The Rice CK2 Kinase Regulates Trafficking of Phosphate Transporters in Response to Phosphate Levels

Jieyu Chen,⁎ a Yifeng Wang, a Fei Wang, a Jian Yang, a Mingxing Gao, a Changying Li, a Yingyao Liu, a Yu Liu, a Naoki Yamaji, b Jian Feng Ma, b Javier Paz-Ares, c Laurent Nussaume, d Shuqun Zhang, a Keke Yi, e,f Zhongchang Wu, a,1 and Ping Wu a

⁎ State Key Laboratory of Plant Physiology and Biochemistry, College of Life Sciences, Zhejiang University, Hangzhou 310058, China
a Institute of Plant Science and Resources, Okayama University, Kurashiki 710-0046, Japan
b Centro Nacional de Biotecnologia, Consejo Superior de Investigaciones Científicas, Campus de Cantoblanco, 28049 Madrid, Spain
c Centro Nacional de Biotecnologia, Consejo Superior de Investigaciones Científicas, Campus de Cantoblanco, 28049 Madrid, Spain
d Unité Mixte de Recherche 7265 Commissariat à l’Energie Atomique/CNRS/University of Aix-Marseille, Institute for Biotechnology and Environmental Biology/SBVM/Laboratory of Plant Development Biology, Commissariat à l’Energie Atomique, Cadarache, St. Paul lez Durance F-13108, France
e State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Institute of Virology and Biotechnology, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
f Key Laboratory of Plant Nutrition and Fertilizer, Ministry of Agriculture, Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, China

ORCID ID: 0000-0001-6383-3817 (Z.W.)

Phosphate transporters (PTs) mediate phosphorus uptake and are regulated at the transcriptional and posttranslational levels. In one key mechanism of posttranslational regulation, phosphorylation of PTs affects their trafficking from the endoplasmic reticulum (ER) to the plasma membrane. However, the kinase(s) mediating PT phosphorylation and the mechanism leading to ER retention of phosphorylated PTs remain unclear. In this study, we identified a rice (Oryza sativa) kinase subunit, CK2β3, which interacts with PT2 and PT8 in a yeast two-hybrid screen. Also, the CK2α3/β3 holoenzyme phosphorylates PT8 under phosphate-sufficient conditions. This phosphorylation inhibited the interaction of PT8 with PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR1, a key cofactor regulating the exit of PTs from the ER to the plasma membrane. Additionally, phosphorylation starvation promoted CK2β3 degradation, relieving the negative regulation of PT phosphorylation-insufficient conditions. In accordance, transgenic expression of a nonphosphorylatable version of OsPT8 resulted in elevated levels of that protein at the plasma and enhanced phosphorus accumulation and plant growth under various phosphorus regimes. Taken together, these results indicate that CK2α3/β3 negatively regulates PTs and phosphorus status regulates CK2α3/β3.

INTRODUCTION

Phosphorus (P), as a component of key macromolecules, including nucleic acids (the largest organic P pool in plants) and phospholipids (important elements of membranes), is one of the essential mineral nutrients required by all organisms. P also influences photosynthesis, respiration, and the regulation of a wide array of cellular processes (Raghothama, 1999). Plants preferentially absorb P in the form of inorganic phosphate (Pi), which is poorly mobile in soils and often not readily available to plants. Thus, the level of available Pi is a major determinant of plant growth and productivity in many soils (Veneklaas et al., 2012; Zhang et al., 2014). However, plants have evolved an array of adaptive responses, involving developmental, physiological, and biochemical changes, to cope with growth in Pi-depleted soils. These responses are oriented toward improving Pi acquisition and use efficiency and to protecting plants from the stress caused by Pi starvation (Raghothama, 1999; Zhang et al., 2014).

The uptake of Pi is mediated by plasma membrane (PM)-localized Pi transporters (PTs) belonging to the PHT1 family, which shares similarity with the yeast high-affinity phosphate transporter PHO84 (Nussaume et al., 2011). Nine PHT1 genes have been identified in Arabidopsis thaliana and 13 in rice (Oryza sativa) (Raghothama, 1999; Goff et al., 2002). Gene expression analysis showed that most PHT1 family members are temporally and spatially upregulated in response to Pi starvation (Karthekeyan et al., 2002; Mudge et al., 2002; Misson et al., 2004; Shin et al., 2004). Their expression patterns extend beyond the root, in line with their roles in both Pi uptake and translocation: crucial functions for maintaining the internal P homeostasis in plants. For instance, in rice, the low-affinity phosphate transporter PT2 plays an important role in Pi translocation from root to shoot (Ai et al., 2009), whereas the high-affinity transporter PT8 plays a role in uptake, with half of the Pi uptake capacity dependent on PT8 (Chen et al., 2011; Jia et al., 2011). Therefore, increasing Pi transporter activity is one of the most important plant responses to Pi starvation (Raghothama, 1999; Nussaume et al., 2011).

1 Address correspondence to wzchang@zju.edu.cn.

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (www.plantcell.org) is: Zhongchang Wu (wzchang@zju.edu.cn). Articles can be viewed online without a subscription. www.plantcell.org/cgi/doi/10.1105/tpc.114.135335
In addition to transcriptional control, the activity of PTs, as PM-localized proteins, is also regulated posttranscriptionally. PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR1 (PHF1) plays a major role in regulating the trafficking of PTs from the endoplasmic reticulum (ER) to the PM (González et al., 2005; Chen et al., 2011). In addition, posttranslational control of PHT1 family members at the level of protein stability involves both PHOSPHATE2 (PHO2) and NITROGEN LIMITATION ADAPTATION (NLA), two components of the ubiquitin-mediated degradation pathway (Huang et al., 2013; Lin et al., 2013; Park et al., 2014). Superimposed on these mechanisms, Pi transporters may undergo phosphorylation that negatively regulates the exit of PHT1 members from the ER (Nühse et al., 2004; Hem et al., 2007; Bayle et al., 2011). However, the nature of the kinase(s) involved in the control of PHT1 activity and the underlying molecular mechanism(s) remain unclear.

