Chapter 51

Roles of Flavonoids in Symbiotic Root–Rhizosphere Interactions

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51.1 INTRODUCTION

51.1.1 Flavonoid Synthesis and Occurrence in Plants

Flavonoids are metabolites of the phenylpropanoid pathway, which are synthesized from *p*-coumaroyl-CoA and malonyl-CoA and share their precursors with the lignin biosynthetic pathway (Stafford, 1990). Flavonoids have been found in all plants, and so far over 10,000 flavonoids have been identified in different plant species (Ferrer et al., 2008). The diversity of flavonoids is achieved through the generation of several basic flavonoid structures, including flavonols, flavan-3-ols, flavones, flavanones, isoflavonoids, isoflavans, and pterocarpans (Fig. 51.1). A diversity of end products is derived from the modification of these basal structures, e.g. by glycosylation, methylation, hydroxylation, malonylation, acylation, prenylation, or polymerization (Winkel-Shirley, 2001). These modifications can alter the solubility, mobility, degradation, and function of flavonoids inside the plant and in the rhizosphere.

Flavonoid synthesis has been well studied, and the majority of enzymes have been identified (Dixon and Steele, 1999; Winkel-Shirley, 2001; Du et al., 2010). The synthesis of flavonoids starts on enzyme complexes that are located at the cytosolic side of the endoplasmic reticulum (Jorgensen et al., 2005). Flavonoid intermediates can subsequently be channeled into the vacuole for storage, often after being glycosylated by enzyme complexes located at the tonoplast (Aoki et al., 2000; Winkel, 2004). The accumulation of final flavonoid end products is often specific for particular cell types. In roots, flavonoids often accumulate at the root tip and in root cap cells. Flavonoid accumulation in specific cell types of the root, for example, in precursor cells of nodules, have been linked to specific functions in root development (Mathesius et al., 1998a; Mathesius, 2001). Intracellularly, flavonoids can be found in the cytoplasm, the vacuole, the nucleus, the cell wall, or in cell membranes (Hutzler et al., 1998; Erlejman et al., 2004; Saslowsky et al., 2005; Naoumkina and Dixon, 2008). Several transcription factors, in particular, those of the MYB and bHLH families, control the localization and synthesis of flavonoids in different tissues and in response to the environment (Koes et al., 2005). However, in most cases, the regulation of cell specificity remains unknown.

Despite the cell specificity of flavonoid synthesis, there is also evidence that flavonoids can be transported within and between cells and tissues. Flavonoids are thought to move via vesicle-mediated transport or membrane-bound transporters of MATE (multidrug and toxic extrusion compound) or ABC (ATP-binding cassette) families within cells (Zhao and Dixon, 2009). Transport of flavonoids between cells over long distances is less well understood. In *Arabidopsis*, it was demonstrated that external application of flavonoids led to their transport toward distal tissues (Buer et al., 2007). This mode of transport is most likely mediated by

Molecular Microbial Ecology of the Rhizosphere, Volume 1, First Edition. Edited by Frans J. de Bruijn.

