Chapter 10 Phosphorus Nutrition: Rhizosphere Processes, Plant Response and Adaptations

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10.1 Introduction

Phosphorus (P) is an essential element required for cellular function and when deficient has a significant impact on plant growth and fecundity. Poor availability of P in soil and consequent P deficiency represents a major constraint to crop production globally (Runge-Metzger 1995). Soil P status is also a key factor that controls the competitive dynamics and species composition in different natural ecosystems (McGill and Cole 1981; Attiwill and Adams 1993), and thus may have significant impact on biodiversity (Wassen et al. 2005). Many plant species have evolved in P-limited environments and, as a consequence, are known to possess a number of adaptive features that can enhance the acquisition of P from soil (Raghothama 1999; Vance et al. 2003; Richardson et al. 2007). Most plants have evolved to respond to P starvation by increasing the ability of their root systems to acquire P from the soil (White et al. 2005; Hammond and White 2008; Lynch and Brown 2008; White and Hammond 2008; Fang et al. 2009). Plant root cells take up P as orthophosphate (H₂PO₄⁻, abbreviated here as Pi), whose concentrations in the soil solution is extremely low (<10 μ M). The mass flow of Pi in the soil solution is insufficient to supply the P requirements of a plant (Kirkby and Johnston 2008). Hence, roots must proliferate throughout the soil to acquire sufficient P for plant nutrition. Although some soil P is present as labile Pi bound to soil particles, most is present as sparingly soluble inorganic salts, such as calcium (Ca) phosphate in

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alkaline soils or aluminium (Al) and iron (Fe) phosphates in acidic soils, or as complex organic compounds in soil organic material or soil organisms (Hinsinger 2001; Oberson and Joner 2005; Turner 2007; Kirkby and Johnston 2008). Organic P generally accounts for around 50% of soil P, and is largely comprised of monoesters with lesser amounts of diesters and phosphonates (Newman and Tate 1980; Hawkes et al. 1984; Condron et al. 1990). In order to be available to plants, inorganic P must be either desorbed or solubilised, and organic P must be mineralised to release Pi. Once in the soil solution, Pi is acquired rapidly by plant roots such that its concentration in close proximity to the root surface is estimated to be in the order of ~0.05 to 0.2 μ M (Barber 1984), which is significantly less than elsewhere in the soil environment, where soil solution concentrations are typically in the range of 1–5 μ M (Bieleski 1973). Slow Pi diffusion through soil to the roots is the ultimate limitation to P supply to the root surface, and can thus restrict P acquisition.

The conserved responses of plants to P starvation that increase P acquisition include:

- 1. Acidification of the rhizosphere and secretion of low molecular weight organic anions and phosphatase enzymes into the soil to mobilize Pi from inorganic and organic P sources (Marschner 1995; Hinsinger 2001; Jones et al. 2003; Delhaize et al. 2007; Jain et al. 2007b; George and Richardson 2008).
- 2. Investment of a greater proportion of plant biomass in the root system, and alterations in the morphology of the root system to enable greater exploration of the soil volume and the exploitation of localized patches of high Pi availability (White et al. 2005; Hermans et al. 2006; Hammond and White 2008; Lynch and Brown 2008).
- 3. Increasing the capacity of root cells to take up Pi, thereby reducing Pi concentrations in the rhizosphere, increasing the rate of diffusion of Pi towards the rhizosphere and stimulating the release of Pi from labile sources (Marschner 1995; Bucher 2007; Jain et al. 2007b).

In addition, most plants foster symbiotic relationships with mycorrhizal fungi to increase their ability to explore the soil volume and mobilize P from remote inorganic and organic sources (Bucher 2007; Smith and Read 2007; Jansa et al. 2011). All these responses are coordinated by a small number of regulatory systems controlled by both the P status of the shoot and Pi availability in the rhizosphere (White et al. 2005; Amtmann et al. 2006; White and Hammond 2008; Hammond and White 2008).

In this chapter, we will discuss the current state of knowledge regarding (1) how plants react to limited P availability by changing their physiological response in root growth and rhizosphere biochemistry traits, (2) how they coordinate this response to P limitation, and (3) how they respond to the re-supply of P once P becomes available again. Gaps in knowledge will be identified and priorities for future research will be discussed.

10.2 Root and Rhizosphere Responses of Plants to P Deficit

10.2.1 Morphological Adjustment of Roots to P Deficiency

Most species partition a greater proportion of their total dry matter into root growth when grown under P deficiency (Bradshaw et al. 1960; Hill et al. 2006). A number of studies indicate that the capacity to adjust root mass ratio in favour of root growth is expressed most effectively by species that have evolved in fertile soils (Christie and Moorby 1975; Boot and Mensink 1990), and consequently this adjustment is considered characteristic of plants that can compete effectively in high-nutrient environments (Chapin 1980). Many species adjusting to low P conditions concurrently increase specific root length (SRL) to achieve longer or more branched roots per unit of root dry matter (Christie 1975; Fitter 1985; Hill et al. 2006) and increase their root hair length and density (Itoh and Barber 1983). Increased SRL can be achieved by reducing root mass density (Fitter 1985; Fan et al. 2003) and/or by decreasing root diameter (Hill et al. 2006). In addition, a common physiological response is root agravitropism or topsoil foraging, putting roots where concentrations of P are relatively large (Lynch 2005). The formation of specialised root structures that increase P acquisition is an alternative means by which plants adjust to low soil P levels. Most notable of these are the cluster (or proteoid) roots (dense bottle-brush-like clusters of rootlets) formed on white lupin (Lupinus albus) (Gardner et al. 1981; Dinkelaker et al. 1995; Keerthisinghe et al. 1998; Neumann et al. 1999). The formation of cluster roots by white lupin is induced and regulated by the P status of the shoot rather than the P concentration of the root system or the soil solution (Keerthisinghe et al. 1998; Shane et al. 2003; Shen et al. 2005). In particular, cluster roots significantly increase root-surface area and thus soil contact, and are usually found on species that are either non-mycorrhizal or weakly mycorrhizal (Skene 1998).

