knowledge of the topology and regulation of this pathway in plants [Shirley, 1996; Whinkel-Shirley, 2001; Saito and Yamazaki, 2002; Xie and Dixon, 2005]. Here we revisit the most relevant information about the genetic and enzymatic components of phenylpropanoid metabolism with special emphasis on the (iso)flavonoid pathway. We also summarize the critical biological roles played by these secondary metabolites in different aspects of the life cycle of plants. Finally, we discuss the current status and future perspectives of metabolic engineering of the phenylpropanoid pathway to enhance the nutraceutical value of plant-based foods, improving structural properties of lignocellulosic biomass for industrial applications, and discovering new bioactive (iso)flavonoids with pharmaceutical application.

PHENYLPROPANOID METABOLISM IN PLANTS

Phenylpropanoid Biosynthesis in Plants: Enzymology and Pathway Topology

The phenylpropanoid pathway gives rise to a myriad of polyfunctional bioactive molecules that accumulate in plants as monomeric (e.g., hydroxycinnamic acids, monolignols, anthocyanins, flavonols, flavones, auronol, stilbenes, isoflavones) or polymeric [e.g., proanthocyanidins (PA), phlobaphenes, lignins] compounds. Flavonoids in particular are built on a conserved C₁₅ (6:3:6) structure, with a diversity of conjugation and substitution patterns in the C-ring (Fig. 21.1). The nature of these modifications serves as the basis to define flavonoid groups, many of which have distinctive physicochemical properties and biological activities [Frankel et al., 1995; de Beer et al., 2002; Rice-Evans and Miller, 1996; Rice-Evans et al., 1996; Springob et al., 2003]. Additional hydroxylation and methylation substitutions at positions 3', 4', and 5' of the B-ring further delineate specific compounds within a given flavonoid group. Flavonoids are present in all plant taxa with the noticeable exception of algae [reviewed by Raushier, 2006], consistent with the proposal that gain-of-function traits associated with flavonoid accumulation were critical to increased reproductive fitness and survival of early land plants. Phenylpropanoid biosynthesis requires the coordinated action of a multiplicity of enzymes and enzymatic complexes to channel carbon from intermediates of primary metabolism to the different end products of the pathway [Winkel, 2004]. The topology of the biosynthetic pathway as well as structural similarity of the end products can be traced from relatively recent

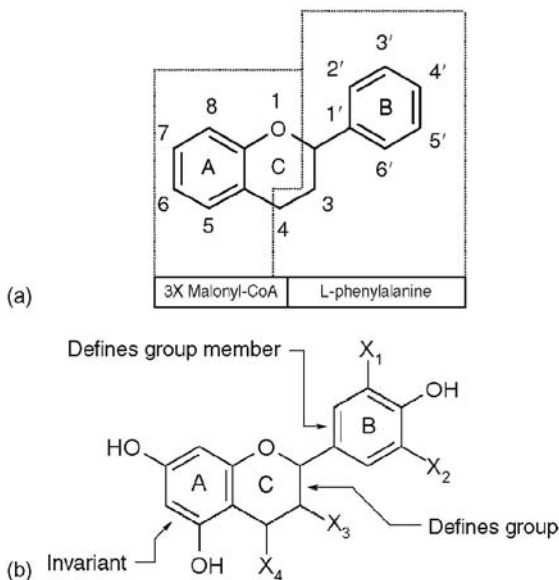


Figure 21.1 Basic C15 (6:3:6) structure of flavonoids and numbering system for carbon positions in the three rings. The B-ring carbon skeleton derives entirely from L-phenylalanine. Ring A and C is originated in the condensation reaction with three malonyl-CoA moieties, B, C. Common patterns of conjugation and substitutions in the B- and C-rings defining the different flavonoid groups.

gymnosperm and angiosperm lineages, to the more ancient taxa of extant bryophytes (mosses) [Rausher, 2006].

The deamination of L-phenylalanine to trans-cinnamic acid, which is catalyzed by phenylalanine ammonia lyase (PAL, EC 4.3.1.5) (Fig. 21.2), represents the first committed step of the general phenylpropanoid pathway. The resulting cinnamate is converted to *p*-coumaric acid in a hydroxylation reaction mediated by the P450 mono-oxygenase cinnamic acid 4-hydroxylase (C4H, EC 1.14.13.11). A series of sequential reactions controlled by hydroxylases, SAM-dependent *O*-methyltransferases, and dehydratases convert *p*-coumarate into a pool of free (e.g., caffeic, ferulic, 5-hydroxyferulic and sinapic acid) and sterified (e.g., with organic acids) hydroxycinnamic acids [Boerjan et al., 2003]. Activation of hydroxycinnamic acids with coenzyme A in an ATP-dependent thioesterification reaction, catalyzed by 4-coumaroyl-CoA ligase (4CL, EC 6.2.1.12) [Heldt, 1999], is required for biosynthesis of the monolignol precursors of lignins [Boerjan et al., 2003] and the initial step of (iso)flavonoid and stilbene biosynthesis.

The irreversible condensation reaction between a starter hydroxycinnamoyl-CoA molecule and three acetate extender units derived from malonyl-CoA constitute the first committed step of flavonoid and stilbene biosynthesis [Springob et al., 2003] (Fig. 21.2). The reactions catalyzed by two type III

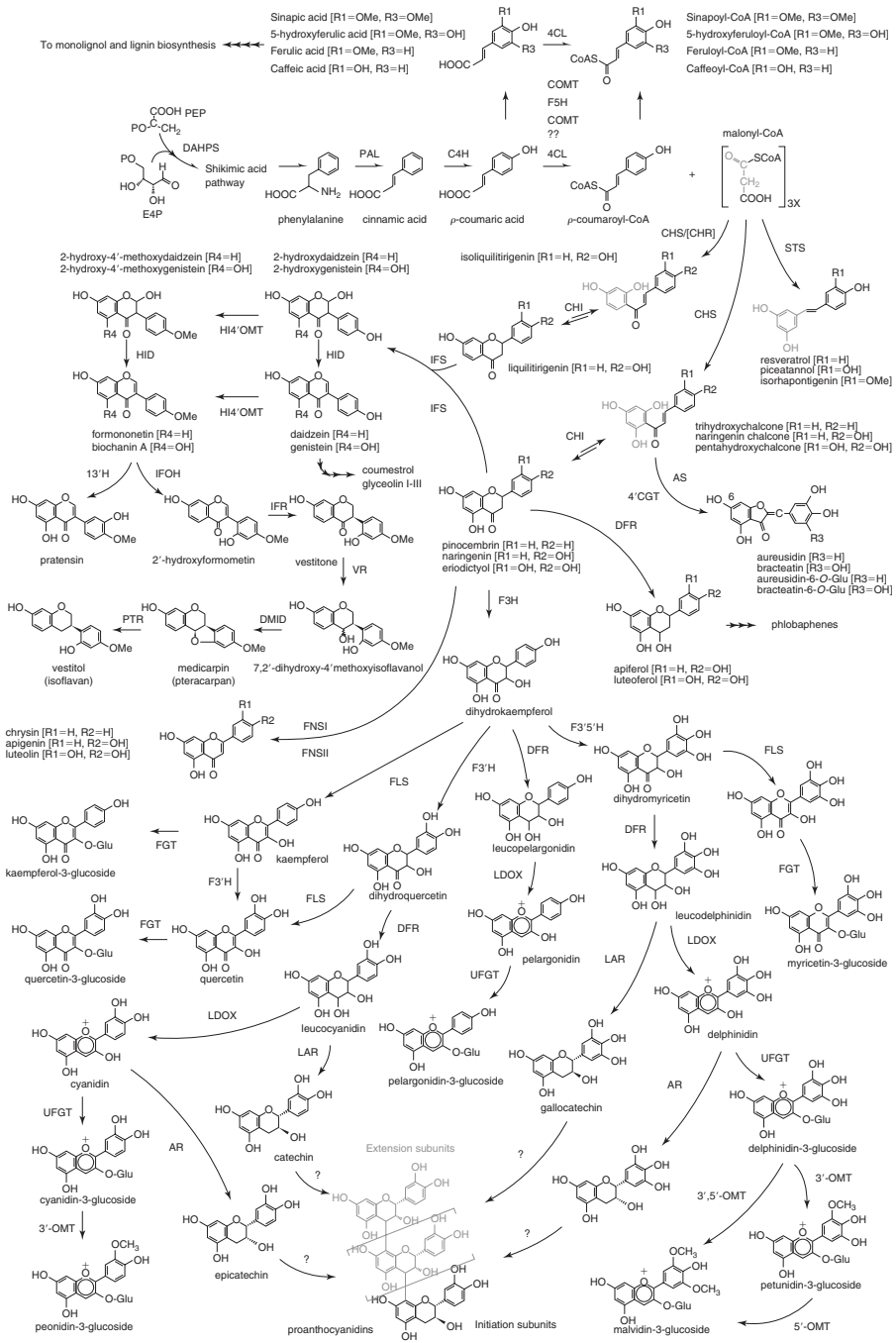


Figure 21.2 Schematic representation of the general phenylpropanoid, flavonoid, and isoflavonoid pathways in plants (see text for legends).

polyketide synthases (PKS), chalcone synthase (CHS, EC 2.3.1.74), and stilbene synthase (STS, EC 2.3.1.95) yield a linear tetraketide intermediate [Watts et al., 2006; Halls and Yu, 2008], which after subsequent aldol condensation, decarboxylation, and a final aromatization step, is converted to the C15 (6:3:6) chalcone skeleton that is common to all flavonoids or to the C14 (6:2:6) stilbene structure [Watts et al., 2006].

Stilbenes, and in particular trans-resveratrol, are found in at least 72 plant species from 31 different genera and 12 botanical families [Counet et al., 2006]. Among the most publicized examples with relevance to the human diet are grapes (*Vitis* sp.) [Li et al., 2006a; Creasy and Creasy, 1998], cranberries (*Vaccinium macrocarpon*) [Wang et al., 2002], peanuts (*Arachis hypogea*) [Lee et al., 2004], and cocoa (*Theobroma cacao*) [Counet et al., 2006]. STS activity converts the acetyl-CoA esters of the hydroxycinnamic acids (i.e., *p*-coumaric, caffeic, and ferulic acids) to their respective stilbenes, namely resveratrol (3,5,4'-trans-trihydroxystilbene), piceatannol (3,3',4',5-tetrahydroxystilbene), and isorhapontigenin (3,4',5-dihydroxy-3'-methoxystilbene). STS isoforms from different plant species vary in their affinity for hydroxycinnamoyl-CoAs [Schoppner and Kindl, 1984; Kodan et al., 2002]. For example, the peanut STS cannot properly fold feruoyl-CoA-derived linear tetraketide intermediates, resulting in the accumulation of tri- and tetraketide lactones [Watts et al., 2006], while STS from *Pinus* spp. prefers cinnamoyl-CoA over *p*-coumaroyl-CoA [Kodan et al., 2002; Raiber et al., 1995]. Native American and European grapes (*Vitis* spp.) constitute an excellent model for characterization of stilbene biosynthesis and metabolism. Stilbenes accumulate at high levels in grape leaves and stems (Langcake, 1981) and at lower concentrations in berry skins and seeds [Li et al., 2006a]. Steady-state levels can be greatly changed by fungal elicitors [Langcake and Pryce, 1977a], ultra violet (UV) radiation [Langcake and Pryce, 1977b; Cantos et al., 2002], and phytohormones [Tassoni et al., 2005]. The trans-isomer of resveratrol is typically the most abundant stilbene species found in different tissues [Li et al., 2006a; Ali and Strommer, 2003; Versari et al., 2001; Waterhouse and Lamuela-Raventos, 1994]. In lower quantities, grapes also produce other stilbene aglycones such as cis-resveratrol [Moreno et al., 2008], trans-piceatannol or trans-astringinin (3',4',3,5-tetrahydroxystilbene) [Cantos et al., 2002], and pterostilbene (3,5-dimethoxy-4'-hydroxystilbene) [Langcake, 1981]. A recently characterized multifunctional glucosyltransferase from the native American grape *Vitis labrusca* [Hall and De Luca, 2006] accepts a range of structurally similar substrates, including resveratrol, flavonols, and hydroxycinnamic acids and might be involved in the biosynthesis of the 3-*O*-monoglucosides trans-piceid (trans-resveratrol-3-*O*- β -glucoside) and trans-astringin (trans-piceatannol-3-*O*- β -glucoside) [Cantos et al., 2002]. Glucosylation may play a critical role in protecting stilbenes from polyphenol oxidase-mediated oxidative degradation [Regev-Shoshani et al., 2003]. Several plant species [Sotheeswaran and Pasupathy, 1993], including grapes [Langcake, 1981; Langcake and Pryce, 1977a,b; Cantos et al., 2002], accumulate oligomeric stilbenes with potent

phytoalexin properties. In grapes, certain stilbene oligomers, known as viniferins [Langcake and Pryce, 1977a,b; Langcake, 1981; Cantos et al., 2002], arise from the oxidative coupling of trans-resveratrol moieties [Ros Barceló et al., 2003]. The reaction is likely to be catalyzed by a still uncharacterized 4-hydroxystilbene peroxidase [Calderon et al., 1992; Ros Barceló and Pomar, 2002; Ros Barceló et al., 2003, Pezet et al., 2004] that oxidizes trans-resveratrol to form stilbene dimers (ϵ -viniferin), trimers (α -viniferin), and tetramers (Γ -2-viniferin) [Ros Barceló et al., 2003].

The 2',4',6',4-tetrahydroxychalcone (naringenin chalcone or chalcone) resulting from the CHS reaction is converted to the (2*S*)-flavanone naringenin spontaneously or by a stereo-specific cyclization reaction catalyzed by chalcone isomerase (CHI, EC 5.5.1.6) [Springob et al., 2003] (Fig. 21.2). Naringenin is a biosynthetic intermediate for a range of flavonoid species, including flavones, isoflavonols, flavanols, anthocyanins, phlobaphenes, flavan-3-ols, and proanthocyanidins. CHS activity can also drive the stepwise condensation of three molecules of malonyl-CoA with cinnamoyl-CoA to yield pinocembrin chalcone, with caffeoyl-CoA to yield eriodictyol chalcone (2',4',6',3,4-pentahydroxychalcone), and with feruloyl-CoA to yield homoeriodictyol chalcone [Yan et al., 2005]. The action of CHI on these chalcone substrates results in the production of their respective (2*S*)-flavanones: (2*S*)-pinocembrin, (2*S*)-eriodictyol, and (2*S*)-homoeriodictyol [Yan et al., 2005]. Other flavanones can result from the activity of P450-dependent monooxygenases on naringenin. For example, eriodictyol results from hydroxylation at position 3' of the B-ring by flavonoid 3'-hydroxylase (F3'H, EC 1.14.13.21) [Springob et al., 2003].

