



Investigating the molecular basis of drought tolerance in Populus: The WATBIO Populus core experiment

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Introduction

- **Populus core experiment:** Investigation of drought stress responses of selected *Populus* genotypes
- **Unifying research aim of participating groups:** Analysis of development of tissues and organs under drought in order to identify mechanisms important to maintain growth under limited water availability
- **Main hypothesis:** *Populus* genotypes originating from different environments harbour adaptation mechanisms that can be exploited to produce new germplasm for sustained biomass production under stress

Methods

Drought stress experiment with *Populus nigra*

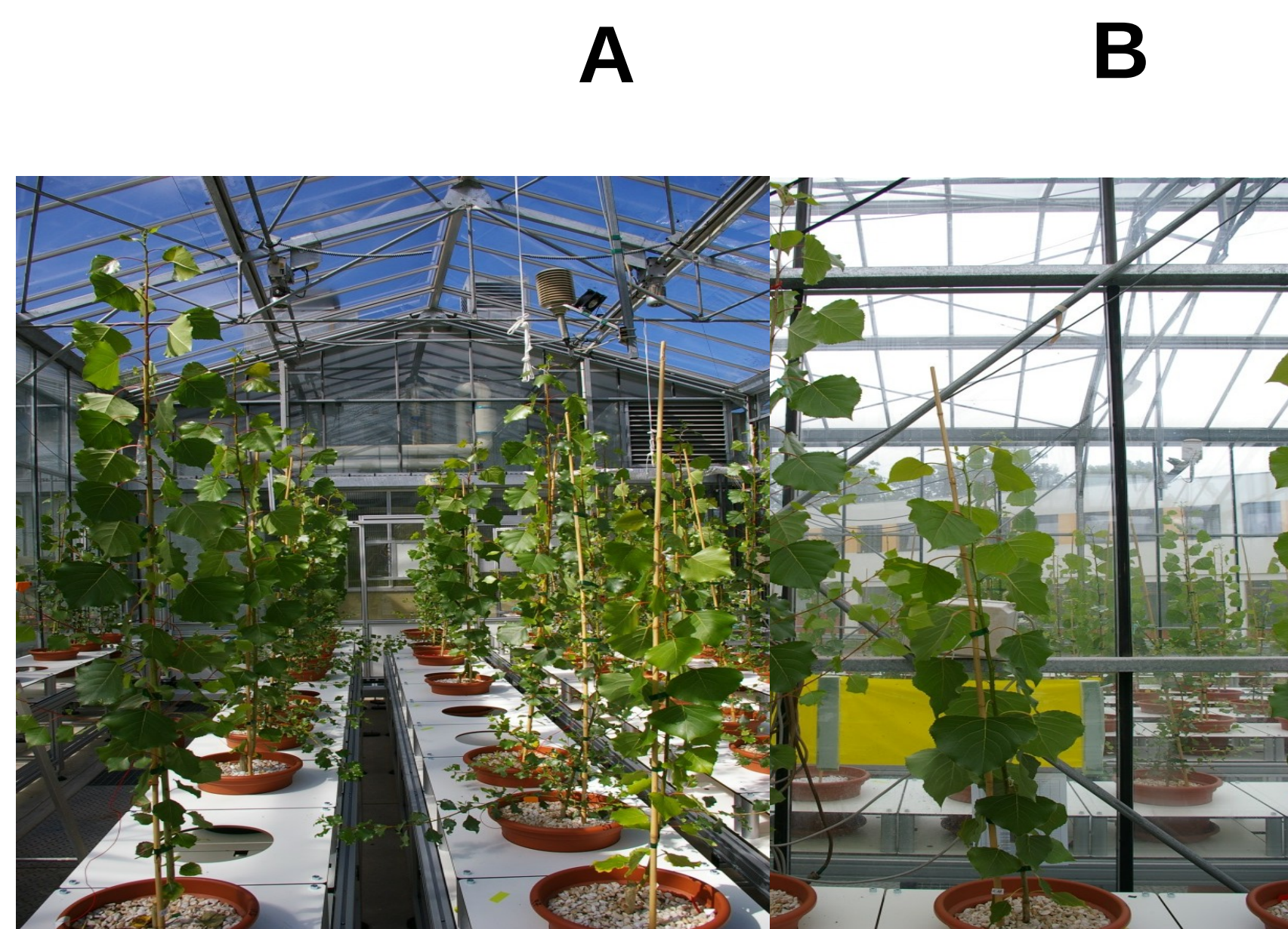


Fig. 1 | Growth of *Populus nigra* trees in a greenhouse with an automated watering system at INRA Nancy (A, B). Trees of three genotypes (“Spain”, “France”, “Italy”) were exposed to a control or moderate drought treatment for five weeks. B) Two representative plants of genotype “Italy” at the end of the experiment (left, control; right, drought treated).