10.2.2 Formation of Root Hairs in Response to P Deficit

Root hair development may be sparse in high-P conditions, but both density and length increase when plants are grown on a low-P supply (Bates and Lynch 1996; Gahoonia and Nielsen 1997), thus increasing the capacity for P acquisition (Itoh and Barber 1983; Föhse et al. 1991). The benefit of increased root hair density reaches a plateau when the P-depletion zones around each root hair begin to overlap, with the optimal relationship between root hair density and length dependent on the P-diffusion coefficient of the soil (Ma et al. 2001). In a study of ten grassland species, Hill et al. (2006) concluded that root-morphology adjustments helped plants to maintain root length under a range of low-P conditions, consequently improving the potential for P uptake from P-deficient soil. However, the intrinsic morphological characteristics of each species (particularly an extensive,

fine root system), as opposed to the ability to adjust root morphology, was the most important determinant of whether a plant had a low P fertiliser requirement for maximum growth rate (Hill et al. 2006).

The use of root hair mutants has demonstrated that the presence of root hairs increases the root soil contact, evidenced by enhanced rhizosheath (soil adhering to roots) production (Haling et al. 2010; Brown et al. 2010) and this, in association with the consequent enhanced root surface area, has been demonstrated to enhance tolerance of Al-toxic (Haling et al. 2010) and P-deficient conditions (Brown et al. 2010). The major mechanism by which root hairs are beneficial to P acquisition is likely to be the greater volume of soil exploited by long root hair varieties, as evidenced by differential zones of depletion around roots of various barley root-hair mutants (Fig. 10.1) (Gahoonia and Nielsen 1997).

10.2.3 Release of Extracellular Organic Anions

Many studies have shown that organic anions modify the chemistry of the rhizosphere and mobilise various forms of inorganic and organic P. This is achieved by an increase in the dissolution of sparingly soluble P minerals, reduced sorption of P by alteration of the surface characteristics of soil particles, desorption of Pi from sorption sites (ligand exchange and ligand dissolution), and through the chelation of cations (e.g. Al and Fe in acidic soils or Ca in alkaline soils) that are commonly associated or complexed with Pi in soil (Bar-Yosef 1991; Jones and Darrah 1994; Lan et al. 1995; Jones 1998). Organic anions may also promote the growth of rhizosphere microorganisms that improve plant P acquisition. The importance of



Fig. 10.1 Depletion of NaHCO₃-extractable inorganic P (mmol P/kg soil) from the rhizosphere of two barley cultivars (*Hordeum vulgare* cvs Zita and Salka) with different root hair morphologies. The cultivars are compared to an unplanted control soil (from Gahoonia and Nielsen 1997)

organic anions in increasing the availability of organic P, and its subsequent mineralisation by phosphatases, has also been identified recently (Jones 1998; Otani and Ae 1999; Hayes et al. 2000a; Hens et al. 2003; Li et al. 2003).

It is evident that exudation of organic anions from plant roots is facilitated by transport proteins (Neumann et al. 1999; Ryan et al. 2001). At concentrations commonly found in the rhizosphere (10–100 μ M; Jones 1998) citrate and oxalate have a greater potential for P mobilisation than other organic anions. In fact, high rates of citrate exudation from cluster roots of white lupins are associated with a large capacity for P mobilisation in soil by this species (Vance et al. 2003; Richardson et al. 2007). Other plant species vary in the nature and amounts of organic anions they exude from roots (Veneklaas et al. 2003; Wouterlood et al. 2004; Pearse et al. 2006). But, generally increased organic anion efflux from roots stimulated by P-deficient conditions (Hedley et al. 1982; Lipton et al. 1987; Hoffland et al. 1989; Kirk et al. 1999), is a common phenomenon.

The heterologous expression of genes for enzymes involved in organic anion synthesis in roots has been investigated as a means to increase exudation of organic anions from roots. Overexpression of a bacterial gene encoding citrate synthase (CS) in tobacco (*Nicotiana tabacum*) has been reported to increase citrate efflux from roots of transgenic lines compared to control plants (de la Fuente-Martínez et al. 1997). However, using similar gene constructs and in some cases the same transgenic lines, Delhaize et al. (2001) could not confirm these results. Moreover, tobacco plants that overexpressed a tobacco CS, or were downregulated for isocitrate dehydrogenase expression, showed no significant increase in citrate efflux even though in some cases the plants had greater internal citrate concentration (Delhaize et al. 2003). Notwithstanding this, it is apparent that there is potential to enhance organic acid exudation by targeting the citrate synthesis biosynthetic pathway. Overexpression of a plant gene for mitochondrial CS in *Arabidopsis thaliana* enhanced citrate efflux, with an associated small improvement in P acquisition (Koyama et al. 2000).

