Full title:

HPS4/SABRE regulates plant responses to phosphate starvation through antagonistic interaction with ethylene signalling

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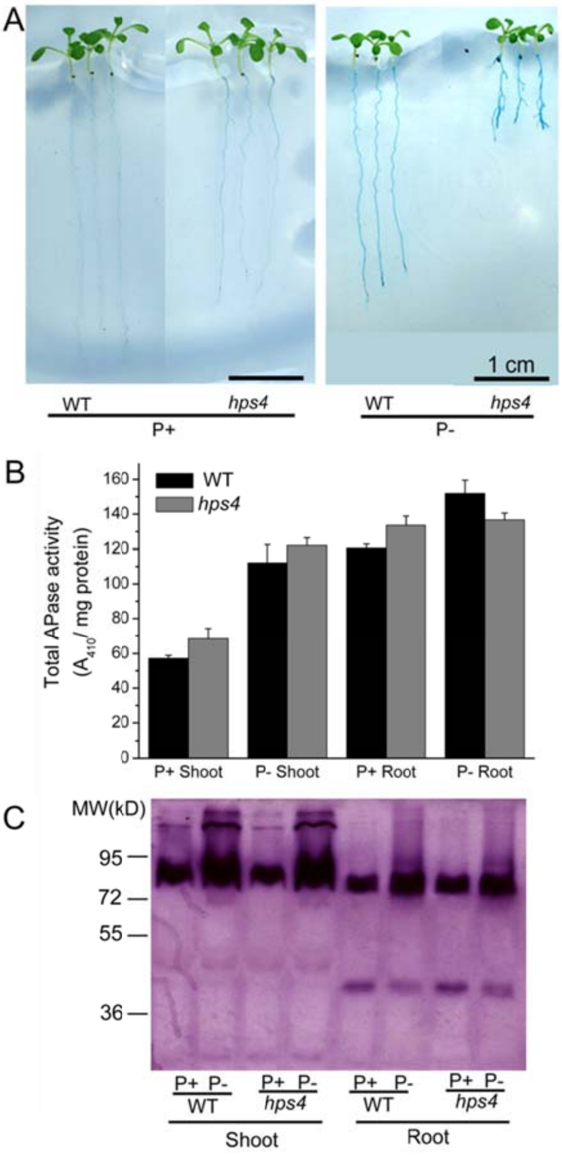
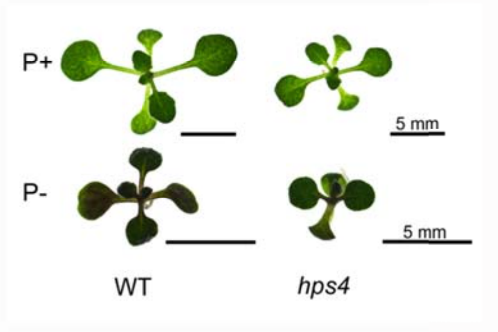
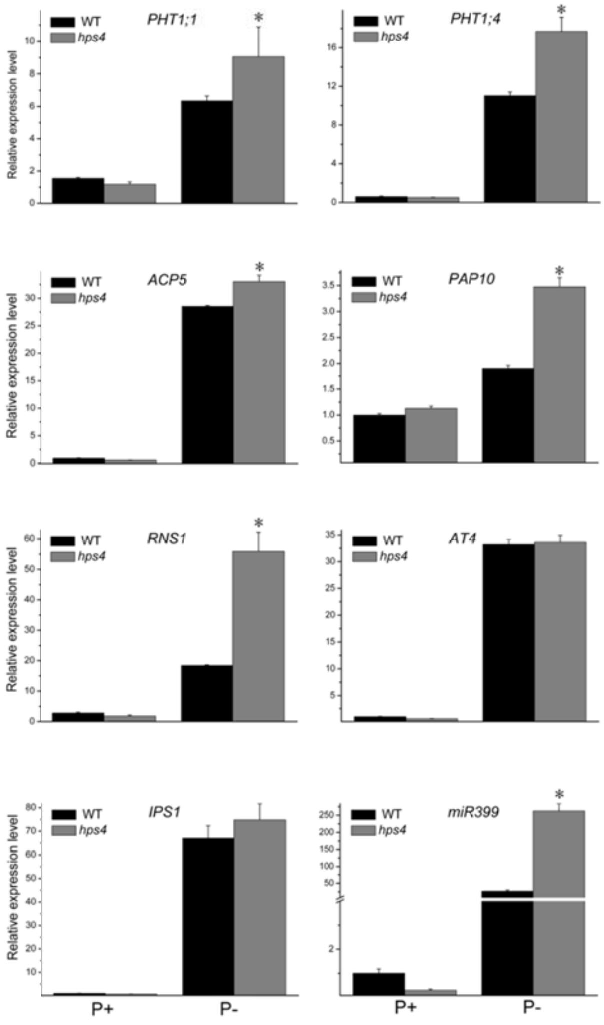
Supplementary Figure S1