Flavones are ubiquitous in plant organs and tissues of more than 70 different botanical families [Harborne and Baxter, 1999]. Aglycons and glucosides of this flavonoid subgroup participate in important biological functions such as protection against UV radiation, co-pigmentation with anthocyanins, plant-insect interactions, stimulation of arbuscular mycorrhizae colonization, and mediation of the establishment of symbiotic relationship between legumes and nitrogen-fixing rhizobia [reviewed by Martens and Mithöfer, 2005]. Flavones are also of great relevance for human nutrition and health [Martens and Mithöfer, 2005]. The first committed step in flavone biosynthesis starts with the conversion of the (2*S*)-flavanones pinocembrin, naringenin, and eriodictyol to their respective flavones chrysin (5,7-dihydroxyflavone), apigenin (5,7,4'-trihydroxyflavone), and luteolin (5,7,3',4'-tetrahydroxyflavone) (Fig. 21.2). In most plant families [Heller and Forkmann, 1993], this reaction is performed by a membrane-bound NADPH-dependent cytochrome P450 monooxygenase known as flavone synthase II (FNSII, EC 1.14.11.22) [Akashi et al., 1999; Martens and Forkmann, 1999]. Interestingly, members of the Apiaceae (or Umbelliferae) botanical family (e.g., parsley, cilantro, fennel, carrot, etc.) convert flavanones to flavones with a soluble 2-oxoglutarate/Fe²⁺-dependent dioxygenase known as flavone synthase I (FNSI, EC 1.14.11.22) [Lukacin et al., 2001; Martens et al., 2001]. The final biological and pharmacological activity of

different flavones is defined by specific modifications to the basic flavone structure, including hydroxylation, *O*- and *C*-methylation, isoprenylation, and methylenedioxy substitutions [Martens and Mithöfer, 2005].

Isoflavones are found especially in legumes but also in several other plant species [Dewick, 1982], particularly when elicited by pathogen attack [Geigert et al., 1973] or herbivore induced wounding. Isoflavone biosynthesis branches out from the flavonoid pathway (Fig. 21.2). The legume-specific chalcone reductase (CHR, EC 1.1.1.1) converts an intermediate of the multistep reaction catalyzed by CHS to yield 4,2',4'-trihydroxychalcone (deoxychalcone or isoliquiritigenin) [Deavours and Dixon, 2005; Bomati et al., 2005]. This CHS/CHR coupled reaction is unique to legumes and constitutes the main entry point to the biosynthesis of several bioactive isoflavonoids, coumestans, pterocarpan, and isoflavans [Dixon and Paiva, 1995] (Fig. 21.2), with roles in phytoalexin-mediated defense against pathogens and herbivores as well as in signaling with symbiotic N-fixing bacteria. The CHI-catalyzed conversion of isoliquiritigenin to 7,4'-dihydroxyflavanone (syn. liquiritigenin) and naringenin chalcone to naringenin generates substrates for the cytochrome P450 2-hydroxyflavanone synthase, also known as isoflavanone synthase (IFS, EC 1.14.13.86) [Jung et al., 2000]. Isoflavone synthase catalyzes both the hydroxylation at C2 and the unique 1,2 aryl migration from C2 to C3 of the flavanone intermediate to yield 2,7,4'-trihydroxy-isoflavanone or 2-hydroxyflavanone [Akashi et al., 2003; Deavours and Dixon, 2005]. As a result, liquiritigenin (4',7-dihydroxyflavanone) or naringenin yield their respective 4'-hydroxy isoflavones daidzein (4'-7-dihydroxyisoflavone) and genistein (4',5,7-trihydroxyisoflavone) after a dehydration step catalyzed by 2-hydroxyisoflavanone dehydratase (HID, EC 4.2.1.105) [Hakamatsuka et al., 1998; Chen et al., 2001; Akashi et al., 2003, 2005; Deavours and Dixon, 2005; Shimamura et al., 2007]. Another isoflavonoid normally found in legumes, glycitein, is likely to be derived from isoliquiritigenin through a still uncharacterized reaction [Latunde-Dada et al., 2001]. 2-Hydroxyflavanones can be methylated by 2,7,4'-trihydroxyisoflavanone 4'-*O*-methyltransferase (HI4 OMT, EC 2.1.1.46) [Akashi et al., 2003; Deavours and Dixon, 2005; Shimamura et al., 2007] to form 2,7-dihydroxy-4'-methoxyisoflavanones [Akashi et al., 2003] that can be in turn converted by the HID activity to the 4'-methoxy isoflavones formononetin (or 4'-*O*-methyl daidzein) and biochanin A (or 4'-*O*-methyl genistein) [He and Dixon, 2000]. The biosynthetic steps catalyzed by IFS, HID, and HI4 OMT appear to be organized as a multienzyme complex or metabolon [Winkel, 2004]. Naringenin is a precursor to both anthocyanin and proanthocyanidins biosynthesis, and its conversion to genistein is a key factor in the competition for substrate between the isoflavone and flavonoid biosynthetic pathways. For example, accumulation of genistein in IFS overexpressing *Arabidopsis* plants was limited by the predominant channeling of naringenin via the flavonoid pathway [Liu et al., 2002].

The biosynthesis of pterocarpan, which include well-known phytoalexins such as medicarpin in alfalfa (*Medicago sativa*) [Baker et al., 1989; Higgins, 1972; Oommen et al., 1994; He and Dixon, 2000] (Fig. 21.2), pisatin in pea

(*Pisum sativum*) [Akashi et al., 2003], and glyceollin I-III in soybean (*Glycine max*) [López-Meyer and Paiva, 2002; Burrow et al., 2001; Dixon and Paiva, 1995; Guo et al., 1994a; Stoessl, 1982], is strongly induced in leaves elicited by fungal pathogens. Pterocarpan biosynthesis initiates with the conversion of formononetin to 2'-hydroxyformononetin (7-hydroxy-4'-methoxydaidzein) in a dehydration reaction catalyzed by 4'-methoxyisoflavone 2'-hydroxylase (EC 1.14.13.53) [Hinderer et al., 1987] (Fig. 21.2). Isoflavone reductase (IFR, EC 1.3.1.45) further reduces 2'-hydroxyformononetin to the isoflavanone vestitone [López-Meyer and Paiva, 2002]. An additional reduction catalyzed by vestitone reductase (VR, EC 1.3.1.45) converts vestitone to 7,2'-dihydroxy-4'-methoxyisoflavanol (or DMI) [Guo et al., 1994a]. In a final step, DMI dehydratase (DMID, EC 4.2.1) catalyzes DMI dehydration and cyclation of an ether ring to yield (–)-medicarpin [Akashi et al., 2006]. In vitro studies have demonstrated protein–protein interaction between VR and DMID [Guo et al., 1994b] suggesting a possible metabolon organization for these two consecutive reactions. In legumes, glucosyl- and malonyl-glucose [Kudou et al., 1991; Yu et al., 2003] conjugates of isoflavones (daidzein, glycitin, and genistein) [Graham, 1991; Burrow et al., 2001] and pterocarpan [López-Meyer and Paiva, 2002] are stored in the vacuole. Pterocarpan is the initial substrate for the biosynthesis of another group of compounds with phytoalexin and feed-deterrent properties [Russell et al., 1978] known as isoflavans [Akashi et al., 2006]. In *Lotus japonicus*, pterocarpan reductase (PTR, EC 1.1.1.246) catalyzes the stereospecific NADPH-dependent reduction of the pterocarpan (–)-medicarpin to the isoflavan (–) vestitol [Akashi et al., 2006] (Fig. 21.2).

Aurone flavonoids, such as aureusidin, contribute to yellow petal pigmentation of certain flowers such as snapdragon (*Antirrhinum majus*) and dahlia (*Dahlia variabilis*) [Ono et al., 2006]. In *A. majus* two enzymatic activities are essential for the biosynthesis of aurones from chalcones: the polyphenol oxidase homolog aureusidin synthase (AS1, EC 1.21.3.6) [Nakayama et al., 2000; Nakayama, 2002] and chalcone 4'-*O*-glucosyltransferase (4'CGT, EC 2.1.1.154) [Nakayama, 2002; Ono et al., 2006] (Fig. 21.2). The *A. majus* AS1 catalyzes the oxidative cyclization of naringenin chalcone, eriodictyol chalcone and their respective 4'-*O*-glucosides to aureusidin, bracteatin, and their corresponding 6-*O*-glucosides [Nakayama et al., 2000; Sato et al., 2001; Nakayama et al., 2001; Ono et al., 2006]. Both enzymes have distinctive subcellular domains. While AS1 activity is restricted to the vacuolar domain, 4'CGT has been localized to the cytosol [Ono et al., 2006]. The proposed topology for this pathway suggests that chalcones are 4'-*O*-glucosylated in the cytoplasm and then transported to the vacuole where AS1 convert them to aurone aglycones and 6-*O*-glucosides [Ono et al., 2006].

In plants accumulating anthocyanins, flavonols, and proanthocyanidins, naringenin is stereospecifically hydroxylated at position 3 of the C-ring (C3) by the 2-oxoglutarate-dependent dioxygenase flavanone 3-hydroxylase (F3H, EC 1.14.11.9) to yield the 3-hydroxy-trans-flavanone (syn. dihydroflavonol) dihydrokaempferol [Springob et al., 2003] (Fig. 21.2). Dihydroquercetin (3',4',5,5',7-

pentahydroxyflavanone) is formed after a hydroxylation reaction mediated by F3H or F3'H on eriodictyol or dihydrokaempferol, respectively [Springob et al., 2003]. Another P450-dependent monooxygenase, flavonoid 3',5'-hydroxylase (F3'5'H, EC 1.14.13.88) hydroxylates positions 3' and 5' of the B-ring of a flavanone or a dihydroflavonol. Thus, F3'5'H activity can hydroxylate naringenin to dihydroquercetin or dihydrokaempferol to dihydromyricetin [Springob et al., 2003]. The F3'H activity would result in cyanidin-type anthocyanidin/flavan-3-ols (3'-hydroxylation) while that of F3'5'H in delphinidin-type anthocyanidin/flavan-3-ols (3',5'-hydroxylations). The dihydroflavonol pool can be channeled through two major metabolic routes, one leading to colorless flavonols and the other to anthocyanins and proanthocyanidins. The first committed step in flavonol biosynthesis is catalyzed by the 2-oxoglutarate-dependent oxygenase flavonol synthase (FLS, EC 1.14.11.23) (Fig. 21.2). The reaction yields the flavonol aglycones kaempferol, quercetin, and myricetin. In addition, the *Arabidopsis* and *Citrus spp.* FLS can convert flavanones (e.g., naringenin, eriodictyol, and 5'-hydroxy eriodictyol) to dihydroflavonols [Prescott et al., 2002; Lukacin et al., 2003]. Dihydroflavonols can be further reduced to form the 2*R*,3*S*-trans-flavan-3*S*,4*S*-cis-diols (syn. leucoanthocyanidins) 2,3-trans-3,4-cis-leucopelargonidin, 2,3-trans-3,4-cis-leucocyanidin and 2,3-trans-3,4-cis-leucodelphinidin [Marles et al., 2003]. This NADPH-dependent reduction reaction is catalyzed by dihydroflavonol 4-reductase (DFR, EC 1.1.1.219). DFRs from different plant species have high substrate specificity [Marles et al., 2003; Xie et al., 2004a]. A single amino acid change from Asn133 to Asp133 in the *Medicago truncatula* DFR drastically reduced specificity for dihydrokaempferol [Xie et al., 2004a]. An identical substitution in the petunia (*Petunia hybrida*) DFR [Johnson et al. 2001; Xie et al., 2004a] creates an even stronger phenotype preventing the accumulation of pelargonidin-derived anthocyanins [Johnson et al., 2001; Springob et al., 2003]. DFR from *Dahlia variabilis*, *Gerbera hybrida*, *Zea mays*, and *M. truncatula* can also convert flavanones to flavan-4-ols [Fischer et al., 1998, 2003; Halbwirth et al., 2003; Xie et al., 2004a], the monomeric components of 3-deoxyproanthocyanidins or phlobaphenes (Fig. 21.2).

Leucoanthocyanidins are oxidized by another 2-oxoglutarate-dependent oxygenase known as anthocyanin synthase or leucoanthocyanidin dioxygenase (ANS or LDOX, EC 1.14.11) to yield the anthocyanidins pelargonidin, cyanidin, and delphinidin. Both leucoanthocyanidins and anthocyanidins are substrates for the biosynthesis of flavan-3-ols, the monomeric constituents of proanthocyanidins or condensed tannins. Proanthocyanidins are oligomers or polymers of flavan-3-ols subunits with roles in plant protection against pathogens, insects, and mammalian herbivores as well as in the control of seed permeability and dormancy [Debeaujon et al., 2000]. Proanthocyanidins that yield cyanidin as a result of acid hydrolysis are known as procyanidins [Porter et al., 1986]. Similarly, proanthocyanidins with at least one extension subunit of a (4') [e.g., (epi)afzelechin] or (3',4',5')-hydroxylated B-ring [e.g., (epi)gallocatechin] flavan-3-ol are known as propelargonidins and prodelphinidins, respectively.

The initial steps in proanthocyanidin biosynthesis are catalyzed by anthocyanidin reductase (ANR, EC 1.3.1.77) [Devic et al., 1999; Xie et al., 2003, 2004b] and leucoanthocyanidin reductase (LAR, EC 1.17.1.3) [Tanner et al., 2003]. Both ANR and LAR provide the 2,3-cis and 2,3-trans-flavan-3-ol monomers that could function either as a starter or extension subunit [Xie and Dixon, 2005] during proanthocyanidin polymerization. Leucoanthocyanidin reductase, a member of the isoflavone-reductase-like group of the plant reductase-epimerase-dehydrogenase (RED) supergene family, catalyzes the reduction of leucoanthocyanidins to their respective 2,3-trans-(+)-flavan-3-ols [Tanner et al., 2003; Marles et al., 2003]. This NADPH-dependent reduction reaction converts the leucoanthocyanidins leucopelargonidin, leucocyanidin, and leucodelphinidin to their respective alternative initiating subunits 2,3-trans-(+)-afzelechin, 2,3-trans-(+)-catechin, and 2,3-trans-(+)-gallocatechin [de Pascual-Teresa et al., 2000; Tanner et al., 2003]. The LAR activity is absent in *Arabidopsis* and was first cloned from the tropical forage legume *Desmodium uncinatum* [Tanner et al., 2003; Skadhauge et al., 1997a]. Since then, LARs have been identified in grapes [Bogs et al., 2005], apple [*Malus domestica*, Pfeiffer et al., 2006], *Lotus corniculatus* [Paolucci et al., 2007], and tea [*Camelia sinensis*, Punyasiri et al., 2004]. Anthocyanidin reductase catalyzes the NADPH-dependent reduction of an anthocyanidin to 2,3-cis-2*R*,3*R*-flavan-3-ol. The first cloned and enzymatically characterized ANR were the *Arabidopsis thaliana* BANYULS (BAN) [Devic et al., 1999] and its *M. truncatula* homolog [Xie et al., 2003; Pang et al., 2007]. In *Arabidopsis*, ANR activity results in the conversion of the LDOX product cyanidin to 2,3-cis-(−)-epicatechin, the most abundant PA subunit in the seed coat of this species [Abrahams et al., 2002; Xie et al., 2003]. Although with different substrate specificity, *in vitro* characterization of the *Arabidopsis* and *Medicago* ANRs has shown that the enzyme accepts either cyanidin, pelargonidin, or delphinidin to generate (−)-epicatechin, (−)-epiafzelechin, and (−)-epigallocatechin, respectively [Xie et al., 2004b]. The identification of ANR explained the origin of the 2,3-trans stereochemistry of anthocyanidins, flavonols, and catechin and the 2,3-cis configuration of most PA extension units found in plants [Winkel, 2006]. ANR have also been identified in grapes [*Vitis vinifera*, Bogs et al., 2005], *L. corniculatus* [Paolucci et al., 2007], tea [*C. sinensis*, Punyasiri et al., 2004], *Ginkgo biloba* [Shen et al., 2005], and persimmon [*Dyospyros kaki*, Ikegami et al., 2007] among others. Both ANR and LAR represent a major metabolic cross-road between anthocyanidin and PA biosynthesis [Pang et al., 2007]. Substrate competition became evident when the ectopic expression of the *V. vinifera* [Bogs et al., 2005] and *M. truncatula* [Xie et al., 2003] ANRs in tobacco increased proanthocyanidins content while at the same time reduced anthocyanins levels in pigmented petals. Likewise, the seed coat of the *Arabidopsis* ban mutant lacks proanthocyanidins and hyperaccumulate anthocyanins [Devic et al., 1999; Debeaujon et al., 2003]. In grapes [Bogs et al., 2005] and bilberry (*Vaccinium myrtillus*) [Jaakola et al., 2002], anthocyanin biosynthesis is temporarily compartmentalized from proanthocyanidin and flavonol biosynthesis. In both

species proanthocyanidins and flavonol biosynthesis in developing fruits precedes the accumulation of anthocyanins during the ripening stage. As a result, there appears to be no direct competition between these two branches of the flavonoid pathway for common substrates.

