Genome discovery of deep frost-tolerant eucalyptus for breeding and molecular ecology

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ProCoGen final open conference
Promoting Conifer Genomic Resources
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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.

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In contrast to some instinctive expectations, frost tolerance becomes increasingly a concern in areas experiencing rapid climate changes. Eucalypts leading breeders as well as landowners are seeking for cold-tolerant germplasm for expanding plantations towards colder areas as well as to secure wood and biomass production at places already subjected to severe sudden frosts. From an ecological point of view, eucalypts constitute with oaks another model system of species complexes with clinal variations among ecotypes of huge interest for understanding forest tree adaptation to the environment and climate change and ecosystem/community genetics (Kremer *et al.* 2014, Whitham *et al.* 2006, Crutsinger 2015). FCBA has been breeding frost-tolerant eucalyptus for about 50 years, focusing on E gunnii and E dalrympleana. FCBA varieties have been used for decades as models for genomic and physiological investigations by the Plant Science Laboratory (LRSV, in Toulouse, team 2), leading to significant results regarding the dissection of molecular processes related to cold response and wood formation. Remarkably, several key genes involved in the biosynthesis of lignin and the regulation of the secondary cell wall formation were first cloned in *E. gunnii*. The earliest public releases of large sets of ESTs in *Eucalyptus* were from *E. gunnii*. Recently, the first genetic map and some *de novo* genome sequencing has been performed for one reference *E gunnii* genotype. We propose to go further, sequencing also a *E dalrympleana* whole genome and resequencing a number of individuals from natural populations as well as the breeding population. Comparative studies with the E. grandis reference genome will improve our understanding of the molecular bases, evolutionary history and genomic organization of frost tolerance and wood production in *Eucalyptus*. In addition, these genome sequences will constitute a highly valuable resource to further dissect the gene flow between and within species of the *Eucalyptus* species complex of the Tasmania central plateau and shed a new light on the associated ecosystems.

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