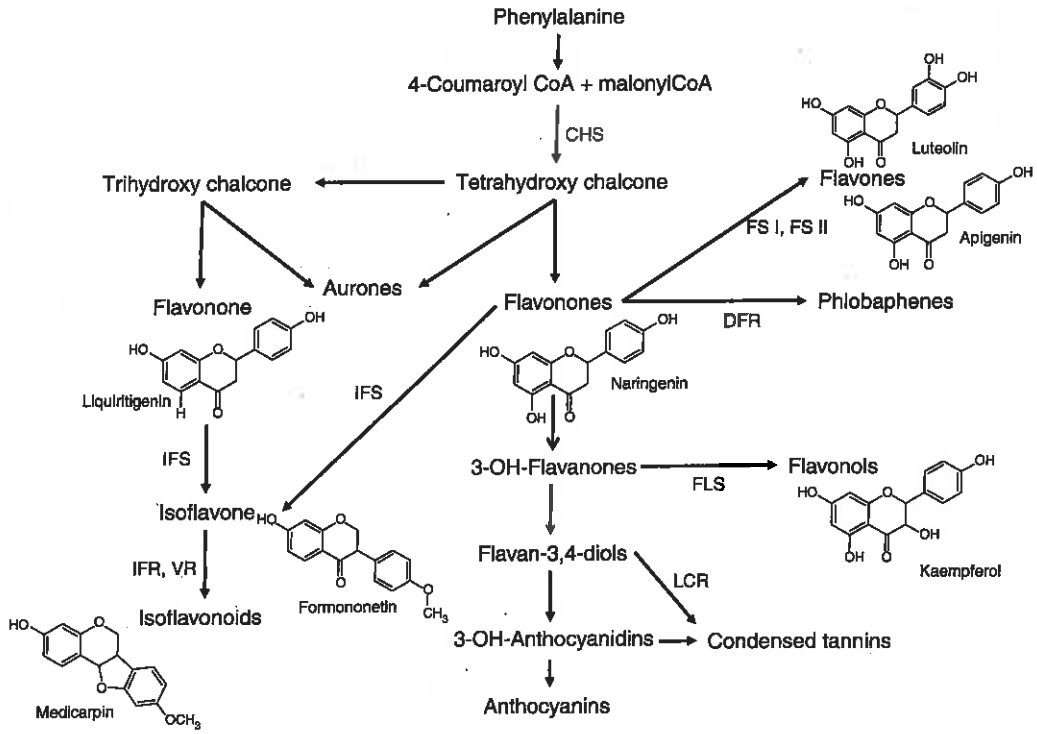

Figure 51.1 Major branches of the flavonoid biosynthesis pathway. The major branches of the flavonoid pathway as well as critical enzymes are shown. CHS, chalcone synthase; DFR, dihydroflavonol 4-reductase; FS I/II, flavone synthase I/II; FLS, flavonol synthase; IFS, isoflavone synthase; IFR, isoflavone reductase; LCR, leucoanthocyanidin reductase; VR, vesitone reductase. Examples of a few structures of compounds discussed in the text are provided.

members of the ABC transporter families. In addition, glutathione could be a vehicle for long-distance flavonoid transport. So far, the exact mechanisms of flavonoid transport within and between cells remain poorly understood.

51.2 FLAVONOID FUNCTIONS IN THE RHIZOSPHERE

While many flavonoids have functions within the root, a proportion of flavonoids is exuded into the rhizosphere soil (Cesco et al., 2010). Flavonoid exudation is poorly understood, although some recent progress has been made toward the identification of potential flavonoid transporters. Flavonoid exudation is likely to be an active process that is often triggered by biotic elicitors (Schmidt et al., 1994; Armero et al., 2001). ABC transporters are likely candidates for flavonoid transporters as *Arabidopsis* ABC transporter mutants were shown to have altered root exudate profiles, although they likely affect multiple compounds (Badri et al., 2008). Sugiyama and colleagues showed that the exudation of the isoflavonoid genistein from soybean root plasma membrane vesicles was ATP-dependent and most likely catalyzed by an ABC-type transporter (Sugiyama et al., 2007). The ABC transporter mutant *abcg30* affected several phenylpropanoid exudates, although it remains unclear whether this transporter directly transports the altered phenolics (Badri et al., 2009). The location or regulation remains unknown for most of the transporters catalyzing flavonoid exudation into the rhizosphere. In addition to active exudation, flavonoids can also be released passively from decomposing root cap and border cells (Hawes et al., 1998, Shaw et al., 2006).

Many studies have determined the types and estimated the concentrations of flavonoids in root exudates, although most of these were from plants grown in solution, not in soil (summarized by Cesco et al., 2010). Both aglycone and glycoside forms of flavonoid have been found in root exudates (see also Chapter 22). Their concentrations in exudate solutions vary widely between species and are furthermore affected by plant growth condition, sampling techniques, and nutrient availability. There is little information available on the actual concentrations of flavonoids in the rhizosphere, or how these concentrations change in space and time. In addition, flavonoid exudation varies along the root, with larger amounts being reported to be exuded from

the root tip (Graham, 1991, Hawes et al., 1998). During cluster root formation in lupins, there is strict spatial and temporal regulation of isoflavonoid exudation, along with citrate release, to coincide with the maturation of the cluster roots (Weisskopf et al., 2006, Tomasi et al., 2008). Techniques that could be used in the future to better estimate flavonoid concentrations in roots and in the rhizosphere include solid-phase root zone extraction with the use of microtubes that can be placed along the root or in soil (Mohney et al., 2009, Weidenhamer et al., 2009).

The fate of flavonoids in the rhizosphere depends on various conditions in the soil. Depending on their structural modifications, the solubility and mobility of flavonoids in the soil varies. For example, while glycosylation improves flavonoid solubility in water, it is likely that microorganisms and root exoenzymes quickly deglycosylate flavonoid glycosides, leaving the more hydrophobic aglycone (Hartwig and Phillips, 1991). Flavonoid persistence in the soil varies and is likely to be hours to days, depending on their structure (Shaw and Hooker, 2008). Flavonoids can be absorbed into the cell wall or into soil particles with cationic binding sites, thus becoming unavailable (Shaw and Hooker, 2008). Persistence in nonsterile soil is often much shorter than in sterile soil, suggesting that flavonoids are degraded by microorganisms. Certain bacteria can metabolize flavonoids as a carbon source, and others can specifically modify flavonoids. For example, rhizobia can partially break down *nod* gene inducing flavonoids to produce flavonoids more or less as active as *nod* gene inducers (Rao and Cooper, 1995).

Flavonoids can also alter the rhizosphere soil by acting as antioxidants and metal chelators. The chelation and reduction of metal ions can alter nutrient concentration in the soil, and this might be important for the availability of iron and phosphorus. For example, an isoflavonoid identified from root exudates of *Medicago sativa* dissolved ferric phosphate, thus making, both, phosphate and iron available to the plant (Masaoka et al., 1993). The flavonoids genistein, quercetin, and kaempferol can also alter iron availability by chelating iron otherwise unavailable in iron oxides and by reducing Fe(III) to Fe(II) (Cesco et al., 2010).

The synthesis and release of flavonoids respond strongly to abiotic and biotic signals in the rhizosphere (Dixon and Paiva, 1995). For example, flavonoid synthesis is affected by nitrogen (Coronado et al., 1995) and phosphorus (Juszczuk et al., 2004) supply in the soil. Flavonoid synthesis is specifically induced by symbionts and pathogens (see the following sections) and responds to signaling molecules of these organisms. The following sections highlight some examples of the diverse functions of flavonoids in the rhizosphere.

51.3 MULTIPLE ROLES OF FLAVONOIDS IN NODULATION

Legumes in general have the ability to form symbiotic relationships with nitrogen-fixing bacteria called *rhizobia*. This ability is shared with some nonlegume families, also known as *actinorhizal plants* that associate with the nitrogen-fixing actinomycetes, in particular the *Frankia* species. Rhizobia are housed in specialized root organelles called *nodules* where they convert atmospheric nitrogen into a form that can be absorbed by the plants. In exchange, the host plant provides a source of carbon to the bacteria (see Chapter 44). The development of nodules involves exchange of signals between the bacteria and the host (see Chapter 45). Flavonoids play an integral role in this symbiotic relationship as chemoattractants, inducers of genes including *nod* genes, determinants of host specificity, regulators of root development, and defense response from the host plant (Cooper, 2004).

The role of root-exuded flavonoids as regulators of *nod* genes in rhizobia has been well established. A multitude of products from *nod* genes are important to synthesize species-specific Nod factors or lipochitin oligosaccharides required for nodule formation in the host (Spaink, 1995). The transcription of these genes is regulated by NodD, a transcription factor of the LysR family of transcriptional regulators (see Chapter 45). It is thought that when a suitable flavonoid binds to NodD, it enhances the access of RNA polymerase and improves the transcriptional ability of the *nod* genes at the site in the promoter where NodD is localized (Peck et al., 2006, Li et al., 2008). Flavonoids also induce an elevation in concentration of intracellular calcium in the rhizobia that induces NodD proteins for Nod factor synthesis (Moscatiello et al., 2010). The initial inducers for *nod* genes were discovered to be the flavones luteolin, isolated from *M. sativa* and 7,4′-dihydroxyflavone (DHF) from *Trifolium repens* (Peters et al., 1986, Redmond et al., 1986). Many other flavonoids have since been discovered to have *nod* gene inducing roles (as summarized by Cooper, 2004). It should be noted that a combination of flavonoids is thought to be more effective in inducing *nod* genes as opposed to a single compound (Bolanos-Vasquez and Warner, 1997, Begum et al., 2001). The host specificity of legume–rhizobia symbiosis is, in part, conferred by a combination of specific exudation of flavonoid mixtures from the host and selective perception of flavonoids from the rhizobial NodD proteins. Not all flavonoids are *nod* gene activators. For certain rhizobium species, some flavonoids show *nod* gene repressing activity. In *Sinorhizobium meliloti*, Nod factor production was negatively controlled by the isoflavonoids, medicarpin, and coumestrol (Zuanazzi et al., 1998). An optimal level of Nod factor production is thought to be maintained by