Although the enzymatic steps leading to the biosynthesis of initiating and extension flavan-3-ol subunits have been characterized in several plant systems, the biochemical mechanisms by which extension subunits are incorporated into growing proanthocyanidin polymers remains elusive [Dixon et al., 2005; Xie and Dixon, 2005]. It is still unclear whether the actual polymerization of flavan-3-ols is an enzymatic or a nonenzymatic process [Xie and Dixon, 2005]. Models suggest the possible involvement of polyphenol oxidase (PPO) in the formation of flavan-3-ols-derived quinone intermediates. Carbocations derived from these intermediates can react with flavan-3-ols to form C4–C6– and C4–C8-linked PA dimers and oligomers [Xie and Dixon, 2005]. Different plant species have distinctive proanthocyanidin monomer composition. In wine grapes both (+)-catechin and (–)-epicatechin are common proanthocyanidin starter units depending upon the tissue and developmental stage at which proanthocyanidins are isolated [Souquet et al., 1996; Kennedy et al., 2000, 2001; Downey et al., 2003a]. In *Arabidopsis*, however, the absence of LAR activity in seeds leads to proanthocyanidins that contain exclusively epicatechin starter units. The most commonly found flavan-3-ol extension subunits are in the 2,3-trans configuration with distinctive hydroxylation patterns in the B-ring depending on the presence of active cytochrome P450s F3'H and F3'5'H [Menting et al., 1994; Kaltenbach et al., 1999; Schenbohm et al., 2000]. For example, the most frequent extension subunits in wine grapes [Souquet et al., 1996, 2000] and *L. corniculatus* [Foo et al., 1996] are epicatechin and epigallocatechin. Expression of the grape F3'H and F3'5'H correlates spatially and temporally with the accumulation of (3',4')- and (3',4',5')-hydroxylated flavonols, flavan-3-ols (and PAs) and anthocyanins [Bogs et al., 2006]. The absence of F3'5'H activity in *Arabidopsis* leads to PAs that are homo-oligomers of the (3',4')-hydroxylated flavan-3-ol epicatechin [Debeaujon et al., 2000; Abrahams et al., 2003]. The degree of polymerization, stereochemistry, and number of phenolic hydroxyl groups appears to be critical to define PA beneficial bioactivity in relation to human health [Xie and Dixon, 2005].

Different enzyme families are involved in additional modifications to the basic structure of different flavonoid species, including glycosyl and acetyltransferases, methylases, and peroxidases [reviewed by Winkel, 2006]. These modifications are essential to provide stability, physicochemical properties, and distinctive bioactivity. Glycosylation enhances solubility and might be essential for facilitating transmembrane transport and vacuolar storage [Koes et al., 2005]. UDP-glucose, UDP-galactose, and UDP-rhamnose are among the most common nucleotide sugar substrates used to transfer one to several glycosyl moieties to positions 2, 3, 5, 6, and 7 of the flavonoid backbone (Fig. 21.1). In the European grape (*V. vinifera* L.), anthocyanidins are glucosylated by UDP-glucose:anthocyanidin 3-O-glucosyltransferase, also named UDP-glucose:

flavonoid 3-*O*-glucosyltransferase (UFGT, EC 2.4.1.91) at the 3-*O*-position of the C-ring and rarely at the 5-*O*-position of the B-ring. Anthocyanidin 3, 5-*O*-diglucosides are almost exclusively found in native American *Vitis* sp. [Peynaud and Ribéreau-Gayon, 1970; Baldi et al., 1995]. The glucosyltransferase activities involved in glycosylation of flavonol conjugates may be different from those glucosylating anthocyanidins [Ford et al., 1998]. For example, the 3-*O*-glucosyltransferase activity of the grape UFGT is significantly greater with cyanidin than quercetin [Ford et al., 1998]. In addition, UFGT transcripts are only found after the onset of ripening and accumulation of anthocyanins in the skin of colored berries [Boss et al., 1996a, 1996b; Goes da Silva et al., 2005], while glycosylated flavonols are actively synthesized in flowers and immature berries [Downey et al., 2003b]. Moreover, a glucosyltransferase with specific activity toward (–)-epicatechin was recently isolated from *M. truncatula* seed coats [Pang et al., 2008]. Anthocyanidin glycosylation constitute a major rate-limiting step for anthocyanin accumulation in grapes [Boss et al., 1996a, 1996b]. In fact, mutations impairing UFGT transcription appear to be the origin of white wine grape cultivars [Kobayashi et al., 2002, 2004; Walker et al., 2007].

Anthocyanidin glucosylation is not only a major control point in anthocyanin biosynthesis but also a prerequisite for additional substitutions like methylation at positions 3' and 5' and acylation of glucose moieties [Springob et al., 2003]. In grapes, peonidin-3-glucoside and delphinidin-3-glucoside are further modified by methylation at position 3' to yield peonidin and petunidin, respectively (Fig. 21.2). This reaction is mediated by a SAM-dependent 3'-*O*-methyltransferase (3'-OMET, no EC). A 3-*O*-methyltransferase (3-OMT) from *Serratula tinctoria* preferentially methylates the flavonol quercetin [Huang et al., 2004]. Considering the high specificity of plant *O*-methyltransferases toward their substrates [Baily et al., 1997], acylation of anthocyanins must take place at a later step in anthocyanin biosynthesis. Acylation of grape anthocyanins involves different hydroxycinnamic acids (e.g., *p*-coumaric and less frequently caffeic and acetic acids). The relative abundance of acylated anthocyanins is generally lower than that of their glucosylated precursors but are critical substitutions to increase anthocyanin solubility in water, enhance stability against β -glucosidase-mediated degradation, and favor co-pigmentation interactions [Boulton, 2001; Springob et al., 2003].

Enzymatic complexes involved in flavonoid precursors [Achnine et al., 2004] and flavonoid biosynthesis are associated with the cytoplasmic side of the endoplasmic reticulum (ER) [Stafford, 1974, 1981, 1991; Hrazdina et al., 1978, 1987; Hrazdina and Jensen, 1992; Winkel-Shirley, 1999; Liu and Dixon, 2001; Saslowsky and Winkel-Shirley, 2001]. However, flavonoids accumulate in multiple subcellular compartments and some are even extruded out of the cellular domain. Examples are flavonoids sequestered in the vacuole of specific cell layers and organs where they function as insect attractants or herbivore deterrents [Koes et al., 1994; Mol et al., 1998], extruded flavonoids that participate in allelopathic interactions or the establishment of symbiotic relationships with soil rhizobia [Martinoia et al., 1993; Paiva, 2000], cytosolic

flavonoids that interfere with cell-to-cell auxin transport [Buer and Muday, 2004], and nucleous-localized flavonoids [Buer and Muday, 2004; Saslowsky et al., 2005] that may participate in regulation of gene transcription [Peer and Murphy, 2006]. Significant progress in the understanding of transport mechanisms has been made in recent years, although still key mechanistic aspects remain elusive. As a result, several molecular models currently exist to explain intracellular trafficking, active transmembrane transport, and vacuolar sequestration of flavonoid conjugates [reviewed by Kitamura, 2006; Grotewold, 2004]. Flavonoid activation by conjugation with hydrophilic moieties such as sugars, acyl residues, and glutathione is essential for stability and transport mechanism specificity [Hopp and Seitz, 1987; Klein et al., 1996]. Several glutathione-*S*-transferase-like proteins essential for vacuolar flavonoid sequestration have been characterized in different plant species including the maize bronze2 [BZ2, Marrs et al., 1995], the petunia AN9 [Alfenito et al., 1998], the soybean GST26A [Alfenito et al., 1998], the carnation flavonoid3 [FL3, Larsen et al., 2003], and the *Arabidopsis* TT19 [Kitamura et al., 2004]. Only the latter appears to function in the vacuolar sequestration of proanthocyanidin precursors in addition to anthocyanin conjugates [Kitamura et al., 2004]. The apparent absence of a free flavonoid–glutathione conjugate pool led to propose a mechanistic model where glutathione-*S*-transferases-like proteins act as carriers of nonglutathionated flavanoids [Mueller et al., 2000] that are directly delivered to a specific type of tonoplast-bound ATP-dependent/proton-gradient independent ATP-binding cassette (ABC) transporters known as glutathione *S*-X pumps [Rea et al., 1998; Theodoulou, 2000] (Fig. 21.3). These carriers participate in the transmembrane trafficking and the vacuolar sequestration of a variety of glutathione conjugates [Martinoia et al., 1993; Klein et al., 2006; Koes et al., 2005; Lepiniec et al., 2006]. Examples of this class of transporters are the maize multidrug resistance-associated protein 3 [MRP3, Goodman et al., 2004] and the *Arabidopsis* MRP1 and 2 [Lu et al., 1997, 1998]. An alternative model of flavonoid transmembrane transport is based on the activity of H^+ -antiporters [Klein et al., 1996] (Fig. 21.3) that depend on proton gradients actively created by membrane-bound H^+ -ATPases and H^+ -translocating inorganic pyrophosphatases (H^+ -PPiases) [Maeshima, 2001]. A well-characterized example is the *Arabidopsis* TT12 that encodes for a tonoplast-localized member of the multidrug and toxic compound extrusion (MATE) transporter family [Debeaujon et al., 2001; Marinova et al., 2007a]. TT12 acts as an anthocyanin and flavan-3-ol glycoside/ H^+ -antiporter that cannot transport anthocyanidins, glycosylated flavonols, flavan-3-ol monomers aglycones, or dimers [Marinova et al., 2007a]. The *tt12* mutation impairs proanthocyanidin accumulation in the vacuole of seed coat cells and accumulates catechin and leucocyanidins in the cytoplasm [Debeaujon et al., 2001]. A similar phenotype is observed in the *Arabidopsis* *aha10* mutant encoding for the autoinhibited H^+ -ATPase isoform 10 (AHA10) [Baxter et al., 2005]. This H^+ -ATPase is predominantly expressed in developing seeds and plays a role in creating the electrochemical gradient required by TT12 to transport PA precursors into the

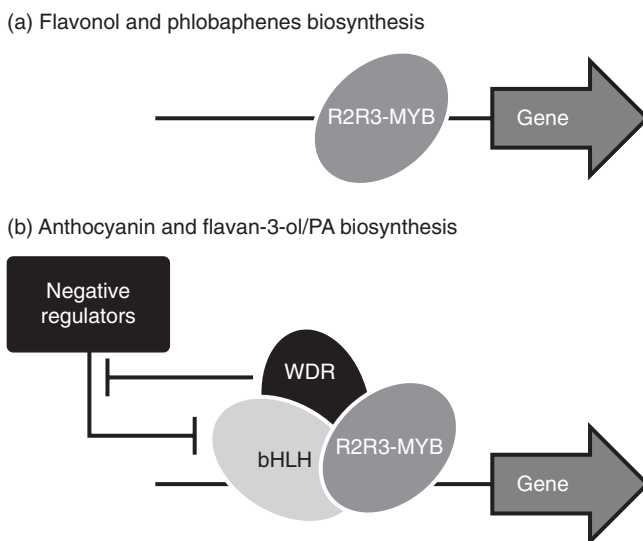


Figure 21.3 Models of R2R3-MYB, bHLH, and WDR transcriptional control of different branches of the flavonoid pathway. (Adapted from Quattrocchio et al., [2006] and Lepiniec et al., [2006].)

vacuolar domain [Baxter et al., 2005]. The tomato (*Lycopersicon esculentum*) MTP77 is another example of a MATE-type transporter involved in flavonoid transport [Mathews et al., 2003]. Recently, a third type of transporter with similarity to the organic anion carrier mammalian bilitranslocases has been linked to the vacuolar transport of flavonoids in carnation (*Dianthus caryophyllus*) petal microsomes [Passamonti et al., 2005] and developing grape (*V. vinifera*) berry tissues [Braidot et al., 2008]. In addition to the active transport model of conjugated flavonoids, vacuolar sequestration of flavonoids may involve the fusion of ER-derived vesicles containing anthocyanins or proanthocyanidin precursors [Peckert and Small, 1980; Yazaki et al., 2008] (Fig. 21.3). By this mechanism, flavonoids synthesized in the cytoplasmic side of the ER might be actively transported into the ER lumen [Grotewold, 2001] and secreted as ER-derived small vesicles [Poustka et al., 2007]. These vesicles may then fuse to the tonoplast, releasing their content into the vacuolar domain [Stafford, 1989], or form anthocyanin-accumulating subvacuolar structures known as anthocyanoplasts or anthocyanin vacuolar inclusions (AVIs) [Poustka et al., 2007]. The *Arabidopsis* glutathione-*S*-transferase-like protein TT19 may participate in the vesicle-to-vacuole trafficking of anthocyanins and flavan-3-ols since the tt19 mutant accumulates proanthocyanidin precursors in small vesicle-like structures [Kitamura et al., 2004]. This ER-to-vacuole flavonoid trafficking appear to be common to the secretion pathway followed by proteins targeted to vacuolar storage [Poustka et al., 2007].

Transcriptional and Posttranscriptional Regulation of Phenylpropanoid Biosynthesis in Plants

The flavonoid pathway in plants is arguably one of the most in-depth characterized metabolic network, both at the level of structural enzymes and regulatory genes [reviewed by Quattrocchio et al., 2006; Lepiniec et al., 2006]. The pathway is largely under the combinatorial transcriptional control of a diverse set of transcription factor families [Springob et al., 2003; Winkel-Shirley, 2001, 2002] (Table 21.1) that regulate expression in response to internal and external cues at specific stages in development or in certain tissues and cell types [Gonzalez et al., 2008].

Several model systems have been used to dissect this transcriptional regulatory network including loss- and gain-of-function mutants in proanthocyanidin biosynthesis in *Arabidopsis thaliana* seeds [Debeaujon et al., 2003; Lepiniec et al., 2006], phlobaphenes in maize [Goff et al., 1992; Grotewold et al., 1991], and flavonoid pigments in flowers [Quattrocchio et al., 2006]. For example, among the 20 different loci affecting seed coloration in the *Arabidopsis* transparent testa (tt) mutants, 6 correspond to transcription factors (table 21.1) [Lepiniec et al., 2006]. Distinctive transcriptional control over the expression of different enzymatic steps in the flavonoid pathway has been recognized in different plant species. *Arabidopsis* bHLH and MYB tt mutants are impaired in the expression of genes in later steps of the pathway (e.g., DFR and LDOX) without modifying messenger ribonucleic acid (mRNA) levels of PAL and CHS genes [Shirley et al., 1995; Pelletier et al., 1997, 1999; Zhang et al., 2003; Gonzalez et al., 2008]. Based partially on these experimental observations, the flavonoid pathway in dicotyledonous species appear to be organized in two distinctive clusters of co-regulated genes known as early (EBG) and late (LBG) biosynthetic genes [Shirley et al., 1995; Mol et al., 1998; Nesi et al., 2000; Pelletier et al., 1997, 1999; Zhang et al., 2003; Quattrocchio et al., 2006; Takos et al., 2006b]. However, this may not be the case for monocotyledonous species like maize, where it has been shown that all genes coding for structural enzymes of the pathway are coordinately transcribed [Irani et al., 2003].

