

DESCRIPTION FOR THE GENERAL PUBLIC

Global climate change alters environmental conditions, and thus affects reproduction of plants from seeds. Environmental factors such as temperature, light intensity and water availability are key factors controlling seed germination and, as a result, affect the reproductive success of plants. In the proposed project we plan to investigate the ecophysiology of seed germination in European beech (*Fagus sylvatica* L.) in order to evaluate the potential of this species to adapt to environmental changes. European beech grows in a wide range of environments and has developed a variety of adaptive mechanisms. One of the most important mechanisms is deep physiological dormancy of seeds, ensuring seed survival through the winter and plant germination in spring, when the conditions are most suitable for the development of seedlings in temperate climate. The environmental diversity over the wide natural distribution range of beech has led to the development of different populations adapted to local climates. The variation of beech seed germination and its plasticity under variable environmental conditions are not currently known. The aim of this proposal is to determine the relationships between the germination parameters of beech seeds and different environmental conditions, and to identify the molecular mechanisms responsible for such adaptations. Because of deep physiological dormancy, germination of beech seeds must be preceded by a cold stratification. In this project, we plan to combine several levels of research: 1. Analysis of European beech diversity in Poland in terms of the depth of seed dormancy and germination. We will collect seeds from several populations of beech growing in various habitats (climatic conditions, geographical and topographical situation) in Poland. This analysis will aim to investigate the inter-population differentiation of the depth of seed dormancy and germination capacity. Current weather data will be gathered for the locations of the populations. We plan to collect seeds from the same populations in subsequent years. Germination tests will allow relating seed dormancy and germination to environmental conditions. Comparison of data from consecutive years will reveal whether the adaptation, reflected by the depth of dormancy, is plastic. 2. Analysis of the differences in gene expression among populations differing in depths of seed dormancy. We plan to investigate the differences among seed lots of different origins through the analysis of gene expression at the level of the transcriptome and proteome, especially focusing on proteins undergoing post-translational modification to regulate their activity. In these studies, the overall variability in dormancy depth will be analysed on mRNA level using the next-generation sequencing methods. To precisely determine the role of individual genes in controlling dormancy depth the quantitative real-time PCR will be used. The phosphoproteome, nitroproteome, nitrosoproteome, acetylome and ubiquitome will be investigated in order to determine their role in the regulation of dormancy depth. 3. Analysis of chromatin structure and histones modification on the promotor region of genes involved in beech seed dormancy depth regulation. In order to check whether the nucleosome occupancy alters the promoter region of genes identified in previous tasks, the MNase-qPCR and ChIP-qPCR analysis with specific antibodies recognising the histone 3 modifications will be used. The successful completion of this research task allows us to indicate epigenetic mechanisms that could be involved in regulation of beech seed dormancy and germination processes. It is expected that the data obtained in the project will allow the recognition of the factors regulating the adaptation and survival of individual populations of trees under the conditions of global warming.