the *nod* gene activators and repressors acting together. This also prevents elicitation of defense responses by the plant (Savouré et al., 1997, Zuanazzi et al., 1998).

The profile of flavonoid exudates from the root changes during the symbiosis. Several legumes that have been inoculated with rhizobia show differences in flavonoid exudates from the roots. This may be important to fine-tune the synthesis of Nod factors during the different stages of symbiosis (Dakora et al., 1993, Schmidt et al., 1994). Additionally, flavonoids can be metabolized by the rhizobia causing alterations in the transcriptional activity of *nod* genes (Rao and Cooper, 1995).

The role of flavonoids in the rhizosphere is not limited to regulating gene expression in rhizobia. Some flavones and flavonones such as luteolin and apigenin that induce *nod* genes have also been shown to evoke a strong chemoattractant response from the rhizobia, with different flavonoids attracting different *Rhizobium* species (Aguilar et al., 1988, Dharmatilake and Bauer, 1992).

Flavonoids contribute to host specificity in actinorhizal symbioses although no canonical *nod* genes have been found in *Frankia* (Normand et al., 2007). The actinorhizal plants accumulated flavonoids within the nodules (Laplaze et al., 1999). Some uncharacterized flavonoids from the seeds of actinorhizal plants also enhance or inhibit symbiosis (Benoit and Berry, 1997). The fruits of the host plant *Myrica gale* positively affected the growth and nitrogen fixation with compatible *Frankia* strains while having inhibitory effects on noncompatible strains (Popovici et al., 2010), suggesting that flavonoids could play a role in the selection of compatible bacteria by the host. Similarly, in legumes, the phytoalexin medicarpin produced by clover and medic species inhibits the growth of incompatible, but not that of compatible, rhizobia strains (Pankhurst and Biggs, 1980). This selectivity may be due to some (iso)flavonoids inducing resistance to phytoalexins in rhizobia (Parniske et al., 1991), which allows the legume host to mount a defense against pathogens while promoting rhizobial infection.

The flavonoids regulate more than just the *nod* genes in rhizobia. These include genes for exopolysaccharide synthesis, which is important for regulating defense responses in the host (Dunn et al., 1992). The type III secretion system and many exported proteins that are important for nodulation in some rhizobia have also been shown to respond to flavonoid exudates from the host plant (Krishnan et al., 2003). Proteome analysis has also revealed many uncharacterized proteins that are induced or repressed by flavonoids from the host (Guerreiro et al., 1997).

The initial response of the division of root cortical cells and root hair deformation is induced by the perception of Nod factors from rhizobia (see Chapter 45). Some flavonoids have been discovered as negative regulators of auxin transport and could thus cause accumulation of auxin at the nodule initiation site to stimulate cell division and nodule organogenesis (Mathesius et al., 1998b, Boot et al., 1999, Wasson et al., 2006). The exact mechanism through which flavonoids redirect auxin transport during nodule initiation is unknown, but the perception of Nod factors by the plant is thought to induce endogenous flavonoids that could cause inhibition of auxin transport locally (Mathesius et al., 1998a). In the legume *Medicago truncatula*, silencing of different branches of the flavonoid biosynthesis pathway showed that flavonols such as kaempferol are the most probable candidates for auxin transport inhibitors (Zhang et al., 2009). Other flavonoids such as isoflavonoids may also be involved in the development of determinate nodules (Subramanian et al., 2006).

