

## **Testing the hypothesis of mitochondrial DNA evolution using hybrid zone of forest tree species and de novo sequence genome assemblies.**

Evolutionary biologists have a unique opportunity to look back in time and see the origins of species, their complex history, changes in number and distribution, and many more mysteries of their life. All this would be impossible without suitable molecular markers that are based on differences in DNA sequence between individuals. Especially important for tracking changes in species demography and population structure are markers of mitochondrial origin, almost universally used across the tree of life. Although biologists have used those markers routinely to study differentiation between populations and species, the evolution of those organelles themselves is still poorly known. Particularly complex and understudied are plant mitochondria mostly due to their extraordinarily large genomes – in some cases even 200 times larger than animal ones. In recent years many questions regarding certain aspects of plant mitochondrial evolution were asked, for example, whether they can influence the fitness of their carriers, how often deviations from single-parent transmission of those organelles happen, and most importantly – do they recombine? The later idea was proposed to explain certain properties of mitochondrial DNA of species found in so-called hybrid zones – areas where two or more different species can co-occur, crossbreed and produce viable offspring. However, to this day this idea was never directly tested. The project will take advantage of recent developments in DNA sequencing technology which allows generating whole mitochondrial genomes of plants. Then, advanced DNA sequence analysis of individuals from the hybrid zone of closely related pines will be used to answer essential question regarding evolution of mitochondrial genomes. To do so, the project will sequence several mitochondria of three pine species and then use comparative genomic methods to detect possible signatures of recombination events in their history. Thanks to the generation of whole mitochondrial DNA sequences of those pines, the project will develop new markers and use them to assess how novel and putatively recombinant variants can spread across populations within hybrid zones. The project will advance current understanding of evolution of mitochondrial genomes and shed light on their structural complexity. It will provide new knowledge to advance evolutionary biology, population genomics, genome biology and molecular ecology studies in plants.