

Supplementary Material

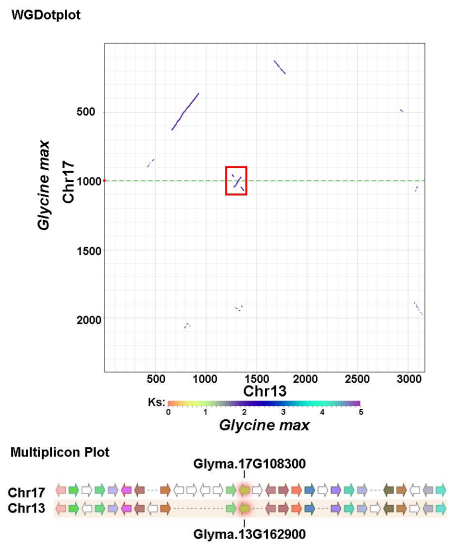
The role of the chloroplast localised phosphate transporter *GmPHT4;10* gene in plant growth, photosynthesis and drought resistance

Liwei Liu^A, Xu He^A, Shuwen Wang^A, Xueting Qin^A, Songhao Che^A, Lei Wu^A, Dongchao Wang^B, Ping Tian^B, Xiaoshuang Wei^B, Zhihai Wu^B, Xue Yang^{A,}, and Meiyang Yang^{A,*}*

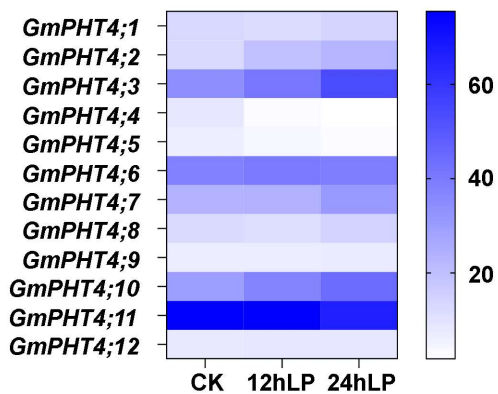
^ACollege of Life Sciences, Jilin Agricultural University, Changchun, Jilin 130118, China.

^BCollege of Agronomy, Jilin Agricultural University, Changchun, Jilin 130118, China.

*Correspondence to: Xue Yang College of Life Sciences, Jilin Agricultural University, Changchun, Jilin 130118, China Email: xueyang840316@163.com Meiyang Yang College of Life Sciences, Jilin Agricultural University, Changchun, Jilin 130118, China Email: jlaumeiyang@163.com



Supplementary Fig. S1 The collinearity analysis of Chromosome 17 with *GmPHT4;10* gene and Chromosome 13 with *GmPHT4;7* gene



Supplementary Fig. S2 Transcriptome expression of soybean PHT4 subfamily members after 12 hours and 24 hours of phosphate deficiency treatment. The transcriptome data can be found online at: <https://www.ncbi.nlm.nih.gov/sra/PRJNA871448>. Accession number : PRJNA871448, NCBI SRA database.

Supplementary Table S1. All primers used in the article

Gene name	Primers	Primer sequences (5'-3')	Applications
<i>GmPHT4;10</i>	<i>GmPHT4;10</i> -F	5'-AACACAGCTAAATATTCTTCCTTG-3'	Gene cloning
	<i>GmPHT4;10</i> -R	5'-CAGAATAATGAATGATTGGAACCTT-3'	Gene cloning
	<i>SGmPHT4;10</i> -F	5'-CGCGTCGACATGGCCAGGCTCACGCT-3'	Subcellular localization
	<i>SGmPHT4;10</i> -R	5'-TGCACTGCAGTCAGTTTAGCTCAGAAAACTTTGAG-3'	Subcellular localization
	<i>QGmPHT4;10</i> -F	5'-ACCACACCCTCAGGCTCAGA-3'	Gene expression patterns
	<i>QGmPHT4;10</i> -R	5'-AGGTCTCATGCTGCTTCTCCAT-3'	Gene expression patterns
	<i>V-GmPHT4;10</i> -F	5'-CGCGGATCCATGGCCAGGCTCACGCTGAGAC-3'	Eukaryotic expression
	<i>V-GmPHT4;10</i> -R	5'-TGCACTGCAGTCAGTTTAGCTCAGAAAACTT-3'	Eukaryotic expression
<i>CYP2</i> (TC224926)	<i>CYP2</i> -F	5'-CGGGACCAGTGTGCTTCTTCA-3'	Gene expression patterns
	<i>CYP2</i> -R	5'-CCCCTCCACTACAAAGGCTCG-3'	Gene expression patterns
<i>P_{4;10}</i>	<i>P_{4;10}</i> -F	5'-TGACATTCATGATAAAACACTTTTT-3'	Gene promoter cloning
	<i>P_{4;10}</i> -R1	5'-GTTATGCGTTGTGCATATTCC-3'	Gene promoter cloning
	<i>P_{4;10}</i> -R2	5'-GGCAGGCTATTTTAACCAGC-3'	Gene promoter cloning
	<i>V-P_{4;10}</i> -F	5'-CCGGAATTCTGACATTCATGATAAAACACTTTTT-3'	Eukaryotic expression
	<i>V-P_{4;10}</i> -R1	5'-GGAAGATCTGTTATGCGTTGTGCATATTCC-3'	Eukaryotic expression
	<i>V-P_{4;10}</i> -R2	5'-GGAAGATCTGGCAGGCTATTTTAACCAGC-3'	Eukaryotic expression

