



HAL
open science

Can genomics simplify current breeding without the cost of a genome-wide approach?

Laurent Bouffier, Marjorie Vidal, Jérôme Bartholomé, Christophe C. Boury,
Christophe Plomion

► To cite this version:

Laurent Bouffier, Marjorie Vidal, Jérôme Bartholomé, Christophe C. Boury, Christophe Plomion. Can genomics simplify current breeding without the cost of a genome-wide approach?. ProCoGen Dissemination Workshop "from our labs to yours forest", Dec 2015, Orléans, France. 75 p. hal-02743400

HAL Id: hal-02743400

<https://hal.inrae.fr/hal-02743400>

Submitted on 3 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.



Distributed under a Creative Commons Attribution 4.0 International License

ProCoGen final open conference
Promoting Conifer Genomic Resources
30th November – 2nd December 2015
Orléans, France

Conifers are key ecological species dominating many terrestrial landscapes, and they are among the largest terrestrial carbon sinks. Of significant economic importance, conifers are key sources for timber, paper and bio-energy worldwide. At social and scientific levels, there is an increasing awareness of the global change challenges affecting conifers.

In parallel, technological and methodological improvements have been attained and have benefited the conifer taxa, notably on high throughput analytical tools able to describe the variability and plasticity at different levels of integration (from genes up to phenotypes). These new advances can be used not only to improve our understanding of fundamental conifer adaptive biology, but also to address practical problems for the forest industry as well as problems related to the management of conifer forests in the context of global change.

Several international research initiatives have crystalized around these new advances, like next-generation DNA sequencing technologies, with a focus on unraveling fundamental and practical problems of conifer adaptability and domestication. **ProCoGen** is a project funded by the EC 7FP that develops integrative and multidisciplinary genomic research in conifers, using high-throughput platforms for sequencing, genotyping and doing functional analysis. The objective of **ProCoGen** is to unravel genome organization and to identify genes and gene networks controlling important ecological and economic traits, such as those related to environmentally driven tree reaction for growth, drought and cold stress tolerance, and thus provide tree breeders with tools for precise selection. **ProCoGen** as well as other parallel initiatives worldwide have produced already substantial findings deserving broad dissemination among scientist for fostering awareness and further collaboration in conifer research.

With this goal in mind, a **ProCoGen** final open conference will be held in Orleans (France) from November 30th to December 2nd 2015. The aim of this international event will be to serve as a showcase of main results achieved in the project, along with other internationally relevant achievements brought in by key invited speakers and general attendees. External researchers from similar initiatives worldwide, from complementary disciplines ranging from genomics, to molecular and population genetics, tree physiology and developmental biology, biochemistry, molecular and cell biology, bioinformatics and conifer breeders, are invited to present and discuss recent and relevant results on structural, functional, comparative and translational genomics of conifer species. Emphasis will be given to broaden the coverage of key actors, from public research institutes and Universities to privately funded research organizations. External and **ProCoGen** keynote speakers, oral and poster presentations form external attendees and **ProCoGen** members will be included in



the program. The number of participants will be limited to 100-120. No registration fees will be demanded. A conference website will be available for registration and abstract submission.

This open conference will be held along with a **ProCoGen** Training Workshop on “*Practicalities of marker and genome-assisted selection*” and with a **ProCoGen** Dissemination Workshop on “*Transfer of genome-related tools to breeding programs*”. The TWS and DSW will be held on December 3th 2015 and December 4th 2015, respectively.



Can genomics simplify current breeding without the cost of a genome?

Laurent Bouffier^{1,2}, Marjorie Vidal^{1,2,3}, Jérôme Bartholomé^{1,2}, Christophe Boury^{1,2}, Christophe Plomion^{1,2}

¹ INRA, BIOGECO, UMR 1202, 33610 Cestas, France

² University Bordeaux, BIOGECO, UMR 1202, 33400 Talence, France

³ FCBA, Biotechnology and Advanced Silviculture Department, Genetics & Biotechnology team, 33610 Cestas, France

Genomic selection is not a short term perspective for maritime pine. However, molecular markers can be of first importance to enhance innovative breeding strategies. They should be progressively implemented in the maritime pine breeding program. The first step for this implementation is in progress with the genotyping of a part of the clonal archives in order to check identities and pedigrees. Then, forward selections in polycross trials associated with pedigree recovery will be carried out this year to both constitute the breeding population and establish seed orchards. This talk will present the tools developed for identity checking and how we plan to use these molecular markers to enhance innovative breeding strategies.