# Physiological and transcriptional responses of poplar to water deficit

Annegret Kohler, Marie-Béatrice Bogeat-Triboulot, Christine Delaruelle, Erwin Dreyer, Jean-Marc J.-M. Guehl, Francis Martin

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[1]KOHLER Annegret, [1,2]OLIE Valérie, [2]BOGEAT-TRIBOULOT Marie-Béatrice, [1]DELARUELLE Christine, [2]DREYER Erwin, [2]GUEHL Jean-Marc & [1]MARTIN Francis

*[1]UMR INRA-UHP, Interactions Arbres/Micro-organismes , INRA-Nancy, France*

*[2]UMR INRA-UHP, Forest Ecology and Ecophysiology, INRA-Nancy, France*

## Introduction

Drought greatly affects the growth and development of plants. In order to understand the molecular basis of the response of poplar trees to water-deficit and identify candidate genes, we carried out an integrated approach combining functional genomics and ecophysiological approaches on *Populus trichocarpa x deltoides* cv Beaupré .

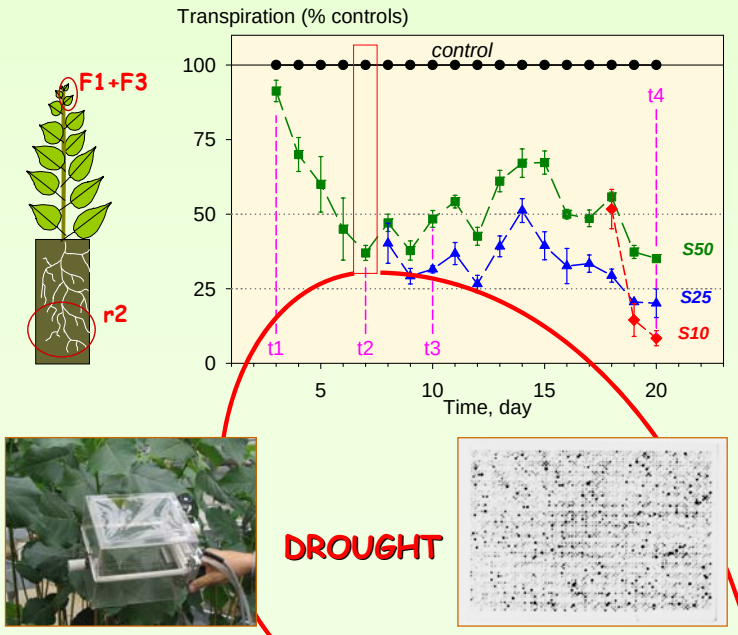
## Material and methods

*The response to drought was assessed using experimental conditions that closely approximate stress development in the field. Drought level was monitored through transpiration rate. 3 stress levels (50, 25 and 10% of control transpiration) were combined to 4 durations (t1, t2, t3 and t4 corresponding to 3, 7, 10 and 20 days, respectively).*

*Physiological status was characterised at each time point on the harvested plants. Growing leaves and roots were collected for transcriptome analysis (2-3 replicates).*

*cDNA arrays contained 4608 ESTs from adventitious roots and leaves of* Populus trichocarpa x deltoides *cv Beaupré (Kohler, 2003).*

*Signal intensities lower than 2x mean of (background + standard deviation) were eliminated and central normalization was performed on the remaining data. A Bayesian statistical method (CyberT), based on the t-test, was used to test for statistically significant differences in gene expression.*




### Ecophysiological analysis

| Transpiration rate | Leaf water potential | Growth rate | Photosynth. (leaf F3) | Stomatal conductance (leaf F3) | Relative water content (GF1 / R2) | Full turgor osmotic pressure (GF1 / R2) |
|---|---|---|---|---|---|---|
| ↘ - 63% | predawn → mid-day ↘ - 3 b. | height → root ↗ + 70% | ↘ - 60% | ↘ - 80% | leaf → root ↘ -30% | leaf ↗ +20% root ↗ +10% |

### Transcriptome analysis

#### Up-regulated transcripts

**Stress/Defense-related**
SOD: superoxide dismutase (L)
Aluminium-induced (L)
Peroxidase (L)
Metallothionein PtdMT2a (L,R)
Wound-induced (L,R)

**Protein synthesis**
Ribosomal Proteins (40S, 60S) (L,R)
Elongation factor 1 alpha (L)

**Cell wall modification**
Extensin (R)
Prolin-rich protein (L)
CAD (R)

**Lipid metabolism**
GDSL-motif Lipase (L)
8-Delta sphingolipid-desaturase (R)

**Signalling**
14-3-3 protein (L)
GTPase (L)
Protein phosphatase 2C (L)

**Glycolyse**
Glyceraldehyde-3-phos. dehydrogenase (R)
Pyruvate kinase (R)

#### Down-regulated transcripts

**Photosynthesis**
PSII 5kd protein precursor (L)
RUBISCO small subunit (L)

**Stress/Defense-related**
Metallothionein PtdMT1a, PtdMT1b (R)

**Water transfert**
Aquaporin TIP (L)

**Differentially expressed transcripts**

| | ↗ | ↘ |
|---|---|---|
| Leaves | 40 (1%) | 9 (0.2%) |
| Roots | 30 (0.7%) | 10 (0.2%) |

(total number of analyzed cDNA elements: 4062)

## Summary

3 levels of analysis : physiology, transcriptome and proteome (cf. Meddour poster)

| | Physio. | Transcripts | Proteins |
|---|---|---|---|
| **Water transfer** Transpiration aquaporin | ↘ | ↘ | |
| **Photosynthesis** PSII rubisco subunit | ↘ | ↘ ↘ | ↗ |
| **Root growth/energy** (pyruvate kinase) | ↗ | ↗ | ↘ |
| **Stress / defence** SOD wound induced | | ↗ ↗ | ↗ ↗ |
| **Lipid metabolism** GDSL motif lipase | | ↗ | ↗ |
| **Protein synthesis** ribosomal proteins | | ↗ | ↘ |

**Kohler A, Delaruelle C, Martin D, Encelot N, Martin F. 2003.** The poplar root transcriptome: analysis of 7000 expressed sequence tags. *FEBS letters* **542**: 37-41