ProCoGen

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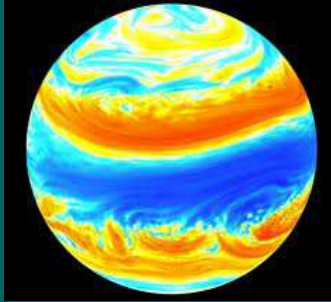
Why Conifers?

- Conifers include 600–700 species worldwide

- Pinaceae is the largest extant family with approximately 220 – 250 species

- Dominate the temperate regions of the northern hemisphere & their distribution ranges from sub arctic to tropic

- Represent the largest terrestrial carbon sink

- Immense economic and ecological importance

- Conifer plantations for wood production account for 60% of worldwide reforestation and cover nearly 800 000 square kilometres (FAO, 2007 State of the World's Forests)

Threats

Global climate change

Depletion by certain diseases, pests and fires

Harvesting at a faster rate than regeneration either naturally or artificially

Challenges

- Conifers have a large genome size (20-30 Gbp), more than 7 times the size of the human genome

- High frequency of repetitive sequences

Key

Recent advancements in:

Microarray and high-throughput sequencing techniques

Next-generation sequencing

Bioinformatic tools

ProCoGen

EU large scale integrating project under Knowledge-Based

Bio-Economy (KBBE)-7th Framework Programme (FP7)

Duration: 4 years

1st of Jan. 2012

Total cost: EUR 7 786 898
EU contribution: EUR 5 978 303

Coordinator:

Prof. Carmen DÍAZ SALA, University of Alcala, Spain

Dr. Maria-Teresa Cervera, INIA-CIFRO, Spain

Objectives

To develop an 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

Integrating European and Transatlantic Initiatives

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

Swedish Spruce Genome Project

Europe
Previous *EC grant* projects: TreeSnips, NoE Evoltree, Treebreedex, DIGENFOR
Ongoing *EC grant* projects: NovelTree, FoResTTrac, SustainPine

Canada
Genome Canada grants
Treenomix 1 & 2 *UBC*
Arborea 1 & 2 *ULaval*
SMarTForest *Ulaval/UBC*

