An integrated approach to bud set in poplar : phenotypes, candidate genes, and QTLs

Antje Rohde, Tom Ruttink, Sophie Dillen, Nicolas Marron, Francesco Fabbrini, Véronique Storme, Véronique V. Jorge, Anne Rae, Isabella Paolucci, Muriel Gaudet, et al.

HAL Id: hal-02756516
https://hal.inrae.fr/hal-02756516

Submitted on 3 Jun 2020

Population Genetics and Genomics of Forest Trees: From Gene Function to Evolutionary Dynamics and Conservation

A joint conference of IUFRO Working Groups **2.04.01** (*Population, ecological and conservation genetics*) and **2.04.10** (*Genomics*), and COST Action **E-28** (*Genosilva: European Forest Genomics Network*)

PROGRAMME and CONFERENCE ABSTRACT BOOK

October 1-6, 2006
Alcalá de Henares, Madrid (Spain)

Universidad de Alcalá

INIA
Instituto Nacional de Investigación
y Tecnología Agraria y Alimentaria

IUFRO

cost

An integrated approach to bud set in poplar: phenotypes, candidate genes, and QTLs

Antje Rohde[1], **Tom Ruttink**[1], **Sophie Dillen**[6], **Nicolas Marron**[6], **Francesco Fabbrini**4, **Véronique Storme**[1], **Véronique Jorge**[2], **Anne Rae**[3], **Isabella Paolucci**[4], **Muriel Gaudet**[4], **Gail Taylor**[3], **Reinhart Ceulemans**[5], **Marijke Steenackers**[6], **Maurizio Sabatti**[4], **Catherine Bastien**[2], and **Wout Boerjan**[1]

The seasonal cycle of growth and dormancy is a distinct character of perennial plants and represents one of the most basic adaptations of trees to their environment. The recurrent transitions of meristems into and out of dormancy are of primary significance to plant productivity and survival. These transitions are tightly linked to the yearly dates of bud flush and bud set that in turn delimit the growth season.

In poplar, perception of a short-day signal leads to apical bud set and dormancy induction. Because bud set is of prime importance in determining season length in a changing environment, we dissected this developmental program at the phenotypical, genetical and molecular levels. Taking advantage of the poplar genome sequence, we integrate candidate genes obtained in large-scale gene expression studies with information of QTLs determined in three poplar pedigrees.
Expressional candidate genes were identified in the apex/bud during short-day-induced bud set, using cDNA-AFLP and micro-arrays. Apical buds of plants were sampled at weekly intervals during six weeks of short days, after which apical buds are fully dormant and cannot resume growth without prior cold treatment. The set of significantly differentially expressed genes comprises 1350 genes.

For phenotypic measurements in the field, a new bud-set scoring system was developed: bud set is phenotyped with seven developmentally distinct stages. This system allows accounting for the onset of the bud-set process as well as for its dynamics, as opposed to most earlier studies that rely on the date of accomplished bud set only. Applying this system, high-resolution phenotypic data were obtained in three poplar pedigrees, grown in two environments, and a collection of 450 Populus nigra accessions.

QTLs for different bud-set-related traits have been determined in the three pedigrees and have been positioned onto the poplar genome sequence. Integrated with the position of the expressional candidate genes, they identify genomic regions of relevance for bud set.
Together, this integrated approach provides a comprehensive overview of bud set in terms of the molecular processes associated with aspects of bud development and elucidates the genetic architecture of bud set. Genes or genomic regions identified through this combined approach are tested for their adaptive relevance in association genetics approaches (see abstract of Zaina et al.).

transcuptomic Sur tremula x alba !
inclu del(2) transgenics

NOTES:

CONTACT INFORMATION:
[1] Department of Plant Systems Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University, Technologiepark 927, 9052 Ghent, Belgium.
[2] INRA Forest Tree Improvement, Genetics and Physiology Unit, BP 20619 Ardon, 45166 Olivet, France.
[3] School of Biological Sciences, University of Southampton, Bassett Crescent East, Southampton, SO16 7PX UK.
[4] Department of Forest Resources and Environment (DISAFRI), University of Tuscia, Via San Camillo de Lellis snc, 01100 Viterbo, Italy.
[5] University of Antwerp, Department of Biology, Universiteitsplein 1, 2610 Wilrijk, Belgium.
[6] Research Institute for Nature and Forest, Gaverstraat 4, 9500 Geraardsbergen, Belgium.
e-mail: antje.rohde@psb.ugent.be
The popyomics consortium:
www.soton.ac.uk/~popyomic/