

DESCRIPTION FOR THE GENERAL PUBLIC

Within the range of species occurrence and in response to environmental gradients, plants have developed populations in which individuals differ from each other, e.g., in morphological structure and ability to survive in a given environment. Closely related plant species can also interbreed in their contact zones, creating hybrids, which often show better adaptation to the environment in a given population than the parental species. Such adaptation is one of the key features of living organisms, however, the genetic basis of differentiation of hybrid types and populations of pure parental species subject to various environmental pressures are largely unknown. The proposed research concerns the analysis of the processes of local adaptation and differentiation of populations at the DNA level, and will use the contact zones of three closely related pine species of great ecological and/or economic importance in Poland including Scots pine, dwarf mountain pine and peat bog pine. The research will involve three native hybrid populations with different species composition, located in the south of Poland. In addition, the project will use reference populations of pure species from lowland, mountain, and peatland areas in Europe to investigate how adaptation to different environmental conditions affects patterns of population genetic variation. Comparison of this variability in a group of over a thousand trees, including hundreds of hybrid individuals analyzed for thousands of genetic markers, including those potentially responsible for population differentiation, will allow us to better understand the processes and identify genes that affect adaptive variability in hybrid zones and pure species stands. The obtained data on the distribution of the patterns of genetic variation segregated from generation to generation in the studied populations is of key importance for the correct modeling of their possible responses to climate change. The project will provide strong scientific outcomes in molecular ecology and population genomics, and the results will have practical implications in the development of conservation and management of the natural genomic resources of those important forest tree species, which are under strong pressure from ongoing environmental changes.