

pH of leaf apoplast is relevant for transcription of ABA-synthesizing key gene *vp14* and for stomatal aperture in *Zea mays* L.

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Supplementary data

Supplementary Table S1. Long-term effect of one-time infiltration on rate of photosynthesis and transpiration. 'Control', infiltration of 0.4 ml of an aqueous 25 µM OG solution; 'MES pH_{apo} 4.0 (osmotic control)', infiltration of 0.4 mL of a mixture of 7.5 mM MES at pH 4.7 and 25 µM OG; 'MES pH_{apo} 6.5', infiltration of 0.4 mL of a mixture of 5 mM MES at pH 6.5 and 25 µM OG; 'MOPSO pH_{apo} 6.5', infiltration of 0.4 mL of a mixture of 7.5 mM MOPSO at pH 6.5 and 25 µM OG. Mean ± SD of six independent (n = 6) biological replications. Tukey-HSD test revealed no statistical significance ($P \leq 0.05$) between values from all groups, as indicated by ns.

Treatment (hours after infiltration)	Transpiration rate (mmol H ₂ O m ⁻² s ⁻¹)		Photosynthetic rate (µmol CO ₂ m ⁻² s ⁻¹)
	0 h	24h	
Control	5.3±1.2 ns		9.82±0.7 ns
		6.0±1.3 ns	11.42±0.5 ns
		6.2±1.3 ns	12.25±0.6 ns
		5.5±1.5 ns	10.36±0.4 ns
MES pH _{apo} 4.0 (osmotic control)	5.2±1.4 ns		10.20±0.3 ns
		5.9±1.2 ns	11.14±0.8 ns
		6.0±1.3 ns	11.91±0.2 ns
		6.3±1.4 ns	12.60±0.4 ns
MES pH _{apo} 6.5	5.1±1.6 ns		9.51±0.9 ns
		5.9±1.0 ns	11.37±0.6 ns
		6.1±1.4 ns	12.08±0.7 ns
		6.0±1.5 ns	11.54±0.6 ns
MOPSO pH _{apo} 6.5	5.4±1.2 ns		10.23±0.6 ns
		5.9±1.4 ns	11.65±0.5 ns
		6.0±1.2 ns	11.79±0.5 ns
		6.2±1.2 ns	12.35±0.6 ns

Supplementary Table S2. Specificity of the *Zmvp14* primer pair was demonstrated by sequencing the real-time quantitative RT-PCR product.
 Column 1, primer pair. Column 2, DNA sequencing result. Columns 3-7, sequence was alignment against NCBI's reference mRNA sequences (refseq_rna; blastn), search was limited to *Zea mays* L. (taxid:4577). Identical sequencing results were found in our study were identical primer pair was used previous (identical sequencing result shown in the previous work by (Geilfus *et al.*, 2018).

<i>Zea mays viviparous 14 (Zmvp14) primer pair</i>	Sequencing summary of real-time quantitative RT-PCR products (N, any base; primer sequences highlighted grey)	Significant alignments of sequences (NCBI blastn on <i>Zea mays</i> L. [taxid:4577]; database: refseq_rna)				
		Genbank sequence ID	Description	Max score/ Total score	Query coverage (%)/ Ident (%)	E value
f 5'-3' TTCTCGGAGGAGGAACAG AGGA r 5'-3' CCAACTGTAACTCTGGTG TGC	TTTCTCGGAGGAGGAACAGAG GAGCCAGGCCATGGATCAGGGG AGAAGTCACCAGAGGGAGCCC AGATCAGTTCCCCGGGGTCTT CNCTGTCNCCNNNCACNGCA CACNAGAGTTACAGTTGGA	NM_001112432.3 (No other Blast hits found)	<i>Zea mays</i> <i>viviparous14</i> (<i>vp14</i>), mRNA	187/187	99/ 94	4e-47

Supplementary Table S3. pH_{apo} transient reduces transpiration rate, stomatal conductance and photosynthetic rate. 'Control', infiltration of 0.4 ml of an aqueous 25 µM OG solution; 'MES pH_{apo} 4.0 (osmotic control)', infiltration of 0.4 mL of a mixture of 7.5 mM MES at pH 4.7 and 25 µM OG; 'MES pH_{apo} 6.5', infiltration of 0.4 mL of a mixture of 5 mM MES at pH 6.5 and 25 µM OG; 'MOPSO pH_{apo} 6.5', infiltration of 0.4 mL of a mixture of 7.5 mM MOPSO at pH 6.5 and 25 µM OG. Mean ± SD of six independent (n = 6) biological replications. Statistical significance between values from all groups ($P \leq 0.05$) as calculated by the Tukey-HSD test is indicated by small letters for transpiration rate and capital letters for stomatal aperture.