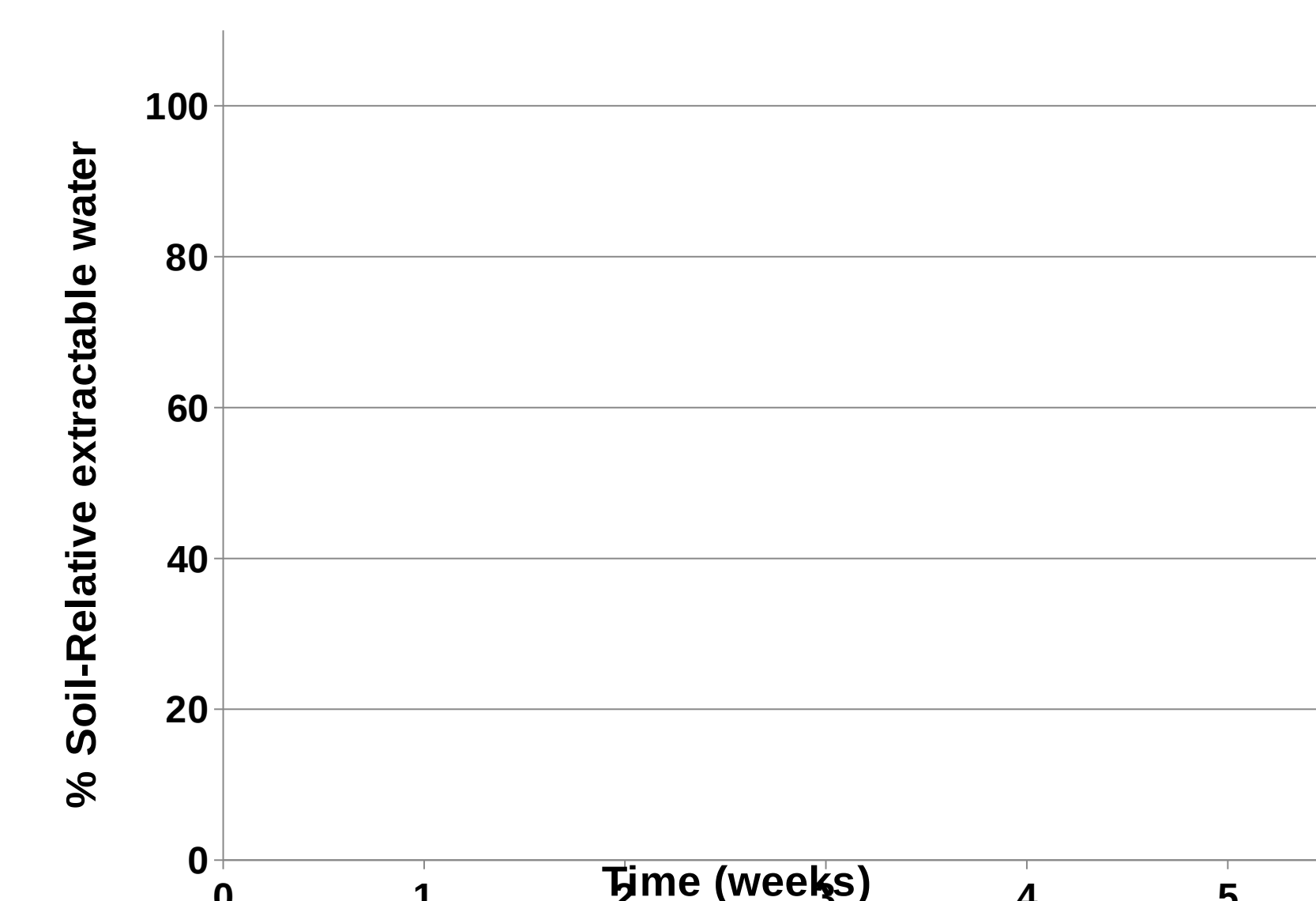
