OsPTF1, a Novel Transcription Factor Involved in Tolerance to Phosphate Starvation in Rice[1][w]

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We report here on a novel transcription factor with a basic helix-loop-helix domain for tolerance to inorganic phosphate (Pi) starvation in rice (*Oryza sativa*). The gene is designated *OsPTF1*. The expression of *OsPTF1* is Pi starvation induced in roots while constitutively expressed in shoots, as shown by northern-blot analysis. Overexpression of *OsPTF1* enhanced tolerance to Pi starvation in transgenic rice. Tillering ability, root and shoot biomass, and phosphorus content of transgenic rice plants were about 30% higher than those of the wild-type plants in Pi-deficient conditions in hydroponic experiments. In soil pot and field experiments, more than 20% increase in tiller number, panicle weight, and phosphorus content was observed in transgenic plants compared to wild-type plants at low-Pi levels. In Pi-deficient conditions, transgenic rice plants showed significantly higher total root length and root surface area, which results in a higher instantaneous Pi uptake rate over their wild-type counterparts. Microarray analysis for transgenic plants overexpressing *OsPTF1* has been performed to investigate the downstream regulation of OsPTF1.

Phosphorus (P) is an essential macronutrient for plant growth, development, and reproduction. Plants absorb P almost exclusively in the inorganic form (Pi). Pi concentration is limited in both low- and high-pH soils due to its propensity to form insoluble aluminum and iron phosphate in acidic soils and calcium and magnesium phosphate compounds in alkaline soils (Bar-Yosef, 1991). Pi starvation elicits developmental and biochemical adaptation in plants, including an increase in root hair length and number, root-to-shoot ratio, and induction of high-affinity Pi transporters, phosphatases, and RNases (Schachtman et al., 1998; Raghothama, 1999; Ma et al., 2001). Similar adaptive responses to Pi starvation also occur in bacteria and fungi. In *Escherichia coli*, the PHO regulon comprises at least 15 genes involved in the acquisition of Pi (Torriani, 1990). Yeast (*Saccharomyces cerevisiae*) PHO regulon is mainly controlled by the phosphorylation and dephosphorylation of the transcription factor PHO4. PHO4 is a basic helix-loop-helix (bHLH) transcription factor, which generally interacts with the second transcription factor, PHO2, to induce the expression of downstream genes, such as high-affinity phosphate transporters, during Pi starvation (O'Neill et al., 1996).

Physiological and molecular studies have identified several putative members of a Pi starvation-inducible rescue system in higher plants (for review, see Abel et al., 2002). The regulatory gene, *PHR1*, which participates in the Pi starvation response, has been isolated from Arabidopsis (*Arabidopsis thaliana*; Rubio et al., 2001). The *PHR1* gene encodes a Myb transcription factor with homology to PSR1 from Chlamydomonas (Wykoff et al., 1999). The finding of *PHR1* implies that a PHO-like regulation system may exist in higher plants, and PHR1 may be a central factor for controlling the Pi-signaling system in plants. However, more evidence is needed to elucidate the molecular pathways controlled by *PHR1* for the adaptive responses to low-Pi regimes in plants. Increasing evidence has shown the existence of a complicated transcriptional regulation system that responds to Pi starvation in higher plants (for review, see Hammond et al., 2004). Two types of transcriptional regulations in response to Pi starvation have been reported, including the transient induction of response genes during early stages of stress and the high induction during later stages of stress (Wang et al., 2002; Hammond et al., 2003). The promoters of early response genes are enriched in two sequence motifs, the PHO-like (CDHGTGG; D:G, T, or A; H:C, T, or A) and the TATA box-like (TATAAATA) elements, which are different from the binding motif of PHR1 (Hammond et al., 2003). A systematic transcriptional change in response to Pi starvation was described by microarray analysis in Arabidopsis (Wu et al., 2003). In that study, several transcription factors were identified to be regulated by Pi starvation at different time points and in different plant parts.

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