Several of the 125 R2R3-MYB transcription factors in *Arabidopsis* [Riechmann and Ratcliffe, 2000; Stracke et al., 2001] exert systemic and tissue-specific transcriptional control over structural genes of the general phenylpropanoid and flavonoid pathways [Quattrocchio et al., 1998; Springob et al., 2003]. Promoter regions of frequently co-regulated genes such as CHS, CHI, F3H, and FLS in *Arabidopsis* [Hartman et al., 2005] and other plant species [Hartman et al., 1998] harbor the consensus sequence 5'-AcCTACCa-3' corresponding to the cis-acting element known as MYB recognition element (MRE). This conserved motif is recognized by members of the MYB family [Feldbrügge et al., 1997; Hartmann et al., 2005]. Both flavonol and phlobaphene biosynthesis in monocotyledonous species seem to be under the sole control of R2R3-MYBs (Fig. 21.4). Three MYBs of the subgroup 7 with significant sequence

Table 21.1 Plant Transcription Factors Involved in Phenylpropanoid Biosynthesis Regulation and Their Known Regulons

TF family	Monocotyledonous		Transcription factor loci				Structural enzymes											Reference					
	Maize	Barley	Arabidopsis	Penunia	Anthrinnum	Grape	Lotus	Eucalyptus	PAL	ACL	CHS	CHI	F3H	F3'H	DFR	FLS	LDOX		ANR	LAR	UFGT	Transp	
bHLH																							Nesi et al., 2000
bHLH																							Pay and Gruber, 2001
bHLH				AN1			TANI																Spell et al., 2000
bHLH				JAF13																			Spell et al., 2000
bHLH																							Goff et al., 1992
bHLH																							Comnelli et al., 2008
bHLH																							Gonzalez et al., 2008
MYB																							Martin et al., 1991; Goodrich et al., 1992; Martin and Gonzalez, 1993
MYB	Sh, Lc, R	ANT1/9																					Martin et al., 2003
MYB																							Wang et al., 2007
MYB																							Kobayashi et al., 2002; Walker et al., 2007
MYB																							Devar et al., 2006
MYB	P1																						Leruy et al., 2007
MYB																							Shives and Casika, 1981; Gutenwald et al., 1991, 1994
MYB																							Chopra et al., 1999
MYB	C1																						Quattrocchio et al., 1999
MYB																							Palz-Ann et al., 1987
MYB																							Mehrens et al., 2005; Stracke et al., 2007
MYB																							Mehrens et al., 2005; Stracke et al., 2007
MYB																							Stracke et al., 2007
MYB																							Bowitz et al., 2000; Tohge et al., 2005a; Gonzalez et al., 2008
MYB																							Gonzalez et al., 2008
MYB																							Gonzalez et al., 2008
MYB																							Preston et al., 2004
MYB																							Schwinn et al., 2008
MYB																							Schwinn et al., 2006
MYB																							Schwinn et al., 2006
MYB																							Mas et al., 2006a; Gonzalez et al., 2008
WRKY																							Mas et al., 2006b
WRKY																							Mas et al., 1997
WRKY																							Mas et al., 2004
Zinc finger																							Spanner et al., 2001
WRKY																							Johnson et al., 2002

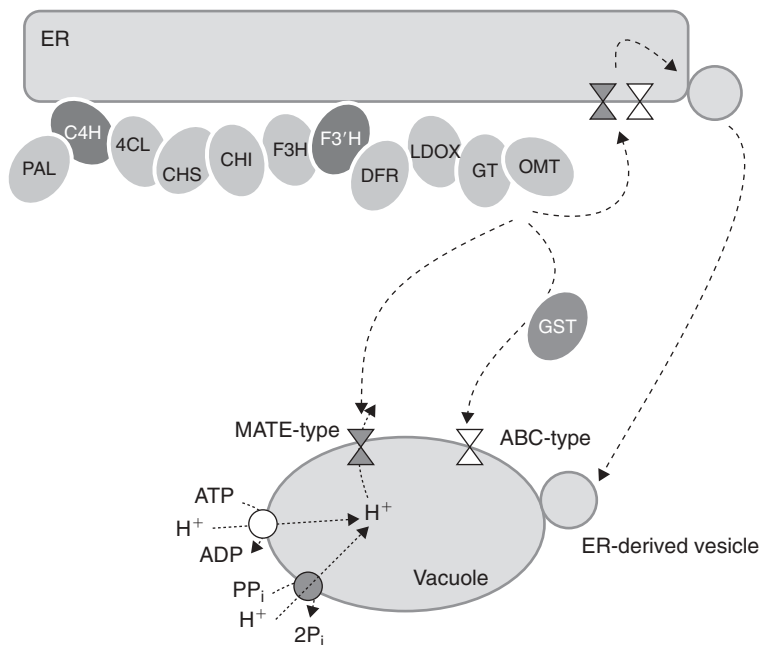


Figure 21.4 Phenylpropanoid and (iso)flavonoid pathway topology, subcellular localization and transport mechanisms. (Adapted from Winkel-Shirley, [2004], Kitamura, [2006] and Marinova et al. [2007b].)

similarity to the maize *P* gene regulate flavonol biosynthesis in different *Arabidopsis* organs [Stracke et al., 2007]. MYB12 or production of flavonol glycosides1 (PFG-1) regulon includes the EBGs 4CL, CHS, CHI, F3H, F3'H, the LBG FLS, and two putative flavonol:glucosyltransferases [Mehrtens et al., 2005; Stracke et al., 2007] (table 21.1). Flavonol content in the *myb12* mutant is significantly reduced but not completely suppressed [Mehrtens et al., 2005], suggesting that other factors may partially contribute to the activation of this branch of the flavonoid pathway. Two additional structurally similar MYBs, MYB11 (PFG2), and MYB111 (PFG3) activate the same set of EBG and LBG acting additively with MYB12 [Stracke et al., 2007]. In fact, flavonols are absent in the *myb11 myb12 myb111* triple mutant phenocopying the CHS (*tt4*) mutant [Stracke et al., 2007]. Although functionally redundant, these MYBs have specific spatial and temporal expression patterns that prevent the occurrence of overlapping functions. While MYB11 expression is generally low in seedlings, MYB12 controls flavonols biosynthesis in roots and MYB111 in cotyledons [Stracke et al., 2007]. The relative abundance of flavonoid glycosides in different *Arabidopsis* tissues would depend on the combinatorial control of these MYBs on the transcription of flavonol:glucosyltransferases [Stracke et al., 2007]. Similarly, both the R2R3-MYBs pericarp color1 (P1) in

maize [Styles and Ceska, 1989] and its orthologous Y1 in sorghum [Chopra et al., 1999] control biosynthesis of 3-deoxy flavonoids and phlobaphenes [Grotewold et al., 1991]. P1 is similar to the *Arabidopsis* MYB12 [Dias et al., 2003] and when ectopically expressed in *Arabidopsis* exerts control over flavonol biosynthesis [Mehrtens et al., 2005]. In vitro, the ability of P1 to bind the consensus sequence ACCT/AACC [Grotewold et al., 1994] depends on the disruption under reducing conditions of a disulfide bond formed between two conserved cysteine residues [Heine et al., 2004]. Therefore, the P1 control over CHS, CHI, and DFR transcription [Grotewold et al., 1994] not only depends on factors affecting P1 expression but also on the cellular redox status.

While flavonol and phlobaphene biosynthesis would depend solely on MYBs [Grotewold et al., 1994], transcriptional regulation of anthocyanin and proanthocyanidin biosynthesis depend on protein–protein interactions and assembly of heterologous complexes between R2R3-MYBs and members of the R/B subgroup of the bHLH transcription factor family [Goff et al., 1992; table 21.1 and Fig. 21.3]. Physical protein–protein interaction takes place between the conserved R3 repeat in the MYB protein and the N-terminus region of the bHLH protein [Goff et al., 1992]. The first interaction of this kind was described in maize, where the C1 (MYB) and R (bHLH) gene products physically interact to activate anthocyanin biosynthesis [Goff et al., 1992]. In petunia, the bHLH AN1 interact with the MYBs AN2 or AN4 to form a transcriptional activation complex that regulates DFR expression [Spelt et al., 2000]. Another R/B bHLH, the petunia JAF13, may also interact in vivo with AN2 regulating expression of DFR [Quattrocchio et al., 2006]. Ectopic expression of the maize Sn (bHLH) in the forage legume *L. corniculatus* induced PA accumulation in specific cell layers of vegetative tissues as a result the increased expression, and likely, activity of the LBGs DFR, ANS, ANR, and LAR [Paolucci et al., 2005, 2007 and references therein]. This result suggests that the rate-limiting step of proanthocyanidin and anthocyanin biosynthesis in certain legumes might be the expression of a native bHLH gene [Paolucci et al., 2007]. Presence of an active transcriptional activation domain in the MYB factor is critical for activity of the complex as a positive regulator of flavonoid biosynthesis. For example, while the ectopic expression of the *Arabidopsis Landesberg erecta* MYB114 upregulated anthocyanin biosynthesis, the opposite phenotype was observed with the ecotype Columbia homolog lacking an active transcriptional activation domain [Gonzalez et al., 2008].

In addition to MYBs and bHLHs, several members of a transcription factor family characterized by the presence of five highly conserved WD-repeats [WDR; Carey et al., 2004; de Vetten et al., 1997; Walker et al., 1999] are also involved in transcriptional regulation of anthocyanin and proanthocyanidin biosynthesis [Debeaujon et al., 2003] (Fig. 21.3). The petunia AN11 encodes a WDR protein that may exert control over floral anthocyanin pigments by post-transcriptional regulation of R2R3-MYB or bHLH activity [de Vetten et al., 1997]. Orthologous WDR proteins such as the *Arabidopsis* TTG1 [Walker et al., 1999; Lepiniec et al., 2006; Baudry et al., 2006] and the maize Pale

Aleurone Color1 (PAC1) [Selinger and Chandler, 1999] are also involved in the regulation of flavonoid pigment accumulation. TTG1 protein is not essential for DNA target recognition by the TT2 (R2R3-MYB)/TT8(bHLH) transcriptional complex [Baudry et al., 2004; Nesi et al., 2001] but might be necessary to stabilize the complex [Payne et al., 2000] by preventing the effect of negative regulators [Quattrocchio et al., 2006]. Several examples of combinatorial interactions between different components in the heterotrimeric complex exist in different model species. In *Anthirrinum majus*, the MYBs Rosea1, Rosea2, and Venosa control accumulation and patterning of anthocyanin pigment in flowers [Schwinn et al., 2006]. These three MYBs have different activation activity for different target genes. Consequently, subtle differences in expression or potential to interact with activation partners of the bHLH and WDR family cause striking differences in the natural variation of floral pigmentation in *A. majus* accessions [Martin et al., 1991; Schwinn et al., 2006]. A similar combinatorial effect on anthocyanin biosynthesis is observed in maize as a result of the interaction between C1/P1 and R/B proteins [Paz-Ares et al., 1987; Ludwig et al., 1989, 1990; Lloyd et al., 1992; Cone et al., 1993]. In *Arabidopsis*, BAN (ANR) and TT3 (DFR) expression is impaired in tt2, tt8, and ttg1 mutants [Walker et al., 1999; Nesi et al., 2000; Baudry et al., 2004]. The heterotrimeric MYB/bHLH/WDR transcription activation complex formed by TT2/TT8/TTG1 directly binds to the BAN promoter, tightly regulating its developmental and spatial activity [Baudry et al., 2004; Lepiniec et al., 2006]. Similarly, VvMYBPA1, one of the 108 R2R3-MYB factors in the grape genome [Matus et al., 2008] and a close homolog the *Arabidopsis* TT12, is able to bind and activate the promoters of VvANR and VvLAR [Bogs et al., 2007]. The accumulation of proanthocyanidins in different *Arabidopsis* organs as a result of the ectopic expression of VvMYBPA1 [Bogs et al., 2007] is another of several examples of the high degree of functional conservation observed in different component of this regulatory network across plant species [Goodrich et al., 1992; Dong et al., 2001; Bradley et al., 1998]. TT8 can also interact with other MYB factors, such as PAP1 and PAP2, to specifically activate anthocyanin biosynthesis [Baudry et al., 2004; Zimmermann et al., 2004]. Other transcription factors identified as positive regulators of flavonoid biosynthesis include the BSISTER MADS box domain TT16 [Nesi et al., 2002], the zinc finger of the WIP subfamily TT1 [Sagasser et al., 2001], and the WRKY TTG2 [Johnson et al., 2002].

Some transcription factors can also act as negative transcriptional regulators of flavonoid biosynthesis. For example, the maize bHLH Intensifier1 (IN1) was identified as a recessive mutation enhancing kernel pigmentation [Burr et al., 1996; Baudry et al., 2004]. R2R3-MYB negative regulators have also been identified in dicotyledonous species. The strawberry (*Fragaria x ananassa*) FAMYB1 represses the LBG LDOX and flavonoid:UDP-glucosyltransferase (GT) [Aharoni et al., 2001]. The *Arabidopsis* MYB4, on the other hand, suppresses C4H expression [Jin et al., 2000]. Both R2R3-MYB negative regulators harbor residues required for direct protein-protein interaction

with bHLH factors [Grotewold et al., 2000; Quattrocchio et al., 2006] suggesting that they may act titrating out positive regulators. Other negative regulators include the flavonoid biosynthesis repressor the *Arabidopsis* Increased Chalcone Synthase Expression1 [ICX1; Wade et al., 2003], the petunia R3-MYB MYBX [van Houwelingen et al., 1998], and the *Eucalyptus globulus* MYB1, a putative repressor of lignin biosynthesis [Legay et al., 2007].

Part of the complexity and diversity observed in regulatory and structural components of the phenylpropanoid pathway resides in the occurrence of whole-genome or segmental duplication events, followed by evolution and functionalization of diverse loci. Gene family expansion [Matus et al., 2008] and gain- or loss-of-function mutations both in the coding [Helariutta et al., 1996; Walker et al., 2007] as well as in the promoter region [De Meaux et al., 2006; Kobayashi et al., 2002, 2004] contribute to enhance the diversity of enzymatic activities as well as in the spatial and developmental transcriptional activation of the pathway. With the exception of *Arabidopsis*, where all structural enzymes of the flavonoid pathway but F³H are encoded by single copy genes [Pelletier et al., 1999], there are multiple examples of region-specific intrachromosomal duplication or genome-wide polyploidization contributing to the diversity of flavonoid genes. In legumes, genes involved in flavonoid biosynthesis appear as clusters of multigene families. For example, CHS family is represented by eight genes in soybean [Clough et al., 2004; Tuteja et al., 2004] and six in Phaseolus [Ryder et al., 1987]. Different paralogs have unique expression patterns [Tuteja et al., 2004] and responsiveness to environmental stimuli [Shimizu et al., 1999]. The *Lotus japonicus* genome harbors a tandem cluster of three paralog R2R3-MYBs orthologous to the *Arabidopsis* TT2. Transient expression experiments showed their functional equivalence since all were able to activate the LjANR promoter when coexpressed with TT8 and TTG1 [Yoshida et al., 2008]. The native expression domain and responsiveness to specific stress factors differ among the LjTT2s paralogs [Yoshida et al., 2008]. LjTT2c and LjTT2b are constitutively expressed at high levels in all organs while LjTT2a is induced in response to wounding [Yoshida et al., 2008]. Similarly, the *Arabidopsis* activators of anthocyanin biosynthesis MYB113 (At1g66370), MYB114 (At1g66380), and PAP2 (At1g66390) [Stracke et al., 2001] occur in a cluster tandem [Gonzalez et al., 2008]. They all have distinctive activation properties and expression domains in relation to their paralog PAP1 [Toghe et al., 2005; Gonzalez et al., 2008]. Sense-antisense interaction between members of multigene families can also have strong consequences on activation of the flavonoid pathway as a result of cell type and organ-specific gene silencing [Tuteja et al., 2004].