The local changes in auxin accumulation in nodulating roots can also be due to auxin breakdown by peroxidases that can be regulated by certain flavonoids. For example, in white clover (*Trifolium repens*), the isoflavonoid formononetin accumulates in the nodule primordia where it accelerates auxin breakdown. Other flavonoids can also inhibit auxin breakdown such as the derivatives of DHF and free DHF, which accumulate in the vacuoles of the cortical cells that later form the nodule primordia (Mathesius, 2001). The mixture of flavonoids causing local changes in auxin may be critical in regulating cell divisions during nodule development. The roles of flavonoids in the initiation of nodulation are depicted in Figure 51.2.

51.4 EFFECTS OF FLAVONOIDS ON QUORUM-SENSING-REGULATED BACTERIAL BEHAVIORS

Several of the behaviors of rhizosphere bacteria are coordinated by cell-to-cell signals called *quorum-sensing signals* (QSS) (Fuqua et al., 2001; see also Chapters 50 and 70–76). Most bacteria synthesize QSS and the so far best-studied signals are the acyl homoserine lactones (AHLs) that are used by many gram-negative bacteria. QSS diffuse across the bacterial membrane and can bind to internal receptors once their concentration exceeds a certain threshold (Fuqua et al., 1994). This can activate the expression of hundreds of genes, including many important in plant–microbe interactions, for example, in biofilm formation, motility, conjugation, nitrogen fixation, and the synthesis of degradative enzymes, exopolysaccharides, and toxins (Gonzalez and Marketon, 2003, von Bodman et al., 2003).

Several molecules were identified, which interfere with bacterial quorum sensing, including halogenated furanones synthesized by red algae (Manefield et al.,

