

## Workshop on “Advancements in Conifer Genomics”

### IUFRO Tree Biotechnology meeting, 09.06.2015, Florence, Italy



The [IUFRO Tree Biotechnology](#) meeting was attended by around 280 people from 42 different countries. An open discussion workshop on “Advancements in Conifer Genomics” was organised at the end of session I on “Tree Genomics and Climate Change” by the representatives of the conifer genomics initiatives: Dr. Carmen Diaz-Sala (Spain), Dr. Maria-Teresa Cervera (Spain), Dr. Nathaniel Street (p.p. Dr. Pär Ingvarsson, Sweden), John Mackay (Canada) and Jill Wegrzyn (USA). They gave a short presentation about their project updates, current and future activities, and convergence among initiatives.

Dr. Nathaniel Street represented the [Spruce Genome Project](#) from Sweden on behalf of Pär Ingvarsson. He presented a short update on the *Picea abies* genome sequencing project. Extra fosmid pool data is being added to increase the coverage of the [previous assembly](#). New algorithms are being tested for achieving the best possible assembly. Continuous efforts are being made to obtain a genetic map. RNA sequencing is also being done for functional studies. He mentioned that a new version of the Norway spruce assembly would be available in autumn this year (2015), and the next step would involve finding genes in single scaffolds for further analysis. Genomic resources and general expression catalogues developed on this project have been made accessible via the [Congenie](#) web pages which are updated regularly.



New developments in the [PineRefSeq](#) project were presented by Dr. Jill Wegrzyn, co-PI of this project. She described the whole genome shot-gun sequencing strategy being followed for *Pinus taeda*, *Pseudotsuga menziesii* and *P. lambertiana* genome sequencing, and mentioned the current progress status of the same. A third [version 1.01](#) of the loblolly pine assembly has been made available on TreeGenes database. Version 2.0 is planned to be released by the end of 2015, which will be integrating PacBio sequencing data and fosmid pool resources, using SOAPdenovo2 and an updated version of Masurca.



Assembly strategy for *P. lambertiana* remained similar to *P. taeda* with the main difference being the usage of SOAPdenovo2 for better scaffolding and time efficiency. [Version 0.5](#) of *Pseudosuga menziesii* assembly data has also been released last month. The data generated on this project is being stored in the TreeGenes database for web-based search. GenSAS is also being employed for whole genome structural annotation.

Dr. Maria-Teresa Cervera briefly described the [ProCoGen](#) project, emphasising the collaborative efforts with international initiatives. She described the sequencing approach being followed for *Pinus sylvestris* and *Pinus pinaster*. Currently the assembly of the sequences is in progress and the first release is expected by the end of 2015. Population analysis of samples collected along the entire natural distribution range of these two species is being done using SNPs discovered on this project. Transcriptomic data is being analysed to understand the gene regulatory networks associated with growth and adaptive traits in *Pinus sylvestris*, *Pinus pinaster* and *Picea abies* (publications available on [ProCoGen](#) website). Comparative mapping is also in progress using data from the ongoing conifer genomics initiatives.



Dr. John Mackay threw light on recent Canadian projects: the [AdapTree](#) project aims at understanding genetics of local adaptation in conifer species; the [Taiga](#) project aims at identifying tree aggressors using genomic approaches; the [Tria](#) project, is dedicated to development of science-based strategies for combating the mountain pine beetle; [SmartForest](#), which was built upon genomic research conducted during the [Treenomix](#) and [Arborea](#) projects, focuses on further development of spruce marker technologies for sustainable forestry. He gave a brief presentation on SmartForest project updates, highlighting progress in *Picea glauca* sequencing and genomics. A shot-gun approach was followed to sequence a single diploid genotype of *Picea glauca* from western North America ([Biol et. al 2013](#)). An improved assembly and gene family analysis has been recently published online ([Warren R. L. et al. 2015 in press](#)) where a second draft assembly has been added by sequencing another genotype from eastern North America, thus representing two genotypes from distant geographic regions. Over 50 papers have been published on various aspects of genomics during the course of this project. Future plans would involve collaboration with ProCoGen. Prospective research proposals would aim at developing reference transcriptomes for seven conifers of eastern Canada; sequencing of black spruce; comparative analysis of SNPs and structural variations; comparative transcriptomic profiling e.g. for studying differences at population level; and studies on abiotic and biotic stress.



The presentations were followed by an open discussion on future research and challenges. The following suggestions and proposals were put forward by the chair and participants:

Improvement of contiguity of the assemblies

Collaboration for improving assemblies

Working towards inclusion of more tree species and developing tools for comparative analysis

Developing cost effective tools for genotyping for population analysis for breeding programmes

Intensifying transfer of information to tree breeding and other applied fields

Establishment of functional analysis platforms

Making the data integration from various databases more user-friendly and consistent

Addressing issues pertaining to environmental changes and globalisation

Development of a reference quality genome: would be highly time-consuming and the gaps in the assembly still pose a challenge. It was proposed that one could work on physical mapping and long read technologies, perhaps starting with forming consortiums and intensifying work on few selected genomes, to develop highly refined assemblies which could then be applied to larger number of species. This would be beneficial to all and would also be cost effective and efficient.

Applicability of ongoing genomic research on species of the northern hemisphere to species of the southern hemisphere was also discussed. For instance integrating *Pinus radiata*, which is of commercial interest, could find funding more easily. Depending on the purpose for e.g. wood formation or adaptability, one could form consortiums to address these issues more specifically.

To conclude the session, Dr. Diaz-Sala gave a brief presentation on research and collaboration possibilities within the framework of Horizon 2020, as well as other possibilities of project financing like ERA Net, JPI, EUREKA, COST etc. Dr. Wegrzyn talked about the financing possibilities within the USA and sources for funding international collaborations.