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Natural variation of root hydraulics in *Arabidopsis* grown in normal and salt-stressed conditions.

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► **To cite this version:**

Moira Sutka, Guowei Li, Julie Boudet, Yann Boursiac, Patrick Doumas, et al.. Natural variation of root hydraulics in *Arabidopsis* grown in normal and salt-stressed conditions.. *Plant Physiology*, 2011, 155 (3), pp.1264-76. 10.1104/pp.110.163113 . hal-00576512

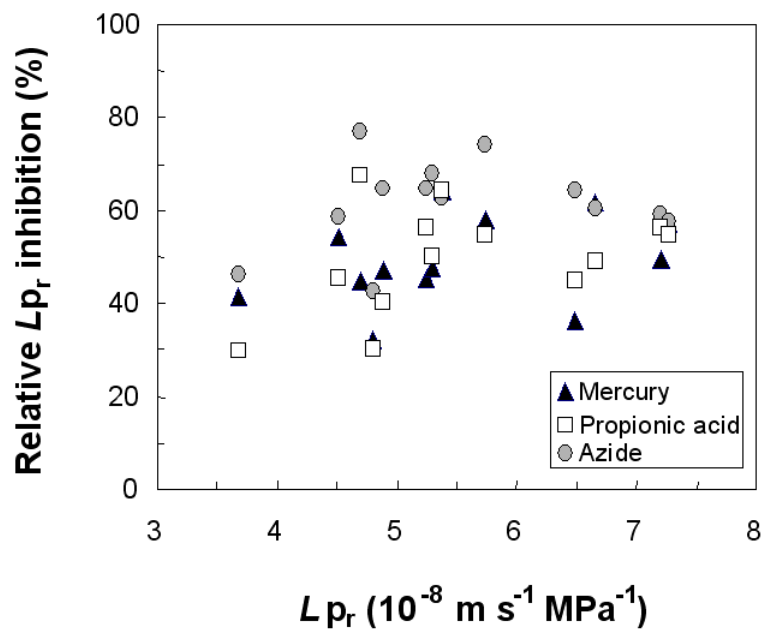
HAL Id: hal-00576512

<https://hal.science/hal-00576512v1>

Submitted on 29 May 2020

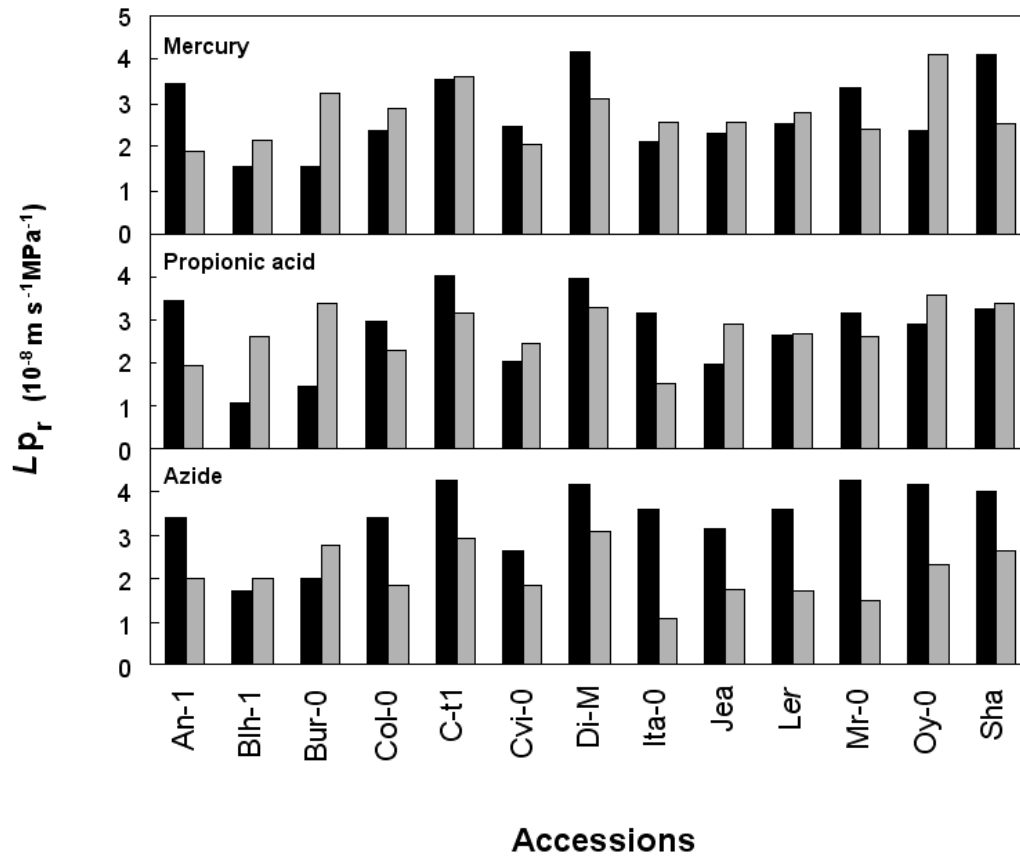
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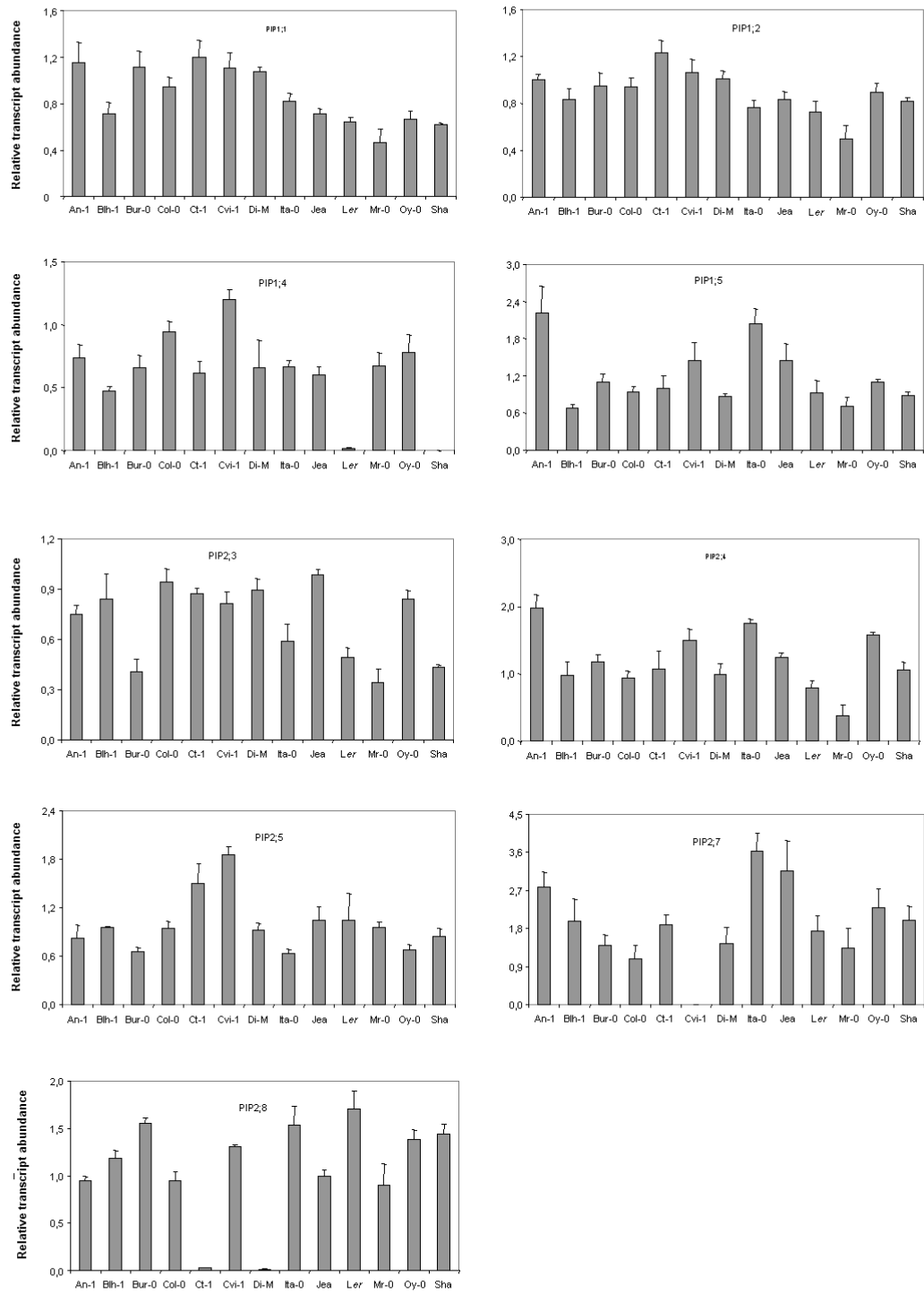
Supplemental Figure 1. Relationship among the 13 accessions between L_{p_r} and its relative inhibition by mercury (▲), propionic acid (□), and azide (●).