Phenylpropanoid Pathway, Subcellular Localization, and Metabolic Channeling

Phenylpropanoids and flavonoids found in plants are predominantly derived from the aromatic amino acid L-phenylalanine originated in the shikimic acid

pathway. Although biosynthesis of aromatic amino acids occurs preferentially in plastids [Weaver and Herrmann, 1997], the initial precursors erythrose-4-phosphate (E4P) and phosphoenolpyruvate (PEP) originate via different metabolic pathways localized in distinctive subcellular compartments. The glycolytic intermediate, PEP is mainly imported from the cytosolic pool since plastids produce insufficient amounts of this precursor [Bagge and Larsson, 1986; Hrazdina and Jensen, 1992]. The plastidial transketolase (TK, EC 2.2.1.1.) activity converts fructose-6-P and 3-phosphoglyceraldehyde to xylulose-5-P and E4P that can be readily channeled to L-phenylalanine biosynthesis in the plastid [Hrazdina and Jensen, 1992]. L-Phenylalanine must be exported from the plastid to the cytosol to reach the multienzyme enzymatic complex of the phenylpropanoid pathway believed to be localized to the cytoplasmic side of the ER [Achnine et al., 2004; Stafford, 1974, 1981, 1991; Hrazdina et al., 1978, 1987; Hrazdina and Jensen, 1992; Winkel-Shirley, 1999a; Liu and Dixon, 2001; Saslowsky and Winkel-Shirley, 2001]. The core general phenylpropanoid and flavonoid pathways appear to be organized as a multienzyme complex or metabolon mediated by direct protein–protein interaction between enzymes catalyzing sequential reactions [Winkel-Shirley, 1999a, 1999b, 2001; Winkel, 2004] (Fig. 21.3). Direct protein–protein interaction between structural enzymes have been demonstrated using a combination of techniques including yeast two-hybrids, immunoprecipitation assays and affinity chromatography [Burbulis and Winkel-Shirley, 1999; Guo et al., 1994b; Winkel, 2004]. A metabolon structure would increase biosynthetic efficiency by optimizing local substrate concentration and conditions at the reaction site, channeling common precursors to competing biosynthetic branches, avoiding toxic effects of some intermediates, and preventing feedback inhibition [Ovádi and Saks, 2004; Winkel-Shirley, 1999a; Winkel, 2004]. The current molecular model anchors the flavonoid pathway metabolon to the ER by means of the transmembrane domains of P450-dependent monooxygenases such as C4H and F3'H [Winkel-Shirley, 1999a; Winkel, 2004] (Fig. 21.3). However, even in F3'H defective *Arabidopsis* mutants, CHS and CHI co-localize to the cytoplasmic side of the ER, suggesting that other proteins might be also involved in anchoring the whole metabolon to the ER [Saslowsky and Winkel-Shirley, 2001; Winkel, 2004].

Considering the complexity that arises from metabolic compartmentation and the extent of enzymatic activities needed to channel primary intermediates to secondary metabolites, a highly coordinated transcriptional regulatory network is required to orchestrate expression of structural genes coding for enzymes and transporters. Indeed, molecular evidence suggests that abiotic [Logemann et al., 2000] and biotic [Hermsmeier et al., 2001] stress factors co-induce transcription of committed enzymes of the oxidative pentose phosphate pathway (OPPP) [Batz et al., 1998; Logemann et al., 2000], shikimic acid [Batz et al., 1998], and phenylpropanoid pathway [Logemann et al., 2000]. In parsley (*Petroselinum crispum*), UV light stimulated and increased the partitioning of carbon from primary to secondary metabolism by enhancing expression of enzymes involved in carbohydrate, shikimic acid, fatty acid degradation, and

flavonoid pathways [Logemann et al., 2000]. Activity levels and transcription of 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (DAHPS, EC 4.1.2.15), the first committed step in aromatic amino acid biosynthesis, was induced under conditions of N and amino acid starvation [Weaver and Herrmann, 1997], light [Henstrand, 1992], wounding [Dyer, 1989], and elicitors [Henstrand, 1992] in coordination with enzymes of the phenylpropanoid metabolism [Weaver and Herrmann, 1997], especially PAL and CHS. Similarly, glucose-6-P dehydrogenase (G6PD, EC 1.1.1.49), a rate-limiting step in the OPPP, is also induced by UV light and elicitors [Batz et al., 1998]. The activity of different flavonoid transport systems is also tightly regulated. For example, GST-like proteins are commonly co-expressed with structural anthocyanin biosynthetic genes [Mathews et al., 2003]. In addition, the activity of MATE-type vacuolar flavonoid/H⁺-antiporters may depend on the existence of a functional flavonoid pathway and posttranslational modifications induced by binding to a still uncharacterized flavonoid biosynthetic intermediate [Marinova et al., 2007b]. This experimental evidence provides only a glimpse of the complex mechanisms in place exerting exquisite control over metabolite fluxes from precursors derived from primary metabolism to the final accumulation of phenylpropanoids in different subcellular compartments.

BIOLOGICAL FUNCTION OF PHENYLPROPANOIDS IN PLANT GROWTH, DEVELOPMENT, AND INTERACTIONS WITH THE ENVIRONMENT

Phenylpropanoids Structural and Signaling Functions in Plant Reproductive Biology

A functional flavonoid pathway in anthers and pistils is required for proper development of the pollen grain, pollen tube growth, fertilization, and seed biogenesis [Burbulis et al., 1996; Ylstra et al., 1992]. This requirement is widespread among all land plants [Jorgensen, 1993]. Different genes involved in flavonoid biosynthesis are expressed during the development of the pollen grain [Alves-Ferreira et al., 2007], and they seem to be under the transcriptional control of R2R3-MYB transcription factors [Preston et al., 2004]. Phenylpropanoids and long-chain fatty acids are among the constituents of sporopollenin, the main polymeric component of the extracellular lipidic matrix of the outer coat (or exine) of pollen grains [Piffanelli et al., 1998; Hsieh and Huang, 2007]. Among the different cell layers of the anther, the sporophytic tapetum cells have the highest specific activities of phenylpropanoid biosynthetic enzymes [Piffanelli et al., 2004]. Flavonoid aglycones synthesized in the tapetal cells are translocated by ER-derived vesicles known as tapetosomes [Hsieh and Huang, 2007] to the immature pollen grain exin where they undergo additional modification [Taylor et al., 1997; Piffanelli et al., 1998]. Flavonol deficient plants are often self-sterile due to lack of proper pollen germination [Taylor and

Jorgensen, 1992; Mo et al., 1992; Kim et al., 1996] or establishment of a functional pollen tube [Pollak et al., 1995; Ylstra et al., 1994; Schijlen et al., 2007]. For example, the maize and petunia CHS mutants [Mo et al., 1992], the tapetum-specific silencing of PAL and CHS in petunia and tobacco [van der Meer et al., 1992; Matsuda et al., 1996], or the silencing of CHS in tomato [Schijlen et al., 2007] cause partial or complete male sterility as a result of abnormal pollen development and pollen tube growth. These reproductive defects are conditional and can be rescued in vitro by chemical complementation with flavonols, in particular quercetin and kaempferol [Ylstra et al., 1992, 1996; Mo et al., 1992; Kim et al., 1996] or by wild-type stigma exudates [Taylor and Jorgensen, 1992; Ylstra et al., 1994; Vogt et al., 1994]. In *Arabidopsis*, however, the flavonoid deficient mutant tt4-1 is fertile and able to set a reduced number of seeds after self-fertilization [Shirley et al., 1995; Ylstra, 1996], probably as a consequence of lower pollen germination [Kim et al., 2006]. These experimental results suggest contrasting roles for flavonoids in plant reproduction depending on the species considered. Some species have a strict dependency on flavonoids to ensure fertilization while others seem to have evolved alternative determinants of fertility [Taylor and Grotewold, 2005] or have completely lost the requirement for flavonoids to set seed [Taylor et al., 1997]. In addition to their structural role, flavonoids seem to exert their effect on pollen grain development and pollen tube growth by regulating transcription of genes involved in the fertilization process. An example is the reported effect of the flavonol kaempferol on the transcriptional regulation of several pollen-specific genes [Guyon et al., 2000], including a SHY leucine-rich repeat protein required for pollen tube penetration into the ovules [Guyon et al., 2004]. In addition to the effects on pollen grain development and functionality, a recent report described the occurrence of parthenocarpic (or fruit biogenesis in the absence of fertilization) seedless fruits in flavonoid-deficient tomato plants lacking CHS activity [Schijlen et al., 2007]. This novel effect on parthenocarpic fruit development suggests a role for auxin-flavonoid interaction on plant reproduction [Schijlen et al., 2007] yet to be elucidated. In sum, although different mechanisms and requirements seem to be in place for different plant species, phenylpropanoids and flavonoids in particular clearly play a critical role in plant reproductive biology.

Flavonoids as Mediators of Transcriptional and Posttranslational Regulation of Protein Activity

Nuclear localization of flavonoid biosynthetic enzymes [Saslowky et al., 2005] and flavonoids [Buer and Muday, 2004; Saslowky et al., 2005] suggests their direct or indirect involvement in regulating gene transcription processes [Pelletier et al., 1999; Polster et al., 2003; Feucht et al., 2004; Peer and Murphy, 2006]. For example, naringenin chalcone and apigenin modulate flavonoid biosynthesis by exerting control over transcription of structural enzymes of the flavonoid pathway [Pelletier et al., 1999]. Possible molecular mechanisms include flavonoid binding to histone proteins [Polster et al., 2003; Feucht

et al., 2004], topoisomerases [Boege et al., 1996], and DNA polymerase [Mizushima et al., 2003] as well as inhibition of phosphorylation signaling cascades when binding to specific phosphokinases [reviewed by Peer and Murphy, 2006]. Flavonoid protein-binding properties are not only relevant in transcription regulation but also play a critical role in other plant reproductive and developmental processes such as the regulation of polar auxin transport and pollen development.

FLAVONOID–AUXIN TRANSPORT INTERACTION AND MODULATION OF PLANT GROWTH

Mutations that impair flavonoid biosynthesis can have dramatic effects on plant growth and development by acting as endogenous negative regulators of auxin cellular efflux and polar (basipetal or acropetal) transport in vivo [Jacobs and Rubery, 1988; Brown et al., 2001; Buer and Muday, 2004; Peer et al., 2004; Taylor and Grotewold, 2005; Besseau et al., 2007; Woodward and Bartel, 2005]. Severe phenotypes are normally associated with reduced primary root growth and increased lateral root formation [Brown et al., 2001], delayed gravitropic responses [Buer and Muday, 2004], and increased number of secondary inflorescences [Brown et al., 2001]. In addition, reduced plant biomass often negatively correlates with flavonoid hyperaccumulation and lower polar auxin transport (PAT) rates [Besseau et al., 2007]. Auxins are mainly produced in the shoot apical meristem and to a lesser extent in other developing organs, such as leaf primordia and developing leaves [Ljung et al., 2001; Avsian-Kretchner et al., 2002]. In shoots, auxin movement is mainly basipetal, while in roots both basipetal and acropetal movements occur in distinctive and spatially separated tissue layers [Woodward and Bartel, 2005]. Cell-to-cell trafficking and long-distance transport from synthesis sites is a complex and highly regulated process that requires the interaction of multiple proteins in a tissue-specific manner. In *Arabidopsis*, auxin cellular influx is regulated by the amino acid permease-like auxin influx carrier protein1 (AUX1)/Like-AUX1 protein [Bennett et al., 1996; Marchant et al., 1999; Parry et al., 2004]. Cellular efflux, on the contrary, seems to be under the control of at least two distinctive types of carrier proteins: the *Arabidopsis* Pin-formed (PIN) family of auxin efflux facilitators [Gälweiler et al., 1998; Utsuno et al., 1998] and members of the ATP-binding cassette (ABC) transporter family known as ATP-dependent multidrug resistance-like (MDR)/P-Glycoprotein (PGP) [Noh et al., 2001; Multani et al., 2003]. MDR/PGP seems to form complexes with a type of regulatory proteins known as naphthylphtalamic acid (NPA) binding proteins (NBPs) [Jacobs and Rubery, 1988; Murphy et al., 2000; Muday and DeLong, 2001]. NBPs have been characterized as membrane-associated aminopeptidases [Murphy et al., 2002] with low binding affinity to NPA while MDR/PGP carriers are considered high-affinity NBPs [Murphy et al., 2002; Noh et al., 2001].

Initial evidence for the involvement of flavonoids in auxin transport regulation emerged from *in vitro* experiments showing that certain flavonoids, in particular, flavonol aglycones such as quercetin and kaempferol, competed with the auxin efflux inhibitor 1-naphthylphthalamic acid (NPA) for auxin transporters binding sites [Jacobs and Rubery, 1988]. These results were later confirmed by *in planta* analysis of PAT in *Arabidopsis* mutants with altered flavonoid biosynthesis. Flavonoid deficiency leads to higher rates of PAT [Brown et al., 2001] while the contrary is observed in flavonoid hyperaccumulating plants. Loss of apical dominance in *tt4* (CHS) mutant [Brown et al., 2001] correlates with high basipetal PAT rates [Brown et al., 2001; Peer et al., 2004; Buer and Muday, 2004]. Chemical complementation bypassing the CHS step restored flavonoid biosynthesis and wild-type auxin transport rates [Buer and Muday, 2004]. On the other hand, flavonol hyperaccumulating mutants such as *tt3* (DFR) and *tt7* (F3'H) [Peer et al., 2004] and plants with reduced hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase (HCT) activity, a rate-limiting step in lignin biosynthesis [Hoffman et al., 2004; Besseau et al., 2007], have significantly lower PAT rates. When HCT and CHS were simultaneously suppressed, absence of flavonoid biosynthesis reestablished wild-type polar auxin transport and normal development in spite of reduced lignin biosynthesis [Besseau et al., 2007]. This result clearly demonstrates that the reduced size and aberrant growth phenotype of HCT-silenced plants resulted from the effects of flavonoid hyperaccumulation on PAT. The MORE AXILLARY BRANCHES1 (MAX1) [Booker et al., 2005], a member of the cytochrome P450 family of monooxygenases, acts as a positive regulator of the flavonoid pathway and represses vegetative bud outgrowth in *Arabidopsis* [Lazar and Howard, 2006]. The *max1* mutant shows increased lateral branching and loss of apical dominance, giving plants a “bushy” appearance [Stirnberg et al., 2002]. A model by which MAX1 would regulate bud repression by a flavonoid-dependent auxin retention mechanism has recently been proposed [Lazar and Goodman, 2006]. By this mechanism, MAX1 activity would increase steady-state levels of flavonoids in stems and buds affecting expression and localization of auxin influx and efflux carriers and directional auxin transport.

