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STSM Topic: Genetic diversity - a source of information useful in breeding and conservation of forest

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Report

The levels of genetic variability and diversity significantly influence the adaptive abilities of the forest populations and species and needs to be understood for effective implementation of preservation programmes and the balanced management of forest trees. Knowledge of the genetic variability distribution in the native populations is important for the preservation of gene resources and for collecting and exploiting forest reproductive material (FRM) (Geburek, Turok 2005).

The purpose of my STSM was to develop my knowledge of the various tools for analysing genetic variability, which is the basis for the adaptation of forest trees, to develop my analytical laboratory skills and appreciate the applications of the statistical methods that are essential for the study of population genetics.

During my scientific mission in the laboratory of Dr Vendramin at the IGV-FI/CRN I had the opportunity to take a part in the whole research procedure to establish the genetic diversity of different species using SSR markers. I worked with the *Abies alba*'s tissue and *Picea opeatica*'s tissue that are representative of the most important species in Polish forest management – fir and spruce. I was involved in the following levels of analysis:

- 1) Preparation of samples for molecular analysis: DNA extraction from plant material using Qiagen kit procedure to a plates;
- 2) Evaluation of the quality and quantity of the DNA extracts;
- 3) Optimization of DNA amplification and multiplex PCR;
- 4) Separation of the PCR products on the automated sequencer and fragment analysis of SSR;

The infrastructure and equipment in the laboratory of Dr Vendramin at IGV-FI/CRN is very sophisticated and I was given the opportunity to use all the necessary tools for genetic analysis namely: a centrifuge, PCR thermocyclers, automatic DNA sequence (Applied Biosystem 3500) and GeneMapper Software to visualize and score the sequences of DNA.

The assessment of the genetic structure of populations is important for evaluation of the demographic processes influencing the pattern of nucleotide diversity in forest populations throughout the whole of Europe. Only the collaboration by institutes in different countries gives researchers the opportunity to obtain plant materials of trees to undertake a globally analysis of their genetic structure and to carry out interdisciplinary research.

This STSM gave me, as an Early Stage Researcher, knowledge of the modern genetic methods that will be used to analysis the differences in the Polish populations of forest trees and the possibility of further collaboration with Dr Vendramin's laboratory at the IGV-FI/CRN. I would like to greatly thank the Cost Office and Mr G.G. Vendramin for giving me this opportunity.

Geburek and Turok 2005. Conservation and management of forest genetics resources in Europe. Arbora Publisher, Zvolen and IPGRI, Rome, p: 3-10