

The rootstock genotypes determine drought tolerance by regulating aquaporin expression and phytohormone balance

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SUPPLEMENTARY MATERIAL:

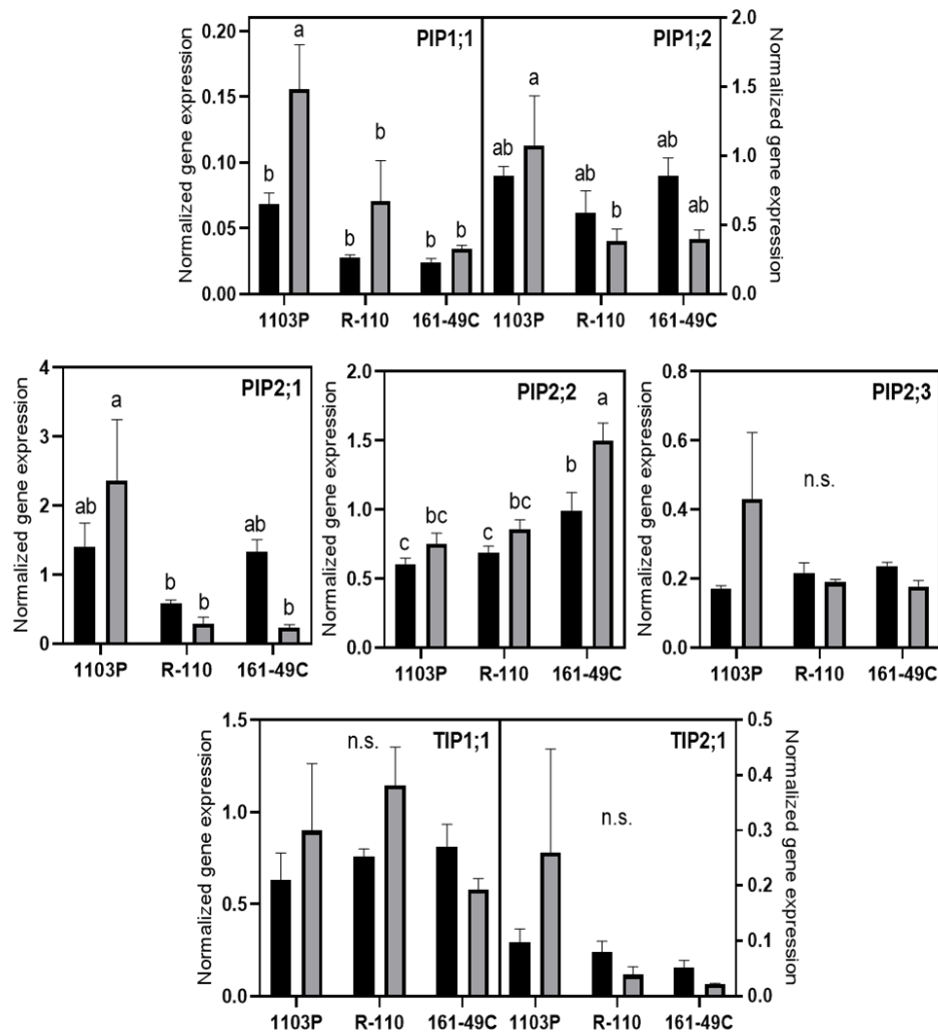


Figure S1: $2^{-\Delta\Delta Ct}$ of studied aquaporin genes for each rootstock under well water (WW) (black) and water stress (WS) (grey). Different letters indicate statistically significant differences by one-way ANOVA with Duncan's multiple comparison test ($p < 0.05$) for each aquaporin gen studied.

Table S1. Mean values of several vegetative growth components of the different rootstocks: clusters, pruning weight, spurs per vine, shoots per vine, 100 berries weight, total clusters weight and cluster weight.

		Clusters	Pruning weight (kg ha ⁻¹)	Spur (spur vine ⁻¹)	Shoots (shoots vine ⁻¹)	100 berries weight (g)	Total clusters weight (kg vine ⁻¹)	Cluster weight (g cluster ⁻¹)
1103P	Irrigation	17.40 ± 7.02	2592	5,80 ± 0,84	13.00 ± 1.73	220.30	3.65	209.57
	Drought	15.67 ± 5.24	1173	7.00 ± 1.58	14.20 ± 4.38	185.90	3.57	227.66
R-110	Irrigation	19.33 ± 1.51	2089	6.00 ± 0.71	13.80 ± 2.17	226.40	3.70	191.38
	Drought	16.83 ± 3.60	821	5.60 ± 1.14	11.80 ± 1.79	191.80	2.65	157.43
161-49C	Irrigation	16.50 ± 5.65	1790	6.40 ± 0.89	14.00 ± 2.12	239.70	3.48	211.11
	Drought	16.17 ± 5.15	562	5.80 ± 1.30	12.60 ± 3.21	161.30	2.18	135.05
Significance	TR	n.s.	-	n.s.	n.s.	-	-	-
	RT	n.s.	-	n.s.	n.s.	-	-	-
	TR x RT	n.s.	-	n.s.	n.s.	-	-	-

Values are means ± standard error of six vines per treatment. Significant differences for treatment (TR), rootstock (RT) and TR × RT were analyzed by two-way ANOVA (ns, not significant; *, $p \leq 0.05$; **, $p \leq 0.01$; ***, $p \leq 0.001$). The bar (-) indicates there were not enough replicates to perform statistical analysis.

Table S2. Primer sequences of each aquaporin gene studied as well as the reference where the sequences were obtained.

<i>Vitis</i> gene	Primer		Reference
PIP 1.1	Forward:	5'-GAGTGGTGCTGGGCGTTGATC-3'	Gambetta et al. [109]
	Reverse:	5'-GTGGAATGCTACAGACATTAC-3'	
PIP 1.2	Forward:	5'-CGCCATCGTCTACAACAAAG-3'	Vandeleur et al. [38]
	Reverse:	5'-CAGGCTCTGGTCTTGAATGG-3'	
PIP 2.1	Forward:	5'-GGCATTCTGCGGGGACACAT-3'	Dayer et al. [40]
	Reverse:	5'-CTTTGACGAGACCCACACCA-3'	
PIP 2.2	Forward:	5'-AACTAAAAACCCACAACACCC-3'	Gambetta et al. [109]
	Reverse:	5'-CATCATCATAATCATCTCTGG-3'	
PIP 2.3	Forward:	5'-GCCATTGCAGCATCTATCA-3'	Pou et al. [30]
	Reverse:	5'-TCCTACAGGGCCACAAATTC-3'	
TIP 1.1	Forward:	5'-GTTGTTGTCTCAACCCATTTC-3'	Galmés et al. [72]
	Reverse:	5'-ATCACC AACCTCATTCATATGC-3'	
TIP 2.1	Forward:	5'-GGAGGAAGAGCAAGTTGTGC-3'	Pou et al. [30]
	Reverse:	5'-GCACATCACCAACCTCATTC-3'	
Ubiquitin	Forward:	5'-GTGCTGTCAACTGCAGGAAA-3'	Pou et al. [30]
	Reverse:	5'-GTAGCCATGGCACATCCAAT-3'	
ELF	Forward:	5'-CGGGCAAGAGATACCTCAAT-3'	Dayer et al. [40]
	Reverse:	5'-AGAGCCTCTCCCTCAAAAGG-3'	
Actin	Forward:	5'-GCCTCCGATTCTCTGCTCTC-3'	Vandeleur et al. [76]
	Reverse:	5'-TCACCATTCAGTTCATTGTAC-3'	