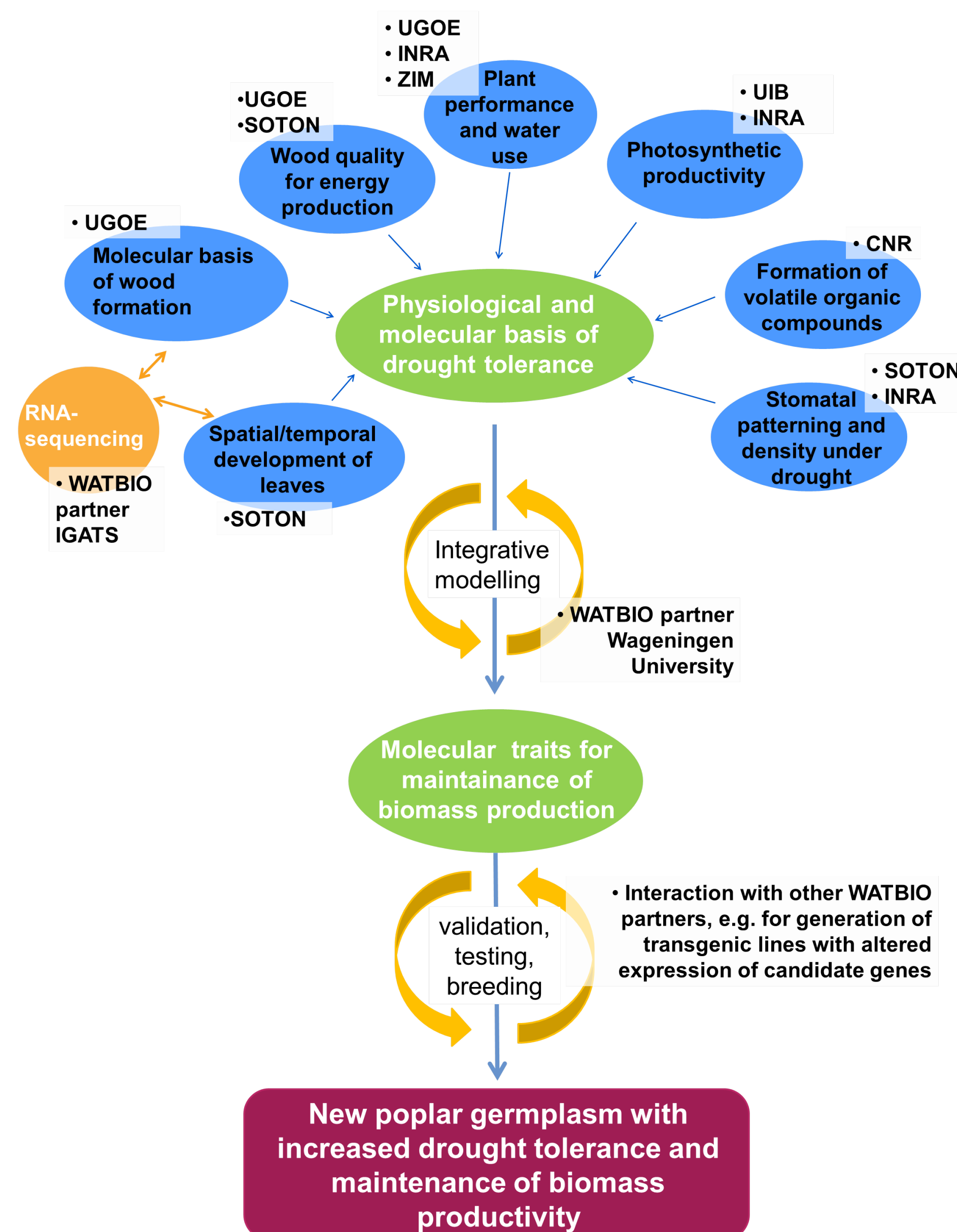


