

Supplementary material

Relation between water status and desiccation-affected genes

in the lichen photobiont *Trebouxia gelatinosa*

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Table A.1. Primers for quantitative real-time PCR analysis.

Gene	Primers	Forward sequence	Reverse sequence	Reference
Ascorbate peroxidase	APX	CAGGGTTCACAAGGACAGGT	TCAGCAAACAGGCACTCATC	Montagner, 2017
Desiccation related protein 1	DPR1	CAAAATGGCGATGTTGTCAC	CAACGTTGAAGATGCCAATG	This study
Desiccation related protein 2	DPR2	AAATTGCCACGTCAACTTC	GAGGAGCAGCACCCCTGTAG	This study
Desiccation related protein 6	DPR6	CCAGATCGACCTCTCTGCTC	GCCAACAGGGTCTTGTCAGT	This study
Desiccation related protein 11	DPR11	CATATGGCGAGGGTATTGCT	TGTGCGATTTCACTCTCAGC	Montagner, 2017
Desiccation related protein 13	DPR13	AGGACATCAGACAGGGATGG	AATTGCCAACAAAGCCAAAC	This study
Expansin 1	EXP1	GACAGGACTCCAGCTTTTGC	CTGAGGGGAGATGACGTTGT	Candotto Carniel et al., 2016
Heat shock protein 70	HSP70	CAGTCACTGCCTTCTCA	CAAGTCAGCCAATGCAAAGA	Montagner, 2017
Light harvesting complex II	LHCII	CTGATGACCCAGATGCCTTT	GGTCCTTGCCTGTCACAAT	Candotto Carniel et al., 2016
Mn-superoxide dismutase	MnSOD	CACCCAGCTTGCTGACTACA	GGTCAAAGTGCCTGGAAT	Montagner, 2017
Ribosomal protein L6	RPL6	AGGAGCTAGCTAGGGGCATC	TCTCGTGCTTTGGGAAGTCT	Candotto Carniel et al., 2016

Table A.2. Duration (h: hours; m: minutes) of the desiccation treatment of *Trebouxia gelatinosa* for each sampling point. Relative water content (RWC; n = 6), water content (WC; n = 6) and water potential (Ψ) in each sampling point are reported. #according to Candotto Carniel et al., 2016.

	T0	T1	T2	T3	T4	T5	T6	T7	T8
Time	0h	4h	7h10m	7h40m	8h25m	9h40m	10h10m	10h35m	silica
RWC (%)	-	-	-	-	100 ± 9	54 ± 9	44 ± 9	13 ± 6	1 ± 1
WC (g H₂O g⁻¹ DW)	6.1 ± 0.32	2.9 ± 0.11	1.9 ± 0.16	1.6 ± 0.21	1.5 ± 0.13	0.8 ± 0.13	0.7 ± 0.15	0.2 ± 0.10	0.01 ± 0.01
Ψ (Mpa)	-0.76	-1.29	-2.14	-2.01	-2.75	-12.67	-16.01	-45.50	-474 [#]

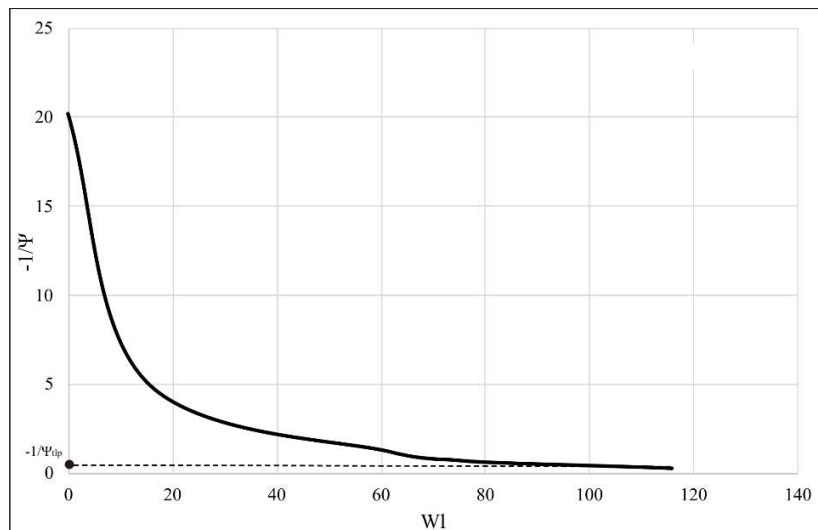


Fig. A.1 Representative PV curve. The cumulative water loss ($WI = TW - FW$) was plotted versus $1/\Psi$, and experiments were concluded when this relationship became linear ($R^2 > 0.98$) (Tyree and Hammel, 1972). Ψ_{tlp} was estimated as the flex point transition between the curvilinear and linear parts of the relationship.

