

COMPARATIVE MAPPING IN SALICACEAE: A TOOL FOR IDENTIFYING IMPORTANT GENES CONTROLLING ADAPTIVE TRAITS

Véronique Jorge¹, Francesco Fabbrini², Patricia Faivre-Rampant³, Matthias Fladung⁴, Muriel Gaudet², Ulf Lagercrantz⁵, Jean-Charles Leplé¹, Michele Morgante⁶, Birte Pakull⁴, Maurizio Sabatti², Véronique Storme⁷, Gail Taylor⁸, Nicola Vitacolonna⁹, Jennifer DeWoody⁸, Catherine Bastien¹

¹ INRA, Unité Amélioration, Génétique et Physiologie Forestières, BP 20619, Ardon, 45166 Olivet Cedex, France

² Dipartimento di Scienze dell'Ambiente Forestale e delle sue Risorse (DISAFRI), Università della Tuscia, Via S. C. De Lellis snc, 01100 – Viterbo, Italy.

³ INRA, unité de Recherche en Génomique Végétale, 2 rue Gaston Crémieux, CP5708, 91057 Evry Cedex, France.

⁴ vTI-Institut für Forstgenetik, Sieker Landstr. 2, 22927 Großhansdorf, Germany.

⁵ Dept. of Evolutionary Functional Genomics, Evolutionary Biology Centre, Uppsala University, Norbyv. 18D, SE-752 36 Uppsala, Sweden.

⁶ Dipartimento di Scienze Agrarie e Ambientali, Università di Udine, via delle Scienze 208, 33100 Udine, Italy

⁷ VIB Department of Plant Systems Biology, Ghent University, Technologiepark 927, 9052 Gent, Belgium.

⁸ University of Southampton, Bassett Crescent East, SO16 7PX, United Kingdom.

⁹ Dipartimento di Matematica Informatica, Università di Udine, via delle Scienze 208, 33100 Udine, Italy

Comparative QTL mapping for adaptive traits among populations and species can lead to the identification of genomic regions conserved over a long evolutionary period and therefore potentially harboring genes of great importance for adaptive processes. At the same time, non-conserved QTLs could be responsible for local adaptation or interspecific differentiation. The availability of *Populus* as a model system for tree and woody perennial plant biology has largely been driven by the rapid development of genomic and molecular biology resources for this genus, culminating in the completion of a draft sequence of the *Populus trichocarpa* (black cottonwood) genome. Numerous genetic maps are available in different *Populus* and *Salix* species and QTLs for adaptive traits (such as phenology and disease resistance) and sex have been mapped. All these maps showed a very good synteny with the *P. trichocarpa* genome; however, very few markers are currently shared between these maps. The objective of our study is to take advantage of the information on the *P. trichocarpa* genome sequence to perform QTL projection and identify candidate genes.

Genetic maps from 7 pedigrees, belonging to 4 *Populus* spp. were aligned with the help of common simple sequence repeat and gene markers. Three additional published maps from *Salix* spp. were partially anchored to the *P. trichocarpa* genome sequence. QTL meta-analysis and projection of QTL intervals on the genome sequence were performed when sufficient genome anchoring markers were available. These analyses allowed identifying large genome regions containing several hundred of candidate genes. Thanks to the availability of biological knowledge accumulated in public data bases (e.g. Gene Ontology) and high-throughput enrichment tools, we have explored these gene lists by functional analysis if QTL regions are statistically enriched in some functional categories compared to the entire genome.

Keywords: genetic mapping, QTL, candidate genes, *Populus* spp., *Salix* spp.

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