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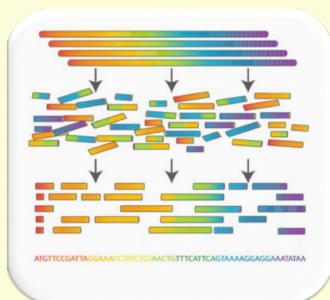
## ABSTRACT

“Promoting a functional and comparative understanding of the conifer genome – implementing applied aspects for more productive and adaptive forests” – ProCoGen is a research project funded by the European Commission 2012-2015 in order to investigate and increase our knowledge on the mechanisms underlining the expression of important adaptive and productive traits in our forest species. The latest technological advancements and innovations in genetic engineering and molecular biology can provide tree breeders with tools for precise selection and help gear up for the future global climatic change scenario. They can also facilitate the maintenance of high quality standards of European forests as sustainable production tools. ProCoGen not only aims at integrating the activities of 20 European research groups, across 11 European nations involved in conifer genome research, but also aspires to strengthen international collaboration with two research groups in Canada. ProCoGen has a total budget of about €7.7million and is supported by EC funding of € 5.9million under the 7th Framework Programme for Research and Innovation. This poster summarizes scientific project achievements to date, such as development of genomic resources (sequencing and re-sequencing in *Pinus sylvestris* and *P. pinaster*), discovery of adaptive capacities (transcriptomics and metabolomics analyses, differential gene expression studies), comparative genomics (COS marker development and exome capture), computational genomics (genome assembly, SNP identification, phylogenomics), and translational genomics (breeding simulation, genomic selection, fingerprinting and traceability), as well as efforts to disseminate project results.

## OBJECTIVES

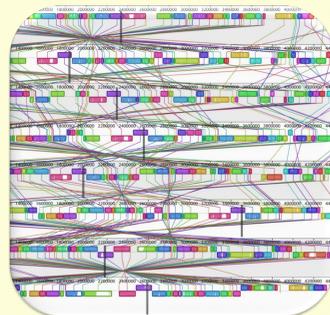
- To develop integrative and multidisciplinary genomic research in conifers, using high-throughput platforms for sequencing, genotyping and functional analysis
- To unravel genome organization and to identify genes and gene networks controlling important ecological and economic traits

## OVERVIEW of work progress in 30 months



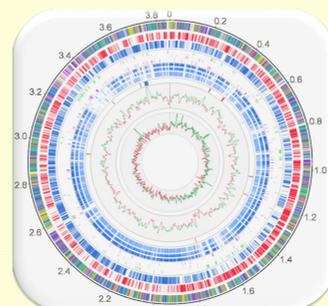
**Genomic resources** Sequencing of *Pinus sylvestris* and *Pinus pinaster* are in progress. The preliminary results have been used for comparative studies using data available from other conifer species. SNPs (single nucleotide polymorphisms) are being traced using probes from the unigenes assembly of *Pinus taeda*. A SNP database for *Pinus pinaster* has been set up and is adding on to the existing Sustainpine database established on the Sustain pine project.

**Adaptive capacity** Protocol for transcriptomic analysis of conifers using laser capture micro-dissection and 454 pyrosequencing has been developed by Cañas et al. (2014) as a part of this work package. Preliminary transcriptomic analysis has shown differential gene expression in 14 different cell and tissue types under study. Epigenetic studies on somatic embryos of *Pinus sylvestris* showed temperature dependent alteration of gene expression. ProCoGen supported the epigenetic studies on *Pinus pinea* as well (Sáez-Laguna et al. 2014).



**Comparative genomics** A pilot exome capture has been designed to be tested on different Pinaceae species. Broad scale comparison and microsynteny studies have been performed between *Picea abies* and *P. glauca* (De La Torre & Ingvarsson 2013).

**Computational genomics** Bioinformatic tools have aided the development of COS markers based on available sequence data from six different conifer species. A preliminary catalogue of SNPs from *Pinus pinaster* has also been compiled.



**Translational genomics & breeding tools** A proof of concept experiment is being developed for the implementation of genomic selection in maritime pine. The first preliminary study has given insight into genome wide diversity patterns and linkage disequilibrium in breeding populations (Plomion et al. 2014).

**Dissemination and integration** Apart from publications in peer reviewed international journals, ProCoGen partners have also been actively participating and disseminating the outcomes of this project at various national and international events. This project has also been offering interactive platforms and possibilities of transferring knowhow through workshops, staff exchange programme and via internet. So far, two training and two dissemination workshops have been held. Most of the presentations can be viewed or downloaded from the project homepage.

## PUBLICATIONS

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Poster information compiled by Dr. Vedhu Krystufek (BFW Vienna)

Images: "Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects." *Biol. Procedures Online* (2009) Commins, J., Toft, C., Fares, M. A.; Georg Frank, BFW, Vienna Austria & Dry earth on Sonora desert Tomas Castelazo; Figure 1 from Darling AE, Miklós I, Ragan MA (2008). "Dynamics of Genome Rearrangement in Bacterial Populations," *PLOS Genetics*. DOI:10.1371/journal.pgen.1000128; Monnet C, Loux V, Gibrat J-F, Spinnler E, Barbe V, et al. (2010) *The Arthrobacter arilaitensis Re17 Genome; Polytree nursery pine breeding; Didier Bert INRA, France.*