

Promoting a functional and comparative understanding of the conifer genome- implementing applied aspects for more productive and adapted forests



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SUMMARY

In the midst of a climatic change scenario, the genetics of adaptive response in conifers becomes essential to ensure a sustainable management of genetic resources and effective breeding. Conifers are the target of major tree breeding efforts worldwide. Advances in molecular technologies such as, next-generation DNA sequencing, could have an enormous impact on the rate of progress and achievements made by tree breeding programmes. These new technologies might be used not only to improve our understanding of fundamental conifer biology, but also to address practical problems for the forest industry as well as problems related to the adaptation and management of conifer forests. In this context, ProCoGen will address genome sequencing of two keystone European conifer species. Genome re-sequencing approaches will be used to obtain two reference pine genomes. Comparative genomics and genetic diversity will be closely integrated and linked to targeted functional genomics investigations to identify genes and gene networks that efficiently help to develop or enhance applications related to forest productivity, forest stewardship in response to environmental change or conservation efforts. The development of high-throughput genotyping tools will produce an array of pre-breeding tools to be implemented in forest tree breeding programmes. ProCoGen will also develop comparative studies based on orthologous sequences, genes and markers, which will allow guiding re-sequencing initiatives and exploiting the research accumulated on each of the species under consideration to accelerate the use of genomic tools in diverse species. ProCoGen will integrate fragmented activities developed by European research groups involved in several ongoing international conifer genome initiatives and contribute to strengthening international collaboration with North American initiatives (US and Canada).

Objectives

To develop integrative and multidisciplinary genomic research in conifers, using high-throughput platforms for sequencing, genotyping and functional analysis, to unravel genome organization to identify genes and gene networks controlling important ecological and economic traits, such as those related to control and reduction of climatic change impact in relation to growth, drought and cold stress.

Developing genetic resources

- Sequencing the complete genomes of two conifer species (*Pinus sylvestris*, *Pinus pinaster*) integrating out comes of international conifer genome sequencing initiatives
- Re-sequencing for SNP discovery to capture the extent of variation in each species

Discovery of adaptive capacities to ensure basic and applied outcomes

Genomic based approaches for studying functional regulation of growth and adaptive responses to abiotic stresses. This project will complement the research efforts of other FP7 projects, which already addressed the response of conifers to biotic stress

Comparative genomics for understanding conifer evolution, effective management and breeding

Integration of genomic resources developed in different conifer species in Europe and North America to perform comparative studies for understanding their evolution and an effective transfer of information to enable the study of other conifer species

Translational genomics: quantitative genomics for breeding and resource management

To identify and quantify associations between variation at the genotypic and the phenotypic levels to enable genome assisted breeding and natural resource management

Genome annotation

Structural annotation - will identify and map protein-coding genes, transposable elements and non-coding genes on the assembled genome. Gene families will be built for further downstream bioinformatics analyses.

Functional annotation - software tools will be used to link potential regulators and targets, in order to infer transcriptional regulatory networks

Integrating European and Trans-Atlantic Initiatives

Linked Resources

USA (*Pinus taeda*)

- DOI Grant: Investigation of pine genome structure using BACs/ BAC sequencing MS State
- DOI Grant: EST discovery in conifers UGA
- DOI Grant: Comparative ReSeq. in Pinaceae and Loblolly Pine Genome Project
- USDA Grant: PineRefSeq UC Davis

Collaborated Resources

Swedish Spruce Genome Project (*Picea abies*)

Europe (*Picea abies*, *Pinus sylvestris*, *Pinus pinaster*, *Picea sitchensis*)

- Previous EC Grant projects: TreeSnips, NoE Evoltree, Treebreedex, DIGENFOR
- Ongoing EC Grant projects: NovelTree, FoResTTTrac, SustainPine

Canada (*Picea glauca*, *Picea mariana*, *Picea sitchensis*)

Genome Canada Grant:

- Treenomix 1 & 2 UBC
- Arborea 1 & 2 Ulaval
- SMartForest Ulaval & UBC

IMPACT

ProCoGen will contribute towards the expected impact of the call by developing an integrative research programme on conifer species combining the use of the most appropriate high-throughput (HT) technologies with advanced bioinformatics to generate new knowledge to improve forest productivity through targeted breeding programs based on better adapted material to regional climatic threats, forest stewardship in response to environmental change as well as conservation efforts. This project will build upon previous networking efforts of European initiatives on forest ecosystems and aims at integrating presently fragmented activities of European research groups. This integrative project will greatly contribute to strongly reinforce the forefront position of the European research on conifer genomics and bioinformatics.

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Pinus pinaster



Pinus sylvestris



Picea abies



Picea sitchensis

ProCoGen model tree species represent two pine sub families and different European regions

Photos sources (from top to bottom): *Pinus pinaster* male cones, Maresko Bloock; *Pinus sylvestris* vnc. Anasta Sillip and cones, Sillip; *Picea abies*, Leo Michels; *Picea sitchensis*, Gerald and Bart Coust; California Academy of Sciences



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