Genes that encode channels involved in the transport of organic anions may be another target for a gene technology approach to improving tolerance to P deficit. Citrate-permeable channels in the plasma membrane of cluster roots of white lupin have been identified (Zhang et al. 2004), and a gene encoding a malate channel has been cloned from wheat (Sasaki et al. 2004). When expressed in transgenic barley (GP-ALMT1), this gene (*TaALMT1*) resulted in increased exudation of malate, albeit in an Al-activated manner (Delhaize et al. 2004), and has been demonstrated to be beneficial to the P nutrition of plants when grown in acidic soils (Fig. 10.2) (Delhaize et al. 2009).

10.2.4 Release of Extracellular Phosphatase

A number of studies have demonstrated significant rates of organic P mineralisation in proportion to soil phosphatase activity (Trasar-Cepeda and Carballas 1991;



Fig. 10.2 Expression of the wheat aluminium resistance gene (*TaALMT1*) in transgenic barley enhances phosphorus uptake per unit root and reduces the root/shoot ratios of plants grown on an acid soil with a range of phosphorus supplies. Effect of phosphorus supply on phosphorus uptake

Lopez-Hernandez et al. 1998; Oehl et al. 2001; George et al. 2002). In natural ecosystems, mineralisation of soil organic P is thought to provide the major proportion of P to plants (Fox and Comerford 1992; Polglase et al. 1992). Similarly, in organic-based farming systems, and where green-manure crops are used for fertilisation, high rates of organic P cycling have been observed (Oberson et al. 1996, 2001; Nziguheba et al. 1998; Maroko et al. 1999; Oehl et al. 2004).

The hydrolysis of organic P is mediated by the action of phosphatase enzymes in the extracellular environment, a process that is necessary for the subsequent uptake of Pi by plant roots (see Nannipieri et al. 2011). At present there is no evidence for direct uptake of dissolved organic P compounds by plants, although organic P substrates may be hydrolysed within the root apoplast (Duff et al. 1994; George et al. 2008). Extracellular phosphatase activity of plant roots is induced under conditions of P deficiency and is associated with either root cell walls (McLachlan 1980; Dracup et al. 1984; Barrett-Lennard et al. 1993; Hayes et al. 1999; Hunter and McManus 1999) or is released directly into the rhizosphere (Tarafdar and Claassen 1988; Tadano et al. 1993; Li et al. 1997; Gaume et al. 2001). The cloning of genes encoding extracellular phosphatases from *A. thaliana* (Haran et al. 2000) and *L. albus* has provided direct evidence for extracellular secretion and regulation of phosphatase expression in response to P deficiency (Wasaki et al. 2000; Miller et al. 2001).

Extracellular secretion of phosphatases from roots is correlated with the ability of plants to obtain P from organic P sources when grown under sterile conditions (Tarafdar and Claassen 1988; Hayes et al. 2000b; Richardson et al. 2000; George et al. 2008). For example, wheat and a range of pasture species are able to utilise P from various monoester (e.g. glucose-6-phosphate) and diester (e.g. ribonucleic acid) forms, but show limited capacity to acquire P directly from *myo*-inositol hexakisphosphate (Richardson et al. 2000; George et al. 2008), despite inositol phosphates being an abundant form of organic P in many soils. It is likely that the biological importance of the different forms of organic P will be dictated by their turnover rates. Direct hydrolysis of organic P and subsequent utilisation of the mineralised Pi by roots has also been demonstrated in soil-grown plants. Depletion of various pools of extractable organic P from the rhizosphere has been linked with greater phosphatase activities around plant roots (Chen et al. 2002; George et al.

Fig. 10.2 (continued) by roots (**a**), root/shoot ratios (**b**), and shoot phosphorus concentrations (**c**) of transgenic barley (*GP*, triangles) and transgenic barley expressing *TaALMT1* (*GP-ALMT1*, *circles*) grown on an unamended acid ferrosol (*open symbols*) or on the same soil that had been limed (*closed symbols*). Phosphorus uptake per unit root was calculated from total shoot phosphorus only, because the phosphorus contents of roots could not be accurately determined because of adhering soil. Plants were harvested 26 days after sowing and the data for each show the treatment means (n = 4) and least-significant difference (*LSD*) (P = 0.05; untransformed data). *Asterisks* indicate where the means of the genotypes grown on the acid soil with a particular phosphorus treatment differences between genotypes were apparent using log10-transformed data (from Delhaize et al. 2009)

2002, 2006). However, the relative contribution of extracellular phosphatases derived from roots and from microorganisms in the utilisation of soil organic P is unclear because the numbers and activity of bacteria and fungi are greater within the rhizosphere than in the bulk soil (Chen et al. 2002; Richardson et al. 2005). In addition, there is some evidence that phosphatases derived from soil fungi have a greater affinity for organic P compounds compared to phosphatases derived from plant roots (Tarafdar et al. 2001). Either way, it is evident that the mineralisation of organic P occurs in the rhizosphere and could make an important contribution to the orthophosphate requirement of plants for growth.

