Climate change is proceeding at an unprecedented rate, which leads to a considerable loss of biodiversity and, consequently, disturbs functioning and stability of ecosystems. Forests harbour a major part of the world's biodiversity and thus represent one of the most important terrestrial ecosystems. They have considerable potential to help with climate changes. However, given the expected rapid rate of these changes, the future of the forests is under great concern. Due to longevity, many tree species may not be able to adapt fast enough to keep up with rapid climate changes, which may cause their decline or extinction. Species can respond to climate changes through three strategies, i.e. range shift, phenotypic plasticity and adaptation. The adaptation potential of trees primarily depends on the existing genetic variability. For these reasons, maintaining the widest level of genetic variability is important. Understanding how species might respond to the ongoing environmental changes is one of the most pressing questions in biology. Can we predict species responses? Thanks to the available modelling techniques, it is possible. Currently, a novel approach, which combines traditional predictive models based on species occurrence data and future climatic scenarios and adaptive variability, has been proposed. Applying this approach results in more accurate predictions of the species response to climate changes.

In this project, we focus on the adaptive genetic variation, which is a key determinant of the evolutionary response of species to climate changes. Specifically, we are going to estimate the possible contribution of crossing between species (hybridization) as a mechanism which reinforces the adaptive potential of species to climate changes. To investigate this topic, we have selected two closely related species, European beech and Oriental beech, two important elements of forest in Europe and Western Asia. The species have different distributions and ecologies but yet hybridize in the area of ranges overlapping (contact zone) in southeastern Europe. In the face of climate changes, considerable range shift is expected for the two species. In the coming decades it can affect the contact zone in terms of its spatial dimensions and the rate of genetic exchanges between the species. A severe reduction of suitable areas for European beech at the southern limit of the species distribution in Europe is particularly worrying. Given the increasing concerns for the persistence of the European beech, the more drought-resistant Oriental beech seems to be an alternative for European beech. However, the application of management solutions towards mitigating climate change, such as assisted migration or assisted gene flow raises justified concerns that need to be carefully addressed. Investigation of an extent of the interspecific hybridization and its potential role is required to assess the risks and avoid failures of future management of the species.

In the project, we will use whole-genome re-sequencing and integrative approaches which combine population genomics with advanced spatial modelling techniques based on the genetic adaptive variability of species. First, we will determine the genomic bases of European beech and Oriental beech divergence and verify whether the detected pattern is associated with adaptation to different environments. By examination of dynamics and direction of gene exchange between the species, we will determine whether genes transferred between the studied species in the contact zone are involved in adaptation to climatic conditions. Subsequently, we will identify the distribution patterns of genetic adaptive variation across the two beech species ranges. The obtained results will be used for genomic modelling of the evolutionary responses of species under future climate change. This will help to answer the questions related to the possible role of hybridization in the species adaptation to novel environmental conditions. Potentially, the hybridization may lead to the enhancement of the adaptive potential of European beech due to transfer of beneficial genes from Oriental beech. However, it may also lead to its genetic swamping and final replacement by Oriental beech, which is better adapted to projected climate change in southeastern Europe.

An important innovative component of the project is the inclusion of a genomics modelling approach that can capture adaptive evolutionary response of species and consider the hybridization as a mechanism enhancing this response. Up to now, hybridization has never been incorporated into the predictive models and little is known about the implications of this process in species response to climate change. Our project will undoubtedly broaden the rapidly evolving field of landscape genomics, providing data on the role of hybridization in the evolutionary response of tree species to climate change. Understanding the impact of this process has a great potential for forest ecology, management and conservation of genetic diversity of tree species. In contrast to some important species, such as oaks, poplars or pines, the evolutionary and ecological consequences of hybridization in the two beech species have not been studied yet. Therefore, our study will also push forward our understanding of hybridization in trees.