The graph shows a plot of relative inhibition data (Figure 2) against mean L_{p_r} (Figure 1).



Supplemental Figure 2. Absolute inhibition (black bars) and residual values (grey bars) of Lp_r after exposure of roots to mercury, propionic acid or azide inhibiting treatments (see text and Figure 2 for experimental details).

Absolute values were recalculated from mean Lp_r (Figure 1) and relative inhibition (Figure 2) data.



Supplemental Figure 3. Relative transcript abundance of *PIPs* in 13 accessions.

Data complimentary to Figure 4, showing the complement of expression data of the 13 *PIP* genes. Same legend as in Figure 4. $PIP1;1 : \sigma_{RE} = 0.28$, $PIP1;2 : \sigma_{RE} = 0.20$, $PIP1;4 : \sigma_{RE} = 0.27$, $PIP1;5 : \sigma_{RE} = 0.41$, $PIP2;3 : \sigma_{RE} = 0.32$, $PIP2;4 : \sigma_{RE} = 0.36$, $PIP2;5 : \sigma_{RE} = 0.35$, $PIP2;7 : \sigma_{RE} = 0.50$, $PIP2;8 : \sigma_{RE} = 0.50$.

Supplemental Table 1. *Correlation analysis of PIP transcript abundance vs. Lp_r*

The table shows the Pearson correlation coefficient (R_{Pearson}) derived from a linear regression between Lp_r values and relative transcript abundance of the indicated genes. The corresponding Spearman's rank correlation coefficients (R_{Spearman}) are also indicated. Significant correlations ($P < 0.05$) are indicated in bold red.

Gene	R_{Pearson}	R_{Spearman}
–		
<i>PIP1;1</i>	0.105	-0.066
<i>PIP1;2</i>	0.267	0.148
<i>PIP1;3</i>	-0.095	0.060
<i>PIP1;4</i>	-0.191	-0.165
<i>PIP1;5</i>	-0.245	-0.236
<i>PIP2;1</i>	0.016	0.137
<i>PIP2;2</i>	0.277	0.286
<i>PIP2;3</i>	0.037	0.088
<i>PIP2;4</i>	-0.154	-0.165
<i>PIP2;5</i>	-0.001	-0.0165
<i>PIP2;6</i>	-0.435	-0.445
<i>PIP2;7</i>	-0.035	0.027
<i>PIP2;8</i>	-0.589	-0.473
<i>PIP2;6 + PIP2;8</i>	-0.601	-0.637

Supplemental Table 2. *Water relation and morphological parameters of root cortical cells under control and salt stress conditions.*

Accession Condition ^a		P_e ^b (MPa)	$T_{1/2}$ ^c (s)	ϵ ^d (MPa)	$L_{p_{cell}}$ ^e ($10^{-6} \text{ m s}^{-1} \text{ MPa}^{-1}$)	n ^f	cell length ^g (μm)	cell diameter ^g (μm)
Blh-1	control	0.40 ± 0.01	0.79 ± 0.06	10.18 ± 0.96	1.02 ± 0.12	20	240.7 ± 8.1	42.1 ± 0.9
	salt	0.20 ± 0.02	2.00 ± 0.25	6.24 ± 0.52	0.71 ± 0.09	21	(45)	(45)
Col-0	control	0.32 ± 0.01	1.07 ± 0.07	5.48 ± 0.05	1.14 ± 0.08	22	155.0 ± 4.5	38.7 ± 0.8
	salt	0.16 ± 0.01	2.42 ± 0.18	2.70 ± 0.17	0.90 ± 0.09	20	(52)	(52)
Ct-1	control	0.53 ± 0.15	1.09 ± 0.09	6.55 ± 0.54	1.05 ± 0.18	17	170.8 ± 5.7	44.1 ± 1.0
	salt	0.19 ± 0.02	1.10 ± 0.15	4.14 ± 0.39	1.43 ± 0.19	14	(38)	(38)
Di-M	control	0.36 ± 0.01	1.02 ± 0.07	7.72 ± 0.058	0.97 ± 0.07	27	194.4 ± 7.2	42.6 ± 0.5
	salt	0.22 ± 0.01	1.98 ± 0.18	5.38 ± 0.26	0.71 ± 0.06	21	(36)	(36)
Mr-0	control	0.38 ± 0.02	0.98 ± 0.09	6.09 ± 0.70	1.43 ± 0.24	16	182.8 ± 5.4	43.6 ± 0.9
	salt	0.16 ± 0.01	1.09 ± 0.13	4.15 ± 0.43	1.66 ± 0.024	17	(54)	(54)

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^aControl: plants were maintained in a standard hydroponic culture medium and the excised root segment to be punctured was transferred into a standard cell pressure probe solution for 10-40 min prior to measurement. Salt: roots of intact plants were bathed for 4 h in a hydroponic culture medium complemented with 100 NaCl and the excised root segment was bathed in a cell pressure probe solution complemented with 100 mM NaCl for 10-40 min prior to measurement.

^bMean stationary turgor pressure \pm SE.

^cHalf-time of water exchange \pm SE.

^dMean volumetric elastic modulus \pm SE.

^eCell hydraulic conductivity \pm SE.

^fNumber of cells used for measurements of water relation parameters in the indicated conditions.

^gMean morphological parameters \pm SE measured on the indicated number of cells (in bracket) in roots bathing in a standard hydroponic culture medium. These parameter values were used for calculation of $L_{p_{cell}}$ in both standard and salt stress conditions.

Supplemental Table 3 Sequences of TIP-specific primer pairs used for real time RT-PCR amplification.

Gene	Primer	Amplicon size (bp)
<i>TIP1;1</i>	Forward*: 5'- ⁸²⁷ CTCCCAACCACAGACTACTGAA ⁸⁴⁸ -3'	136
	Reverse: 5'- ⁹⁶² GCACGATCATAAACCCCTTG ⁹⁴³ -3'	
<i>TIP1;2</i>	Forward: 5'- ⁹⁹⁴ GCATCGTAATGGGTTTCTGG ¹⁰¹³ -3'	128
	Reverse: 5'- ¹¹²¹ TACAATTGCACAAAAGCCTTCC ¹¹⁰⁰ -3'	
<i>TIP2;2</i>	Forward: 5'- ⁹⁰⁶ AGCTCCCACCACAGAAAGCTA ⁹²⁶ -3'	103
	Reverse: 5'- ¹⁰⁰⁸ TTTGGAAGAAACGAGGACCA ⁹⁸⁹ -3'	
<i>TIP2;3</i>	Forward: 5'- ⁹⁴² GTGAGATCCGAGTGTAATTGACTG ⁹⁶⁵ -3'	119
	Reverse: 5'- ¹⁰⁶⁰ TTTTCTTTTCTCTACATACAATCTTGC ¹⁰³⁴ -3'	

All primers were designed within or close to the 3'untranslated transcribed region. The numberings refer to positions from the initiating ATG codon in the genomic sequences.