Research efforts have been focussed on improving the ability of plants to acquire P directly from common forms of soil organic P, such as inositol phosphates. A number of studies have developed transgenic plants with heterologous expression of microbial phytases (Richardson et al. 2001; Zimmermann et al. 2003; Lung et al. 2005; Xiao et al. 2005). Transgenic plants that produce microbial phytase and release it from their roots have novel ability to hydrolyse P from *myo*-inositol hexakisphosphate and, when grown under controlled conditions, showed enhanced growth and P nutrition (Fig. 10.3) (Richardson et al. 2001; Mudge et al. 2003;

	No P	<i>myo</i> -Inositol he (sodium·	xakisphosphate ·phytate)	Na ₂ HPO ₄
Trifolium subterraneum	ex::phyA	Null segregar	t ex::phyA	ex::phyA
Shoot dry weight (mg/plant)	28.1	40.7	51.8	47.9
Shoot phosphorι (μg P/shoot)	ıs 48.3	103.5	299.0	305.3
Exuded root phytase activity ^a (nKat/g root dry v	- vt)	1.3	107.9	-
2.4				

^aActivity for wild-type plants was 0.6 nKat/g root dry weight.

Fig. 10.3 Growth, phosphorus nutrition and activity of phytase exuded from the roots of transgenic *Trifolium subterraneum*. The images show plants that release the *Aspergillus niger* phytase (ex::phyA) as an extracellular enzyme and the corresponding null-segregant transgenic control line. Plants were grown for 28 days in sterile agar either without added phosphorus (no P) or with phosphorus supplied as sodium phytate (*myo*-inositol hexakisphosphate) or disodium phosphate (Na₂HPO₄) at 0.9 mM (with respect to phosphate) (taken from George et al. 2004) Zimmermann et al. 2003; George et al. 2004). However, when grown in a range of soils, these plants have generally shown limited capacity to access additional P over that of control plants (George et al. 2004, 2005b). These results highlight the complexity inherent in attempting to improve multimechanistic tolerance traits by a single gene approach. Whilst potential exists for manipulating P-use efficiency at a genetic scale, success will often be limited by poor understanding of the control of the mechanisms imposed by different soil environments.

10.3 Coordinating Plant Responses to Variations in P Supply

In P-replete plants, small metabolites, nucleic acids and phospholipids contribute approximately equally to leaf P content (Marschner 1995; Dörmann and Benning 2002; White and Hammond 2008). When plants lack sufficient P, they restrict their use of P to essential cellular functions and improve the ability of their root systems to acquire P from the soil.

Many of the responses of plants to P starvation appear to be initiated, or modulated, by a decrease in the delivery of Pi to the shoot and the consequent reduction in the Pi available for shoot metabolism (Fig. 10.4, response 1). This has a direct effect on photosynthesis, glycolysis and respiration, which is reinforced by transcriptional reprogramming (Plaxton and Carswell 1999; Hammond et al. 2003,



Fig. 10.4 Regulatory networks coordinating plant responses to variations in P supply. *Numbers* indicate different plant responses and are explained in the text (from White and Hammond 2008)

2005; Misson et al. 2005; Hermans et al. 2006; Wasaki et al. 2006; Morcuende et al. 2007; White and Hammond 2008). The changes in carbohydrate metabolism result in the accumulation of organic acids, starch and sucrose in leaves of P-starved plants (Fig. 10.4, response 2) (Hermans et al. 2006; Morcuende et al. 2007). Metabolism is rerouted by employing reactions that do not require Pi or adenylates and, under severe P starvation, intracellular phosphatases and nucleases are produced to remobilize P from cellular metabolites and nucleic acids (Plaxton and Carswell 1999; Hammond et al. 2003; Wasaki et al. 2006; Morcuende et al. 2007; Müller et al. 2007).

Increased leaf sucrose concentrations lead indirectly to (1) a reduction in photosynthesis through decreased expression of genes encoding many photosystem subunits and small subunits of RuBisCo (Lloyd and Zakhleniuk 2004; Amtmann et al. 2006; Hermans et al. 2006; Rook et al. 2006; Morcuende et al. 2007), (2) an increase in leaf sulfolipid and galactolipid concentrations through the upregulation of genes involved in their biosynthesis (Dörmann and Benning 2002; Hammond et al. 2003; Benning and Ohta 2005; Misson et al. 2005; Franco-Zorrilla et al. 2005; Gaude et al. 2008), and (3) the production of anthocyanins through a transcriptional cascade involving the transcription factors TTG1-TT8/EGL3-PAP1/PAP2 (Fig. 10.4, response 3) (Lloyd and Zakhleniuk 2004; Teng et al. 2005; Amtmann et al. 2006; Solfanelli et al. 2006). An increased leaf sucrose concentration also results in the upregulation of genes encoding transport proteins delivering organic acids and sucrose to the phloem, which facilitates the movement of these compounds to the root (Fig. 10.4, response 4) (Hermans et al. 2006). Details of the genes and transcription factors identified in genomics studies can be found in a range of databases that are exemplified by the Database of Arabidopsis Transcription Factors (Guo et al. 2005).

One consequence of the increased delivery of organic acids and sucrose to plant roots is an increase in the root/shoot biomass ratio (Fig. 10.4, response 5) (Hermans et al. 2006; Hammond and White 2008). In addition, the sucrose delivered to the root acts as a systemic signal to initiate changes in gene expression that alter root biochemistry and the morphology of the root system (Franco-Zorrilla et al. 2005; Liu et al. 2005; Amtmann et al. 2006; Hermans et al. 2006; Karthikeyan et al. 2007; Tesfaye et al. 2007; Hammond and White 2008). Increased root sucrose concentrations appear to upregulate genes encoding riboregulators, Pi transporters, RNases, phosphatases and metabolic enzymes in combination with the PHR1 transcriptional cascade (Fig. 10.4, response 6), whereas its effects on lateral rooting occur through modulation of auxin transport (Fig. 10.4, response 7) (Jain et al. 2007a; Pérez-Torres et al. 2008) and those on root hair development are contingent upon changes in auxin transport and the local production of ethylene (Fig. 10.4, response 8) (Jain et al. 2007a).