The exact mechanisms by which certain flavonoids interfere with auxin transport are yet to be elucidated [Taylor and Gotewold, 2005; Bailly et al., 2008]. In fact, the experimental evidence suggests that flavonoids may exert their inhibitory effect on auxin transport via different mechanisms depending on the auxin efflux carrier system considered. Certain flavonoids directly bind to low- [Jacobs and Rubery, 1988; Murphy et al., 2000; Muday and DeLong, 2001] and high-affinity NBP [Noh et al., 2001; Geisler et al., 2005; Bouchard et al., 2006]. It has been recently shown that the functional protein-protein interaction and modulation of auxin transport activity of two ABCB/P-glycoproteins, PGP1 and MDR1, by the membrane-anchored immunophilin-like TWISTED DWARF1 (TWD1) is specifically disrupted by NPA and flavonoid binding [Bailly et al., 2008]. This result provides the first distinctive

mechanistic mode of action model of flavonoids action on modulation of PAT rates. In addition, low PIN protein levels and disruption of their characteristic asymmetrical subcellular localization [Gälweiler et al., 1998] was observed in flavonoid biosynthetic mutants [Peer et al., 2004]. The altered localization may result from the direct interference of flavonoids on vesicular trafficking proteins [Muday et al., 2003; Taylor and Grotewold, 2005] or on auxin transport [Peer et al., 2004; Taylor and Grotewold, 2005]. The serine/threonine kinase PINOID (PID) [Friml et al., 2004] governs the polar subcellular localization of PIN1 and might be a direct target of flavonoid action [Taylor and Grotewold, 2005] suggesting a possible role for flavonoids in regulating the phosphorylation/activation state of auxin transport proteins (De Long et al., 2002). Flavonoid may also have direct effects on steady-state levels of cellular auxin pools. For example, up-regulation of flavonoid biosynthesis induced by nod factors during nodule organogenesis in white clover may inhibit peroxidase-mediated breakdown of auxin pools [Mathesius, 2001]. Regardless the exact mechanism in place, the tight regulation of flavonoid biosynthesis in response to environmental cues [Winkel-Shirley, 2002] and its effect on modulating cell-to-cell and long-distance PAT rates as well as localized auxin steady-state levels make them potent transducers that can trigger profound changes in plant architecture to ensure proper adaptation.

Functional Role of Phenylpropanoids in Plant Responses to Abiotic Stresses

Flavonoids accumulate in diverse plant organs, defined tissues and specific cell types as part of normal development [Lee, 2002; Lee et al., 1987] or in response to abiotic/biotic stress factors altering cellular and organism homeostasis [reviewed by Chalker Stack, 1999; Winkel-Shirley, 2001, 2002; Gould, 2004; Shimizu et al., 1999; Shimada et al., 2000]. Common abiotic stressors able to elicit flavonoid accumulation include excess UV-B light [Gould, 2004], drought [Farrant, 2000; Sherwin and Farrant, 1998; Iandolino, 2004], salinity [Walia et al., 2005], osmotic stress [Chalker-Scott, 1999, 2002], cold [Christie et al., 1994; Solecka and Kacperska, 2003], altered carbon to nutrient balance [Lillo et al., 2008; Iandolino, 2004], wounding [Gould et al., 2002, Tamari et al., 1995], and elevated heavy-metal exposure [Hale et al., 2002; Krupa et al., 1996]. Abiotic stress effectors modulate transcription of phenylpropanoid and flavonoid genes [Winkel-Shirley, 2002] via a complex network of receptor mechanisms, signaling cascades, and the activity of multiple transcription factors that ultimately integrate the response to external and internal cues [Chen et al., 2002; Davies and Schwinn, 2003]. An example is the promoter of the maize C1 transcription factor that harbors two conserved cis-acting elements that are critical for abscisic acid (ABA) responsiveness and light-dependent induction [Kao et al., 1996; Sidorenko et al., 2000].

Throughout evolution, plants have evolved complex mechanisms to cope with environmental factors that can compromise plant survival and reproduction. At the metabolic level, most abiotic stressors have profound effects on the

steady-state levels and relative abundance of several metabolites [Coruzzi and Bush, 2001; Coruzzi and Zhou, 2001]. Plants can sense and respond to these stress-dependent metabolic changes triggering a cascade of responses. Well-established examples are the increase in steady-state levels and sensitivity to the phytohormone ABA [Riera et al., 2005] as well as in the levels of reducing sugars and sucrose in leaves [Kerepesi and Galiba, 2000; Ackerson, 1981] in response to drought, osmotic, and salt stresses. Both ABA and glucose up-regulate the full complement of *Arabidopsis* genes involved in flavonoid biosynthesis [Li et al., 2006b] via the combinatorial effect of MYB and MYC-type (bHLH) transcription factors [Abe et al., 1997]. Different sugar-specific sensing mechanisms mediate effector perception and signaling cascades that leads to transcriptional and posttranscriptional regulation of gene expression [Koch, 1996]. Both glucose perception by a hexokinase (HXK)-dependent [Xiao et al., 2000] and HXK-independent mechanism [Smeekens, 2000; Rolland et al., 2002] regulate expression of distinctive sugar responsive gene sets. Expression of genes involved in flavonoid biosynthesis, like PAL and CHS, is modulated by glucose via the HXK-independent pathway [Xiao et al., 2000]. Sucrose-specific response pathways have been identified, but sucrose sensor mechanisms have not been completely elucidated [Teng et al., 2005]. Sucrose/ H^+ symporters mediating active phloem loading and unloading of sucrose at source (mature leaves) and sink tissues (e.g., immature leaves, fruits, roots) may function as sucrose-specific sensors [Eckardt, 2003; Barth et al., 2003]. The *Arabidopsis* *suc2/pho3* mutant [Zakhleniuk et al., 2001] lacks a functional sucrose transporter and hyperaccumulate soluble sugar in leaves [Lloyd and Zakhleniuk, 2004]. Sugar-induced anthocyanin accumulation in *pho3* plants results from the up-regulation of transcriptional regulators and all seven structural genes required for anthocyanin biosynthesis [Lloyd and Zakhleniuk, 2004]. Both the *Arabidopsis* [Xiao et al., 2000] and petunia [Tsukaya et al., 1991] CHS are induced by sugars. The promoter region of these genes contain the same cis-acting regulatory elements, known as Suc boxes [Teng et al., 2005], that provide sucrose responsiveness to the β -amylase gene [Tsukaya et al., 1991]. The sucrose-dependent induction of anthocyanin biosynthesis in *Arabidopsis* is mediated by the MYB transcription factor MYB75/PAP1 [Teng et al., 2005; Lloyd and Zakhleniuk, 2004; Borevitz et al., 2000].

Nutrient deficiency activates transcription and accumulation of different flavonoid compounds [Lea et al., 2007; Lillo et al., 2008]. Among other distinctive deficiency symptoms, long-term inorganic phosphorous (P_i) starvation strongly induces genes coding for all steps of the flavonoid pathway, leading to anthocyanin accumulation [Abel et al., 2002; Zakhleniuk et al., 2001; Misson et al., 2005]. In addition, CHS and PAP1 expression levels were synergistically up-regulated by P_i starvation and excess sucrose [Muller et al., 2007]. Induction of flavonoid biosynthesis in response to nitrogen starvation is a well-characterized response commonly used as a robust marker for altered carbon nitrogen balance at the cellular level [Lea et al., 2007; Lillo et al., 2008]. Nitrogen-starved *Arabidopsis* plants increased steady-state levels and changed

the relative abundance of different flavonoids [Stewart et al., 2001]. These nitrogen-deficiency-dependent responses have practical consequences in fruit production. For example, heavy nitrogen fertilizer applications reduces anthocyanin content of table and wine grape berries [Kliewer, 1977; Iandolino, 2004] while soil conditions associated with low nitrogen stimulate anthocyanin accumulation and contribute to improve wine quality [Kliewer, 1977; Seguin, 1986]. The response to nitrogen starvation reflects changes in expression levels of structural genes and enzymatic activities of the flavonoid pathway. For example, nitrogen stress-altered expression and enzymatic activity level of structural genes of the flavonol and anthocyanin biosynthetic pathway in tomato (*L. esculentum*), which resulted in a threefold increase in anthocyanidin and a twofold increase in quercetin-3-*O*-glucoside content [Bongue-Bartelsman and Phillips, 1995]. Co-induction of flavonol and anthocyanin biosynthesis was also observed in nitrogen-deficient *Arabidopsis* seedlings and it was shown to be controlled by the up-regulation of several MYB and bHLH factors regulating flavonoid biosynthesis [Lea et al., 2007]. In these nitrogen-stressed seedlings, the positive regulators of anthocyanin biosynthesis, PAP1 and PAP2 [Borevitz et al., 2000], and flavonol biosynthesis, MYB12 [Mehrtens et al., 2005], were strongly co-up-regulated with several bHLH factors such as GL3 [Lea et al., 2007].

Acclimation to freezing conditions induces major and complex changes in gene expression and steady-state levels of different metabolite pools [Cook et al., 2004; Kaplan et al., 2004; Hannah et al., 2006]. There exists a strong quantitative association between the induction of flavonoid biosynthetic genes and the extent of cold tolerance in *Arabidopsis* accessions [Hannah et al., 2006]. The R2R3-MYB factor PAP2 and the 37 genes of the PAP1 regulon [Toghe et al., 2005] are among the most highly up-regulated genes positively correlated with acclimation to freezing tolerance [Hannah et al., 2006]. While PAP2 expression is independent from sucrose cellular levels [Solfanelli et al., 2006], cold-induced anthocyanin accumulation may partially result from sucrose-mediated regulation of PAP1 activity since sucrose accumulation also correlates positively with freezing tolerance [Hannah et al., 2006].

The UV-absorbing capacity and strong *in vivo* antioxidant potential of simple phenolics and flavonoids make them play a critical role in UV light stress responses. Several *Arabidopsis* mutants defective in flavonoid and hydroxycinnamic acid biosynthesis are highly sensitive to UV radiation [Li et al., 1993; Landry et al., 1995; Bharti and Khurana, 1997; Bieza and Lois, 2001; Booij-James et al., 2000]. The combination of spectral absorption maximum in the UV-B range (208–315 nm) for hydroxycinnamic acids and UV-A (315–400 nm) range for flavonoids provide an effective sunscreen against a wide range of high-energy solar radiation [Landry et al., 1995]. Most colorless flavonoids (e.g., flavonols) and hydroxycinnamic acids accumulate preferentially in epidermal cell layers where they can be most efficient in filtering out UV-B/A solar radiation [Gould, 2004]. On the contrary, most anthocyanins accumulate in sub-epidermic mesophyll cells [Lee and Collins, 2001; Gould,

2004]. Both colorless cytosolic and colored vacuolar anthocyanin species [Lapidot et al., 1999] are efficient scavengers of free radicals [Neill et al., 2002]. It is likely that the colorless cytosolic forms are the ones first participating in scavenging reactive oxygen species (ROS) generated by chloroplasts [Gould, 2004]. Senescence processes and several abiotic stress factors diminish leaf carboxylation potential by reducing photosynthetic pigment content, impairing electron transport, and NADPH₂/ATP biosynthesis as well as enzymatic processes required for CO₂ assimilation [Walia et al., 2004]. UV-light-induced damage to the photosynthetic apparatus results in a characteristic reduction of the quantum efficiency of photosynthesis or photoinhibition [Long et al., 1994]. As light utilization for photochemistry becomes increasingly impaired, filtering of harmful radiation by phenylpropanoids prevents excess electrons from generating ROS such as superoxide, hydrogen peroxide (H₂O₂), hydroxyl radical, and singlet oxygen [Pastori and Foyer, 2002]. These ROS damage thylakoid membranes [Kolb et al., 2001], nucleic acids [Kootstra, 1994, Stapleton and Walbot, 1994], and proteins involved in light (e.g., photosystem II reaction center) and dark (e.g., Rubisco) reactions of photosynthesis [Jordan, 1996; Vass, 1997; Gould, 2004]. Reddening of senescing leaves in deciduous species during the fall season has been linked to photoprotection of cellular components during remobilization of photosynthetic pigments and resorption of nutrients [Feild et al., 2001; Hoch et al., 2001, 2003]. In some plant species, the photoprotective properties of UV-absorbing flavonoids are also essential to shield photolabile defense compounds. For example, the California coast native silver beachweed (*Ambrosia chamissonis*) accumulates high concentrations of a photolabile antimicrobial compound in certain organs and cell types [Page and Towers, 2002]. Tissues that contain this antimicrobial compound are surrounded by cell layers with high concentrations of UV-light-absorbing anthocyanins [Block et al., 1996; Page et al., 1999].

Light-mediated induction of phenylpropanoid biosynthesis appears to be mediated by MYB and bHLH factors. Light of different qualities strongly induces the positive regulators of anthocyanins biosynthesis PAP1, PAP2, as well as several bHLH transcriptional activators including TT8, EGL3, and GL3 [Cominelli et al., 2008] and strongly represses the negative regulator MYB4 [Jin et al., 2000]. Interestingly, PAP1 appears to up-regulate transcription of structural genes of the flavonoid pathway in a light-dependent manner since PAP1 overexpression alone does not induce anthocyanin accumulation in darkness [Cominelli et al., 2008]. This suggests the existence of a more complex network that includes photoreceptors and light-dependent signaling cascades [Jenkins et al., 2001], the requirement of additional light inducible bHLH (e.g. TT8) or basic-leucine zipper (bZIP) (e.g., HY5) transcription factors [Feldbrügge et al., 1994, 1997; Ang et al., 1998; Hartmann et al., 2005; Shin et al., 2007] or the existence of light-dependent posttranslational mechanisms to activate structural enzymes [Cominelli et al., 2008]. The promoter region of several early and late biosynthetic genes including CHS, F3H, and FLS in parsley (*Petroselinum crispum*) [Schulze-Lefert et al., 1989] and *Arabidopsis*

[Feldbrügge et al., 1994, 1997; Hartmann et al., 1998, 2005] harbors a G-box cis-acting element conferring light responsiveness that is a potential target for bHLH and bZIP transcription factors. PIF3, a bHLH transcription factor mediating phytochrome transcriptional cascades, regulates anthocyanin biosynthesis in a HY5-dependent manner [Shin et al., 2007]. Blue-light photomorphogenic responses mediated by cryptochrome flavyn-type photoreceptors or cytokinins, including anthocyanin accumulation, are regulated by HY5 [Vandenbussche et al., 2007]. In vitro binding assays have shown that PIF3 binds to the G-box element (CACGTG) while HY5 can bind both to the G- and Z-box (ATACGTGT) elements [Chattopadhyay et al., 1998; Martinez-Garcia et al., 2000; Yadav et al., 2002]. In *Arabidopsis*, chromatin immunoprecipitation-based assays have shown that both transcription factors bind independent elements in the promoter regions of CHS, CHI, F3 H, F3H, DFR, and LDOX genes [Shin et al., 2007].

To summarize, the responsiveness of phenylpropanoid metabolism to abiotic stressors that can severely and irreversibly affect several plant processes constitute a critical trait to increase reproductive fitness and survival of land plants [Raushier, 2006]. The timely activation of the pathway is tightly regulated by a complex network of receptors, signaling cascades, and transcriptional regulators [Swindell, 2006] that integrate internal and external cues and ensure optimal use of metabolic resources.