CK2, formerly known as casein kinase II, is a heterotetramer composed of two catalytic and two regulatory subunits, CK2α and CK2β, respectively (Niefind et al., 2001). The human genome has two genes encoding catalytic α- or α′-subunits and only one for the regulatory β-subunit (Winkler et al., 1998; Ackermann et al., 2005), whereas plant genomes frequently have multigene families that encode each subunit (Espunya et al., 2005; Salinas et al., 2006). For example, four and two genes in rice encode CK2α and CK2β, respectively. CK2 is involved in a number of biological processes in mammals (Pinna, 2002; Meggio and Pinna, 2003), and CK2α- or CK2β3-MYC was observed in PT2/PT8-GFP immunoprecipitates in both PT2/PT8-GFP and the other three subunits of CK2 kinase in plants. The CK2β3 subunit often serves as an anchor element to bind its targets and interact with the catalytic α-subunits to form a holoenzyme (Ganley et al., 2001; Pinna, 2002). Accordingly, we tested for interactions of α-subunits with the PTs in the presence of CK2β3. The hydrophilic C termini (CT) of PT2/PT8, including the putative phosphorylation sites (Figure 1C; Bayle et al., 2011; Chen et al., 2011), were used in a yeast three-hybrid assay with two different CK2α (α2/α3) catalytic subunits in the presence or absence of CK2β3. CK2β3 was found to be necessary for the interaction between CK2α3 and PT2/PT8-CT in these assays (Figure 1D), suggesting that CK2α3, CK2β3, and the C termini of PT2/PT8 form a complex in yeast. In vivo co-IP assays confirmed this observation, as CK2β3 and CK2α3 were pulled down together with PT2/PT8-CT in plant cells (Figure 1E). The specificity of the CK2α3 subunit was confirmed, as even in the presence of CK2β3, no physical interaction between PT2/PT8-CT and CK2α3 was observed. Altogether, these results showed that the CK2α3/β3 complex interacted with PTs.

**RESULTS**

**The Rice CK2α3/β3 Complex Interacts with PTs**

Previous phosphoproteomic studies have identified phosphorylation of PTs (Nühse et al., 2004), and posttranscriptional regulation has been reported to be involved in the exit of PHT1 from the ER in plants (Bayle et al., 2011). To identify kinases potentially acting on PTs, we fused PT8 (Os10g044700), a high-affinity Pi transporter (Chen et al., 2011; Jia et al., 2011), to the C terminus of ubiquitin. We used the resulting chimeric bait vector PT8-Cub to screen a rice root cDNA library and identified multiple independent cDNAs encoding a putative protein kinase, CK2 (formerly known as casein kinase II) β-subunit (Os07g0495100; Rohila et al., 2006; Ding et al., 2009).

To confirm the initial library screening, we used PT8 and PT2 (Os03g0150800), the principal low-affinity PT for Pi translocation in rice roots (Ai et al., 2009), as bait to test for interaction with the CK2β3 subunit. Additionally, given that CK2 exists as a tetramer of two catalytic α-subunits, α2 (Os07g0114400) and α3 (Os03g0207300), and two regulatory β-subunits, β1 (Os10g0564900) and β3 (Os07g0495100) (Meggio and Pinna, 2003; Bibby and Litchfield, 2005; Rohila et al., 2006), the other three subunits were also used as prey for interaction analysis with PTs in both yeast and plants.

Split-ubiquitin yeast two-hybrid assays indicated that among these CK2 components, only β3 interacted with PT2 and PT8 in yeast cells (Figure 1A). To further validate this two-hybrid interaction between PT and the CK2 components, we conducted coimmunoprecipitation (co-IP) assays using Nicotiana benthamiana leaves infiltrated with either green fluorescent protein (GFP) or PT2/PT8-GFP together with the four CK2 components. β3-MYC was observed in PT2/PT8-GFP immunoprecipitates but not in the GFP control reactions (Figure 1B), whereas no physical interaction signal could be detected between PT2/PT8-GFP and the other three subunits of CK2 kinase in planta.

The CK2β3 subunit often serves as an anchor element to bind its targets and interact with the catalytic α-subunits to form a holoenzyme (Ganley et al., 2001; Pinna, 2002). Accordingly, we tested for interactions of α-subunits with the PTs in the presence of CK2β3. The hydrophilic C termini (CT) of PT2/PT8, including the putative phosphorylation sites (Figure 1C; Bayle et al., 2011; Chen et al., 2011), were used in a yeast three-hybrid assay with two different CK2α (α2/α3) catalytic subunits in the presence or absence of CK2β3. CK2β3 was found to be necessary for the interaction between CK2α3 and PT2/PT8-CT in these assays (Figure 1D), suggesting that CK2α3, CK2β3, and the C termini of PT2/PT8 form a complex in yeast. In vivo co-IP assays confirmed this observation, as CK2β3 and CK2α3 were pulled down together with PT2/PT8-CT in plant cells (Figure 1E). The specificity of the CK2α3 subunit was confirmed, as even in the presence of CK2β3, no physical interaction between PT2/PT8-CT and CK2α3 was observed. Altogether, these results showed that the CK2α3/β3 complex interacted with PTs.
designated PT8-CTS512A and PT8-CTS517A, respectively, mimicking peptides, replacing Ser-512 or Ser-517 by alanine (in peptides serine residues were target sites for CK2, we mutated PT8-CT). The mutation of Ser-517 (but not Ser-512) prevented the phosphorylation of PT8-CT (Figure 2A), indicating that Ser-517 of PT8 is the site of phosphorylation by CK2α3.

To confirm the phosphorylation of PT8 by CK2α3/β3 holoenzyme in vivo, we then performed PT8 phosphorylation assays using solubilized microsomal extracts from rice roots. A PT8-specific antibody (Supplemental Figure 3) was used to detect the phosphorylation status of PT8 via PhosTag SDS-PAGE (Figure 2B). In wild-type roots grown under +P (200 μM Pi), two bands were detected on the PhosTag immunoblots. The lower mobility band was determined to be phosphorylated PT8, as it was sensitive to λ-phosphatase (λ-PPase) treatment (Figure 2B). Furthermore, extracts from the roots of CK2α3 overexpressor (α3-OX) and CK2α3 knockout (α3-Ri) plants displayed enhanced and reduced PT8 phosphorylation, respectively. This validated our in vitro experiments showing that CK2α3 could function as the CK2 catalytic subunit involved in PT phosphorylation.

We also transferred the two subunits into rice protoplasts together to test additive effects of CK2β3, and the results showed that the phosphorylation of PT8 by CK2α3 was enhanced in the presence of CK2β3 (Figure 2C). Phosphorylation by CK2β3 in these bands was further confirmed by their sensitivity to 5,6-dichloro-1-β-D-ribofuranosylbenzimidazole (DRB), a CK2-specific inhibitor. It is noteworthy that CK2β3 did not provide catalytic activity, but it did increase holoenzyme function. Additionally, in vivo phosphorylation analysis of plants overexpressing CK2β3 (β3-OX) alone showed that increasing CK2β3 also enhanced PT8 phosphorylation in transgenic rice (Supplemental Figure 4), which is presumably dependent on endogenous expression of CK2α3. By contrast, downregulation of CK2β3 resulted in reduced PT8 phosphorylation, in agreement with in vivo CK2 function depending on the substrate-anchoring, regulatory subunit as well as the catalytic subunit.