The PHR1 protein is a MYB transcription factor that binds to an imperfectpalindromic sequence (P1BS; GNATATNC) that is present in the promoter regions of many genes whose expression responds to P starvation. These include genes encoding transcription factors, protein kinases, Pi transporters, RNases, phosphatases, metabolic enzymes and enzymes involved in the synthesis of sulfolipids and



Fig. 10.5 Gene Regulatory networks impacting on PHR1-mediated acclimatory responses to P starvation. *Arrows* indicate positive regulation. *Blunt-ended lines* indicate negative regulation

galactolipids (Fig. 10.5) (Rubio et al. 2001; Hammond et al. 2004; Franco-Zorrilla et al. 2004; Misson et al. 2005; Jain et al. 2007b; Fang et al. 2009; Lin et al. 2009). The expression of *PHR1* appears to be constitutive, but the PHR1 protein is targeted by a small ubiquitin-like modifier (SUMO) E3 ligase (SIZ1), whose expression is increased by P starvation (Miura et al. 2005). The activity of SIZ1 acts as a negative regulator of plant responses to P starvation (Miura et al. 2005). The PHR1-mediated increase in Pi transport is contingent upon the activity of PHF1, an ER protein that facilitates the trafficking of PHT1-family Pi transporters, whose expression is upregulated upon P starvation (González et al. 2005). Amongst the targets of the PHR1 protein are members of the miR399 microRNA family and the SPX gene family (Bari et al. 2006; Franco-Zorrilla et al. 2007; Nilsson et al. 2007; Lin et al. 2009). The expression of *miR399s* is specifically and rapidly upregulated by P starvation (Chiou 2007). The target for miR399s is AtUBC24, which is downregulated during P starvation. This gene encodes the ubiquitin E2 conjugating enzyme responsible for the *pho2* mutant phenotype, which is thought to downregulate the transcription of a subset of P-starvation-responsive genes through intermediary transcription factors (Chiou 2007; Fang et al. 2009). Expression of AtUBC24 in roots appears to be regulated systemically by shoot P status and the translocation of miR399s in the phloem (Buhtz et al. 2008; Lin et al. 2008; Pant et al. 2008). The rate of their translocation in the phloem is likely to be influenced indirectly by sucrose loading and unloading in the shoot and root, respectively. Members of the TPSI1/Mt4/At4 family of non-coding transcripts, whose expression is rapidly and specifically induced in response to P starvation, appear to bind and sequester miR399s thereby attenuating miR399-mediated transcriptional responses to P starvation (Franco-Zorrilla et al. 2007). In Arabidopsis, the expression of AtSPX1 and AtSPX3 are greatly increased by P starvation (Duan et al. 2008). Increased expression of *AtSPX1* upregulates transcription of several genes, including *PAP2*, *RNS1* and *ACP5* (Duan et al. 2008). Increased expression of AtSPX3 occurs upon prolonged P starvation and appears to act in feedback regulation of plant responses to P starvation by downregulating the expression of *AtSPX1*, *At4* and genes encoding several Pi transporters, RNases and phosphatases (Duan et al. 2008).

Crosstalk between local and systemic signals (including auxin, ethylene, cytokinin and sucrose) controls the remodelling of root system morphology in response to P starvation (White et al. 2005; Amtmann et al. 2006; Jain et al. 2007a; Karthikevan et al. 2007; Hammond and White 2008; White and Hammond 2008; Fang et al. 2009). The growth rate of primary roots is reduced in P-starved plants by a reduction of meristem activity, which is initiated directly by contact of the root cap with media lacking Pi and requires the activity of multicopper oxidases (Ticconi et al. 2004; Sánchez-Calderón et al. 2006; Svistoonoff et al. 2007; Jain et al. 2007a; Fang et al. 2009). The proliferation of lateral roots of P-starved plants in regions of increased Pi availability is also contingent upon growth of the primary root apex through these regions (Drew 1975), but appears to be initiated by changes in auxin transport and perception (Nacry et al. 2005; Sánchez-Calderón et al. 2006; Jain et al. 2007a; Hammond and White 2008; Pérez-Torres et al. 2008), with greater sucrose availability increasing the responsiveness to auxin (Nacry et al. 2005; Jain et al. 2007a). Specifically, the TIR1 gene, which encodes the auxin receptor component of the ubiquitin protein ligase complex SCFTIR1, is upregulated by P starvation (Pérez-Torres et al. 2008). The upregulation of TIR1 results in the degradation of AUX/IAA auxin response repressors, allowing the expression of ARF transcription factors, such as ARF19, to modulate the expression of genes that enable the initiation and emergence of lateral roots without increasing root auxin concentrations (Pérez-Torres et al. 2008). The initiation of lateral roots is also promoted by reduced cytokinin concentrations in roots of P-deficient plants, which appears to be a secondary consequence of the crosstalk between sugar and local P-signalling cascades (Franco-Zorrilla et al. 2005). This phenomenon is comparable to the proliferation of specialised cluster roots in regions of local Pi enrichment observed in diverse non-mycorrhizal plant species when they lack sufficient P (Lamont 2003; Lambers et al. 2006; Vance 2008). The initiation and elongation of root hairs are stimulated by locally elevated concentrations of auxin and ethylene, and both are stimulated when more sucrose is available to the roots (Jain et al. 2007a; Hammond and White 2008). Finally, the topsoil-foraging phenotype of P-deficient plants appears to be modulated primarily by the sensitivity of root gravitropism to ethylene, which increases with P starvation (Basu et al. 2007).

