

Popular science summary of the project

Scots pine (*Pinus sylvestris* L.) is one of the most important tree species in the world, with respect to both ecology and economy. It forms pure stands as well as mixed forests with other species. The species occupies both lowlands and mountain regions. Scots pine has the largest range of all conifers that expands from the Arctic Circle in the north to Spain and Turkey in the south and from Scotland to the eastern part of Siberia. Genetic variation of Scots pine has been a subject of numerous studies that are crucial to assess variation within the species that results both from historical processes (e.g. migration after the last glaciation or range shifts of particular populations) and adaptive processes that lead to differences among populations that live and adapt to different environmental conditions. Previous studies have clarified the origin of Scots pine in Europe only partially. Nonetheless, genetic variation of Asian populations is poorly understood.

The aim of the project is to assess genetic variation of populations of Scots pine from Eastern Europe and Asia that have never been a subject of such studies. Furthermore, the next goal of the project is to describe mutual relations between Asian and European populations of the studied species. Apart from that, the proposal aims to verify the hypotheses concerning the origin of Scots pine in Central Europe and Fennoscandia. The studies have suggested that Scots pine in these areas may descend from the Balkan Peninsula and/or from Eastern Europe or Asia. The alternative hypothesis assumes that Scots pine in Central Europe and the Balkans descend from southern Siberia.

Fragments of mitochondrial and nuclear DNA will be used in the course of the project as effective markers allowing precise description of genetic variation of the studied populations. These markers will let us define mutual relations between Scots pine in Asia and Europe. Several dozen of populations from Asia, Eastern Europe, the Balkans, Central Europe and Fennoscandia will be analysed. The use of Asian and Eastern European populations, which have not been studied before, as well as new genomic resources and advanced sequencing technologies make the proposed study scientifically attractive and innovative. The research that will be carried out will complement and significantly broaden the current knowledge about genetic variation and the origin of Scots pine in Europe and Asia, making significant contribution to the development of population genetics of tree species. In the light of ongoing climatic changes, such knowledge is essential to perform further research concerning adaptation of particular populations to local environmental conditions.