Fig. 2 | Soil water conditions in a drought stress experiment with *Populus nigra*. Trees of three genotypes were exposed to a control treatment with 90% soil-relative extractable water (soil-REW) or a drought treatment with a target level of 20% soil-REW, which was reached at week 2.

Concept

The involved partners contribute their expertise to achieve the main goal of the WATBIO project



A core set of measurements is carried out

- Biomass yield
- Soil water status
- Plant water status
- Leaf size, total leaf area
- Branching patterns
- Stomatal conductance
- Wood/lignocellulosic quality, saccharification potential

A collection of samples was used for transcriptome profiling by RNA-Seq

- Genotype “Italy”: samples of developing xylem, fine roots, leaves collected weekly during the experiment
- Genotypes “Spain”, “France”, “Italy”: samples of developing xylem, fine roots, and various leaf stages collected at the end of the experiment

Outlook

- Finish integration of gene expression data with phenotypic traits to identify candidate genes for increased drought tolerance
- Test the hypothesis of adaptive divergence within the genus *Populus* by comparing this study with the second *Populus* core experiment carried out in summer 2014 with two genotypes of *P. tremula*

Results

Drought caused a significant reduction of stomatal conductance in genotypes “France” and “Italy”

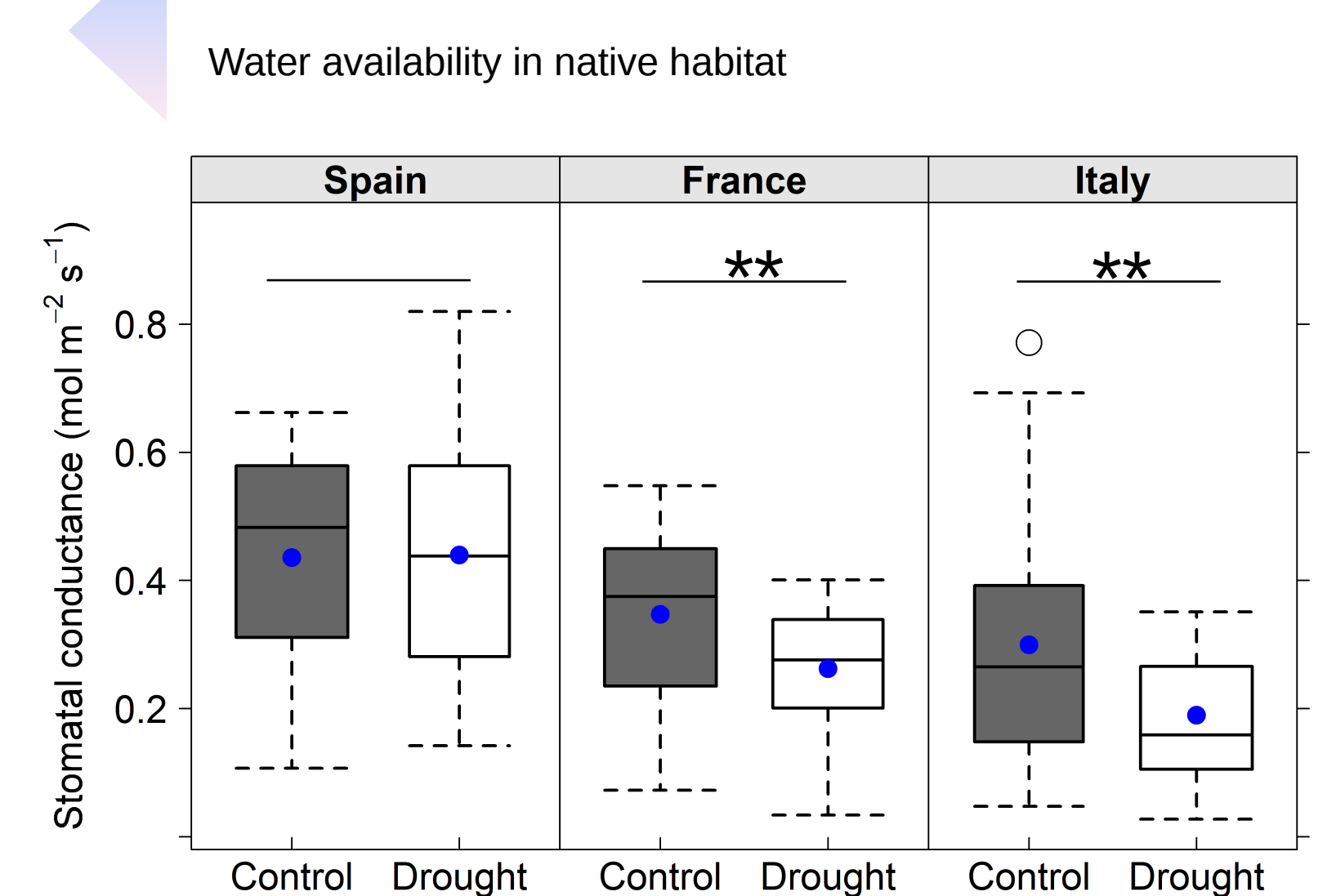


Fig. 3 | Stomatal conductance of three *Populus nigra* genotypes after five weeks of a control or drought treatment (see Fig. 2). Measurements were taken at 2000 $\mu\text{mol m}^{-2} \text{s}^{-1}$ PPFD, $[\text{CO}_2]=400 \mu\text{mol mol}^{-1}$, Temperature 25°C. Blue dots depict the mean, ** denote significant differences between treatments ($P<0.01$, $n=5$).

