Supporting Information

Local and systemic metabolic adjustments to drought in maize: Hydraulic redistribution in a split-root system

Lena Maria Werner, Roman Paul Hartwig, Isabelle Engel, Bastian Leander Franzisky, Stefanie Wienkoop, Martin Brenner, Julian Preiner, Dagmar Repper, Jens Hartung, Christian Zörb, Monika Andrea Wimmer

10.002/jpln.202200279

TABLE S1. Detected compounds in root and rhizosphere solution after 9 days of drought. Shown are the retransformed relative adjusted means. Means with at least one identical letter are non-significant from each other ($p < 0.05$; one-way ANOVA; Fisher's LSD) between the control (well-watered) and the treatments local drought (watered, droughted) and full drought.

	well-watered	Local drought		full drought	well-watered	Local drought		full drought
Compound		**watered**	**drought**			**watered**	**drought**	
Σ amines	0.54	0.51	1.02	0.96	a	a	a	a
Putrescine	0.04	0.07	0.17	0.17	b	ab	a	a
Spermidine	0.47	0.39	0.76	0.71	a	a	a	a
Σ amino acids	5.72	9.75	11.06	9.76	a	a	a	a
Aspargine	0.07	0.11	0.09	0.08	a	a	a	a
Aspartic acid	0.02	0.03	0.04	0.03	a	a	a	a
Glutamic acid	0.25	0.45	0.24	0.15	ab	a	ab	b
Glutamine	0.02	0.03	0.04	0.02	a	a	a	a
Glycine	2.98	1.46	5.57	3.32	a	a	a	a
Isoleucine	0.05	0.03	0.05	0.06	a	a	a	a
Leucine	0.39	1.35	0.55	0.87	a	a	a	a
Lysine	0.20	0.18	0.19	0.16	a	a	a	a
Methionine	0.04	0.15	0.06	0.06	a	a	a	a
Ornithine	0.14	0.19	0.14	0.12	a	a	a	a
Phenylalanine	0.05	0.14	0.03	0.04	ab	a	b	b
Proline	0.33	0.61	1.06	1.79	b	ab	ab	a
Serine	0.19	0.08	0.21	0.20	a	a	a	a
Threonine	0.10	0.40	0.12	0.08	b	a	ab	b
Tryptophan	0.04	0.02	0.01	0.01	a	ab	b	ab
Tyrosine	0.02	0.03	0.01	0.01	a	a	a	a
Valine	0.00	0.00	0.00	0.00	a	a	a	a
Σ organic acids	18.16	21.96	18.15	14.71	a	a	a	a
2-Oxoglutaric acid	0.28	0.65	0.14	0.36	ab	a	b	ab
Citric acid	0.08	0.11	0.10	0.07	a	a	a	a
Fumaric acid	0.07	0.05	0.09	0.12	a	a	a	a

Gluconic acid	0.08	0.08	0.20	0.12	a	a	a	a
Lactic acid	13.60	18.56	15.38	9.43	a	a	a	a
Malic acid	0.11	0.08	0.25	0.04	a	ab	a	b
Oxalacetate	0.00	0.03	0.01	0.00	ab	a	ab	b
Pyruvic acid	0.07	0.13	0.17	0.10	a	a	a	a
Succinic acid	0.43	0.56	0.55	0.59	a	a	a	a
Threonic acid	0.10	0.11	0.14	0.13	a	a	a	a
Σ sugars	72.70	54.86	65.41	70.19	a	a	a	a
Fructose	20.98	13.93	14.91	9.58	a	a	a	a
Glucose	15.33	6.53	10.24	7.67	a	ab	ab	b
Maltose	5.85	5.10	7.86	14.43	b	b	ab	a
Melibiose	9.95	6.40	10.28	9.58	a	a	a	a
Raffinose	0.02	0.08	0.03	0.02	a	a	a	a
Sucrose	8.94	5.34	7.12	8.71	a	a	a	a
Trehalose	3.70	3.30	5.00	9.34	b	b	ab	a
Σ sugar alcohol	1.49	1.69	1.73	1.40	a	a	a	a
Galactinol	0.53	0.45	0.55	0.62	a	a	a	a
myo-inositol	0.72	0.91	0.86	0.66	a	a	a	a
Threitol	0.19	0.21	0.24	0.20	a	a	a	a

TABLE S2. Primers used for qPCR gene expression analysis in roots. Gene expression was performed by qPCR (CFX96 C1000 touch, BioRad) using the iTaq Universal SYBR Green Supermix.

Primer	Function	Forward	Reverse	According to
GADPH	HKG	TTGTTTCCCTTCCTGCTACC	AAACTGCAACCTCACCACAAG	(2)
Actine	HKG	GCCCTGCTGTATGAAATGGA	AAAGGAACCAGCTAAAAGCAAAC	(2)
PIP1.2	GOI	CTATTTTATGCGTTGGGATGT	ACTGAAACCAAGAAAACCCTGA	(1)
PIP2.1	GOI	CGGGTCGCCTTTTTTTTG	CCCTTGAGAGTCACGACATGA	(1)
PIP2.5	GOI	TGTCGTCGTTGGTTGCCT	CACAACAATCACACTAGCTTGGAA	(1)

TABLE S3. Expression of PIP1.2, PIP2.1 and PIP2.5 in roots after 10 days of drought. Each biological replicate was measured in triplicate. Gene expression was calculated according to the $2^{-\Delta\Delta CT}$ (3). Values represent adjusted means and standard errors (n=6). Means with at least one identical letter are non-significant from each other ($p < 0.05$; Fisher's LSD) between the control (well-watered) and the treatments local drought (watered, droughted) and full drought.

Treatment	Adjusted mean	Standard error	
PIP1.2			
WW	1.00		n.s.*
$LD_{watered}$	1.19	0.48	
$LD_{droughted}$	0.80	0.32	
FD	2.10	0.75	
PIP2.1			
WW	1.00		B
$LD_{watered}$	0.92	0.17	AB
$LD_{droughted}$	0.62	0.11	A
FD	0.69	0.10	A
PIP2.5			
WW	1.00		C
$LD_{watered}$	0.48	0.12	AB
$LD_{droughted}$	0.42	0.10	A
FD	0.69	0.14	BC

*Global F test indicated no significant differences between the treatments and the controll with *p*-value > 0.05

(1) Hachez, C., Moshelion M., Zelazny E., Cavez D., Chaumont F. (2006) Localization and Quantification of Plasma Membrane Aquaporin Expression in Maize Primary Root: A Clue to Understanding their Role as Cellular Plumbers. *Plant Mol Biol* **62**, 305–323 doi:10.1007/s11103-006-9022-1

(2) Heinen,R.B., Bienert, G.P., Cohen, D., Chevalier A. S., Uehlein N., Hachez C., Kaldenhoff R., Le Thiec D., Chaumont F. (2014) Expression and characterization of plasma membrane aquaporins in stomatal complexes of *Zea mays* . *Plant Mol Biol* **86**, 335–350 doi:10.1007/s11103-014-0232-7

(3) Schmittgen T.D. and Livak, K.J. (2008) Analyzing real-time PCR data by the comparative CT method. Nature Protocols 3, 1101– 1108 doi:10.1038/nprot.2008.73