Spruce bark beetle (*Ips typographus)* is a key member of the forest ecosystem, and at the same time, one of the most aggressive forest pests that destroys thousands of spruce stands each year. In particular, territories that are not native to spruce (managed forests) or where the spruce is weakened due to storms or droughts, are particularly vulnerable to massive beetle's outbreaks. In such cases a spruce bark beetle attacks healthy trees and causes substantial economic loss. