Physiological and transcriptional responses of Populus euphratica to an increasing drought and a recovery

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Introduction

Populus euphratica is a poplar species famous for its ability to cope with high salinity. It also can grow in deserts when it has access to deep soil water. In order to assess its real degree of drought tolerance and to understand the molecular basis of its response to water-deficit, we studied its physiological and molecular responses to an increasing drought.

Ein Avdat valley (Israel)

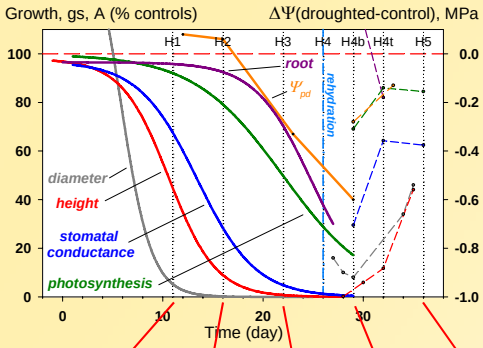
Material and methods

P. eupratica from Ein avdat park (Israël) was *in vitro* multiplied and *ex vitro* acclimated. Plants were grown in a greenhouse and submitted to an increasing drought. While physiology was continuously monitored, leaves and roots were harvested at 4 drought intensities (H1, H2, H3, H4) and 1 recovery point (H5) for biochemical and transcriptome analysis.

17 different normalized and subtracted cDNA libraries were prepared from control and stress exposed trees, and from trees growing in the Ein Avdat valley in Israel. In total 13838 ESTs were obtained from the libraries, and a uni-gene set of 7706 ESTs was reamplified and spotted onto poly-lysine slides.

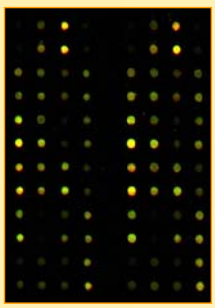
The *P. euphratica* DNA microarrays have been used to determine gene expression profiles in droughted root and leaf samples collected above. All sequences and annotations are available in the Sputnik database at http://sputnik.btk.fi/.

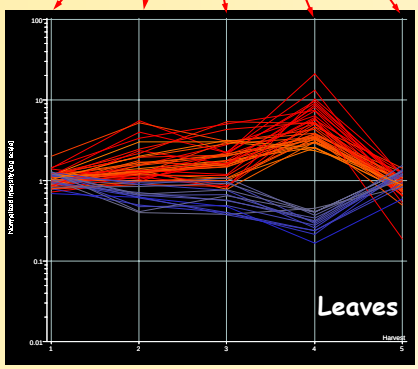
H1 : 10 % soil water content
H2 : 7.5 % SWC
H3 : 5% SWC
H4 : 4% SWC
H5 : recovery point

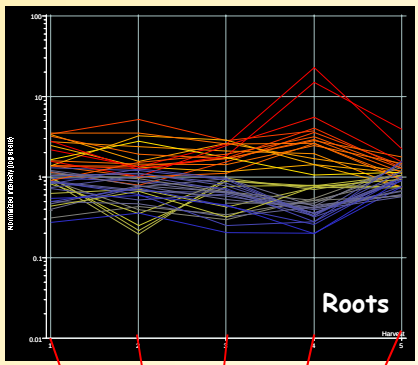


Kinetics of diameter, height and root growth, gas exchange and predawn leaf water potential during an increasing drought and following recovery.

P. euphratica







Gene expression in leaves and roots of stressed *P. euphratica* at 4 drought intensities and following recovery. The Y-axis (log scale) is the ratio [normalized drought channel intensity / control channel intensity]. The displayed genes (each line) were at least two-fold regulated.

Results and discussion

➔ few genes regulated:
55 in leaves (70% up, 30% down)
45 in roots (40% up, 60% down)

➔ changes in transcript levels earlier in roots than in leaves.

➔ good correspondence between physiology and transcript levels for root growth, photosynthesis, …

	Biological process		H1	H2	H3	H4	H5
Leaf	Carbohydrate metabolism	Callose synthase, sucrose synthase, 1-4 α-glucan branching enzyme		↗	↗	↗	
	Response to abiotic or biotic stimulus	Cyclic nucleotide and calmodulin-regulated ion channel		↗	↗	↗	
		Kunitz trypsine inhibitor				↗↗	
		Metallothionein				↘	
		Chalcone synthase				↘	↗
	Amino-acid and protein metabolism	Asparagine synthetase, aldehyde dehydrogenase		↗	↗	↗↗	
		Cysteine protease				↗↗	↘
	Photosynthesis	PSI reaction center subunit VI and X, PSII protein				↘	↗
Root	Cell growth/maintenance	Expansin-like protein	↗	↗	↗	↗	
	Carbohydrate metabolism	Sucrose synthase	↘	↘	↘	↘	
		Mannitol dehydrogenase, mannan endo 1,4-β-mannosidase		↗	↗	↗	
	Transcription	Ethylene response factor 2	↘	↘	↘	↘	
	Unkown	Major storage protein				↗↗	
	Transport	Aquaporin				↘	

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