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Molecular bases of acclimation to water deficit in poplar mature leaves



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Context:

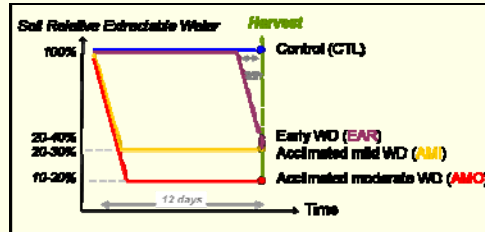
In temperate zones, global change will induce longer and more severe drought episodes. In order to identify candidate genes for water deficit acclimation, we looked for gene expression in response to drought stress in poplar, a model tree species.

Objectives:

- Identify strong drought markers by comparing the response of two genotypes at different stages and intensities of water deficit
- Identify candidate genes for drought acclimation

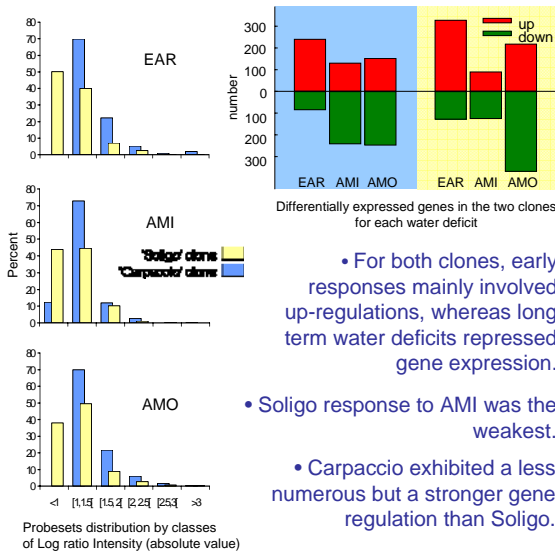
Material and Methods:

Experience was conducted on two genotypes of *Populus deltoides x nigra*, Carpaccio and Soligo, the later being more sensitive to water deficit (Monclus *et al.* 2006). The transcriptome of mature leaves was analysed at different stages and intensities of water deficit (early or following 12 days acclimation; mild and moderate, figure below).



Transcriptome was analysed on the GeneChip Poplar Genome Array (URGV Evry, France) using 2 replicates (a pool of 3 trees each) per modality. Re-annotation of Affymetrix probesets was performed based on poplar gene-models annotation (JGI).

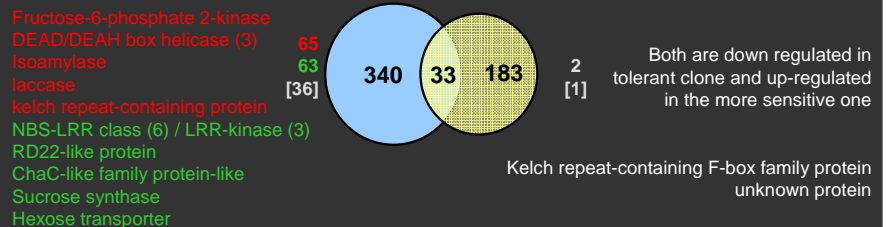
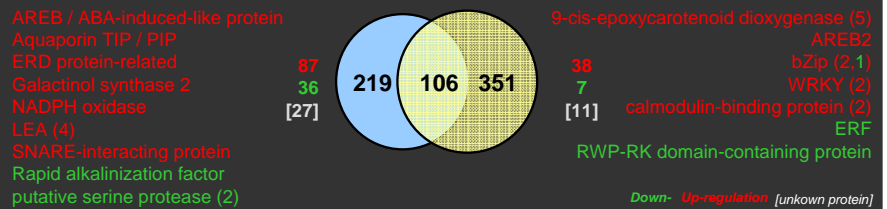
Regulated genes: number and intensity



- For both clones, early responses mainly involved up-regulations, whereas long term water deficits repressed gene expression.
- Soligo response to AMI was the weakest.
- Carpaccio exhibited a less numerous but a stronger gene regulation than Soligo.

Only in the most tolerant clone | Common to both clones

Probesets specifically regulated in the early response



Regulated in the 3 treatments

Carpaccio exclusive response

Unknown protein EAR AMI AMO (2)

ABA 8-hydroxylase (2)

ABC transporter family protein

Receptor-like protein kinase

LRR receptor-like protein kinase 1 / NBS-LRR type

Water deficit markers

Homeobox-leucine zipper protein *

Unknown protein (2)

Galactinol synthase 1

RCI 2A - like *

Protein phosphatase 2C (2) *

Xyloglucan endotransglycosylase *

*Genes commonly regulated by water deficit in *A. thaliana* (Bray, 2004)

Mild water deficit

▲

Acclimation to water deficit

▼

Moderate water deficit

Polyphenol oxidase

Alcohol dehydrogenase

WAK-Like (6)

Sucrose synthase (3)

LRR family protein (6)

LTP

Gibberellin regulated protein

ChaC-like family protein-like (3)

RAV1/ WRKY (2)

Zinc finger homeodomain

LTP

Photosystem family proteins (3)

Kelch repeat-containing protein

Ubiquitin family protein (2)

4-coumarate-CoA ligase-like protein

AP2-EREBP

Response regulator 5 (ARR5)

NBS-LRR type

LEA 5

Glutamine synthetase

Serine hydroxymethyltransferase

UDP-glucosyl transferase family protein

polyubiquitin senescence-associated protein

Proton-dependent oligopeptide transport (2)

The co-analysis of two poplar clones of contrasted tolerance allowed us to discriminate :

- ✓ differentially expressed genes showing a potential adaptative character from genes responding passively to water deficit
- ✓ good water deficit markers which are regulated both in Carpaccio and Soligo.

Affymetrix array results are currently under validation by real-time PCR and by array on an independent experiment.

Candidate genes for water deficit acclimation (Carpaccio specific response) will be validated through an analysis of expression in a wider range of clones by real-time PCR.

Affymetrix arrays are currently performed on other organs such as root apices and stomata to allow meta-analyses.