Understanding the factors influencing intra-species genetic diversity is fundamental to evolutionary ecology, species conservation and managing their gene resources. High population genetic diversity is essential for woody species to respond to the effects of climate change. The rapidly developing field of landscape genomics has great potential to elucidate how neutral and adaptive evolutionary processes interact across the range of a species, resulting in observed genetic variation, phenotypic variation and variation in adaptation within populations. Recognising these relationships is key to predicting how anthropogenic climate change may affect species' genetic diversity, which ultimately determines their persistence.

The observed population die-off episodes of coniferous species emphatically confirm that they are susceptible to droughts caused by global warming. Due to their critical ecological role in forest ecosystems and their significant economic value, most research on woody species in a changing climate has focused on forest trees. However, in some regions and habitats, juniper thickets are dominant components of woody plant communities, increasing biodiversity and providing various ecosystem services. Unfortunately, populations of various juniper species in Europe, including the common juniper, have been declining significantly in recent decades due to climate change.

In the proposed project, landscape genomics methods will be used to investigate how a changing environment and evolutionary history shape the patterns of genetic variation and diversity and the demographic structure of natural populations of the common juniper in its natural range in Europe. The project asks the following research questions:

- What factors determine the spatial distribution of neutral and adaptive genetic diversity of the common juniper in Europe?
- What are the predictors of the vulnerability of common juniper to climate change in Europe?
- What is the diversity of the endophytic fungal community in common juniper in Europe?
- What is the demographic and spatial structure of common juniper populations?

The research will be conducted in 40-45 natural populations of the common juniper in the European range, extending from the Iberian, Apennine and Balkan Peninsulas to Scandinavia. Using genomic methods, the spatial distribution and variability of the adaptation potential of this species to ongoing environmental changes will be recognised. We will assess the effects of ongoing climate change on the long-term survival of juniper and estimate the likely range shifts of this species. We will identify populations and regions with the highest risk of the species withdrawing from plant communities. Analyses of the endophytic fungal community carried out over the geographical range will provide valuable information on the factors shaping the species and functional richness of this group of organisms and its possible impact on the health of the host population. Understanding the demographic structure of natural juniper populations will allow the effect of ongoing climate change on demographic processes to be determined.

The proposed project is a detailed insight into the neutral and adaptive processes shaping the genetic diversity of the common juniper. The results will identify mechanisms and factors for the species' decline in the face of ongoing climate change. Genomic predictions and demographic studies will provide vital information to support conservation efforts for the species.