Given that phosphorylation of PT8 was barely detectable in wild-type plants grown under −P (0 μM Pi) conditions (Figure 2B), the activity of CK2α3/β3 on PT might be regulated by Pi status. To test this hypothesis, proteins were extracted from roots and shoots of transgenic 3SS-CK2α3-FLAG and 3SS-CK2β3-FLAG plants grown under +P and −P conditions. PhosTag immunoblots, using tag-specific antibody, showed no change of CK2α3 protein levels under +P and −P conditions (Figure 2D; Supplemental Figure 5), whereas phosphorylation of CK2β3 was substantially reduced after Pi depletion, and CK2β3 protein accumulation gradually decreased under Pi starvation conditions in a time-dependent manner. After Pi recovery, phosphorylation level and protein abundance of CK2β3 rapidly recovered in both roots and shoots (Figure 2D; Supplemental Figure 5). Treatment with MG132 (10 μM), a 26S proteasome inhibitor, blocked the CK2β3 decline but not the reduction in phosphorylation (Figure 2D), indicative of protein degradation dependent on the ubiquitin/26S proteasome pathway. CK2β subunits that fail to form complexes with catalytic subunits are rapidly degraded (Zhang et al., 2002). In this context, the reduced accumulation of CK2β3 we observed under Pi starvation suggested that unphosphorylated CK2β3 may display decreased binding affinity with CK2α3 to form a stable holoenzyme. In vitro pull-down assays supported this hypothesis (Supplemental Figure 6). Together, all these results revealed nonphosphorylatable forms of PT8-CT). The mutation of Ser-517 (but not Ser-512) prevented the phosphorylation of PT8-CT (Figure 2A), indicating that Ser-517 of PT8 is the site of phosphorylation by CK2α3.

Figure 1. Rice CK2β3 Directly Interacts with PT and Is Necessary for the CK2α3 Interaction with PT.

(A) Split-ubiquitin yeast two-hybrid analysis. Cub, C-terminal ubiquitin (the bait APP-Cub served as a control that could interact with NubI but not with NubG and NubG-CK2 subunits); NubI and NubG, the wild type and the mutated N-terminal fragment of ubiquitin; SD/LW, -Leu-Trp; SD/LWHA, -Leu-Trp-His-Adé.

(B) In vivo co-IP of PT2/PT8 and four CK2 subunits. An α-GFP affinity matrix was used for immunoprecipitation, and the immunoblots were developed using tag-specific antibodies.

(C) Schematic representation of the C-terminal (CT) structure of PT2 and PT8 used in the yeast three-hybrid and co-IP assays. Amino acids 501 to 528 of PT2-CT and 506 to 541 of PT8-CT, containing Ser-512 and Ser-517, respectively, are indicated.

(D) Yeast three-hybrid assay, CK2α2 and CK2α3 were used as prey (AD-α2/α3); pBridge plasmids containing PT2/PT8-CT and additional CK2β3 cloned into MSCI (β3-3BD-PT2/PT8-CT) were used as bait and co-transformed into the AH109 yeast strain. EV, empty vector; SD/LMW, -Leu-Met-Trp; SD/LMWHA, -Leu-Met-Trp-His.

(E) Co-IP of PT8-CT with CK2α3 and CK2β3 in planta.

recombinant GST-α3, GST-β3, and GST-PT8-CT proteins. These assays showed that PT8-CT was phosphorylated in vitro by the catalytic subunit CK2α3 (Figure 2A) but not by the regulatory subunit CK2β3 (Supplemental Figure 2). This is consistent with the previous finding that both the isolated CK2 catalytic α-subunits and the holoenzyme have constitutive activity (Pinna, 2002; Sarno et al., 2002). To test whether the two conservative serine residues were target sites for CK2, we mutated PT8-CT peptides, replacing Ser-512 or Ser-517 by alanine (in peptides designated PT8-CTSS12A and PT8-CTSS17A, respectively, mimicking nonphosphorylatable forms of PT8-CT). The mutation of Ser-517 (but not Ser-512) prevented the phosphorylation of PT8-CT (Figure 2A), indicating that Ser-517 of PT8 is the site of phosphorylation by CK2α3.
that phosphorylation of PTs by CK2 was modulated in response to cellular Pi concentration.

**CK2α3/β3 Affects the ER Exit of PT**

Transgenic lines expressing the phospho-mimicking PHT1;1-GFP (PHT1;1S517A-GFP) exhibited an ER retention pattern in Arabidopsis (Bayle et al., 2011). As rice CK2α3/β3 could phosphorylate the homologous serine site in PT8 (Figures 2A and 2C; Chen et al., 2011), this CK2 could function to modulate the ER exit of PTs. To test this possibility, we examined the subcellular localizations of GFP-tagged PT2/OsPT8. When transiently expressed in rice protoplasts, PT2/PT8-GFP proteins were mainly detected at the PM, as reported previously (Chen et al., 2011). Overexpression of CK2α3 or CK2β3 led to ER retention of PT2/PT8 (Figures 3B and 3C), whereas overexpression of other CK2 components (CK2α2 or CK2β1) had no effect on ER exit of the PTs (Figures 3D and 3E). This suggested a specific regulatory role for CK2α3/β3 in PT trafficking to the PM. Overexpression of CK2α3 or OsCK2β3 alone was sufficient to affect the ER exit of PTs, a result in accordance with the in vivo phosphorylation assay (Figure 2B; Supplemental Figure 4).

To further examine the effects of CK2α3/β3 on the subcellular localization of PTs in planta, a fully functional PT8-GFP driven by its native promoter (Supplemental Figures 7 and 8) was intronspressed into the CK2α3/β3 overexpression transgenic plants (Oxa3/3/Oxβ3; Supplemental Figure 9). In the wild-type background, PT8-GFP displayed a PM localization pattern in root epidermis cells (Figure 3F) similar to that of PHT1;1 in Arabidopsis (Bayle et al., 2011). By contrast, cells coexpressing CK2α3/β3 showed a fluorescence pattern indicative of PT8-GFP retention in the ER (Figures 3G and 3H). These results indicated that the CK2α3/β3 holoenzyme regulates PT exit from the ER to the PM through its phosphorylation.

**Phosphorylation of PT by CK2 Impairs Its Interaction with PHF1**

Phosphorylation of the PT C-terminal domain by CK2 mimicked the effect of mutations in the ER-exit cofactor PHF1 (González et al., 2005; Chen et al., 2011). This suggested that phosphorylation of PT by CK2 might affect its interaction with PHF1. To check this, split-ubiquitin yeast two-hybrid analyses were performed between PHF1 and PT8 as well as mutated versions of PT8 in which Ser-517 was replaced by Ala-517 or Asp-517 (designated PT8S517A or PT8S517D), representing nonphosphorylatable or phospho-mimicking forms of PT8, respectively. Notably, PT8S517D (phospho-mimicking) did not interact with PHF1 in yeast cells, whereas an interaction between PHF1 and wild-type PT8 or nonphosphorylatable PT8S517A (Figure 4A) was observed.

