



HAL
open science

Epigenetic dynamics associated to growth and adaptation

Luc Harvengt, Carmen Díaz-Sala, Maite Cervera, Grégoire Le Provost, Carl Gunnar Fossdal

► **To cite this version:**

Luc Harvengt, Carmen Díaz-Sala, Maite Cervera, Grégoire Le Provost, Carl Gunnar Fossdal. Epigenetic dynamics associated to growth and adaptation. ProCoGen final open conference, Promoting Conifer Genomic Resources, Nov 2015, Orléans, France. 75 p. hal-02741309

HAL Id: hal-02741309

<https://hal.inrae.fr/hal-02741309>

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.



Epigenetic dynamics associated to growth and adaptation

Luc Harvengt¹, Carmen Diaz-Sala², Maite Cervera³, Grégoire LeProvost⁴, and Carl Gunnar Fossdal⁵

¹ FCBA Institut Technologique Forêt Cellulose Bois-construction Ameublement (France)

² University Alcala de Henares, Spain

³ INIA-CIFor, Madrid, Spain

⁴ INRA, France

⁵ NIBIO (previously known as NFLI), Norway

Epigenetic marks have been investigated in Maritime pine full sib families subjected to contrasted levels of artificial drought stress. The same plant material was used in other tasks of the project, mainly transcriptomic studies. P1-UAH & P2-INIA investigated the occurrence of differential methylation in cuttings from a cross between parents from natural population from Spanish regions of contrasted climate. Random methylationsensitive amplification uncovered some hundred anonymous loci experiencing methylation changes during or after the completion of artificial drought stress. P4-INRA studied methylation change at specific loci uncovered through a comprehensive transcriptomic and metabolomic approach in an intensively characterized Landes x Morocco mapping family (results will be lately available). P5-FCBA generated epigenetically –induced maritime pine somatic embryos of a model genotype already extensively characterized at metabolomics and transcriptomic level for further studies. P14-NFLI/NIBIO characterized sRNAs, miRNA and their target mRNA in Norway spruce plant material subjected to contrasting epigenetic-inducing treatment during somatic embryogenesis. Relationships with further plant development and chromatin modification (appreciated through ChIP-Seq) will be presented.