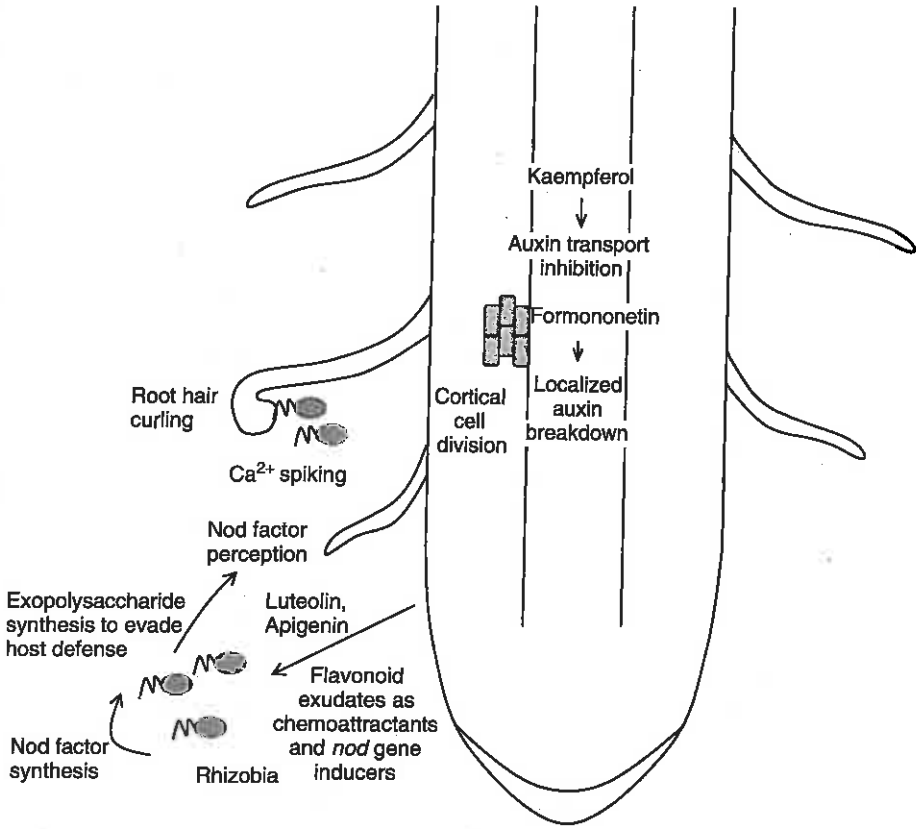

Figure 51.2 Flavonoid functions in the *Rhizobium*–legume symbiosis. Flavonoids are exuded from legume roots and act as *nod* gene inducers and chemoattractants in rhizobia (e.g., luteolin and apigenin). This leads to Nod factor synthesis required for root hair curling and calcium spiking, a necessary step in the early signaling leading to nodule development (see Chapter 45). Rhizobial infection induces synthesis of flavonoids in the root, which are necessary for auxin transport control during nodule development. Kaempferol is hypothesized to control auxin transport, while formononetin could act as a regulator of auxin turnover during nodule development

1999). Higher plants can also produce quorum-sensing mimics that were shown to either inhibit or stimulate AHL-dependent genes in bacterial reporter strains (Teplitski et al., 2000, Gao et al., 2003). While most of these compounds remain unidentified, some have recently been characterized. The first mimic signal identified from plants was lumichrome, a derivative of riboflavine (Rajamani et al., 2008). Another potential AHL mimic is *p*-coumaric acid, a lignin precursor that can be exuded by roots into the soil (Bodini et al., 2009). *p*-Coumaric acid can also be a breakdown product of flavonoids from root exudates (Rao and Cooper, 1995). In addition, some bacteria use *p*-coumaric acid to form *p*-coumaroyl-homoserine lactone (p-coumaroyl-HSL) as a distinct quorum-sensing signal (Schaefer et al., 2008). Thus, *p*-coumaroyl-HSL could sense the presence of a host plant and at the same time control density-dependent behaviors of bacteria. Catechin was identified from the medicinal tree *Combretum albiflorum* as a quorum-sensing mimic, although at concentrations of between 0.125 and 4 mM (Vandeputte et al., 2010). While catechin can also be present in the rhizosphere of plants, for example, as an exudate of the spotted knapweed where it acts as an allelochemical (Weir et al., 2003), its rhizosphere concentration has been contentious (Blair et al., 2005, Duke et al., 2009). Another flavonoid with inhibitory effects on quorum-sensing-regulated reporters in *Escherichia coli*, *Vibrio fischeri* (Vikram et al., 2010), and *Pseudomonas aeruginosa* (Vandeputte et al. 2011) is naringenin. Naringenin is present in the legume root exudates where it can act as a *nod* gene inducer for rhizobia (Novak et al., 2002). It would therefore be interesting to test whether naringenin also affects quorum-sensing-regulated genes in rhizobia.

In legumes, the flavonoid pathway can be activated by exposure to QSS from rhizobia, and it has also been shown that bacterial QSS can stimulate production of QS mimics (Mathesius et al., 2003). This suggests a link between the perception of QSS by plants, activation of flavonoid biosynthesis, and a possible feedback on bacteria by the production of QSS mimics. However, effective concentrations of potential flavonoid mimics in the rhizosphere remain to be tested. A recent study revealed that low micromolar concentrations of *nod* gene inducing flavonoids increased QSS synthesis in three species of rhizobia, and this coincided with the enhanced expression of QSS synthesis genes (Perez-Montano et al., 2011). This suggested that coordination between *nod* gene induction and quorum sensing could be used to enhance the symbiotic behaviors of rhizobia.

51.5 ROLE OF FLAVONOIDS IN MYCORRHIZAL SYMBIOSES

Mycorrhizal fungi colonize the majority of land plants as symbionts and contribute primarily to plant phosphorus nutrition. Mycorrhizal fungi germinate from spores and form hyphae in the soil, which branch in response to certain root exudates. Root exudates also attract the hyphae to a host root. The hyphae penetrate host roots and form ecto- or endomycorrhizal invasion structures (Harrison, 2005; see Chapters 43, 47). Flavonoids present in root exudates were shown to stimulate spore germination, hyphal branching, and root colonization, often in a symbiont-specific manner (Siqueira et al., 1991, Scervino et al., 2005, Kikuchi et al., 2007, Scervino et al., 2007, Steinkellner et al., 2007). Some of the flavonoids that enhance mycorrhizal infection are induced by phosphorus stress (Akiyama et al., 2002). An active stimulator of hyphal growth was identified as the isoflavonoid coumestrol (Morandi et al., 1984), and an *M. truncatula* mutant that overaccumulates coumestrol is hyperinfected by its mycorrhizal partner (Morandi et al., 2009).