BIOLOGICAL ROLE OF PHENYLPROPANOIDS IN MEDIATING PLANT INTERACTIONS WITH OTHER ORGANISMS

Flavonoids as Herbivore Deterrents

The ability of plant proanthocyanidins to tightly bind macromolecules such as proteins and cell wall polysaccharides plays a critical role in plant defense against insect and animal herbivores. Proanthocyanidin abundance in insect diet has been negatively correlated with population size of leaf-chewing herbivores (*Quercus* sp.) [Feeny, 1970; Forkner et al., 2004], larvae growth and development [Nomura and Itioka, 2002; Mutikainen et al., 2002; Barbenhenn and Martin, 1994], and increased parasitism rates [Faeth and Bultman, 1986]. Proanthocyanidin content and biochemical nature determines palatability, digestibility, and nutritional value of forage legumes [Barry and McNabb, 1999; McAllister et al., 2005; Dixon et al. 2005]. Proanthocyanidin–protein complexes are more resistant to the action of proteolytic bacteria in the livestock rumen reducing methane production and bloating [Kingston-Smith and Thomas, 2003; Zucker, 1983]. Proanthocyanidin–protein complexes can then dissociate in the abomasum, increasing the amount of plant protein reaching the small intestine [Barry and Manley, 1984; Mangan, 1988]. The absence of proanthocyanidins in alfalfa (*Medicago sativa*) and clovers (*Trifolium* spp.) [Fay et al., 1980] favors pasture bloating in ruminant animals [Aerts

et al., 1999; Fay et al., 1980] fed exclusively on these pastures. On the contrary, moderate proanthocyanidin amounts ranging from 2 to 4% dry matter prevent fast proteolytic rates during rumen fermentation, thus reducing the risk of bloating [Tanner et al., 1995; McAllister et al., 2005; Dixon et al., 2005 and references therein]. Proanthocyanidin content above 6% dry matter, however, deter herbivores from grazing on leaves, drastically reduce digestibility of proteins and fiber, and negatively impact on ruminant livestock growth rates [Leinmüller et al., 1991; McAllister et al., 2005]. Both insect and mammals have developed numerous strategies to deal with high proanthocyanidin plant organs, including secretion of tannin-binding proteins in the saliva [Shimada, 2006], detoxification mechanisms, and production of excess gastrointestinal mucus, among others [reviewed by McArthur et al., 1995; Dearing et al., 2005]. The nutritional value of forage legume preserved as silage [Wang et al., 2007] or the occurrence of bloating in ruminant livestock grazing exclusively on alfalfa [McAllister et al., 2005; Waghorn, 1990] can be prevented by supplementation with forage plants containing PA [Lees, 1992]. The wide range of variation in proanthocyanidin natural abundance as well as the degree of polymerization, monomer composition, stereochemistry, and the degree of hydroxylation [Haslam, 1981; Clausen et al., 1992; Zucker, 1983] modify the capacity to precipitate proteins and inhibit fiber digestion by cellulolytic ruminal bacteria [McAllister et al., 2005]. As a result, the potential growth gains from dietary supplementation depends on the proanthocyanidin qualitative and quantitative profile of the forage plant selected [Reed and Soller, 1987]. Alfalfa and clovers only accumulate proanthocyanidins in the seed coat [Sharma and Dixon, 2005; Xie et al., 2006]. Numerous breeding approaches including mutagenesis, somaclonal variation, and somatic hybridization have failed to induce proanthocyanidin accumulation in vegetative tissues [Goplen et al., 1980; Gruber et al., 1999]. As a result, transgenic strategies are currently being pursued to improve digestibility of these valuable forage legumes [Morris and Robbins, 1997; Sharma and Dixon, 2005; Xie et al., 2006].

Flavonoids as Pollinator Attractants

Several plant species have evolved floral organs with elaborated morphological structures, unique petal epidermis cellular organization [Kay et al., 1981; Glover and Martin, 1998], and complex pigment biochemistry [reviewed by Grotewold, 2006; Ellestad, 2006] to ensure the attraction of insect pollinators, pollination, seed biogenesis and dispersal [Kevan and Baker, 1983]. Several flavonoids including anthocyanins, flavonols, flavones, and aurones are among the most common phenylpropanoid pigments found in floral organs and fruits [Grotewold, 2006; Ono et al., 2006]. Due to their unique absorption spectra, flavonoids often display complex patterns that become apparent only to specialized visual organs of insect pollinators that are sensitive to the UV range of the spectrum [Giurfa and Menzel, 1997; Gronquist et al., 2001]. In addition, successful pollinations can trigger floral color changes that are

independent of senescing processes as observed in cotton and *Viola cornuta* [Farzad et al., 2000; Weiss 1991, 1995].

The color of monomeric anthocyanin pigments depends on the vacuolar pH [Fukada-Tanaka et al., 2000; Spelt et al., 2002] as well as on the occurrence of intra- or intermolecular interactions between the colored anthocyanin flavylium cation and colorless flavonoids, metal ions, carotenoids, and organic acids [Forkmann, 1991; Ellestad, 2006]. Molecular stacking resulting from these interactions is responsible for changes in the spectral signature of flavonoid pigments via the co-pigmentation phenomena [Ellestad, 2006]. Co-pigmentation enhances absorption (hyperchromic shift) and shifts the wavelength of maximum absorbance (bathochromic shift) of pigment solutions [Boulton, 2001], contributing to color stabilization and generation of distinctive spectral signatures to attract pollinators [Ellestad, 2006; Grotewold, 2006]. In addition to quantitative and qualitative changes in pigment composition, flowers have evolved morphological traits that affect color perception and attractiveness. For example, both the presence of conical-papillate cells in the petal epidermis and to a lower extent the content of anthocyanin pigments drastically influence frequency of pollinator visit and pollination success in *Antirrhinum majus* [Glover and Martin, 1998]. The existence of an intricate genetic network regulating qualitative and quantitative pigment traits [Mol et al., 1998; Weiss, 2000; Martin and Gerats, 1993] and the complex molecular interactions determining flower pigmentation makes the modification of flower color for commercial purposes by breeding or transgenic approaches a challenging proposition [Forkmann, 1991; Chandler, 2003].

Phenylpropanoids as Signaling Molecules in Plant–Plant Interactions: Allelopathy and Parasitism

Allelopathy is defined as the secondary metabolite-mediated interaction between living organisms (plant, fungi, algae, and bacteria) that influence growth and developmental processes in a biological system [International Allelopathy Society, 1996]. Several plants, including modern crops, exude potent allelochemicals that mediate allelopathic interactions, especially with invasive weeds [reviewed by Belz, 2007; Macías et al., 2007]. Crop allelopathy is seen as a natural defense mechanism against invasive weeds with potential for biotechnological applications [reviewed by Belz, 2007; Macías et al., 2007].

In plants, biosynthesis and exudation of allelochemicals follows developmental, diurnal, and abiotic/biotic stress-dependent dynamics. Compounds from 14 different chemical classes have been linked to allelopathic interactions, including several simple phenolic acids (e.g., benzoic and hydroxycinnamic acids) and flavonoids [Rice, 1984; Macías et al., 2007]. The existence of several soil biophysical processes that can reduce the effective concentration and bioactivity of these compounds casts doubts on their actual relevance in allelopathic interactions [Olofsdotter et al., 2002]. However, there are well-documented examples of phenylpropanoid-mediated incompatible interactions among plants. Several Gramineae mediate allelopathic interactions by means of

phenolic and flavonoid exudates [Pérez and Ormeño-Núñez, 1991; Nimbal et al., 1996; Czarnota et al., 2003; Frey et al., 1997]. For example, genetic variability in the content of the flavone 5,7,4'-trihydroxy-3',5'-dimethoxyflavone found in rice root exudates has been associated with allelopathic cultivars [Seal et al., 2004]. Several invasive dicotyledonous species have abundant allelochemical flavonoids like robinetin, in *Robinia pseudoacacia* L. [Nasir et al., 2005], and (–)-catechin in spotted knapweed (*Centaurea maculosa* Lam.) [Bais et al., 2003; Fitter, 2003]. In the latter example, catechin is secreted as a racemic mixture, where the (–)-catechin enantiomer has allelopathic activity and the (+)-catechin acts as a phytoalexin with antibacterial properties against root pathogens [Bais et al., 2002]. The (–) stereoisomer is absorbed through the root system of neighboring plants where it triggers a series of events that ultimately lead to root death [Bais et al., 2002]. Stereochemistry is not the only factor contributing to allelochemical properties. Potency of allelochemical compounds might also depend on the synergistic interaction with metabolites from a wide range of chemical classes [Kong et al., 2004].

The exact molecular mode of action of flavonoid allelochemicals remains elusive [Macías et al., 2007]. Simple phenolic compounds such as benzoic and hydroxycinnamic acid derivatives are widely studied allelochemicals that seem to interfere with plasma membrane functions, enzymatic processes and energy-related systems [Macías et al., 2007]. Depending on their specific lipophilic properties, simple phenolic compounds can penetrate cellular lipid bilayers causing electrolyte leakage conducive to cell death as a consequence of membrane depolarization [Macri et al., 1986] and altered water relations [Barkosky et al., 2000]. Certain phenolics can also affect normal respiratory processes in soil-borne microorganisms [Souto et al., 2000] as well as photosynthetic carbon assimilation in neighboring plants [Barkosky et al., 2000; Yang et al., 2002]. Further detailed identification of allelopathic compounds and their mechanistic mode of action would allow potential biotechnological applications for weed control.

Phenylpropanoids in Plant Defense and Plant–Pathogen Interactions

Several phenylpropanoids including simple phenolics as well as more complex monomeric and oligomeric aromatic compounds derived from the flavonoid, stilbene, and isoflavonoid pathway have toxic properties against a vast array of organisms [Harbone, 1994; Feucht and Treutter, 1999; Grayer and Harborne, 1994; Dixon, 2001]. Phenylpropanoids involved in defense mechanisms can be synthesized constitutively (phytoanticipins) or induced in response to specific elicitors (phytoalexins) [VanEtten et al., 1994; Dixon, 2001; Treutter, 2006]. Phytoanticipins are synthesized during normal development in specific organs and cell layers and can also be up-regulated in response to specific abiotic stress factors or biological elicitors. For example, several flavonoids accumulating in the developing barley seed testa layer provide resistance to different *Fusarium* spp. [Skadhauge et al., 1997b]. In grapes, natural variability in the constitutive and induced stilbene content of vegetative [Borie et al., 2004] and reproductive

[Li et al., 2006a] organs is often linked to the genetic diversity in resistance to gray mold (*Botrytis cinerea*) [Sbaghi et al., 1996; Borie et al., 2004] and decay caused by *Rhizopus stolonifer* [Sarig et al., 1997].

Levels of monomeric and oligomeric stilbenes in grape (*V. vinifera*) berry and vegetative tissues are greatly influenced by the genetic background [Li et al., 2006a] and eliciting factors [Borie et al., 2004]. Resistance of grape cultivars to downy mildew (*Plasmopara viticola*) is correlated to the induced accumulation of the oligomeric ϵ - and δ -viniferin but not to resveratrol or its glucoside piceid [Pezet et al., 2004; Dercks and Creasy, 1989]. In apple (*Malus domestica*), horticultural practices such as N fertilization can enhance plant growth and productivity. At the same time, they can reduce flavonoid biosynthesis and enhance susceptibility to specific pathogens [Rühmann et al., 2002; Rühmann and Treutter, 2003; Leser and Treutter, 2005]. The molecular and biochemical mechanisms underlying the induction of phenylpropanoid phytoalexins accumulation in specific tissues or cell layers in response to biotic or abiotic stress factors [Paiva et al., 1994] may depend on the elicitor effector involved [He and Dixon, 2000; Naoumkina et al., 2007]. In the model legume *Medicago truncatula*, medicarpin accumulation elicited by yeast extracts correlated with the up-regulation of the entire set of genes in the phenylpropanoid/isoflavonoid pathway [Naoumkina et al., 2007]. On the other hand, the wounding signal methyl-jasmonate, exclusively up-regulated β -glucosidases (and likely malonyl-lesterases) and ABC transporters to mobilize vacuolar pools of (malonyl)glucosyl-isoflavonoids [Naoumkina et al., 2007]. The aglycones of these isoflavonoids can then be converted to bioactive medicarpin by a set of co-up-regulated pterocarpan biosynthetic genes [Naoumkina et al., 2007].

Gain-of-function transgenic strategies designed to introduce phytoalexin-dependent resistance traits by up-regulating expression of different rate-limiting steps in isoflavonoid and stilbene biosynthesis often result in enhanced resistance to plant pathogens. Alfalfa leaves accumulate isoflavonoid phytoalexins exclusively upon elicitation [Paiva et al., 1994]. Elicited alfalfa leaves constitutively overexpressing its own isoflavone 7-*O*-methyltransferase [He and Dixon, 2000] or a *M. truncatula* isoflavone reductase [Deavours and Dixon, 2005] had greater steady-state levels of several isoflavone glucosides and medicarpin resulting in enhanced resistance to *Phoma medicaginis* [He and Dixon, 2000]. Likewise, resistance to this pathogen is achieved in transgenic alfalfa plants with constitutive accumulation of a trans-resveratrol-glucoside resulting from the heterologous expression of the peanut stilbene synthase [Hipskind and Paiva, 2000]. In addition to changes in the levels of endogenous phytoalexins, the oxygen-dependent oxidation of (poly)phenolic compounds to their respective quinone forms mediated by plant and microbial polyphenol oxidases (PPO, EC 1.10.3.1, and laccase, EC 1.10.3.2) and peroxidases (EC 1.11.1.7) plays a critical role in defining function and biological activity of phenylpropanoid phytoalexins [reviewed by Pourcel et al., 2007]. Antisense suppression of PPO activity in tomato (*L. esculentum*) induced a dramatic increase in susceptibility to *Pseudomonas syringae* [Thipyapong et al., 2004]

while overexpression was conducive to enhanced bacterial disease resistance [Li and Steffens, 2002]. Microorganisms have also evolved oxidation-dependent detoxification mechanisms to circumvent phytoalexin antimicrobial activity. For example, pathogenicity of isolates of the necrotroph *B. cinerea* correlates with the relative laccase-mediated capacity to conduct oxidative dimerization of resveratrol and pterostilbene (3,5-dimethoxy-4'-hydroxystilbene) found in grapevine tissues [Sbaghi et al., 1996; Cichewicz et al., 1999]. The pathogen and strain-specific presence of detoxification mechanisms may explain the enhanced resistance to *Phytophthora infestans* but not to *B. cinerea* observed in transgenic tomatoes overexpressing the grape stilbene synthase [Thomzik et al., 1997].

Although still relatively uncharacterized, several possible phytoalexin modes of action mechanisms have been proposed. Barley Pas and dihydroquercetin confer resistance mainly by direct or indirect inactivation of fungal enzymes involved in cell wall disassembly and degradation [Skadhauge et al., 1997b]. The grape hydroxystilbenes resveratrol and pterostilbene impair *B. cinerea* conidia respiration and germination while promoting abnormal subcellular organization [Pezett and Pont, 1990a, 1995; Adrian et al., 1997]. The specific toxicity of different stilbenes might be related to their lipophylic characteristics and their potential to disrupt normal cell and organelle membrane functions [Pezet and Pont, 1990b, 1995]. Further identification of known and novel phytoalexins, their mechanistic mode of action, and elucidation of biosynthetic routes are critical steps required to breed or engineer phenylpropanoid-based pathogen-resistant traits in crops.

Flavonoids and the Rhizobium–Legume Symbiosis

All higher organisms are dependent on external sources of reduced nitrogen for survival. One of the main sources of reduced nitrogen in the biosphere is the symbiotic interaction between bacteria, known generally as rhizobia, and the roots of legume plants.

Flavonoids are key regulators of this remarkable developmental and metabolic collaboration, in which otherwise saprophytic soil bacteria (the rhizobia) give up their independent lifestyle and take up residence within cells of a modified legume root organ, known as the nodule. Within the nodule the plant provides energy in the form of photosynthate to the bacterium, in exchange for fixed nitrogen in the form of ammonia. Flavonoids have roles at several steps in this symbiotic relationship, from initial signal exchange at the root surface during the earliest stage of interaction through the induction of nodule organogenesis in the root cortex.

