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► To cite this version:

Ana Carvalho, Clara Graça, Victor Carocha, Susana Pêra, Grégoire Le Provost. Novel and known microRNAs identified in vascular tissues in Scots pine and Maritime pine. ProCoGen final open conference, Promoting Conifer Genomic Resources, Nov 2015, Orléans, France. 75 p., 2015, ProCoGen final open conference. Promoting Conifer Genomic Resources. hal-02743542

HAL Id: hal-02743542

<https://hal.inrae.fr/hal-02743542>

Submitted on 3 Jun 2020

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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



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.



Novel and known microRNAs identified in vascular tissues in Scots pine and Maritime pine

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Among conifers, Pines have high economic importance mainly due to wood and resin production. In the last decade, several transcriptomic and proteomic resources were made available providing opportunities to identify major molecular players involved in xylogenesis and biotic and abiotic responses. Nevertheless, the understanding of post-transcriptional regulation mediated by miRNA in Pines remains scarce. MicroRNAs are small non-coding RNAs (21-24bp) that act by down-regulating mRNA expression either by cleavage or by translational repression, through direct base-pairing to target sites. Genome-wide identification of miRNAs and the perception of the impact of their regulatory roles on plant development and stress responses is susceptible to benefit the definition of strategies for wood quality improvement or stress response strategies. Here, we will present the first results on the identification of miRNA present in vascular tissues (developing xylem and phloem) and needle epidermis of two pine species (*P. pinaster* and *P. sylvestris*) of major economic and ecological importance in European forest. High-throughput sequencing of the 5 small RNAs libraries generated a total of 6,4M raw reads, from which 5.6M are considered mappable, with a size modal distribution (21nt, 32% of the reads). 5,832 miRNA candidate loci, including 44 known miRNAs already identified in other species (1,3 M reads) and 1,291 new high-confidence miRNA candidates (9,9M reads). The majority of the known miRNAs was already identified in *P. taeda* and *P. densata*. Seventy four miRNA sequences with highest abundance (number of reads higher than the average of 1059 reads) were selected for testing their presence in the several sampled tissues and genomes. Additionally, degradome sequencing analysis allowed us to detect 357, 312, 534, 1790 and 428 interactions between target genes and putative miRNAs for *P. pinaster* and *P. sylvestris*. The genomic resources presented here stand out with great relevance for the understanding of post-transcriptional regulation underlying the development of the vascular tissues and stress responses in conifers.

Acknowledgements

The authors thank the European project FP7-KBBE-2011-5/289841 (PROCOGEN). AC and VC thank FCT for SFRH/BPD/68932/2010 and SFRH/BD/72982/2010 Grants, respectively, co-financed by FSE/POPH-QREN. CG and SP thank the research grants in the frame of PROCOGEN. JAPP acknowledges the research contract in the frame of the EU BIO-TALENT (The Creation of the Department of Integrative Plant Biology) project submitted under FP7-ERACHairs-Pilot Call-2013 (Grant agreement n°621321).