Flavonoids are also induced in the root during invasion and arbuscule formation (Harrison and Dixon, 1994). Flavonoids accumulate before the start of infection and this varies with the stage of infection and the infecting symbiont (Harrison and Dixon, 1993, Larose et al., 2002). One of the activities of flavonoids during early infection is to regulate defense reactions, and it has been speculated that mycorrhizal symbionts trigger a temporary defense response in the host roots that involves the induction of flavonoid phytoalexins (Harrison and Dixon, 1993). Flavonoids could also control the extent of mycorrhization at later stages of the symbiosis through an autoregulation process (Larose et al., 2002). Split-root studies showed that the isoflavonoid formononetin and its glycoside are systemically downregulated by rhizobia or mycorrhizae, concomitant with autoregulation of both symbioses (Catford et al., 2006).

Interestingly, lupins, which are not colonized by mycorrhizal fungi, produce pyranoisoflavones that inhibit hyphal branching of mycorrhizal fungi, suggesting that flavonoids could act as, both, stimulators and inhibitors of fungal symbionts in the rhizosphere (Akiyama et al., 2010). However, host plants also synthesize flavonoids that inhibit hyphal branching (Tsai and Phillips, 1991). Therefore, it is likely that, both, hosts and nonhosts can influence the establishment of symbiosis by modification of the profile of flavonoids in root exudates. While flavonoids have clearly been shown to enhance mycorrhizal infection by stimulating spore germination, hyphal branching, and infection, their presence is not essential for the symbiosis, as mycorrhizal infection is not abolished in flavonoid-deficient carrot and maize plants (Becard et al., 1995).

51.6 PERSPECTIVES

While the role of flavonoids in model plant–microbe interactions has been well studied (Fig. 51.3), we lack knowledge on nonmodel organisms including the large number of unculturable bacteria and fungi in the soil (Chapter 16). Crucially, many of the studies carried out in model organisms were performed under sterile laboratory conditions; studies in real rhizospheres will have to be carried out to test flavonoid persistence in the soil, their active concentrations, and their metabolism

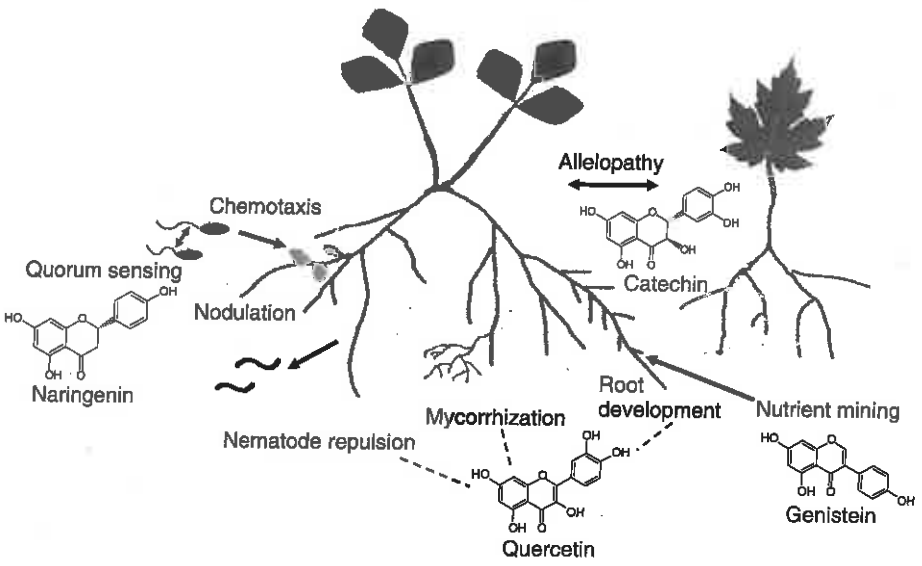

Figure 51.3 Overview of flavonoid functions in rhizosphere interactions. Flavonoid functions in symbiotic interactions include *nod* gene inducers and chemoattractants in rhizobia, possible quorum-sensing regulators in bacteria, and stimulators of mycorrhizal spore germination and hyphal branching. Flavonoids can also affect root development, control fungal pathogens and the attraction of parasitic nematodes, and act as allelochemicals on other plants. Examples of biologically active flavonoids mediating the different interactions are shown.