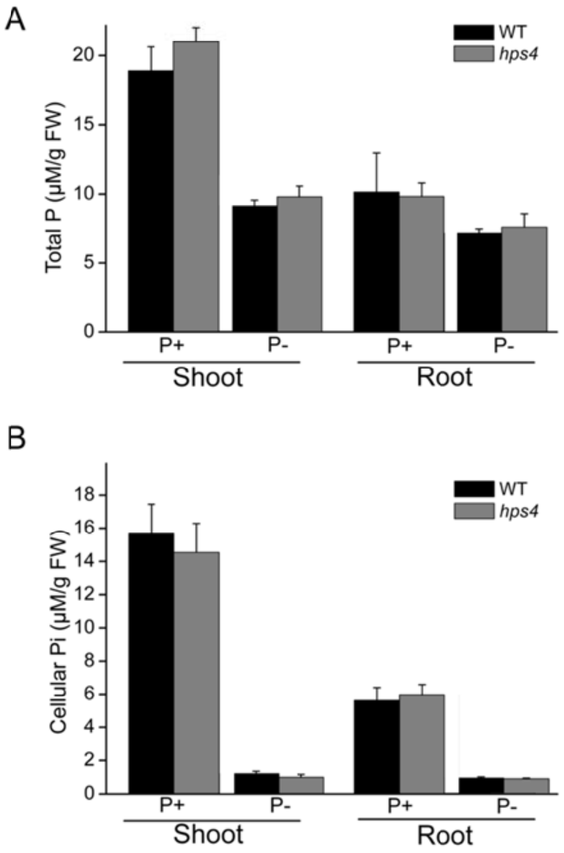
Supplementary Figure S2



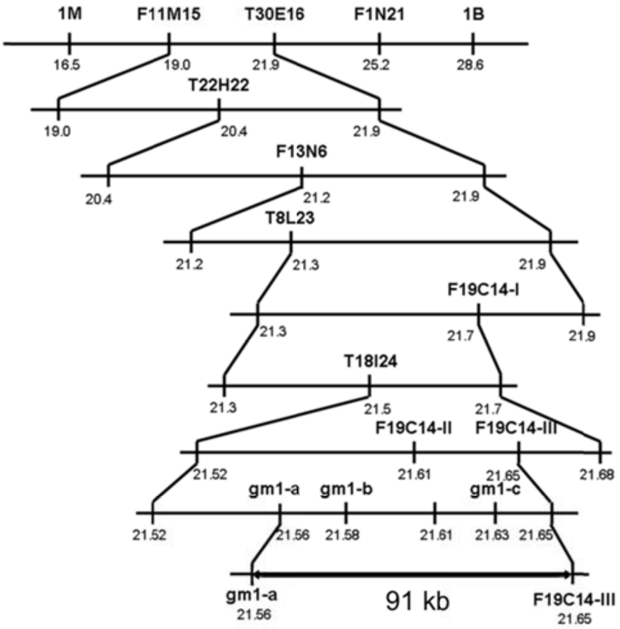
Supplementary Figure S3



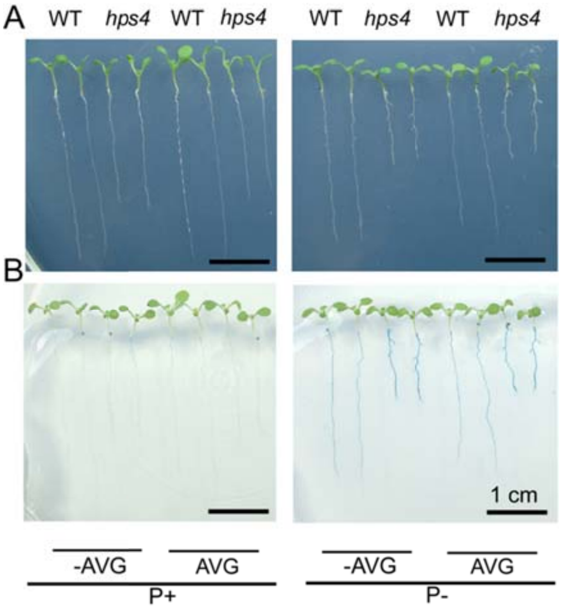
Supplementary Figure S4



Supplementary Figure S5



Supplementary Figure S6



Legends for Supplementary Figures

Supplementary Fig. S1. APase activity in 9-day-old WT and *hps4* seedlings grown on P+ and P- medium. (A) APase activity detected on the root surface by BCIP staining. (B) APase activity determined by quantitative analysis in total shoot and root extracts . (C) APase activity determined by in-gel enzyme assays.   MW: Molecular weight.

Supplementary Fig. S2. Anthocyanin contents in 14-day-old WT and *hps4* seedlings grown on P+ and P- medium. *Arabidopsis* seeds were sown directly on P+ and P- medium, and the seedlings were photographed at 14 DAG.

Supplementary Fig. S3. Analysis of PSI gene expression in 9-day-old WT and *hps4* seedlings. The 9-day-old seedlings of the WT and *hps4* grown on P+ or P- medium were used for quantitative real-time PCR analysis. The names of the genes examined are indicated at the top of each panel. Values are the means and SD of three biological replicates and represent fold-changes normalized to transcript levels of the WT on P+ medium. Means with asterisks are significantly different from the WT ($p<0.05$, two sample *t*-test).

Supplementary Fig. S4. Total phosphorus and cellular Pi contents in 9-day-old WT and *hps4* seedlings grown on P+ and P- medium. The experiments were repeated three times with similar results. Values represent the means and SD of three replicates. Means with asterisks are significantly different from the WT ($p<0.05$, two sample *t*-

test).

Supplementary Fig. S5. The strategy for fine mapping of the *HPS4* gene. The molecular markers used in the fine mapping are shown along with their chromosomal positions. The numbers below each horizontal line are the AGI coordinate on the chromosome. Distance unit: Mb.

Supplementary Fig. S6. The effect of AVG treatment on primary root growth and APase activity of *hps4* and the WT. The seeds of the WT and *hps4* were directly sown on P+ medium. At 3 DAG, the seedlings were transferred to P+ and P- medium with or without addition of 0.2 µM AVG. The seedling samples were photographed after growing another 4 days. (A) Morphology of the seedlings of the WT and *hps4* grown on Pi-sufficient (P+) and Pi-deficient (P-) medium. (B) Detection of APase activity by BCIP staining on the root surfaces of WT and *hps4* seedlings shown in (A).

Supplementary Table 1. Sequence of Primers used for map-based cloning

BAC name	Primer name	Primer sequence (5’ to 3’)
F11M15	F11M15-F	GATTTGATTCGAGTCCGTAT
	F11M15-R	TGTAGGGGAGAATGGAACC
T22H22	T22H22-F	CAGAAAAAGAGATCAAGGGA
	T22H22-R	ACCAAAAGAAGAGAGGGAG
F13N6	F13N6-F	TCGTTGGACAGTCATAGGC
	F13N6-R	CATCTGTTTCATCCGTCAAG
T8L23	T8L23-F	GAAGAGACGGACAAGCATT
	T8L23-R	GGGGTTGGTTTGTTGTTT
F19C14	F19C14-F	CCGTGGAGTGGTTGTGTC
	F19C14-R	ATCCCAAGCCGAAACTAT
T18I24	T18I24-F	TATGGAGTTTTTTTGGCG
	T18I24-R	ATTATGCCATTGCTTGACA
F19C14	F19C14-II-F	AACTGGATGGATTCGTGAT
	F19C14-II-R	GCTACTTCGGTCAATCTTTT
F19C14	F19C14-III-F	GGGGACAAAAACTTACTGG
	F19C14-III-R	CAAACAAGTGCAGAAATGG
	gm1-a-F	AAAACCGCCTAAGCATCT
	gm1-a-R	TCTCCAAATCCCAATATCTC
	gm1-b-F	ATGATGTGCCAATAAACCG
	gm1-b-R	TCTTCAAATAATGGCGACTC
	gm1-c-F	CGCCAATTACACACATCC
	gm1-c-R	GTCGGTATCAAGGGCTAAC

Supplementary Table 2. Sequence of Primers used for quantitative real-time PCR

Locus	Gene	Orientation	Primers sequence
AT3G18780	*ACT2*	F	GACCTTGCTGGACGTGACCTTAC
		R	GTAGTCAACAGCAACAAAGGAGAGC
AT5G03545	*At4*	F	TGGCCCCAAACACAAGAG
		R	CGAACATTCACAATCATAATCTCC
AT3G09922	*IPS1*	F	AGACTGCAGAAGGCTGATTCAGA
		R	TTGCCCAATTTCTAGAGGGAGA
AT5G43350	*PHT1;1*	F	TGATGATCTTGTGCTCTGTCG
		R	ATGACACCCTTGGCTTCGT
AT2G38940	*PHT1;4*	F	CGAAGCTCCTCGGTCGTAT
		R	GGAGAGTCCCAGGCTTTTGT
AT2G02990	*RNS1*	F	TTGTTATCCAAATTCAGGCAAA
		R	AGTTAGGCCAAAGACCATGAAT
AT2G34202	*miR399*	F	AATACTCCTATGGCAGATCGCATTGG
		R	TCCTTTGGCAGAGAAGCATTTTACTTG
AT3G17790	*ACP5*	F	CTTAAGTCCTATTGCAGGCTAGGT
		R	TTGCTAAAAATGATAGGGATGCT
AT2G16430	*PAP10*	F	ATCCTGTTGATGATTCTCCTTCTTG
		R	ATTCATTTATTTGGACGTGACCTTAC
AT1G25220	*ASB1*	F	TTCTCAGATGTCTAGCGTTGGT
		R	TTCTCCTTTGCCACGATCTC
AT4G39950	*CYP79B2*	F	TGACGGATCCCAACAAAAAG
		R	ATGATCGGCCATCCTGTG
AT2G22330	*CYP79B3*	F	CCGTTGGCTACACGACAATA
		R	TTGTAGAGCCAAGCGGTCA
AT1G21430	*YUC11*	F	TGCTCGGAACATTGCTAGAG
		R	TGGAAAGCTTGTTCTTGCTG
AT1G04180	*YUC9*	F	GGGCTATGGAGGGTTAGAACA
		R	ACCAACCACCGGCAAATA
AT4G28720	*YUC8*	F	CAAAACGTTCCTTTCGTTGTT
		R	CGTTTTTGCCATAGAGAAGCA

Locus	Gene	Orientation	Primers sequence
AT2G33230	*YUC7*	F	GGTCGAGTTCTGCAGATTGAT
		R	CCAATCTCACCCAAGTCGTT
AT5G43890	*YUC5*	F	CAGCCAATCCTTTCCTTGTG
		R	TGGAGGTCAGCTTGGATCTT
AT5G11320	*YUC3*	F	CCATACCGGAGTTTCCACAT
		R	TCCCTAAAGATTTCTGTGAGCTTC
AT4G13260	*YUC2*	F	TCCCTAAAGATTTCTGTGAGCTTC
		R	GGGTAAGTAGGGTAGCTTGAAGG