

Table S1 Basic soil properties in 0-30 cm soil layer before the field trials

Soil property	Value
pH	8.5
soil organic matter	10.3 g kg ⁻¹
total N	0.67 g kg ⁻¹
Olsen-P	7 mg kg ⁻¹
exchangeable-K	74 mg kg ⁻¹

The soil type at the study site is a calcareous alluvial fluvo-aquic soil with a loamy and silt texture. The soil samples were analyzed before fertilization. After fresh soil samples were taken, sieved through a 2 mm sieve in the field and then air-dried in the laboratory. Soil pH value was determined by a pH meter using soil to water ratio of 1:2.5 (Peech, 1965). Total nitrogen was analyzed by semi-micro Kjeldahl digestion (Bremner, 1965) followed by ammonium distillation and titrimetric determinations. Olsen-P was extracted with 0.5 mol L⁻¹ NaHCO₃ for 30 min, and analyzed colorimetrically according to Murphy and Riley (1962). Exchangeable-K was done by 1 mol L⁻¹ NH₄OAc for 30 min and analyzed by flame photometer (Chapman, 1965). Organ carbon (OC) was measured by Walkley and Black wet acid dichromate digestion method (Allison, 1965); soil organic matter was calculated as 1.72 x %OC (Walkley and Black, 1934).

References

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Walkley, A. and Black, IA. 1934. An examination of the Degtjareff method for determining soil organic matter and proposed modification of chromic titration method. *Soil Science* **37**, 29-38.

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Table S2 Real time PCR primers

Gene name	Forward (5'-3')	Reverse (5'-3')
<i>TaIPS1.1</i>	TCTCCTGTGAGTACCGGTGACA	ACTGTACACTAGTCGACAACCTTGC
<i>TaPHT1.1&1.9</i>	GAGACCGGCTACTCACGGG	CTAAGCTT CGATGCCATCGTC
<i>TaPHT1.2</i>	TGAGACCGGCTACTCACGG	AATGGAGTCATCGTCGCCAA
<i>TaPHT1.6</i>	TTTTTTATGGTCGGAGAGCGTT	CAGCCCTAATTAACCTGGACAACCT
<i>TaPHT1.8</i>	GATCTTCAGGGACATCAAGTGGATC	TGAACCCGAGGAACTGGATGG
<i>TaPHT1.10</i>	GCGTTCGGGTTCCCTGTATGC	CAGTCGGAGCAATGGTGTCTGT
<i>TaEXPA6</i>	GGCGGCCAGTACAAGGTCTT	GCCCTGAACGAGCGAACTGA
<i>TaEXPB8</i>	CCGGACAATGCTTACTGGTCCA	TGAACAATAGGTAGCGTTTGGTGAG
<i>TaPAP15</i>	GAAGTTTTGCTGGGAACGACA	GCAATAGGCACTTATCGGGTTC
<i>TaPAP16</i>	GTTCGGAAAGTCCACCAATATGC	GACACTAACATGAGCCAAACTCAAA
<i>TaRNS1</i>	AGTTCCTCCGACCTTCTGATGCG	AACAATCGGCTCCCTCCACAT
<i>TaActin</i>	ACCTTCAGTTGCCAGCAAT	CAGAGTCGAGCACAATACCAGTTG

Fig. S1

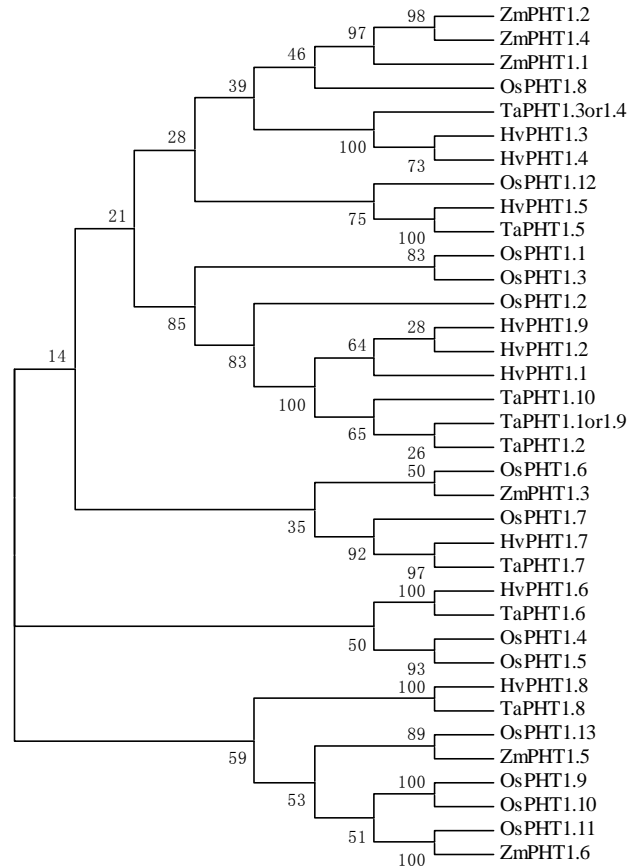


Fig. S1 Phylogenetic analysis of PHT1 proteins from wheat, barley, rice and maize. Phylogenetic tree of 8 TaPHT1 genes, 9 HvPHT1 genes, 13 OsPHT1 genes, and 6 ZmPHT1 genes was constructed by the neighbor-joining method with 1000 bootstrap replicates in the MEGA5 program.

The protein ID numbers of the PHT1 genes are barley (*Hordeum vulgare*) HvPHT1.1, AAN37900; HvPHT1.2, AAO72434; HvPHT1.3, AAO72439; HvPHT1.4, AAO72438; HvPHT1.5, AAO72435; HvPHT1.6, AAN37901; HvPHT1.7, AAO07436; HvPHT1.8, AAO72440; HvPHT1.9, CAP17759; rice (*Oryza sativa*) OsPHT1.1, AAN39042; OsPHT1.2, AAN39043; OsPHT1.3, AAN39044; OsPHT1.4, AAN39045; OsPHT1.5, AAN39046; OsPHT1.6, AAN39047; OsPHT1.7, AAN39048; OsPHT1.8, AAN39049; OsPHT1.9, AAN39050; OsPHT1.10, AAN39051; OsPHT1.11, AAN39052; OsPHT1.12, AAN87745; OsPHT1.13, AAN39054; and maize (*Zea mays*) ZmPHT1.1, AAY42385; ZmPHT1.2, AAY42386; ZmPHT1.3, AAY42387; ZmPHT1.4, AAY42388; ZmPHT1.5, AAY42389; ZmPHT1.6, AAY42390. Protein sequences of TaPHT1s were not published.