

Many factors affect genetic diversity of species - climate change and related adaptation, habitat decline, hybridization. Migration of organisms after the last glaciation to a large extent shaped their current range of occurrence. Numerous threats resulting from the changing climate are especially dangerous for circumboreal species, it is expected that their range may be reduced even by 70% in the future.

The global climatic changes transforming the environment, lowering the water level lead to the disappearance of various habitats and related organisms, which are being replaced by less demanding species. A well-documented example is the disappearance of riparian and alder forests in the Białowieża National Park. Drying of habitats leads to increase of hornbeam (*Carpinus*) population and lowering the diversity of forest undergrowth. The results of environmental monitoring carried out for several decades in these areas indicate a further increase in the number of hornbeams, and consequently a decrease in the number of riparian and alder forests.

Another factor shaping genetic diversity is hybridization - crossing between different species. Hybridization is a key process in evolution of Angiosperms (Angiospermae). Interest in hybridization has a long, more than 100 years, history and its importance was differently discussed – as a process leading to species extinction (extinction by hybridization) and reduction of biodiversity or as a process creating a new genetic and phenotypic diversity and even new species. Taking into consideration the last scientific reports, about 50% of higher plants species is considered as recently formed polyploids (recent polyploids) and in a longer perspective of an evolutionary time scales it is assumed that multiplied genomes with the involvement of hybridization occurs in almost all lineages of higher plants and multiple polyploidization rounds led to formation of the majority of a contemporary species. There is no doubt that hybridization as a link in the chain of steps in allopolyploids origin was the basic process in the evolution of Angiosperms.

In the case of species with specific habitat requirements, for example marsh or peat bog species, transformation of these habitats due to anthropogenic factors and global climate changes may lead to species extinction or genetic pool of these species could be conserved in a newly formed interspecific hybrids. Hybrids as better adapted to disturbed environment than putative parental species are able to expand and displace one or both parental species. A good example of critically endangered species in its European distribution range is a dwarf marsh violet (*Viola epipsila*  $2n=4x=24$ ). In Poland it is protected by law because the number of individuals drastically decreased. The reduction of *V. epipsila* individuals number could result from crosses with a relative marsh violet (*V. palustris*  $2n=8x=48$ ). Highly vital and expansive interspecific hybrids might displace pure individuals of *V. epipsila*.

This project will focus on the genetic diversity of the *Viola epipsila-V.palustris* complex with the participation of interspecific hybridization in its circumboreal range.

The main objective is to elucidate the genetic diversity and population structure of *V. epipsila* and *V. palustris* (sec. *Plagiostigma* Godr., Violaceae) in circumboreal range with focus on postglacial recolonisation and effects from gene flow between both species.

In this project I will determine the frequency of *V. epipsila*, *V. palustris* and their hybrids in populations within their whole circumboreal distribution range using molecular markers (ISSR) and evaluate their genetic diversity. Hybrid origin of selected individuals will be confirmed by comparing their genome sizes with genome sizes of parental species by flow cytometry (genome size of parental species differs, hybrid genome is intermediate) and by testing pollen viability using histochemical test. Reduced pollen viability will confirm the hybrid origin of this forms as both parental species exhibit high pollen viability. Non-coding plastid DNA regions (*trnH-psbA*, *trnS-trnG*, *atpI-atpH*) will allow to estimate a number of haplotypes, to reconstruct a post-glacial migration routes of *V. epipsila*, *V. palustris* and to define the direction of crossing (indicate the maternal species). Research planned in this project will provide the important data based on large sample rate on the impact of global climatic changes on species ranges of occurrence and biodiversity.