To further validate our prediction in planta, co-IP assays were performed using solubilized microsomal extracts. They were prepared from *N. benthamiana* leaves coexpressing PHF1 together with PT8-GFP and its two mutated versions. PHF1 coimmunoprecipitated with PT8-GFP and PT8S517A-GFP but not with PT8S517D-GFP or the GFP control (Figure 4B), suggesting that phosphorylation of PT8 inhibits its interaction with PHF1.

In addition, we found that PHF1 protein abundance increased under the −P condition (0 μM Pi) in a time-dependent manner. This increase was reversed upon Pi resupply (Supplemental Figure 10). The response of PHF1 to Pi starvation was consistent with a function in assisting the exit of more dephosphorylated PT out of the ER under −P. Taken together, these results supported a model in which reduced CK2 and increased PHF1
coordinately enhance the exit from the ER of PTs under Pi starvation conditions.

**CK2α3/β3 Influences Pi Uptake Ability in Rice**

As CK2α3/β3 modulated the ER exit of PTs, it would be expected to also influence Pi uptake. Due to a lack of CK2α3 and CK2β3 T-DNA mutants, we used an RNA interference strategy (Ri) to develop transgenic plants with knockdown of CK2α3 or CK2β3 (Figure 5). Two independent lines of these knockdown plants were grown in +P hydroponic culture (200 μM Pi) for 30 d and used for Pi concentration measurements. As shown in Figures 5A to 5D, knockdown of CK2α3 or CK2β3 (α3-Ri or β3-Ri, respectively) led to necrotic symptoms on older leaf tips (Figure 5B) and retarded growth. α3-Ri and β3-Ri also showed significantly higher Pi concentrations in shoots and roots than that in the wild type (Figure 5E). We further used two independent α3-Ri lines to investigate their Pi uptake ability. Over a 24-h time course, uptake of 33P-labeled Pi by α3-Ri plants was above 30% higher than in the wild type (Figure 5F).

Analysis of α2 and β1 loss-of-function T-DNA insertional mutants (Supplemental Figures 11 and 12) did not reveal significant differences in Pi concentration from the wild-type control (Supplemental Figures 11E and 12E), indicating that there is specificity among CK2 subunits in the regulation of PT intracellular trafficking (Figures 3A to 3E). By contrast, the α2 and β1 mutants showed retarded growth similar to that of α3-Ri and β3-Ri (knockdown lines of CK2α3/β3) (Figure 5A). In this context, whether the growth retardation observed for α3-Ri or β3-Ri is merely a direct consequence of Pi toxicity or reflects the multifaceted role of these subunits cannot be answered at present and merits further investigation.

**Manipulation of PT Phosphorylation Status Affects Its PM Abundance and Pi Uptake Ability**

One expectation of the regulatory steps affecting PT exit from the ER is that PT accumulation at the PM would be dependent on Pi availability. We tested this hypothesis by examining PT8 accumulation at the PM of plants under –P for different time spans. We also checked the PT8 level at the PM after Pi refeeding to Pi-starved plants; in these assays, roots and shoots were analyzed separately (Supplemental Figure 13A). PT8 accumulated with increasing time of Pi-starvation stress. Additionally, PT8 abundance at the PM declined rapidly after Pi restoration, but the decrease of PT8 differed between roots and shoots. We found that this tissue-specific effect of Pi refeeding on PT8 accumulation at
the PM was associated with a higher phosphorylation level of PT8 in shoots (Supplemental Figure 13B).

These findings, as well as the result showing that Riα3 displayed enhanced Pi-uptake ability (Figure 5F) and the observation that phosphorylation of PT8 inhibited its interaction with PHF1, suggested that the nonphosphorylatable PTs should be more abundant at the PM as a result of enhanced ER exit, leading to an increase in Pi uptake ability, as reported previously for plants overexpressing PHF1 (Chen et al., 2011).

To test this notion, transgenic lines were generated with different versions of PT8. The PT8 antibody was then used to detect protein levels in PM-enriched fractions extracted from roots of the wild type, the pt8 mutant (Supplemental Figure 7), and complemented pt8 plants carrying a single copy of the wild-type PT8 (PT8S517) or the nonphosphorylatable PT8 (PT8S517A), designated PT8S517 pt8 and PT8S517A pt8, respectively (Figure 6; Supplemental Figure 14). Immunoblot analysis with the PHF1-specific antibody (ER marker; Supplemental Figure 10A) and the PM marker antibody PIP1;3 (Liu et al., 2013) demonstrated the purity and specificity of the PM-enriched fraction. These assays showed that under a wide range of Pi regimes (from 10 to 200 μM), the PT8 level in the PM fraction of PT8S517A pt8 plants was significantly higher than those in wild-type and PT8S517 pt8 plants, thus confirming that dephosphorylation of PTs favored their targeting efficiency to the PM.

We also examined Pi accumulation and biomass of the genotypes described above grown under different Pi regimes. In general, Pi levels and biomass of shoots and roots in the three PT8S517A pt8 transgenic lines were significantly higher than those of the wild type (Figure 7). Taken together, these studies demonstrated that nonphosphorylatable PT8 (PT8S517A) exhibited higher abundance at the PM than wild-type PT8 (PT8S517) and resulted in enhanced Pi uptake and growth.

**DISCUSSION**

PTs play a key role in Pi uptake and translocation. Multiple lines of evidence indicate that PT proteins undergo several post-translational modifications in addition to transcriptional regulation (Bayle et al., 2011; Huang et al., 2013; Lin et al., 2013; Park et al., 2014). One key regulatory step is ER exit of PTs to the PM, which is regulated positively by PHF1 and negatively by phosphorylation. In this study, we found that the CK2 kinase is responsible for PT phosphorylation and that PT phosphorylation impairs the interaction of PT with PHF1. In addition, we also uncovered the mechanism regulating CK2 activity that is dependent on Pi supply conditions.

**Rice CK2α3/β3 Functions as a Holoenzyme to Phosphorylate Pi Transporters**

Protein kinase CK2 is a ubiquitous Ser/Thr kinase that is evolutionarily conserved in all eukaryotes (Pinna, 2002; Litchfield, 2003; Meggio and Pinna, 2003; Mulekar and Huq, 2014). CK2 has been studied extensively in mammalian systems, where it can phosphorylate more than 300 known substrates, including transmembrane proteins (Ganley et al., 2001; Litchfield, 2003; Meggio and Pinna, 2003; Fu et al., 2013). Characterization of
CK2 in many plant species also demonstrates that this kinase is involved in diverse pathways (Plana et al., 1991; Espunya et al., 1999; Ogiso et al., 2010; Mulekar et al., 2012).