Biomass productivity, and its decrease under drought, differs among genotypes

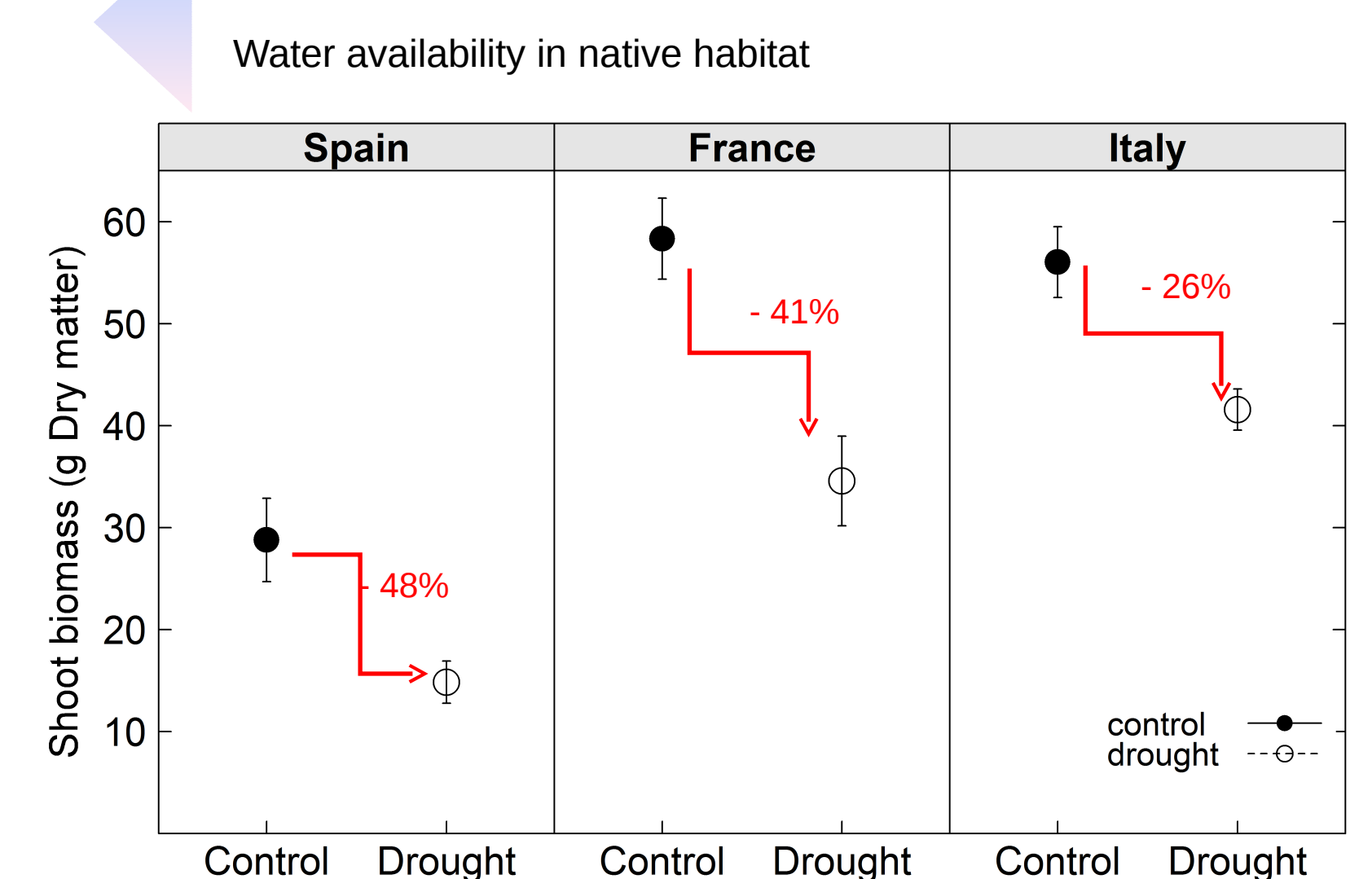


Fig. 4 | Biomass production of three *Populus nigra* genotypes after five weeks of a control or drought stress treatment (see Fig. 2). Data show means $\pm$ SE, $n=6$.

RNA-Seq revealed strong differences in transcript abundances among genotypes, and varying sizes of drought effects among tissues

Tab. 1 | Number of differentially expressed (DE) genes per tissue. Samples were collected at the end of the experiment. Detection of DE genes was carried out with DESeq2 (false discovery rate 0.05).

Tissue	Effect/Contrast	No. of tested genes	DE genes
Dev. xylem	Treatment-x-genotype	23421	0
	Treatment		77
	Genotype		14046
	France/Italy		6117
	Spain/Italy		6196
Fine roots	Treatment-x-genotype	27239	9
	Treatment		1862
	Genotype		11999
	France/Italy		4492
	Spain/Italy		6646
Leaf	Treatment-x-genotype	25010	117
	Treatment		1661
	Genotype		17882
	France/Italy		4557
	Spain/Italy		10362
	Spain/France		10565

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