10.4 Response of Plants to P Re-supply

A root growing in soil is likely to find sites with a high concentration of potentially available P and sites with almost no P (Hodge 2009), though how the plant senses and reacts to this is yet unknown. There will be microsites with active microflora

and/or microflora where competition for nutrients is great. An individual root will then experience local P competition, P-limiting and P-sufficient conditions at different times.

As highlighted above, the physiological state of a P-deficient plant is quite specific and the response is multigenic in nature with, for example, over 1,000 genes being differentially regulated under these conditions in Arabidopsis (Wu et al. 2003; Hammond et al. 2003; Morcuende et al. 2007). Under conditions of P starvation, plants have increased root/shoot biomass ratio (Lynch 1995), alteration of root architecture (Williamson et al. 2001; López-Bucio et al. 2000), many more lateral roots and long root hairs (Bates and Lynch 1996). Also high-affinity P transporters are more abundant (Mudge et al. 2002; Smith et al. 2003) and organic acids and phosphatases are synthesized and secreted (Raghothama 1999; del Pozo et al. 1999; Li et al. 2002). There are fewer P-containing metabolites (Zrenner et al. 2006), phospholipids are replaced in part by sulfolipids and galactolipids (Dörmann and Benning 2002; Kelly et al. 2003), and cells have a reduced level of RNA (Hewitt et al. 2005). Vacuolar Pi has been remobilised, carbohydrates such as starch and sugars have been accumulated and anthocyanin has been produced. In addition, some plants may have begun processes of senescence or flowering (Morcuende et al. 2007).

The hypothetical transcriptional response of plants to P re-supply or upon discovery of a P resource in a heterogeneous environment would be to reverse many of these changes and we consider that this response will take several forms:

- Initially, there is an immediate non-specific response to perturbation of the system, which is likely to be rapid and transient and shows typical characteristics of other perturbation responses, involving increased expression of genes that are likely to protect plants against abiotic and biotic stresses (AbuQamar et al. 2009). It has previously been suggested that these may be cell-autonomous and related to changes in cell membrane potential, initiating cytosolic Ca²⁺ signalling cascades (Hammond et al. 2003; Amtmann et al. 2006). There is considerable crosstalk between abiotic and biotic signalling pathways, and these are often integrated in the cytosolic Ca²⁺ signature.
- 2. Sensing of altered P availability and initiation of regulatory cascades, which will not necessarily be a reversal of those cascades initiated upon P starvation. These responses are also rapid, occurring within 30 min of P re-supply (Amtmann et al. 2006). Although many of these responses are regulated systemically by sucrose concentration in P-deficient plants, upon re-supply of P the necessary gene cascades change regulation far in advance of any changes in sucrose content, suggesting other signalling pathways (Amtmann et al. 2006).
- 3. Reversal of tissue P economy. Morcuende et al. (2007) demonstrated that upon P re-supply there is rapid (<3 h) upregulation of nucleic acid synthesis to promote growth and re-optimise metabolic pathways for energy production and reversal of sulfolipid and galactolipid synthesis, to allow sulfur to become available for protein synthesis.

- 4. Reducing energetic investment in costly P-tolerance mechanisms. Morcuende et al. (2007) demonstrated that expression of genes regulating root growth, organic acid and phosphatases synthesis and efflux are also rapidly downregulated upon P re-supply.
- 5. Upregulation of mechanisms to prevent Pi toxicity such as sequestration and complexation, due to the persistence of Pi-transport proteins.

Results from our own c-DNA microarray experiments, in which A. thaliana was grown in P-deficient conditions then re-supplied with P, generally support these hypotheses of the response of P-starved plants to P re-supply. There was a distinct time-dependent response in the roots (Table 10.1) but this time dependence was not obvious in the leaves (data not shown). Most transcripts reacted after 3 h. Some transcripts increased initially and decreased within 24 h. In the first 45 min of P resupply, the largest proportion of genes differentially regulated are associated with initiating cell production and include genes associated with cell function (3.5%), DNA synthesis (5.2%), protein degradation and synthesis (8.4%), RNA processing and regulation (2.7%) and amino acid metabolism (1.3%). After 3 h of re-supply of P, many of the same genes are still differentially regulated but a number of other processes have started to occur, notably cascades involved in cell wall development and lipid metabolism (3.1%), signalling cascades (8.8%) and sulfur assimilation (4.8%), most likely promoting protein synthesis. Beyond this, and between 0.5 and 2 days after re-supplying P, while the RNA processing, protein metabolism and cell division pathways are still differentially regulated, the DNA synthesis genes have equilibrated and differential regulation of signalling cascades has moderated. Interestingly, it is only at this stage that abiotic stress genes are differentially regulated, much later than anticipated in the hypotheses. It is also at this stage that we see genes involved in carbohydrate metabolism and transporters differentially regulated.