		Treatment		Transpiration rate	Stomatal conductance	Photosynthetic rate
Name	Specification	x-axis in Fig. 1	Description of time point 'Minute' on	(mmol H ₂ O m ⁻² s ⁻¹)	(mmol H ₂ O m ⁻² s ⁻¹)	(µmol CO ₂ m ⁻² s ⁻¹)
Control	Start, before infiltration	10	No alkalinisation, no ABA accumulation	5.3±1.4 ^a	252±42 ^a	10.3±0.8 ^e
	60 min after infiltration	100	No alkalinisation, no ABA accumulation	5.5±1.4 ^a	269±45 ^a	10.5±0.5 ^e
	After re-acidification	200	No alkalinisation, no ABA accumulation	5.4±1.4 ^a	262±40 ^a	10.5±0.4 ^e
	2 h after re-acidification	320	No alkalinisation, no ABA accumulation	5.8±1.1 ^a	283±45 ^a	11.2±0.4 ^e
	4 h after re-acidification	440	No alkalinisation, no ABA accumulation	6.1±0.9 ^a	294±48 ^a	12.1±0.2 ^p
MES pH _{apo} 4.0 (osmotic control)	Start, before infiltration	10	No alkalinisation, no ABA accumulation	5.0±1.3 ^a	244±41 ^a	10.1±0.5 ^e
	60 min after infiltration	100	No alkalinisation, no ABA accumulation	5.4±1.5 ^a	259±39 ^a	10.4±0.6 ^e
	After re-acidification	200	No alkalinisation, a few ABA accumulated	5.4±1.2 ^a	264±43 ^a	10.2±0.7 ^e
	2 h after re-acidification	320	No alkalinisation, no ABA accumulation	5.4±1.3 ^a	267±46 ^a	10.5±0.3 ^e
	4 h after re-acidification	440	No alkalinisation, no ABA accumulation	4.7±1.1 ^a	230±38 ^a	8.3±0.6 ^b
MES pH _{apo} 6.5	Start, before infiltration	10	Before alkalinisation, no ABA accumulation	5.0±1.3 ^a	242±41 ^a	9.9±0.7 ^e
	60 min after infiltration	100	Apoplast alkalinised, no ABA accumulation	5.4±1.3 ^a	256±44 ^a	10.4±0.3 ^e
	After re-acidification	200	Apoplast re-acidified, ABA accumulated	4.7±1.6 ^a	227±39 ^a	8.5±0.3 ^b
	2 h after re-acidification	320	Apoplast re-acidified, ABA accumulated	2.3±0.4 ^b	128±25 ^b	5.2±0.3 ^y
	4 h after re-acidification	440	Apoplast re-acidified, ABA was not measured	1.8±0.3 ^{bc}	97±26 ^{by}	3.1±0.2 ^t
MOPSO pH _{apo} 6.5	Start, before infiltration	10	Before alkalinisation, no ABA accumulation	5.5±1.5 ^a	267±43 ^a	10.6±0.4 ^e
	60 min after infiltration	100	Apoplast alkalinised, no ABA accumulation	5.4±1.2 ^a	258±37 ^a	10.5±0.4 ^e
	After re-acidification	200	Apoplast re-acidified, ABA accumulated	4.8±1.5 ^a	235±40 ^a	8.4±0.3 ^b
	2 h after re-acidification	320	Apoplast re-acidified, ABA accumulated	1.7±0.1 ^c	85±14 ^y	2.9±0.1 ^t
	4 h after re-acidification	440	Apoplast re-acidified, ABA was not measured	1.9±0.3 ^{bc}	102±26 ^{by}	3.1±0.1 ^t

Supplementary Fig. S1. Specificity of the *vp14* primer pair. Real-time qRT-PCR products were separated on agarose gels. Only one single DNA band appeared. *In-silico* analysis using the Primer-BLAST software predicted a band size of ~ 117 bp. Gels contain 2% agarose, Tris-borate-EDTA, 5 µl SYBR Safe pro 100 ml Gel (SYBR® Safe DNA Gel Stain, Invitrogen).

