



HAL
open science

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.

► **To cite this version:**

Jean-Charles Leplé, Philippe Label, Marie-Claude Lesage Descauses, Françoise F. Laurans, Didier Le Thiec, et al.. Whole-genome transcriptomic analysis of xylem tissues for two poplar genotypes of contrasted tolerance to water deficit submitted to various drought conditions.. 2nd Poplar Symposium From Genes to Function, Mar 2009, Göttingen, Germany. n.p. hal-02816667

HAL Id: hal-02816667

<https://hal.inrae.fr/hal-02816667>

Submitted on 6 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

¹Lep le JC, ¹Label P, ¹Lesage-Descauses M-C, ¹Laurans F, ²Le Thiec D, ²Bogeat-Triboulot M-B, ¹Moreau A, ¹Bourgait I, ¹Desplat N, ¹D jardin A, ³Balzergue S, ³Renou JP, ¹Pilate G

¹INRA, UR588 Unit  Am lioration G n tique et Physiologie Foresti res, Centre de recherche d'Orl ans, 2163 Avenue de la Pomme de Pin, CS 40001 Ardon, 45075 Orl ans Cedex 2, France.

²INRA, UMR1137 Ecologie et Ecophysiologie Foresti res, Centre de recherche de Nancy, 54280 Champenoux, France.

³INRA, UMR1165 Unit  de Recherche en G nomique V g tale, Centre de Versailles-Grignon, 2 rue Gaston Cr mieux CP 5708, 91057 Evry, France.

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).