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Physiological and transcriptional responses of poplar to water deficit

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Introduction

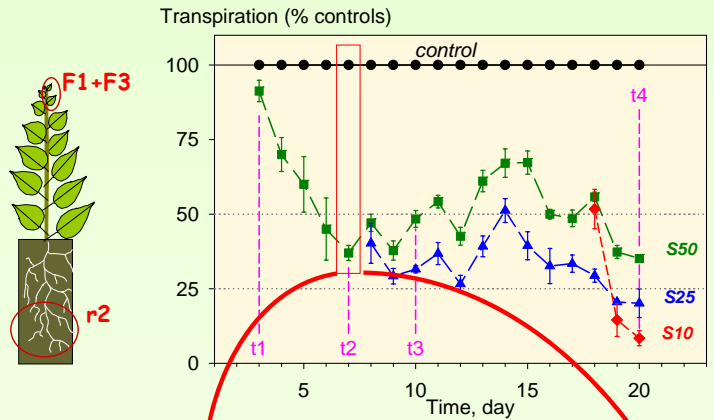
Drought greatly affects the growth and development of plants. In order to understand the molecular basis of the response of poplar trees to water-deficit and identify candidate genes, we carried out an integrated approach combining functional genomics and ecophysiological approaches on *Populus trichocarpa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

Material and methods

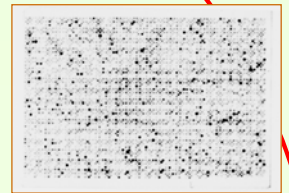
The response to drought was assessed using experimental conditions that closely approximate stress development in the field. Drought level was monitored through transpiration rate. 3 stress levels (50, 25 and 10% of control transpiration) were combined to 4 durations (t1, t2, t3 and t4 corresponding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



DROUGHT



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%

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		↗	↓

Transcriptome analysis

Up-regulated transcripts

Stress/Defence-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/Defence-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)