



Back to nature: candidate genes, population genomics and prediction of maladaptation in natural populations

Santiago C. González-Martínez, Ricardo Alia, Katharina B. Budde, Andrew J. Eckert, Delphine Grivet, Myriam Heuertz, Juan-Pablo Jaramillo-Correa, Maria Mayol, Christophe Plomion, Miquel Riba, et al.

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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 from 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.

Back to nature: candidate genes, population genomics and prediction of maladaptation in natural populations

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Population and ecological genomics hold promise to identify relevant drivers of genetic adaptation to climate, as well as the relevant genes and gene networks associated with this process. Most important variation for adaptation is expected to be polygenic. However, most research to date has been based on single loci. Moreover, there is an urgent need to establish field experiments that help connecting molecular variation with fitness surrogates in a wide variety of natural environments. In this talk, we first provide a conceptual framework for population genomic studies to better understand the genetic bases of adaptation, in particular in reference to recent progress in human genetics. We also highlight the difference between “mutational” and “allelic” variation, which may underlie the highly contrasted results obtained from QTL and association genetics studies in terms of allelic effects, as well as explain the higher than expected success of candidate gene studies (in comparison with larger studies based on less well characterized markers). Second, we develop different case studies in European conifers, providing evidence on molecular adaptation to climate in two widespread species with highly contrasted population structure, the maritime pine (*Pinus pinaster* Aiton) and the English yew (*Taxus baccata* L.). In both cases, common gardens and quantitative genetic analyses of fitness-related traits were fundamental to either identify selection drivers (e.g. continentality in yew) or to validate genotype-environment associations (in maritime pine) by associating allelic make-up with fitness under extreme environmental conditions. For maritime pine, we also present preliminary results on the relevance of polygenic adaptation to climate, and on how studies that consider gene interactions may overcome previous limitations to identify relevant adaptive variation in this species. Finally, current studies at local spatial scales in different conifers and their comparison with rangewide adaptation patterns stress the need to explore different geographical scales of genetic adaptation.