Our results reveal a role of CK2 in plant Pi homeostasis. We found that CK2 binds to high- and low-affinity PTs in rice through the regulatory subunit CK2β3 (Figures 1A to 1C), and

Figure 6. Increased Abundance of Nonphosphorylatable PT8 at the PM.
(A) PT8 protein levels in PM-enriched protein fractions in roots. Proteins extracted from seedlings (15 d old) of the wild type, the pt8 mutant, and transgenic pt8 mutant plants expressing PT8 (PT8517) or the nonphosphorylatable PT8517A mutant from the PT8 promoter were examined by immunoblotting using anti-PT8 antibody (Supplemental Figure 3) after growth at different Pi concentrations (10, 50, 100, and 200 µM). Immunoblots were also probed with antibodies against rice PM PIP1;3 and with anti-PHF1 antibody as controls for PM enrichment and ER contamination. Coomassie brilliant blue (CBB) staining was used as a loading control.
(B) Quantification of the results shown in (A). Relative PT protein (fold) is the ratio of the respective signal under the given Pi level to the loading control (protein gel blotting bands with anti-PIP1;3 antibody). Asterisks indicate statistically significant changes of PT8 signal: *P < 0.05, **P < 0.01, ***P < 0.005, and ****P < 0.0001.

Figure 7. The Nonphosphorylatable PT8 Increases Pi Uptake Ability.
(A) Pi concentrations of the plants shown in Supplemental Figure 14. Wild-type plants, pt8 mutants, and transgenic pt8 mutant plants expressing PT8 (PT8517) or the nonphosphorylatable PT8517A mutant from the PT8 promoter were grown for 30 d in solution culture with 10, 50, 100, and 200 µM Pi (n = 3).
(B) Biomass (dry weight [DW]) of the wild-type and related plants shown in Supplemental Figure 14 (n = 5). Different letters indicate the statistical significance of variations analyzed by Duncan’s multiple range test (P < 0.05); letters inside the bars indicate the significance of variations in each part of individual lines, and letters above the bars indicate the significance of variations for overall plants. Error bars represent SD. FW, fresh weight.
Figure 8. Model for CK2α3β3 Regulation of the ER Exit of PTs.

Under high Pi, phosphorylated CK2α3β3 interacts with CK2α3. This forms an active holoenzyme that phosphorylates PTs, thereby inhibiting the interaction between PTs and PHF1, resulting in ER retention of PTs. Under low Pi, CK2α3β3 is dephosphorylated and degraded. PHF1 interacts with nonphosphorylated PT, facilitating trafficking of PT through the ER and promoting its subsequent accumulation at the PM. The thickness of the arrows represents the intensity of the effects under different conditions. The pathway indicated by the dashed lines requires more evidence. See text for more details. ERAD, ER-associated protein degradation; TGN, trans-Golgi network.

CK2-mediated phosphorylation of PT inhibits the ER exit of PT protein, leading to reduced phosphate uptake ability in rice. These findings expand our understanding of CK2 function in plant growth and development and provide evidence for specific protein kinase effects on transmembrane proteins in plants as in animals (Ganley et al., 2001; Scott et al., 2006; Lambert and Hansen, 2011; Fu et al., 2013).

Genes encoding CK2 subunits show a higher degree of redundancy in plants compared with animals (Espunya et al., 2005; Ogiso et al., 2010; Mulekar et al., 2012). Here, we found that the duplication of CK2 subunits was accompanied by functional divergence, as only CK2α3β3 was active in PT phosphorylation. In accordance, only overexpression of CK2α3/β3 inhibited the ER exit of PTs (Figures 3A to 3E). Consistent with this, rice transgenic lines with knockdown of CK2α3 or CK2α3β3 exhibited higher Pi concentration (Figure 5E; Supplemental Figures 11E and 12E).

Our results also reinforce the general notion that the non-catalytic CK2β subunit can function as an “anchoring element” for the substrate, rather than being responsible for the activation or inhibition of catalytic activity of the CK2α3 subunit (Pinna, 2002). Indeed, we have shown that the CK2α3β3 subunit is necessary to allow an interaction between CK2α3 and PT8 in vivo (Figure 1).

A minimum consensus sequence (Ser-Xaa-Xaa-acidic) for the CK2 target site has been defined (Pinna, 2002; Mulekar and Huq, 2014), and such a sequence also exists in the C-terminal domain of rice PT2 and PT8 (Figure 1C). Additionally, substrate specificity of different subunits could be achieved through their localization to distinct subcellular compartments. Here, we found that in rice, CK2α3 and CK2α3β3 are targeted to the ER compartment (Supplemental Figure 1), where PT exit from the ER was regulated by phosphorylation. Together, these findings indicate that CK2α3/β3 functions as a holoenzyme to phosphorylate PT in its C-terminal domain.

Phosphorylation of PTs Is Dependent on Pi Supply

It is notable that PT phosphorylation by CK2 is responsive to cellular Pi status (Figure 2B). Regulation of CK2 kinase activity has been considered puzzling, since neither of the typical regulatory mechanisms (control by second messenger molecules and switching off of catalytic activity by an interaction partner) for eukaryotic protein kinases held true for the enzyme (Allende and Allende, 1995). Recent crystal structure analysis of CK2 in Drosophila melanogaster supports a “regulation-by-aggregation” model in which CK2 tetramers are arranged as approximately linear aggregates with completely blocked active sites (Schnittler et al., 2014). By contrast, according to our results, Pi deficiency in rice causes downregulation of the phosphorylation and protein level of CK2β3 (Figure 2E; Supplemental Figure 5), excluding the possibility of an aggregation mechanism analogous to that in Drosophila CK2.

In animals, the CK2β subunit is regulated by protein degradation through a YROALDMILD “cyclin destruction” consensus sequence (Allende and Allende, 1995). In addition, phosphomimicking in the human CK2β subunit enhances its stability (Zhang et al., 2002). In line with this result, we found that rice CK2β3 contains a related “destruction” box (YDYALDLILD) in the analogous position (amino acids 139 to 148), and abundance of CK2β3 was reduced when it was dephosphorylated in Pi-starved plants. Our findings support that phosphorylation of the CK2 regulatory subunit may result in enhanced activity of the holoenzyme, in agreement with a previous finding that the CK2β subunit is involved in the assembly of holoenzyme as a possible checkpoint for enzyme activity (Allende and Allende, 1998).

Further investigation is required to identify the detailed mechanism involved in modulating the phosphorylation and degradation of CK2β3 under Pi starvation.

In addition to its crucial role in the regulation of CK2 activity, Pi supply also affects the accumulation of PHO2 and NLA (Lin et al., 2013; Park et al., 2014), which are involved in Pi utilization and (subsequent degradation). Thus, CK2, PHO2, and NLA generate a negative feedback loop for the regulation of PT activity according to plant Pi status. Such a negative loop is paralleled by a similar feedback mechanism for transcriptional control generated between the PHR1 master regulator of Pi starvation responses and several SPX proteins (Lv et al., 2014; Puga et al., 2014; Wang et al., 2014).