<i>atpht4;5</i>	<i>atpht4;5-LP</i>	5'-CCTCCAAAAACAAAGCCTACC- 3'	Homozygous screening
	<i>atpht4;5-LBb1.3</i>	5'-ATTTTGCCGATTCGGAAC- 3'	Homozygous screening
	<i>atpht4;5-RP</i>	5'-GGTGGTTTTTGGTGATGATTG- 3'	Homozygous screening
	<i>atpht4;5-F</i>	5'-CAAGATTTTTGGCGGAAGAA- 3'	Gene knockout identification
	<i>atpht4;5-R</i>	5'-AGAGCCTCACTGAAATAAGTTGGT- 3'	Gene knockout identification

Note: Restrictive enzyme digestion sites are *SalI*, *PstI*, *BamHI*, *PstI*, *EcoRI*, *BglII* and *BglII*, marked with underline.

Supplementary Table S2. Basic information of soybean PHT4 subfamily members

Gene name	Phytozome gene ID	Protein domain family	Map position	Extron no.	Direction	Protein leghth	MW (KDa)	Theory pI
<i>GmPHT4;1</i>	Glyma.02G224200	MFS superfamily	Chr02:41175313..41180091	9	reverse	516	55.7	10.01
<i>GmPHT4;2</i>	Glyma.03G008200	MFS superfamily	Chr03:793191..799880	11	reverse	593	65.5	9.36
<i>GmPHT4;3</i>	Glyma.07G069600	MFS superfamily	Chr07:6307073..6313498	11	reverse	592	65.2	9.37
<i>GmPHT4;4</i>	Glyma.07G144700	MFS superfamily	Chr07:17231556..17235971	8	reverse	504	55.0	9.88
<i>GmPHT4;5</i>	Glyma.07G274200	MFS superfamily	Chr07:44592193..44600634	1	reverse	429	46.6	9.58
<i>GmPHT4;6</i>	Glyma.11G175800	MFS superfamily	Chr11:20331840..20340143	11	forward	517	57.3	9.41
<i>GmPHT4;7</i>	Glyma.13G162900	MFS superfamily	Chr13:27823310..27833361	15	forward	525	57.4	7.16
<i>GmPHT4;8</i>	Glyma.14G190900	MFS superfamily	Chr14:45569552..45574890	9	reverse	515	55.8	9.93
<i>GmPHT4;9</i>	Glyma.17G000300	MFS superfamily	Chr17:17407..21108	1	forward	429	46.5	9.68
<i>GmPHT4;10</i>	Glyma.17G108300	MFS superfamily	Chr17:8486013..8495685	15	reverse	524	57.5	6.83
<i>GmPHT4;11</i>	Glyma.18G066000	MFS superfamily	Chr18:6041786..6050082	11	reverse	491	53.8	9.09
<i>GmPHT4;12</i>	Glyma.20G002000	MFS superfamily	Chr20:213184..219283	11	forward	597	65.7	9.12

Supplementary Table S3. All sequences involved in phylogenetic tree analysis

Species name	Transporter name	Locus (Phytozome v13)
<i>Glycine max</i>	GmPHT4;1	Glyma.02G224200
	GmPHT4;2	Glyma.03G008200
	GmPHT4;3	Glyma.07G069600
	GmPHT4;4	Glyma.07G144700
	GmPHT4;5	Glyma.07G274200
	GmPHT4;6	Glyma.11G175800
	GmPHT4;7	Glyma.13G162900
	GmPHT4;8	Glyma.14G190900
	GmPHT4;9	Glyma.17G000300
	GmPHT4;10	Glyma.17G108300
	GmPHT4;11	Glyma.18G066000
	GmPHT4;12	Glyma.20G002000
<i>Phaseolus vulgaris</i>	PvPHT4;1	Phvul.002G333800
	PvPHT4;2	Phvul.003G171700
	PvPHT4;3	Phvul.008G061900
	PvPHT4;4	Phvul.008G108000
	PvPHT4;5	Phvul.008G263700
	PvPHT4;6	Phvul.010G099800
<i>Medicago truncatula</i>	MtPHT4;1	Medtr3g463080
	MtPHT4;2	Medtr4g030900
	MtPHT4;3	Medtr4g116030
	MtPHT4;4	Medtr5g069630
	MtPHT4;5	Medtr7g066780
	MtPHT4;6	Medtr8g030600
<i>Arabidopsis thaliana</i>	AtPHT4;1	At2g29650
	AtPHT4;2	At2g38060
	AtPHT4;3	At3g46980
	AtPHT4;4	At4g00370
	AtPHT4;5	At5g20380
	AtPHT4;6	At5g44370
	AtPHT1;1	At5g43350
	AtPHT1;2	At5g43370
	AtPHT1;3	At5g43360
	AtPHT1;4	At2g38940
	AtPHT1;5	At2g32830
	AtPHT1;6	At5g43340
	AtPHT1;7	At3g54700
	AtPHT1;8	At1g20860
	AtPHT1;9	At1g76430
	AtPHT2;1	At3g26570
	AtPHT3;1	At5g14040
	AtPHT3;2	At3g48850

AtPHT3;3	At2g17270
AtPHT5;1	At1g63010
AtPHT5;2	At4g11810
AtPHT5;3	At4g22990