Pinus taeda
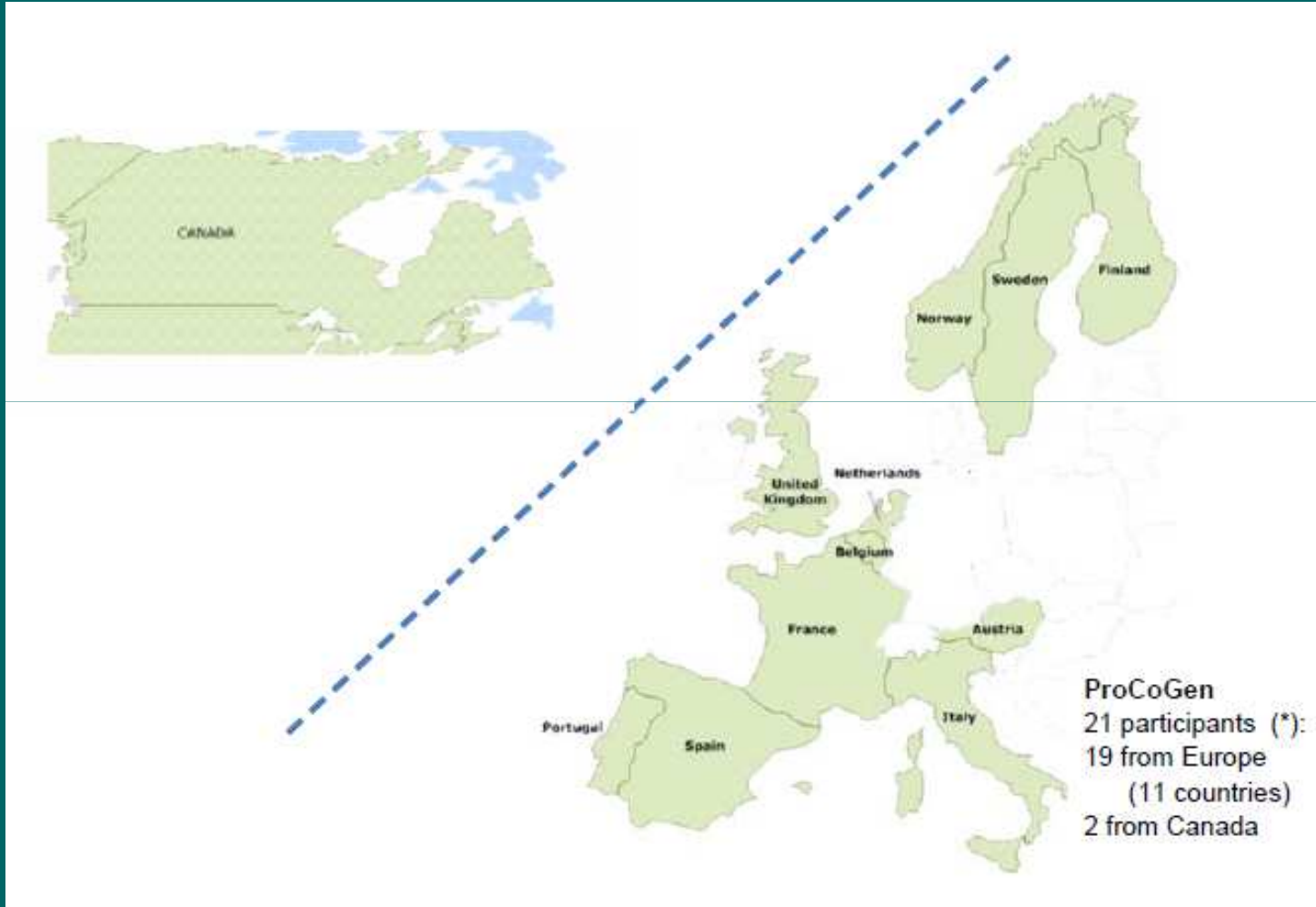(main focus)

Picea abies

Pinus sylvestris

Pinus pinaster

Picea sitchensis

Picea glauca
Picea mariana
Picea sitchensis

Linked Resources

Collaborated Resources

Partners

ProCoGen
21 participants (*):
19 from Europe
    (11 countries)
2 from Canada

ProCoGen model tree species:

Maritime pine (*Pinus pinaster*)
Atlantic and Mediterranean Europe

Scots pine (*Pinus sylvestris*)
Central and Northern Europe

Norway spruce (*Picea abies*)
Central and Northern Europe

Sitka spruce (*Picea sitchensis*)
of high economic interest in UK

Strategy

- Develop an integrative genomic research programme in model conifer species

- Develop new bioinformatic solutions

- Comparative studies in conifers

- Establish an effective molecular-assisted pre-breeding capacity in Europe

- Provide training in emerging technological and translational approaches & dissemination of results
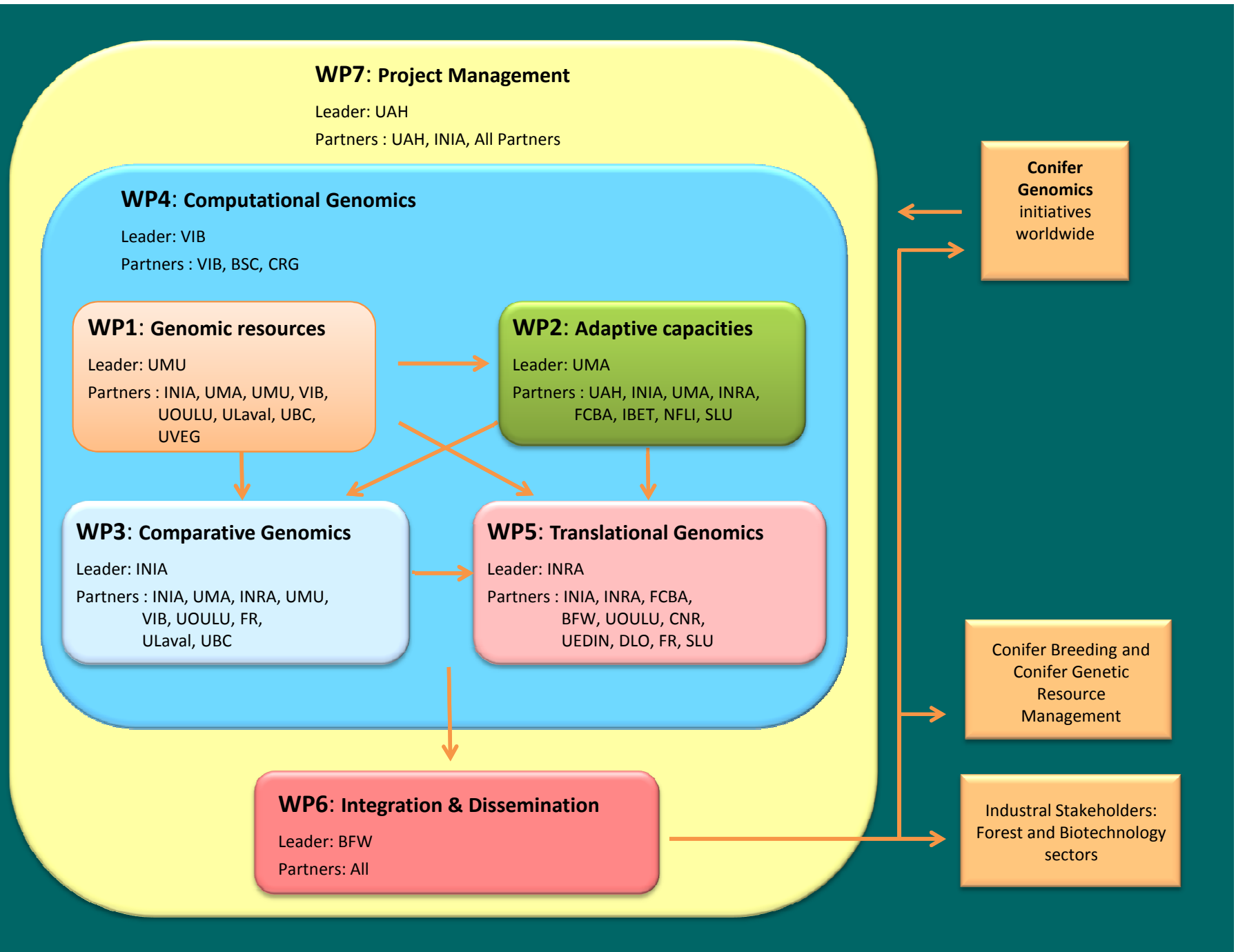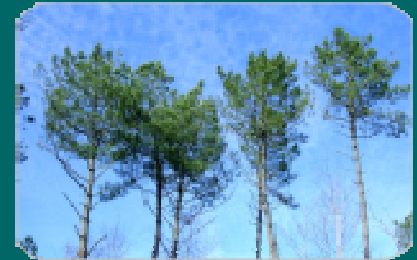
WP 1 Development of Genomic Resources
Leader Dr. Pär K. Ingvarsson (UMU)

Objectives:

a) Two complete conifer genomes will be sequenced

b) A large set of SNPs will be developed for these species through exome re-sequencing from pools of individuals samples

WP 2 Discovery of adaptive capacities to ensure basic and applied outcomes

Leader Dr. Francisco M Canovas (UMA)

Objectives:

Genomics-based approaches for the study of the functional regulation of growth and adaptive responses to abiotic stresses.