A CK2-Integrated Model for PT ER Exit

In this study, we found that phosphorylation of PT prevents its interaction with PHF1 (Figure 4), an integral membrane protein located in the ER that facilitates the ER trafficking of PHT1 family members. Together with the observation that PHF1 functions...
upstream of COPII vesicle formation (Bayle et al., 2011), our data make a critical contribution to our knowledge of the regulation of PT trafficking from the ER by identifying the kinase involved in the phosphorylation process, CK2, and uncovering its functional connection to the ER-exit facilitation function of PHF1. A model summarizing the role of CK2 phosphorylation is provided in Figure 8. It shows that low-Pi stress leads to a reduction of the phosphorylation and abundance of CK2β3, which limits CK2α3 access to PTs for phosphorylation. Therefore, the nonphosphorylated PTs can interact with PHF1 for efficient trafficking from the ER to the PM. By contrast, under Pi-sufficient conditions, phosphorylated CK2β3 is stable and, together with CK2α3, forms an active holoenzyme that phosphorylates PTs to inhibit the interaction between PTs and PHF1, resulting in ER retention of PTs.

The ER is the site for the maturation of secretory and membrane proteins, and improperly folded or excess proteins are frequently retained in the ER and subjected to ER-associated protein degradation (Arvan et al., 2002; Hegde and Ploegh, 2010). Recently, interplay between protein phosphorylation and ubiquitination in ER-associated protein degradation was demonstrated (Wang et al., 2012). Accordingly, it is possible that CK2-mediated phosphorylation of PT under high Pi may lead to ER retention and subsequent ER-associated degradation of PTs.

In summary, there is a regulatory step at the ER whereby PHF1 enables the exit of PTs and phosphorylation by CK2 inhibits it by impeding PT-PHF1 interaction in addition to transcriptional control increasing PT levels in response to low Pi (Karthikeyan et al., 2002; Mudge et al., 2002). The activity of this kinase is affected by Pi supply, because reduced phosphorylation of CK2β3 results in its decreased stability and interaction capacity with CK2α3. Thus, superimposing both regulatory mechanisms, transcriptional and posttranslational, should allow a sharper response to changes in Pi availability for better maintenance of P homeostasis in plants. Conversely, we show that relieving phosphorylation control by expressing a nonphosphorylatable version of PT8 enhances Pi acquisition efficiency and plant growth, providing a possible strategy for improving Pi acquisition efficiency in crops, especially under P-limited conditions.

METHODS

Plant Materials and Growth Conditions

Rice (Oryza sativa cv Nipponbare) as the wild type and transgenic plants were grown hydroponically in full-strength Kimura nutrient solution with high or low Pi in a greenhouse with a 12-h-day (30°C)/12-h-night (22°C) photoperiod, unless specified otherwise. Isolated RNA was treated with RNase-free DNase (Qiagen) for DUALmembrane pairwise interaction kit (Dualsystems Biotech). First-strand cDNA and second-strand cDNA were cloned in frame into the vectors pBT3-N and pPR3-STE, respectively. The coding regions of PT2/PT8 and CK2α3/β3/β3 were cloned in frame in the vectors pBT3-STE and pPR3-N, respectively. The protein-protein interactions were assessed by the growth of yeast colonies on synthetic medium lacking Leu and Trp. The protein-protein interactions were assessed by the growth of yeast colonies on synthetic medium lacking Leu, Trp, His, and Ade. The bait APP-Cub expressing the type I integral membrane protein APP (for amyloid A4 precursor protein) was used as the control that could interact with NubI but not with NubG.

Membrane Protein Isolation

Membrane proteins were isolated from rice seedlings (the tissue used is indicated in the respective experiments), infiltrated N. benthamiana leaves, or harvested protoplasts as follows. Tissues or suspension cells were first mechanically disrupted and suspended in homogenization buffer containing 50 mM Tris, 500 mM sucrose, 10% glycerol, 20 mM EDTA-Na2, 20 mM EGTA, 50 mM NaF, 5 mM β-glycerophosphate, 1 mM phenanthroline, 0.6% polyvinylpyrrolidone (average molecular weight from 30,000 to 40,000), and 10 mM ascorbic acid, with freshly added 1 mM leupeptin, 5 mM DTT, and 1 mM sodium orthovanadate. The resulting homogenate was filtered through a nylon cloth (100-μm diameter) and then centrifuged at 26,000g for 25 min. The resulting supernatant was filtered through two successive filters, 63- and 34-μm diameter. The microsomal pellet was obtained from the supernatant by centrifugation at 84,000g for 25 min. PM proteins were isolated from total microsomal proteins by two-phase partitioning as described previously (Szabó-Nagy et al., 1989). Total microsomal protein and PM protein-enriched fractions were loaded for immunoblot analysis on general gels or by PhosTag SDS-PAGE.

co-IP Assays

Microsomal fractions were prepared from coinfiltrated N. benthamiana leaves as described above. Samples were solubilized by dilution with 5 volumes of PBS containing 1.5% Triton X-100 and incubated for 1 h at 4°C. This was followed by centrifugation at 20,000g for 1 h and incubation with anti-GFP magnetic beads (Chromotek) for 2 h at 4°C. Beads were washed five times with washing buffer (50 mM Tris, pH 7.5, 150 mM NaCl, 0.2% Triton X-100, 1 mM phenylmethylsulfonyl fluoride, and 1× protease inhibitor cocktail [Roche]). Following SDS-PAGE and transfer to nitrocellulose, GFP, PT8-GFP, PT2-GFP, PT8-GFP, PT8S517A-GFP, and PT8S517D-GFP proteins and CK2 subunits were detected by immunoblotting with tag-specific antibodies (Sigma-Aldrich). PHF1 was detected using PHF1-specific antibody (see below).
Yeast Three-Hybrid Assays
The cDNA fragments encoding PT2/8-CT and CK2β3 were inserted into the pBridge vector (Clontech) to generate fusions with the GAL4 DNA-binding domain and Met promoter, respectively. CK2α2/α3 was inserted into the pGADT7 vector (Clontech) to generate pGAD-α2/α3 to serve as prey in yeast three-hybrid assays. The resulting constructs were co-transformed into yeast strain AH109 and selected on dropout medium lacking Leu, Met, and Trp or Leu, Met, Trp, and His.

Recombinant Protein Expression
Fragments encoding mature CK2α3/β3 and PT8-CT as well as alleles of PT8-CT were cloned into expression vector pGEX-4T-1 (GE Healthcare). Fragments encoding mature CK2α3/β3 lacking Leu, Met, and Trp or Leu, Met, Trp, and His were cloned into expression vector pGEX-4T-1 (GE Healthcare). The recombinant vectors were identified by sequencing. Recombinant plasmids were transformed into Escherichia coli TransB (DE3) (Transgen) and then treated with 0.05 mM isopropyl-β-D-thiogalactoside for 12 h under 22°C to induce the expression of fusion proteins. Expressed proteins were purified using GST-affinity chromatography on immobilized glutathione followed by competitive elution with excess reduced glutathione according to the manufacturer’s instructions (GE Healthcare).

