DESCRIPTION FOR THE GENERAL PUBLIC

Current geographic patterns of genetic diversity within species reflect their responses to expansion and contractions of their habitats associated with glacial cycles. During their evolution, forest trees have migrated (by seed dispersal) and adapted to new environments. This 'local adaptation' caused changes in the parts of the genome that control a tree's ability to survive and reproduce in different climates. As a result, forest trees often show strong differences between populations in observable characters (phenotype), for example in height or shape, in timing of growth, or in ability to withstand cold temperatures or water deficit. Although a lot of research has been done on differences in tree phenotype and how this is shaped by the environment, very little is known about the mutations, genes and biochemical pathways involved. However, information about the genes that control adaptive traits would be useful for conservation, restoration and forest management, particularly in the face of future climate change. The aim of the project is to verify hypothesis related to the selective and historical processes that influenced development of species phenotypic variation. The project will focus of Scots pine that is one of the most important plant species forming large forest ecosystems of great ecological, economic and social importance in Europe and Asia. The project will use newest genomic resources and advanced genotyping methods to study thousands of polymorphic sites across the Scots pine genome in a group of a few hundred individuals sampled from populations from different locations. The molecular data will be used for assessment of the species population variation and identification of genomic regions under selection. It is expected that predicted environmental changes will negatively affect productivity and mortality rates of forest trees that constitute over three quarter of terrestrial biomass. The outputs of the project will significantly advance understanding of historical processes in producing patterns of divergence between populations including genetic variation that underlies adaptation and survival of populations in local environments. Therefore, the project results will be especially beneficial for conservation and silviculture in the face of rapidly changing environments. The project data will contribute to evolutionary biology, population genetics and molecular ecology.