

Description for the general public

Forests play a pivotal role in nature, harboring more than half of terrestrial biodiversity. Tree species that creates forests form populations occupying a broad range of environments. Forests need to adapt to this environments to survive and succeed. Research show differentiation between populations in many traits including growth performance, resistance to low temperature or drought. This variation results from adaptive response of populations to environmental gradients and natural selection of individuals that show best performance. Historical processes underlying current distribution range of the species and evolutionary processes related to development of phenotypic differentiation are mostly unknown. However, knowledge about population history of forest tree species including their recolonization routes and admixture patterns of populations of different origin is important for understanding of the genetic basis of adaptive variation and possible responses of forest ecosystems to environmental change. The project will study four ecologically and economically important pine species largely distributed in Europe. Three of them including Scots pine, Dwarf mountain pine and Peat-bog pine occurs also in Poland, and the fourth one, Mountain pine, grows in southern Europe. Polymorphisms at a set of new genetic markers of mitochondrial and nuclear genomes will be studied in dozens of populations from the species distribution range in Europe. Molecular analyses will be conducted with the use of novel DNA sequencing methods and they will provide new data for assessment of population structure and history within the species range. The project will deliver new knowledge about the mechanisms underlying differentiation between populations that is important for conservation and management of forest resources worldwide. The project is pioneer in application of newest genetic data and advanced laboratory and analytical methods for nucleotide polymorphisms study of hundreds of individuals from European distribution range of the species. The results will allow verification of the research hypothesis related to population history and evolution of the investigated taxa. The results will contribute to development of research in population genetics and landscape genomics of forest trees.