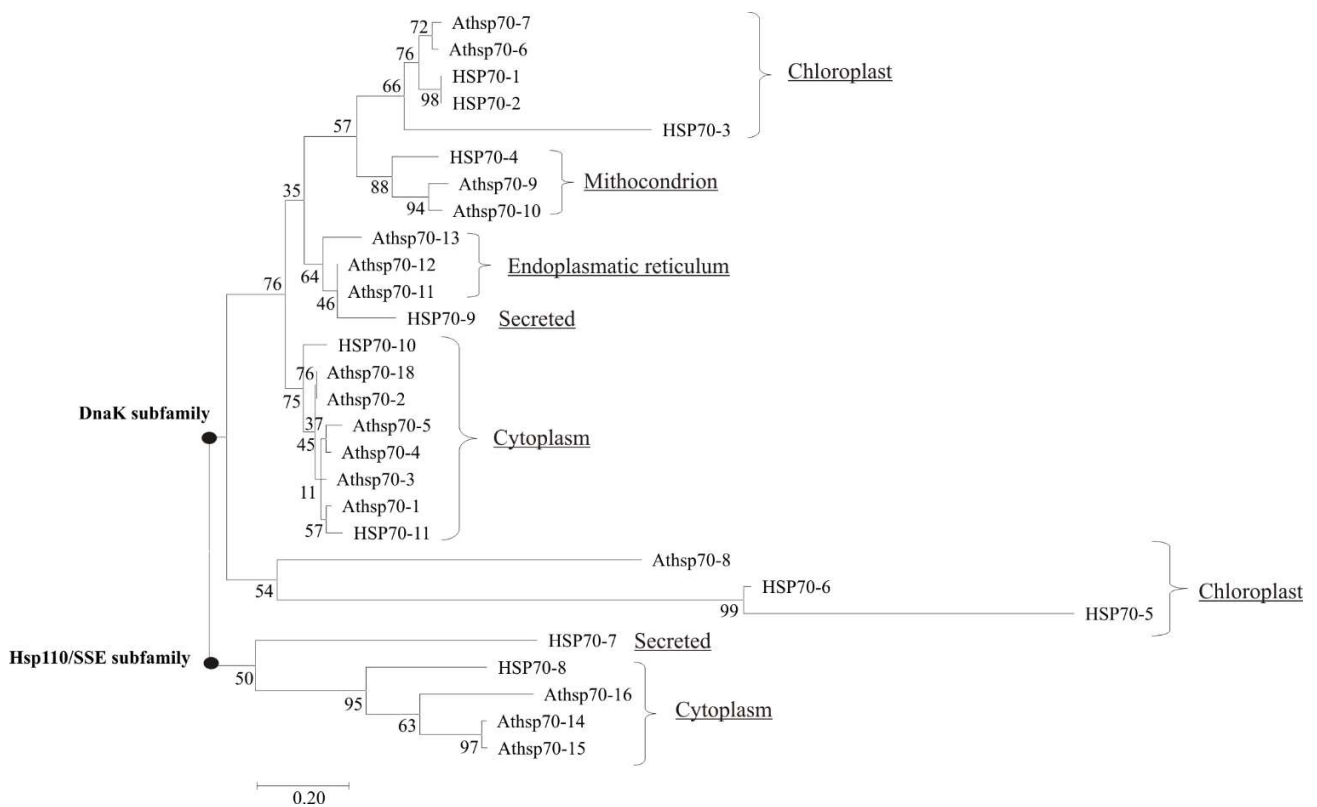


Fig. A.2 Phylogenetic tree showing sequence relations between *Arabidopsis thaliana* (Athsp1-16) and *Trebouxia gelatinosa* (HSP1-HSP11) HSP70 proteins. Predicted cellular localizations of *A. thaliana* (Lin et al., 2001) and *T. gelatinosa* proteins are reported. The tree was inferred with MEGA7 (Tamura et al., 2007) by using the Maximum Likelihood method based on the JTT matrix-based model. The bootstrap consensus tree inferred from 10000 replicates. The percentage of trees in

which the associated taxa clustered together is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.