In Vitro Phosphorylation Assays
In vitro kinase assays in solution were performed essentially as described previously (Meng et al., 2012) with a few modifications. Kinase subunits and substrate proteins were mixed with 1× kinase buffer (100 mM Tris-HCl, pH 8.0, 5 mM DTT, 5 mM EGTA, and 5 mM MgCl2, New England Biolabs) and 1× ATP solution (100 μM ATP and 1 μCi of [γ-32P]ATP; Perkin-Elmer) in a total volume of 50 μL. Equal amounts of GST-tagged PT8-CT and its Ser-to-Ala mutant proteins were incubated with CK2α3 in the presence of [γ-32P]ATP. The reactions were incubated at 30°C for 30 min and then stopped by adding 5× loading buffer and boiling for 5 min. Products were separated by electrophoresis through 12% acrylamide gels, and the gels were stained, dried, and then visualized by exposure to x-ray film.

In Vivo Phosphorylation Assays
Rice seedlings and CK2 overexpression/knockdown transgenic plants were grown for 7 d in full-strength Kimura nutrient solution with high or low Pi, and then the roots of these seedlings were harvested for microsomai fraction extraction. Membrane fractions were subjected to λ-PPase treatment as described previously (Michniewicz et al., 2007) with a few modifications. Treatment was performed with λ-PPase (Sigma-Aldrich) in a total volume of 50 μL, and samples were incubated at 30°C for 30 min. The reactions were stopped by adding 5× SDS loading buffer (Sangon) and boiled. For the in vivo phosphorylation assays performed in protoplasts, the membrane proteins were extracted from protoplasts developed from wild-type callus and callus harboring overexpressed CK2α3 or CK2β3, and simultaneously overexpressed CK2α3 and CK2β3, in the absence and presence of DRB inhibitor. Cells were treated with 50 μM DRB for 12 h. For the control, an equal volume of DMSO, which was the solvent used to prepare the inhibitor stock solutions, was added. Samples were separated on 10% SDS-PAGE, and samples were incubated at 30°C for 30 min. The samples were separated on 10% SDS-PAGE, and the proteins were transferred to nitrocellulose membranes. The membranes were incubated with the primary antibodies (anti-FLAG M2; 1:3000 protein gel blotting) and then incubated with the secondary antibody (anti-mouse or anti-rabbit; 1:5000 protein gel blotting). Detection was performed with the enhanced chemiluminescence reagent (Pierce).

Pull-Down Assays
β3-FLAG was synthesized by N. benthamiana leaves infiltrated with Agrobacterium tumefaciens. For in vitro binding, 20 μL of total N. benthamiana protein was added to 600 μL of binding buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM EDTA, 10% glycerol, 2 mM Na2VO4, 25 mM β-glycerophosphate, 10 mM NaF, 0.05 to 0.1% Tween 20, 1× Roche protease inhibitor, and 1 mM phenylmethylsulfonyl fluoride), followed by 50 μL of glutathione-agarose beads with bound GST-α3 or its alleles, and was incubated at 4°C for 3 h. The beads were washed with binding buffer three times. Bound proteins were eluted with 5× SDS loading buffer and resolved by 12% SDS-PAGE. Individual bands were detected by immunoblotting with tag-specific antibodies. Commercial antibodies were purchased from Sigma-Aldrich (anti-FLAG M2; 1:3000 protein gel blotting) and GE Healthcare (anti-GST; 1:5000 protein gel blotting).

Subcellular Localization of PT2/8 Proteins in Rice Protoplast Cells
Isolation of rice protoplasts and protoplast transient transformation were conducted as described previously (Chen et al., 2011). Observations were made on a Zeiss Axiovert LSM 710 laser scanning microscope. Protoplasts were observed under a 63× objective. For excitation of fluorescence proteins and mCherry, the following lines of an argon ion laser were used: 488 nm for GFP and 543 nm for mCherry. Fluorescence was detected at 493 to 542 nm for GFP and 578 to 625 nm for mCherry.

Construction of Vectors and Generation of Transgenic Plants
The nonphosphorylatable (SS17A) mutation in PT8 and wild-type PT8 were generated with primers using the PT8(327A) pPR3-STE plasmid as template; released fragments were inserted into pCambia1300 vector to generate pCambia1300-PT8/PT8(327A). Plasmids bearing PT8ps-PT8ps/ PT8ps(327A), in which the genes were under the control of the native promoter, were derived from pCambia1300-PT8ps/PT8ps(327A) by replacing the cauliflower mosaic virus 3SS promoter with 2679 bp of genome sequence upstream of the ATG of PT8. Plasmids encoding PT8ps-PT8ps-GFP under control of its native promoter were similarly derived from pCambia1300-PT8ps-GFP by replacing the cauliflower mosaic virus 3SS promoter with 2679 bp of genome sequence upstream of the ATG of PT8. For the RNA interference construct, fragments 179 to 430 bp for CK2α3 and 517 to 763 bp for CK2β3 were cloned in both orientations in pCambia35SS-1300 vector and separated by the second intron of NRT1 of maize (Zea mays) to form a hairpin structure. The binary vectors and the 3SS promoter-driven CK2α3/β3 vectors (see above) were introduced into Agrobacterium strain EHA105 and transformed into wild-type rice (cv Nipponbare) according to the method described previously (Chen et al., 2011).

RNA Isolation, RT-PCR, and Quantitative RT-PCR Analysis
Total RNA from rice samples was isolated using TRIzol reagent (Invitrogen) followed by treatment with DNase I (GiaGen) before quantitative RT-PCR (qRT-PCR) to eliminate genomic DNA contamination. cDNA was synthesized from 5 μg of total RNA using SuperScript III (Invitrogen). qRT-PCR was performed using the SYBR Green I Master (Roche) on the LightCycler 480 Real-Time PCR system (Roche) according to the manufacturer’s instructions. Relative expression levels were normalized to that of the housekeeping gene ACT71. The primers used for RT-PCR and qRT-PCR are listed in Supplemental Table 1.

Determination of Cellular Pi Concentration and Pi Uptake Ability
Cellular Pi concentration was determined as described previously (Chen et al., 2011). 33P uptake analysis was conducted as described previously (Wu et al., 2011).

Development of PHF1 and PT8 Polyclonal Antibodies
Polyclonal rabbit PHF1 antibody was raised against a C-terminal fragment of rice PHF1 corresponding to amino acid residues 375 to 387 (C-KESPPVPEDQNPW-COOH) and affinity purified by Abmart. For an
antibody against rice PT8, the synthetic peptide C-VLQVEIQOEODKLEOMVT-
COOH (positions 264 to 281 of rice PT8) was used to immunize rabbits. The
obtained antisera was purified through a peptide affinity column before use.