So, from this single study it is apparent that the earliest responses of plants to P re-supply is to upregulate cellular molecular machinery, which is quickly followed by cell division and lipid and protein biosynthesis. It is only later that the plant shows a generic stress response and upregulation of specific signalling cascades and P transport. The key result from this and other studies is that the vast majority (~35%) of differentially regulated genes at all time points are of unknown origin, which means that there are a lot of response mechanisms and regulatory cascades associated with P re-supply that are yet to be understood.

10.5 Can P Starvation and Re-supply Responses Be Genetically Manipulated for Agricultural Benefit?

Increased pressure on P fertiliser usage and costs due to the depletion of nonrenewable natural resources (Heffer et al. 2006; Cordell et al. 2009; Gilbert 2009), their potential negative impacts on local environments and water quality (White and

Table 10.1 Diff	ferential regulation of ger	nes in root a	nd shoot	tissue	uodn a	re-sup	pply of P to roots i	in comparison to a sa	alt-stress co	ntrol			
Cell process		Number	Percent	age o	f genes		Cell process		Number	Percen	tage of	gene	
		of genes	differe	ntially	regula	uted			of genes	differe	ntially	regula	ted
			0.75 h	3 h	12 h 4	48 h				0.75 h	3 h	12 h	48 h
Cell	Cell	162	3.5	2.8	2.8 -	1	Nucleotide	Synthesis	12	I	0.2	Ι	I
	Division	24	0.5	I		1	metabolism	Degradation	10	I	0.2	I	Ι
	Cycle	32	0.7	0.1	'	1	RNA	RNA	603	I	I	11.8	I
	Vesicle transport	34	I	0.7	0.6	I		Processing	51	1.1	I	Ι	Ι
	Late embryogenesis	5	0.1	Ι		I		Transcription	27	I	I	0.5	Ι
Cell wall	Cell wall	73	I	1.4	1.4	I		Regulation of	477	1.6	0.9	9.3	0.9
								transcription					
	Precursor synthesis	2	I	Ι		1	DNA	DNA	150	3.0	2.9	I	Ι
	Cell wall proteins	14	I	0.1	0.3			Synthesis/	103	2.2	2.0	0.1	Ι
								chromatin					
								structure					
	Degradation	15	I	I		D.4		Unspecified	23	I	I	I	0.6
	Modification	13	I	0.2		0.4	Protein	Synthesis	129	1.6	2.5	2.3	2.5
Glycolysis	Glycolysis	Ι	I	I	0.3	1		Postranslational	163	0.2	2.9	3.2	3.4
								modification					
	Mitochondrial	39	I	0.6	0.8	0.7		Degradation	367	6.8	7.0	6.7	0.2
	e-transport/ATP												
	synthesis			t •					č				
Lipid	Lipid metabolism	I	I	1./		1		Protein Iolding	17	I	I	0.4	I
	Exotics	18	I	0.3	·	1	Amino acid	Amino acid	69	1.3	1.3	1.2	I
								metabolism					
	Phospholipase D	4	Ι	I	0.1	I		Synthesis	44	Ι	0.2	0.9	0.9
Carbohydrate	Raffinose family	4	I	0.1	1	4.7		Degradation	28	0.5	0.5	I	0.4
(CHO)	Trehalose	7	0.2	0.1		0.3	Hormones	Hormone	118	0.1	2.2	0.4	0.1
metabolism								metabolism					
	Myo-inositol	7	Ι	Ι		I	Signalling	Signalling	248	Ι	4.7	I	I
	CHO metabolism	24	I	0.5		I		Receptor kinases	92	0.2	1.8	0.3	0.7
	Synthesis	10	I	0.2	· I	I		Calcium	40	0.9	T	I	I
												(conti	(pəni

Table IO.1 (cor	(finued)											
Cell process		Number	Percenta	ge of g	enes	Cell process		Number	Percen	itage of	f genes	
		of genes	different	ially re	gulated			of genes	differe	ntially	regula	ted
			0.75 h	3 h 12	h 48 h				0.75 h	3 h	12 h	48 h
Stress	Stress	I		- 3.1	T		Phosphoinositides	4	0.1	I	Т	1
	PR-proteins	4	1	1	0.1		Miscellaneous	3	I	0.1	I	I
	Abiotic	98	I	- 1.5	1	Transport	Transport	191	0.2	0.9	3.7	4.0
	Heat	61	1.0	1.1 1.2	1.2	Nitrogen	Metabolism	5	I	I	0.1	I
	Cold	6	0.1 (.1 -	Ι	Sulfur	Assimilation	252	0.1	4.8	0.1	0.1
	Unspecified	22	0.4 (0.3 0.3	0.4	Miscellaneous	Miscellaneous	252	5.4	0.7	1.1	1.2
Redox	Redox regulation	42	0.2	0.6 0.8	0.8	Not Assigned		1,833	33.9	33.9	35.8	35.0
Polyamine	Metabolism	б		- 0.1	I							
The plants were	grown in a P-poor soil fo	or 8 weeks an	d after tha	t P was	added 1	to increase the P avi	ailability fourfold. At	the same ti	me, oth	er plan	ts were	also es in