One feature of the rhizobium–legume symbiosis is the high degree of specificity that many legumes and their symbiotic partners exhibit. For example, *Sinorhizobium meliloti*, the well-characterized bacterial symbiont of alfalfa and related *Medicago* species, is unable to nodulate its close relative *Pisum sativum* (Mendel's pea), and conversely pea symbionts do not nodulate *Medicago* species. It is now clear that there are multiple molecular determinants

of specificity, including bacterial ligands (known as “Nod factors”) that stimulate host responses and corresponding cognate plant Nod factor receptors [Long 1996; Oldroyd and Downie, 2008]. However, the earliest manifestation of specificity depends on the release of host metabolites into the rhizosphere, where they are perceived by the bacterium and initiate a regulatory and biosynthetic cascade. Metabolites in the host legume are principally products of the flavonoid and isoflavonoid pathway [Peters et al., 1986; Redmond et al., 1986]. Bacterial genetics played a large role in deciphering the nature of early bacterial responses to legume exudates [Long, 1996], and by the early 1990s it was understood that flavonoids were perceived by a family of LysR transcription factors, including NodD1 of *S. meliloti*. NodD proteins are both positive and negative regulators of the expression of a suite of bacterial genes known as the Nod regulon. Products of the Nod regulon include enzymes involved in the synthesis of a second signal, delivered from the bacterium to the plant. The signal molecule, a chitolipooligosaccharide, acts in a plant–host specific manner to trigger a suite of host responses, which includes up-regulation of flavonoid gene transcription and flavonoid biosynthesis in the root epidermis [Van Brussel et al., 1990; Recourt et al., 1992]. The outcome is a flavonoid-based regulatory loop that is presumed to reinforce early signal exchange.

A remarkable degree of specificity is exhibited at the level of flavonoid-induced gene transcription in the bacterium. Peck et al. [2006] demonstrate that NodD homologs from a range of rhizobium species exhibit different specificities for flavonoid-mediated gene induction, consistent with direct physical interaction between NodD transcription factors and flavonoids. Interestingly, flavonoids act generally to stimulate binding of the *S. meliloti* transcription factor, SmNodD1, to nod gene promoters, independent of whether or not the flavonoids activate NodD1-dependent gene transcription. Thus, flavonoids act nonspecifically to enhance NodD1 binding to promoters, and specifically to affect transcriptional activation. Peck et al. [2006] propose a model wherein the inactive flavonoids are competitive inhibitors of nod gene induction, competing with activating flavonoids for NodD interaction and also promoting transcriptionally inactive promoter DNA–NodD complexes.

As mentioned above, the product of Nod gene activation in the bacterium is the synthesis of a ligand called Nod factor. Nod factor perception activates a suite of host responses that include the up-regulation of flavonoid synthesis and the activation of cell division in the root cortex leading to nodule organogenesis. The convergence of work spanning several decades led to the hypothesis that Nod factor-induced flavonoid accumulation might be causal to Nod factor-induced cell cycle activation. Key to this hypothesis were the demonstrations that (i) exogenous flavonoids can regulate polar auxin transport [Jacobs and Rubery, 1998]; (ii) auxin transport inhibitors such as N-(1-naphthyl)-phthalamic acid (NPA) can induce nodule-like structures on legume roots [Hirsch et al., 1989]; (iii) both flavonoid biosynthesis genes [Yang et al., 1992] and flavonoid metabolites [Mathesius et al., 2000] accumulate at the site of incipient cortical cell division; and (iv) cortical cell division is preceded by a

spatially co-incident inhibition of polar auxin transport [Mathesius et al., 1998]. Mechanistically, flavonoid-mediated changes in the auxin transport are thought to alter critical auxin-to-cytokinin ratios at the site of cortical cell activation, leading to nodule primordia (e.g., as supported by the study of Cooper and Long [1994]). Recently, nodule-related cell division has been shown to depend on the plant hormone cytokinin [Gonzalez-Rizzo et al., 2006; Tirichine et al., 2007; Murray et al., 2007]. However, there is no conclusive proof that flavonoids are required for cortical cell activation.

Working with the model legume, *M. truncatula*, Wasson et al. [2006] used RNA interference (RNAi) to reduce the level of chalcone synthase (CHS) transcript and thus flavonoid biosynthesis in *Agrobacterium* rhizogenes-transformed “hairy” roots. The transformed roots exhibited a substantial reduction in the levels of flavonoid metabolites and were unable to form nodules (no cell division) upon inoculation with compatible *Sinorhizobium meliloti*. Reduced flavonoid levels were predicted to impact symbiosis in two ways: first, through precluding induction of bacterial gene expression via the flavonoid-responsive NodD circuit described above, and second by precluding flavonoid-mediated changes in auxin transport in the root cortex. When bacteria were pretreated with flavonoids to ensure efficient Nod gene induction in the bacterium, root hair curling (a classic Nod factor response) was restored, though inner cortical cell divisions were still absent. By contrast, nodule formation could be rescued by treatment of roots with naringenin and liquiritigenin. The CHS RNAi plants exhibited increased polar auxin transport relative to wild type, similar to phenotypes observed for flavonoid-deficient mutants of *Arabidopsis* [reviewed by Peer and Murphy, 2007]. Importantly, inoculation with preinduced *S. meliloti* caused decreased auxin transport in wild-type, but not in the CHS RNAi, plants. The results of Wasson et al. [2006] are consistent with a model wherein the bacterium induces CHS, and the resulting flavonoid biosynthesis inhibits polar auxin transport, which leads to (is necessary for) cell division.

A similar but not identical study by Subramanian et al. [2006], working in soybean, used RNA interference to co-knockdown two isoflavone synthase paralogs (IFS1 and IFS2) and in a separate experiment to knock down chalcone reductase (CHR). The IFS knockdown plants were severely reduced for nodulation, and they had substantially reduced levels of daidzein and genistein, the two main Nod gene inducers in the *Bradyrhizobium*–soybean symbiosis. By contrast, the CHR knockdown plants had reduced levels of daidzein but increased levels of genistein, and these plants nodulated normally. IFS knockdown plants exhibited increased auxin transport, similar to the results described previously for *Medicago* and *Arabidopsis*; conversely, plants silenced for CHR had decreased auxin transport. Thus, the data from Subramanian et al. [2006] support a role for product(s) of IFS in nodulation (presumably daidzein and/or genistein), and a role for product(s) of IFS (presumably daidzein) in polar auxin transport.

To determine whether the reduced polar auxin transport observed in IFS knockdown plants was causal to the absence of nodulation, the authors conducted

two experiments: (1) They used a genistein-hypersensitive strain of *Bradyrhizobium*, which gives efficient Nod factor gene induction even in the IFS knockdown background, and (2) they inoculated wild-type and mutant plants directly with cognate Nod factor. They observed that the genistein-hypersensitive strain restored nodulation to the IFS knockdown plants, suggesting that products of IFS of activity are critical to bacterial Nod gene induction but not to polar auxin transport. In other words, they could dissociate the auxin transport phenotype of the plant from the Nod gene induction phenotype of the bacterium by means of the genistein-hypersensitive bacterial symbiont. The results of the second experiment were consistent with the first; namely, they revealed that purified Nod factor was sufficient to induce cortical cell activation (cell division) in IFS and CHR knockdown plants as efficiently as in wild-type plants. Thus, in contrast to the conclusion of Wasson et al. [2006], Subramanian et al. [2006] concluded that flavonoid-inhibition of auxin transport is not critical to nodulation.

To summarize, it seems clear that flavonoids are important for nodulation and that part of this importance relates to Nod gene induction in the bacterium via the NodD circuit. It also seems clear that endogenous flavonoids can inhibit auxin transport in both *Medicago* and soybean. It is formally possible that flavonoid-regulated auxin transport is important to nodulation in *Medicago* but not in soybean. In fact, these two species exhibit a conspicuous difference in nodule development: in *Medicago* nodule primordia arise from inner cortical cells, while in soybean nodule primordia arise from cells in the outer cortex—perhaps this anatomical distinction reflects an underlying physiological difference in nodule initiation. Alternatively, flavonoid-mediated altered auxin transport may be correlated with, but not essential to, nodulation. The discrepancy between the results of Wasson et al. [2006] and Subramanian et al. [2006] may be a function of biological differences between *Medicago* and soybean or may reflect differences in experimental design such as the choice of genes for RNAi. In any case, these studies highlight the complexity of research at the intersection of flavonoid metabolism and plant physiology. It is well established that flavonoids are endogenous regulators of polar auxin transport [reviewed by Peer and Murphy, 2007] and that they exert their effects by both direct and indirect means; however, while flavonoids are well established as factors in plant growth and development, they are often not essential to these processes. In many cases, such biological nuance complicates qualitative statements about the link between flavonoids and plant function, as may be the case for the rhizobium–legume symbiosis.

TRENDS IN METABOLIC ENGINEERING OF PHENYLPROPANOID METABOLISM IN PLANTS AND MICROORGANISMS

The flavonoid pathway is an important source of small molecules with nutraceutical and drug discovery potential due to their potent bioactivity against several human diseases [reviewed by Lin and Weng, 2006; Ross and

Kasum, 2002; Ververidis et al., 2007a]. Flavonoids are potent antioxidants in vitro and several epidemiological and clinical studies have linked diets with high flavonoid intake with lower rates of cardiovascular disease, cancer, and other age-related diseases. In spite of the dramatic progress in our understanding of the flavonoid pathway, *in planta* biosynthesis of flavonoids for drug discovery imposes several challenges from a pharmaceutical standpoint. Low concentration and limitations to diversify basic chemistry complicate the use of plants as bioreactors to produce specific flavonoids in sufficient amounts for basic research, development, and use in clinical trials [Butler, 2004]. The biochemical synthesis of flavonoids in microorganisms provide a novel approach that would circumvent such limitations [reviewed by Chemler et al., 2006; Leonard et al., 2007b; Ververidis et al., 2007b]. Both yeast and bacteria have been used as model organisms for bioreactor-based flavonoid production [Yan et al., 2005; Miyahisa et al., 2005; Leonard et al., 2006a, 2006b; Zhang et al., 2006]. Introduction of the core flavanone biosynthetic pathway and simultaneous co-expression of several downstream enzymatic activities allowed the biosynthesis of different flavonoids in the gut bacteria *Escherichia coli* [Miyahisa et al., 2005; Leonard et al., 2006a, 2006b; Beckwilder et al., 2006] and the bread and wine yeast *Saccharomyces cerevisiae* [Chemler et al., 2006; Leonard et al., 2005; Yan et al., 2005; Beckwilder et al., 2006]. Further refinements to overcome metabolic bottlenecks [Miyahisa et al., 2005] boosted flavonoid production more than a 1,000-fold when central metabolic pathways in *E. coli* were engineered to increase the endogenous malonyl-CoA pool [Leonard et al., 2007]. The application of ¹³C-isotopomer-based flux analysis [Sauer, 2006] to gain insight on the fluxome of these engineered microorganisms would certainly provide new leads for further optimization of flavonoid biosynthesis.

Efforts to metabolically engineer the phenylpropanoid and flavonoid pathways in plants have been directed toward improvement or introduction of novel phenotypic traits with relevance to human diet, animal feed, or ornamental purposes [Forkmann and Martens, 2001; Tian et al., 2007]. Transgenic approaches have been applied to overcome genetic constraints limiting conventional or marker-assisted breeding. Also, they have been used when the introduction of the new trait cannot be done at the expense of modifying preexistent desirable characteristics of the base germplasm. Transgenic blue/violet carnations, blue roses [Tanaka et al., 2005], and yellow snapdragons and dahlias [Ono et al., 2006] are just a few examples of pathway engineering by ectopic expression of exotic genes of the flavonoid pathway without introducing changes in other desirable phenotypic traits [Forkmann and Martens, 2001]. Pathway engineering has also been applied to increase the nutraceutical value of fruits and vegetables [Dixon and Steele, 1999; de Vos et al., 2000]. For example, overexpression of the maize transcription factors LC and C1 [Bovy et al., 2002] or the petunia CHI [Verhoeven et al., 2002; Muir et al., 2001] increased nutraceutical value and antioxidant potential of tomatoes as a result of dramatic increase in total flavonol content. Soybeans with increased content of beneficial isoflavones were obtained by

ectopic expression of maize C1 and R transcription factors and suppression of F3H to prevent competition from anthocyanin biosynthesis [Yu et al., 2003]. Modification of the (iso)flavonoid profile of edible plant organs by introducing activities that can modify their basic carbon skeleton and bioactivity is certainly the next frontier in metabolic engineering of foods with enhanced nutraceutical value [Tian et al., 2007; Lim et al., 2004]. The phenylpropanoid pathway has also been targeted to engineer traits related to improvement in animal feed quality and industrial processing of plant biomass. Metabolic engineering of lignin biosynthesis has found applications in forage quality improvement and production of ethanol for biofuel. Lignin content [Jung and Vogel, 1986] and relative changes in lignin composition [Buxton and Russell, 1988] associated with forage legume maturity stage correlate negatively with digestibility and nutritional value for ruminant livestock [Albrecht et al., 1987; Casler and Vogel, 1999]. Digestibility of alfalfa was substantially improved in plants with low lignin content and similar monolignol subunit composition. This milestone was achieved by antisense-mediated silencing of cytochrome P450 monooxygenases [Reddy et al., 2005] and methyltransferases [Guo et al., 2001] involved in the biosynthesis of monolignol lignin subunits. Reduction of lignin content in plant lignocellulosic biomass may also improve access of degradative enzymes to cellulose and increase efficiency of enzymatic saccharification processes that release fermentescible sugars for biofuel production [Mosier et al., 2005; Chapple et al., 2007]. Low lignin biomass may avoid hot acid pretreatments that add to processing costs [Mosier et al., 2005] and introduce contaminants that interfere with yeast-based fermentation processes [Almeida et al., 2007]. On a different approach, down-regulation of lignin biosynthesis in alfalfa was achieved using antisense technology to reduce expression of six different genes in the monolignol biosynthetic pathway [Chen and Dixon, 2007]. In these plants, yield of fermentescible sugar increased proportionally with decreasing lignin content [Chen and Dixon, 2007]. The application of this approach to other bioenergy crops (e.g., poplar—*Populus* sp., *Miscanthus* × *giganteus*, switchgrass—*Panicum virgatum*, etc.) may alleviate pressure on food crops currently used for biofuel production and lead to a cost-effective and renewable nonedible plant biomass source for ethanol-based biofuel production [Chapple et al., 2007]. Future progress in metabolic engineering to increase nutraceutical value of edible plant organs, enhance disease resistance, or modify structural properties of plant biomass for industrial applications will depend on progress made on our understanding of transcriptional regulation [Century et al., 2008], transport mechanisms, and factors affecting fluxes from precursor pathways as well as between branches of the phenylpropanoid pathway [Liu et al., 2002; Ro and Douglas, 2004; Schwender, 2008; Farag et al., 2008].

CONCLUSIONS

The phenylpropanoid pathway is the source of hundreds of metabolites that play critical roles in ensuring land plant survival, reproduction, and interaction

with other organisms and their environment. Advances in (iso)flavonoids isolation and characterization [reviewed by Stobiecki and Kachlicki, 2006] as well as identification of full gene complements as a result of whole genome sequencing projects (<http://www.sciencemag.org/plantgenomes/>) and characterization of novel mutants will dramatically expand our mechanistic understanding of the role of these secondary metabolites in plant biology and ecophysiology. Due to the inherent limitations of using plants as bioreactors, pathway engineering will likely focus on introducing traits to enhance tolerance to abiotic/biotic stress factors, improve edible quality and nutraceutical value of fruits and vegetables, and modify industrial processing properties of plant biomass, particularly in relation to cellulose-based biofuel production. Pharmaceutical discovery and production of phenylpropanoid-based drugs will almost certainly rely on progress made on microorganism-based (iso)flavonoids and stilbene biosynthesis.

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