by other organisms. Because of the complexity of the rhizosphere, it is likely that a flavonoid known to perform a certain role in symbiosis could also have effects on pathogens and other plants. Flavonoids act in defense as phytoalexins and phytoanticipins, particularly against fungi (Makoi and Ndakidemi, 2007). Their action in chemoattraction could also be more widespread than in attracting specific symbionts. For example, isoflavonoid exudation from soybean roots can stimulate attraction of its symbionts *Bradyrhizobium japonicum* as well as the pathogen *Phytophthora sojae* (Morris et al., 1998). In addition, flavonoids have effects on nematode behavior, as certain flavonoids act as repellents for specific nematode species and can inhibit their motility and hatching (Wuyts et al., 2006).

Flavonoids have also been shown to have allelopathic activity. For example, isoflavonoids identified from the forage legume *Desmodium unicatum* was found to significantly inhibit postgermination and attachment of *Striga*, a devastating parasitic weed causing huge crop losses in sub-Saharan Africa (Hooper et al., 2010, Khan et al., 2010). The flavanol (−)-catechin, exuded from the roots of the spotted knapweed (*Centaurea maculosa*) that has been invading large parts of North America, was reported to induce reactive oxygen species in susceptible species that led to cell death and degradation of the root system (Bais et al., 2003). However, it remains unclear whether concentrations of (−)-catechin in soil would be high enough to be effective (Blair et al., 2005; Duke et al., 2009). Thus, catechin may also suppress plant growth as a potent allelopathic signal, while it could also inhibit quorum sensing in host-related soil bacteria.

A further area awaiting exploration is the effect of flavonoids on microbial community structures in the rhizosphere (see Chapters 10–22). Flavonoid exudation affects microbial community structure by favoring species that use flavonoids as a carbon source while inhibiting the growth of other organisms through their role as phytoalexins (Rao and Cooper, 1994; Walker et al., 2003). An increase in the exudation of phenolics in the *Arabidopsis abcg30* mutant was demonstrated to have wide-ranging effects on bacterial and fungal community structure, although this mutation also affected other exudates (Badri et al., 2009). In addition, metabolism of flavonoids by rhizosphere bacteria could alter flavonoid availability and activity in the soil and affect other organisms (Shaw et al., 2006). This would be difficult to predict unless studies in real rhizosphere soil are undertaken.

Because the flavonoid pathway is well understood and has been successfully manipulated in transgenic plants (Wang et al., 2011), it appears tempting to influence rhizosphere processes by altering flavonoid exudation. While this might be achievable relatively easily through overexpression or silencing of certain branches of the flavonoid pathway (Fig. 51.1), several drawbacks suggest caution with this approach: First, little is known about flavonoid transporters responsible for flavonoid exudation; thus, overexpression of flavonoid biosynthesis genes could increase flavonoids in the wrong tissue and could have unforeseen effects on plant development (Buer and Muday, 2004; Ringli et al., 2008; Buer and Djordjevic, 2009). In addition, it could alter the flux of other metabolites by competition (Liu et al., 2002; Wang et al., 2011). For example, mutants with an altered flavonoid pathway are affected in lignin biosynthesis, and vice versa, as these pathways share the same precursors (Laffont et al., 2010; Besseau et al., 2007).

As an alternative to genetic manipulation of the flavonoid biosynthesis pathway, one could exploit the huge diversity of flavonoids synthesized by different plant species (Dakora, 1995). For example, culturing of intercropping plants producing *Striga*-inhibiting isoflavonoid exudates has shown success in making actual improvements to crop yields for farmers in sub-Saharan Africa (Hooper et al., 2009).

ACKNOWLEDGMENTS

We gratefully acknowledge the Australian Postgraduate Award to SH and the ARC Fellowship to UM from the Australian Research Council (DP0557692).

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