Accession Numbers
The Michigan State University Rice Genome Annotation Project Database
accession numbers for the genes studied in this work are Os07g0187700
(PHF1), Os03g0150800 (PT2), Os10g0444700 (PT8), Os07g0114400
(CK2α2), Os03g00270300 (CK2α3), Os10g0564900 (CK2β1), and
Os07g0495100 (CK2β3). NCBI accession numbers for the proteins are as
follows: PHF1, NP_001059077; PT2, NP_001048979; PT8, NP_001064708;
CK2α2, NP_0010587522; CK2α3, NP_001049325; CK2β1, NP_001065415;
and CK2β3, NP_001059693.

Supplemental Data
Supplemental Figure 1. Subcellular Localization of CK2α3/β3.
Supplemental Figure 2. CK2β3 Is Unable to Phosphorylate the C-Terminal Ser-517 Residue of PT8.
Supplemental Figure 3. Specificity of the Rice PT8 Polyclonal Antibody.
Supplemental Figure 4. Effect of CK2β3 Overexpression on PT8 Phosphorylation in Vivo.
Supplemental Figure 5. Immunoblotting Analysis for CK2α3/β3 Protein Level in Plants Grown under Pi-Sufficient and Pi-Starvation Conditions.
Supplemental Figure 6. Cellular Pi Sensitivity of the Interaction between CK2β3 and CK2α3.
Supplemental Figure 7. Isolation of pt8 Mutants in Nipponbare Background.
Supplemental Figure 8. Functional PT8-GFP Rescued pt8 Mutant.
Supplemental Figure 9. Phenotype and Pi Concentration of Transgenic Plants Overexpressing CK2α3/β3.
Supplemental Figure 10. Specificity of the PHF1 Polyclonal Antibody.
Supplemental Figure 11. Phenotype and Pi Content Analysis of α2 T-DNA Insertional Mutant.
Supplemental Figure 12. Phenotype and Pi Analysis of β1 T-DNA Insertional Mutant.
Supplemental Figure 13. PT8 Protein Accumulation and Phosphorylation Levels Differ in Roots and Shoots.
Supplemental Figure 14. DNA Gel Blot Analysis and Plant Phenotype of Independent Transgenic Lines of the pt8 Mutant Transformed with PT85517 and PT85517A Expressing Constructs.
Supplemental Table 1. Primers Used in This Study.

ACKNOWLEDGMENTS
We thank Mingxiu Chen for helping develop the transgenic plants. This work
was supported by the National Basic Research and Development Program
of China (Grant 2011CB100303), the Ministry of Science and Technology of
China (Grant 2012AA10A302), the Ministry of Agriculture of China (Grants
2011Z2X08001-005, 2013Z2X08001-005, and 2014Z2X08001005), the Ministry
of Education and Bureau of Foreign Experts of China (Grant B14027), the
National Natural Science Foundation of China (Grant 31320248), and a
Grant-in-Aid for Scientific Research on Innovative Areas from the Ministry
of Education, Culture, Sports, Science, and Technology of Japan (Grant
22119002 to J.F.M.).

AUTHOR CONTRIBUTIONS
P.W. conceived the project. P.W., S.Q.Z., and J.P.-A. designed the experiments. J.Y.C. developed the assay and performed the experiments
together with Y.F.W., F.W., J.Y., and M.X.G. Z.O.W., Y.L., C.Y.L., and
Y.Y.L. analyzed the nutrients. N.Y. and J.F.M. developed the OsPT8
antibody. P.W. wrote the article with improvement from J.P.-A., S.Q.Z.,
L.N., K.K.Y., and J.F.M.

Received December 11, 2014; revised January 30, 2015; accepted
February 7, 2015; published February 27, 2015.

REFERENCES
nase CK2 (CSNK2A2): Genomic organization, promoter identification and
Ai, P., Sun, S., Zhao, J., Fan, X., Xin, W., Guo, Q., Yu, L., Shen, Q.,
porters, OsPht1;2 and OsPht1;6, have different functions and ki-
Allende, C.C., and Allende, J.E. (1998). Promiscuous subunit inter-
actions: A possible mechanism for the regulation of protein kinase
kinase CK2: An enzyme with multiple substrates and a puzzling
Secretory pathway quality control operating in Golgi, plasma-
Bayle, V., Arrighi, J.F., Creff, A., Nespolous, C., Vialaret, J.,
Rossignol, M., Gonzalez, E., Paz-Ares, J., and Nussaume, L.
(2011). Arabidopsis thaliana high-affinity phosphate transporters exhibit
multiple levels of posttranslational regulation. Plant Cell 23: 1523–1535.
the regulatory subunit of protein kinase CK2: CK2 dependent and
CK2 independent roles reveal a secret identity for CK2beta. Int. J.
Wu, P. (2011). OsPHF1 regulates the plasma membrane localization of low- and high-affinity inorganic phosphate transporters and de-
determines inorganic phosphate uptake and translocation in rice.
Physiol. 149: 1478–1492.
Espunya, M.C., Combettes, B., Dot, J., Chaubet-Gigot, N., and
Martínez, M.C. (1999). Cell-cycle modulation of CK2 activity in
Espunya, M.C., López-Giraldez, T., Hernan, I., Carballo, M., and
protein kinase CK2 subunits in the plant cell cycle. J. Exp. Bot. 56:
3183–3192.
Phosphorylation sites required for regulation of cardiac calcium
channels in the fight-or-flight response. Proc. Natl. Acad. Sci. USA
110: 19821–19826.
References:


The Rice CK2 Kinase Regulates Trafficking of Phosphate Transporters in Response to Phosphate Levels
Jieyu Chen, Yifeng Wang, Fei Wang, Jian Yang, Mingxing Gao, Changying Li, Yingyao Liu, Yu Liu, Naoki Yamaji, Jian Feng Ma, Javier Paz-Ares, Laurent Nussaume, Shuqun Zhang, Keke Yi, Zhongchang Wu and Ping Wu

Plant Cell 2015;27;711-723; originally published online February 27, 2015;
DOI 10.1105/tpc.114.135335

This information is current as of July 2, 2017

Supplemental Data /content/suppl/2015/02/10/tpc.114.135335.DC1.html
References This article cites 55 articles, 28 of which can be accessed free at:
/content/27/3/711.full.html#ref-list-1
eTOCs Sign up for eTOCs at:
http://www.plantcell.org/cgi/alerts/ctmain
CiteTrack Alerts Sign up for CiteTrack Alerts at:
http://www.plantcell.org/cgi/alerts/ctmain
Subscription Information Subscription Information for The Plant Cell and Plant Physiology is available at:
http://www.aspb.org/publications/subscriptions.cfm

© American Society of Plant Biologists
ADVANCING THE SCIENCE OF PLANT BIOLOGY