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Transcript profiling of wood transcriptional regulators, wood chemistry and phenotyping in poplar and eucalyptus genotypes growing under drought, salinity and limiting nitrogen conditions

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The possibilities for using lignocellulosic biomass produced from forest crops in order to obtain second generation biofuels is a key issue in the current context of climate change and the promotion of renewable energy sources.

It is therefore important to make progress in the functional characterization of candidate genes (CGs) associated with wood traits relevant to bioenergy as well as to determine the effects of environmental factors (drought, salinity, and nitrogen availability among others) on wood production and chemistry. Fast growing species adapted to coppicing such as *Populus* and *Eucalyptus* spp. are among the most promising forest species for bioenergy production in the short term.

The aim of our project is to compare how three common environmental factors such as drought, salt and nitrogen availability, affect wood composition and transcript profiling of CGs involved in wood formation in different poplar and eucalypt genotypes. Poplar and eucalypt genotypes were selected based on their potential for bioenergy production and their performances under different abiotic stresses. In particular, four poplar genotypes: *P. x canadensis* (Oudenberg); *P. tremula x P. alba*; two *P. alba* clones (J 1-3-18 and Po10-10-20), and four eucalyptus genotypes: *E. camaldulensis* (169); *E. urograndis* (5E); *E. globulus* (Odiel); *E. globulus* (Anselmo) were used.

We found that the environmental factors caused responses of different magnitude and at different levels among the genotypes.

Correlation analysis will allow us to specifically associate changes in the expression of regulatory genes caused by environmental factors with alterations in secondary xylem composition and phenotypic adjustments.

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