Main focus

- Transcriptome sequencing for protein coding gene annotation, transcript expression profiling and transcriptome dynamics

- Small non-coding RNA profiling and the discovery of novel small RNA genes

- Understanding the regulation of transcription

- Epigenetic dynamics of candidate genes associated with traits of interest

WP 3 Comparative Genomics to understand conifer evolution and effective management and breeding
Leader Dr. María-Teresa Cervera (INIA-CIFOR)

Objectives:

Integration of genomic resources developed in different model conifer species

Comparative studies for understanding their evolution

Main focus

- Identification of COS (Conserved Orthologous Set) markers based on transcriptomics data comparison and cDNA relative position in pine and spruce genetic linkage maps.

- Evaluate the level of synteny and conservation of gene order in Pinaceae

- Apply comparative mapping to orthologous gene-based saturated genetic maps.

- Evaluate if the colinearity observed at chromosomal level is further retained at the molecular level based on genome sequence data at BAC level and whole genome level.

- Infer gene and sRNA function based on comparative transcriptomics

WP 4 __Computational Genomics__

Leader Dr. Yves Van de Peer (VIB)

Objectives:

Provide structural and functional annotations in a consistent manner for the available transcriptomic and genomic data.

Inferring transcriptional regulatory networks and genome-wide system biology analyses

Data management for all consortium partners

Main focus

- Assemble, annotate, analyze and manage genomic and transcriptomic data

- COS marker development among the different conifer species

- Gene families construction and analysis as a resource for further downstream analyses

Main focus

- Apply state-of-the-art computational methods to ensure fast and accurate data processing and management

- Disseminate the data produced by different partners through user friendly, dynamic and integrated online portals

WP 5 Translational Genomics: Quantitative genomics enabling breeding and resource management

Leader Dr. Léopoldo Sanchez (INRA)

Objectives:

The aim of this WP is to identify and quantify associations between variation at genotypic and phenotypic levels to enable genome-assisted breeding and resource management.

Main focus

- Generate data and tools to identify and quantify associations between nucleotide polymorphisms and phenotypic trait variation.

- Evaluate different breeding scenarios involving multi-generation Marker-Assisted Selection (MAS) and Genomic Selection (GS) by computer simulations.

- Evaluate by deterministic approaches the economical efficiency of the breeding scenarios involving MAS and GS.

- Implement molecular markers for core collection definition and forest reproductive material management and tracking.

WP 6 Integration with conifer genomics initiatives worldwide & Dissemination and Training

Leader Dr. Berthold Heinze (BFW)

Objectives:

Integration of efforts made on this project with similar large-scale initiatives.

Build an international conifer genomics network comprising of representatives of relevant projects and initiatives.

To ensure proper dissemination of project results to the scientific community worldwide and other stakeholders in the forestry sector.

Main focus

- To link up with the European Forest Institute "Evoltree" specific program (perpetuation of the EC-funded Evoltree project that ended in Oct. 2010, NOVELTREE, TREEBREEDEX, FoResTTraC) and other international projects on conifer genetics.

- To transfer knowledge and technology from leading partners to other project participants.

- To transfer applied outcomes of the project, and promote conifer genomics in general to organisations involved in conifer breeding and management.

- To interact with key European organisations in research and development as multipliers and end-users of the project results.

- To create a pool of technology providers for interaction with forest research.

- To establish a Technology Transfer Cooperative Group as an internet blog.

- To construct the project website

www.procogen.eu

WP 7 **Management**

Leader Dr. Carmen Diaz-Sala (UAH)

Objectives:

Administrative and financial coordination

Survey of activities

Optimise the use of fast evolving technologies and development of new strategies.

Efficient management of the entire organisational setup and ensure conformity to EC rules and procedures.

Contribution to Research

a) Deciphering the genome structure of several model conifer species

b) Identification of molecular plasticity associated with growth and adaptive response

c) Comparison of gene and gene networks governing the response of conifers to climate change

d) Inferring information that can be transferred to other conifer species

e) Designing tools for genome-assisted breeding and resource management

THANK YOU

THE END