Evidence of intense chromosomal shuffling during conifer evolution

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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 form external attendees and **ProCoGen** members will be included in

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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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While recent advances have been gained on genome evolution in angiosperm lineages, virtually nothing is known about karyotype evolution in the other group of seed plants, the gymnosperms. In this work, we used high density gene-based linkage mapping to compare the karyotype structure of two families of conifers (the most abundant group of gymnosperms) separated around 290 million years ago: Pinaceae and Cupressaceae. We propose for the first time a model based on the fusion of 20 ancestral chromosomal blocks that may have shaped the modern karyotpes of Pinaceae (with n=12) and Cupressaceae (with n=11). The considerable difference in modern genome organization between these two lineages contrasts strongly with the remarkable level of synteny already reported within the Pinaceae. It also suggests a convergent evolutionary mechanism of chromosomal block shuffling that has shaped the genomes of the spermatophytes.