The plants were grown in a P-poor soil for 8 weeks and after that P was added to increase the P availability fourfold. At the same time, other plants were also treated with a salt stress to remove any general abiotic stress responses. Phosphorus addition resulted in an extractable P concentration increased by 20 times in the soils. Roots and above ground tissue were sampled initially, after 45 min, 3, 12, and 48 h. c-DNA microarray experiments were carried out to assess the percentage of genes differentially regulated. Missing values indicate non-detectable changes Hammond 2008), and the energy required and carbon dioxide evolved in their production and use (Helsel 1992; Jenssen and Kongshaug 2003), have increased the need to manage P fertiliser input more carefully. Over 85% of P mined is used in food production (Heffer et al. 2006) and peak P production (akin to peak oil) is estimated to occur by 2033 (Raven 2008; Cordell et al. 2009). These pressures will be exacerbated by increasing demand on food production systems as the human population increases, and by fluctuation in oil prices (Cordell et al. 2009). The breeding of new crop varieties that yield well with reduced P fertiliser inputs is now a priority for sustainable agriculture in the future.

Breeding crops that acquire and/or use P more efficiently is one strategy to reduce the use of P fertilisers. Such crops could produce comparable yields with lower inputs of inorganic Pi fertilisers or have reduced physiological P requirements and tissue P concentrations, thus reducing the amount of P removed by the crop and, thereby, the amount of P needed to maintain the availability of Pi in the soil. New varieties can be bred conventionally, based on trait-focused screens of germplasm collections. However, a great deal of information is now available about how plants regulate P homeostasis and acquisition from the soil, particularly at the genetic level (Franco-Zorrilla et al. 2004; Jain et al. 2007b; Hammond and White 2008; White and Hammond 2008: Fang et al. 2009; Lin et al. 2009). Mutants with allelic variation and/or altered expression of genes affecting P acquisition or P use within the plant have been generated. Several of these mutants illustrate strategies for developing crop plants that acquire and/or use P more efficiently.

Mutations that improve P acquisition from the soil could improve crop growth when P availability in the soil is poor. Transgenic plants that secrete microbial phytases into the rhizosphere have the potential to release P from inositol phosphates and show enhanced growth and P nutrition when inositol hexaphosphate is the major source of P (Richardson et al. 2001; Mudge et al. 2003; Zimmermann et al. 2003; George et al. 2004, 2005a). However, when grown in most soils, these plants have comparable growth and P nutrition to control plants (George et al. 2004, 2005b). Similarly, overexpression of a bacterial gene encoding citrate synthase in tobacco has been reported to increase citrate efflux from roots and to increase the availability of P from Ca-P (de la Fuente-Martínez et al. 1997; López-Bucio et al. 2000), but an effect on plant growth and P acquisition is not always observed (Delhaize et al. 2001). The expression of a wheat malate transporter gene (ALMT1) in barley has been shown to be effective in increasing P uptake by transgenic plants, but only in severely acidic soil conditions (Delhaize et al. 2009). Increased expression of specific phosphate transporters has been shown to increase biomass accumulation in tobacco cell cultures under P-limiting conditions (Mitsukawa et al. 1997), but did not enhance P uptake rates or growth of transgenic barley in soil (Rae et al. 2004).

Mutations altering root morphology also have the potential to enable plants to acquire more P. For example, barley genotypes with long root hairs have higher yields than genotypes with no root hairs on soils with low P availability (Brown et al. 2010), and genotypes of bean, maize and brassica with larger root systems have better growth under P-limiting conditions (Rubio et al. 2003; Liu et al. 2004; Hammond et al. 2009). The overexpression of miR399, or the downregulation of

UBC24 (*pho2*) expression, results in greater accumulation of P (Delhaize and Randall 1995; Aung et al. 2006; Bari et al. 2006; Chiou et al. 2006). A T-DNA insertional knockout of AtSIZ1 caused *Arabidopsis* to exhibit exaggerated Pi starvation responses, including cessation of primary root growth, extensive lateral root and root hair development, increase in root/shoot biomass quotient, and greater anthocyanin accumulation, even though intracellular Pi levels in *siz1* plants were similar to those in the wild type. All three mutants exhibit constitutive P-deficiency symptoms, including increased P uptake, which might be beneficial in some agricultural systems.

Mutations that improve crop growth when soil P availability is low, through better physiological utilisation of P, may also be useful in breeding crops for reduced P inputs. For example, OsPTF1, a bHLH transcription factor from rice, whose expression increases in the roots of P-starved plants, has been shown to enhance tolerance to P starvation (Yi et al. 2005). Also, transgenic tobacco cells that lack an alternative oxidase had improved growth under P-limiting conditions (Parsons et al. 1999).

10.6 Concluding Remarks

Management of soil P remains a crucial issue for the economic and environmental sustainability of agriculture and natural ecosystems globally. It is therefore essential that we have appropriate understanding of the mechanisms by which plants are able to acquire P from soil. In this chapter, various processes and physiological traits of plants that facilitate the availability and acquisition of P from soil have been outlined and some possibilities for deploying these traits into agricultural germplasm discussed. Better understanding of these processes and development of improved germplasm may ultimately improve the P-use efficiency of agriculture systems and provide valuable information for wider-scale land and resource management. However, at present it is evident that the full extent of the complexity of the gene-by-gene, and gene-by-environment interactions that are associated with plant P nutrition are not well appreciated, and that our comprehension of the functional redundancy and compatibility of different mechanisms both within individual plants and between coexisting organisms is poor. It is therefore important that a systems approach to P management continues to be developed for a more sustainable agriculture.

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