

Gene flow between populations shapes the genetic variation of future generations. In the case of plants, gene flow occurs through the dispersal of seeds and pollen. However, in the case of strong fragmentation of the population, when plants of the same species occur in spatial isolates, the process of gene flow may be strongly limited or completely absent. The lack of gene exchange often contributes to a decrease in the ability of a population to adapt to new conditions, resulting, for example, from climate change. As a consequence, genetically isolated populations are at risk of extinction.

This project aims to determine the scale (frequency) of gene exchange between populations of common yew scattered in the Dukla Beskids (Western Carpathians). Thanks to the application of genetic methods of parentage analysis (analysis of paternity and maternity), similar to the methods used in forensic genetics, we will determine whether naturally recruiting yew seedlings are the result of the dispersal of seeds and / or pollen between populations.

Yew produces seeds that are surrounded by a fleshy aril, and that are dispersed by birds. According to previous research, the behaviour of feeding birds is related to the amount and size of seeds. Birds were observed to visit more frequently small-crop trees and flight longer after the visit. In addition, small seeds pass a longer time through the digestive system from the moment of ingestion to defecation. Therefore, it is believed that small seeds are spread over greater distances. Whereas, the yew pollen is spread by wind. Hence, the range of pollen dispersal depends on atmospheric factors and topographic conditions. In recent theoretical studies and controlled experimental studies, it was shown that in the case of varied topography (mountainous or hilly terrain) the distance of pollen dispersal depends on the elevation of the starting point (tree). So far, these hypotheses have not been verified in empirical studies.

Thanks to the analysis of seedling parentage and measurement of fecundity (seed production), expressed by the quantitative index and the weight of seeds, we will answer the question whether the distance of seed dispersal depends on fecundity (i.e. the quality of the food base). In addition, we will determine if there is a relationship between the dispersal of pollen and the elevation of the tree. The mathematical models of pollen and seed distribution developed in the project will be useful in predicting the gene flow between populations of the studied species, especially in areas exposed to rapid climate change.