

4th AFORGEN meeting report (19.-21.6.2015)

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AFORGEN is a network of scientists from Europe and the US who share an interest in the genetic resources of high mountain forests. The aim of the network is an intensive exchange of information and the development of a cross-border research network for the study of adaptation processes in alpine forest ecosystems. Forests and trees are the main components of most alpine ecosystems that provide habitat for a variety of macro- and micro-organisms. It is therefore important to study the genetic and genomic mechanisms, so that these key elements are able to carry out their functions. Here latest genetic and genomic technologies. The attention is directed primarily to the Alps in a broader sense, and other mountain regions in the Mediterranean, the temperate, boreal and Arctic regions to be involved. After meetings in South Tyrol, Austria and Switzerland in previous years, the fourth meeting has taken place in Ramsau near Berchtesgaden (South Bavaria). 16 scientists from six countries have participated and presented their latest research. The species of this meeting was *Pinus cembra*, *Pinus sylvestris*, *Larix decidua*, *Picea abies*, *Picea orientalis*, *Abies alba* and *Fagus sylvatica*. The meeting was a good possibility for young researchers to present their work, which was mostly preliminary results and receive valuable feedback from experienced senior researchers and experts in the field.

A phylogeographic and genomic study in stone pine with samples from the entire distribution range was presented (Lendvay et al., WSL), trying to link neutral and SNP variation to paleo data in order to locate possible refugia. To enlarge the picture and “go adaptive” the genetic basis of local adaptation in *Pinus cembra* is studied in the ongoing project “Picadapt” (Rellstab et al., WSL), which aims to detecting signatures of selection by population and landscape genomic approaches. Transcriptome analysis to detect candidate genes connected to climate change variables, SNP genotyping of elevational transects and environmental association analyses will be the main tools used in the project. Another study focused on anthocyanins contents, profiles and characteristics in high elevation conifers (in *P. cembra* and *Larix decidua*) involved in mechanisms for sun protection in alpine forests in the Austrian Alps (Heinze et al., BFW). The main aim of this study was to analyze transcriptomes of flowers/cones at several developmental stages and in needles for comparison and by that to find the underlying genes in the anthocyanin pathway.

An adaptive approach to the sequencing of large conifer genomes (PineRefSeq) was presented stating the challenges of sequencing conifer genomes compared to other plant genomes (Neale et al., UC Davis). The guiding principles thereby will be to develop the needed technologies and adapt to future requirements and to follow an open access policy. The species involved are *Pinus taeda*, *Pinus lambertiana* and *Pseudotsuga menziesii* and the applied tools are whole genome shotgun and fosmid pool sequencing. After identifying the number and function of the genes, the information can be used in marker assisted selection e.g. for disease selection or use the tools for landscape genomic studies.

Further progress in genetic studies of Carpathian pine populations was reported (Tóth et al., University of Budapest). Phylogeographic structure of natural populations will be combined with historical aspects and demography and thereby will provide the basis for studying the molecular background of adaptive traits.

For *Picea sp.* several studies were presented (Sullivan et al., UPSC), one on spruce phylogenomics using whole plastid sequencing in order to disentangle the competing hypothesis of current *Picea* phylogenies. Geostatistical biogeography and coast-to-coast phylogeography of *P. abies* complex with genotyping by sequencing are the future plans in this study. The effectiveness of genetic resource conservation was reported for *Picea orientalis* (Kaya et al., METU), comparing the genetic diversity of managed and conserved stands of the species in Turkey. The study used nuclear microsatellites transferred from other spruce species and compared diversity values between populations of *P. orientalis* and other spruce species. One breeding project focused on “breeding for browsing resistance” in *Picea abies* (Trujillo-Moya et al., BFW). Red Deer may have preferences for certain phenotypes to be browsed and to test for genetic causes of the phenotypic variation in browsing damage, the phenotypic differences will be related to genes putatively associated with browsing “resistance”.

Last but not least a project update for “Adapt” was presented (Frank et al., WSL), focusing on the question if quantitative genetic variation of *Fagus sylvatica* is related to environmental factors. For *Picea abies* and *Abies alba* results were already given at the last meeting. The main aims of the study are to quantitatively assess genetic variation in potentially adaptive traits of spruce, fir and beech in Switzerland, to identify environmental factors related to variation in adaptive traits, to evaluate the risk of maladaptation of today’s populations to future climates and to draw implications for forest management (guidelines for seed movement and seed sources).

An excursion to the national park Berchtesgaden was led by Dr. Roland Baier (deputy head of the ASP), presenting forest management in an alpine national park and natural forest dynamics in the Northern Limestone Alps and discussing genetic implications.

More information on the meeting can be found on the web or by directly contacting AFORGEN network members:

<http://alpforests-gen.fem-environment.eu/home/>



Excursion to the national park Berchtesgaden; walking in spruce dominated forests.