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► To cite this version:

Marie-Béatrice Bogeat-Triboulot, Mikael Brosché, Didier Le Thiec, David Hukin, Andrea Polle, et al.. Physiological and transcriptional responses of *Populus euphratica* to an increasing drought and a recovery. 12. New Phytologist Symposium: Functional Genomics of environmental adaptation in *Populus*, Oct 2004, Gatlingburg, United States. 1 p., 2004. hal-02831576

HAL Id: hal-02831576

<https://hal.inrae.fr/hal-02831576>

Submitted on 7 Jun 2020

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

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Ein Avdat valley (Israel)



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.

Material and methods

P. euphratica 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-llysine slides.

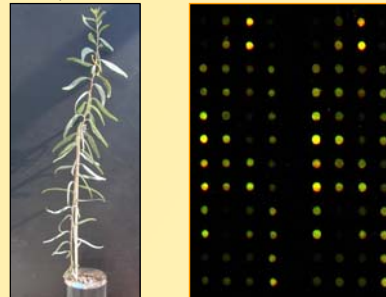
The *P. euphratica* DNA microarrays have been used to determine gene expression profiles in droughted root and leaf samples collected above. All sequences and annotations are available in the Sputnik database at <http://sputnik.btk.fi/>.

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

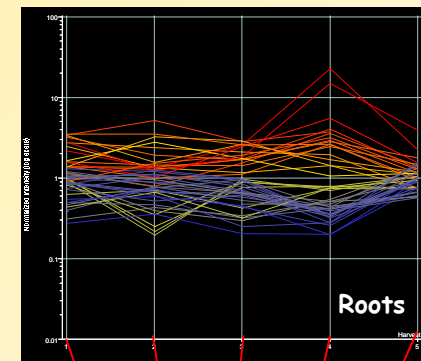
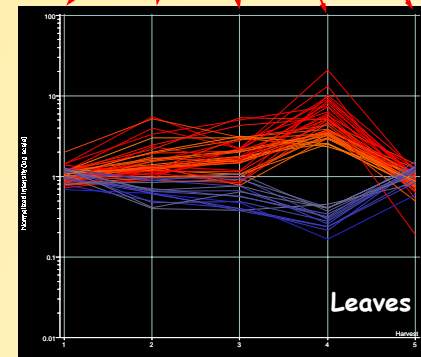
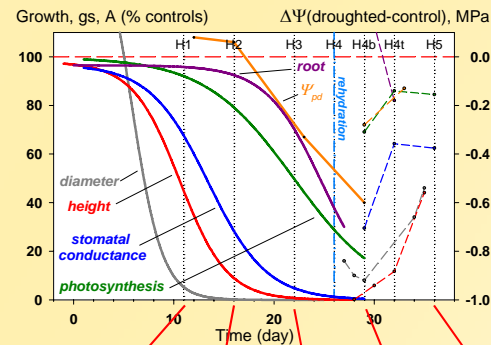
Kinetics of diameter, height and root growth, gas exchange and predawn leaf water potential during an increasing drought and following recovery.



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 trypsin 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 | | | | ↘ | | |

Acknowledgements : This research was carried out in the frame of Establish project with the financial support from the European Communities (contract N° QLK5-CT-2000-01377). Arie Altmann is acknowledged for providing the plants and the picture from Ein Avdat valley.