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## **Whole-genome transcriptomic analysis of xylem tissues for two poplar genotypes of contrasted tolerance to water deficit submitted to various drought conditions.**

Jean-Charles Leplé, Philippe Label, Marie-Claude Lesage Descauses, Françoise F. Laurans, Didier Le Thiec, Marie-Béatrice Bogeat-Triboulot, Moreau Alain, Isabelle Bourgait, Nelly Desplat, Annabelle Dejardin, et al.

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Title: Whole-genome transcriptomic analysis of xylem tissues for two poplar genotypes of contrasted tolerance to water deficit submitted to various drought conditions.

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Abstract: The numerous molecular studies on drought response in plants were mostly focused on short-term responses without considering dose-response effects. Moreover, despite the importance of xylem in tree water relations, assessments of drought-induced gene expression in wood are very scarce. In this work, we investigated xylem correlations between histological characteristics induced by water shortage and drought-induced gene expression. The experimental plan consisted of two *Populus deltoides* x *Populus nigra* hybrid clones (Soligo and Carpaccio) contrasted for their tolerance to water shortage and four water regimes: one short-term response to water deficit and two long-term responses either to mild and moderate water deficit and the well-watered control. For each condition tested, six trees were dedicated to molecular studies and three for ecophysiological and growth measurements. After histological staining of stem cross sections, image analysis was carried out on selected areas corresponding to stressed xylem. Total vessel lumen area was consistently higher in Carpaccio as compared to Soligo, whatever the stress condition. Interestingly, under the most stringent water shortage, Soligo exhibited a significant increase of the cell wall/ray cell fraction and an increase of water use efficiency. Spatial statistics are underway to better describe the variability of these histological variables. In addition, complete debarked stem samples and cambial zones only plus very young differentiating scraped xylem were analyzed on whole-genome Affymetrix poplar arrays. We identified modules of co-expressed genes especially using a new clustering algorithm developed by Maere et al. (BMC Systems Biology 2008, 2:33). A limited number of modules are representative of clone-specific responses but some others are potentially correlated to genotype-treatment interactions. Prospective models to integrate these phenotypic, ecophysiological and gene expression data will be discussed.

This work is part of an ANR - Genoplante 2010 research project entitled: "Molecular bases of acclimation and adaptation to water deficit in poplar" (POPSEC, 2007-2009).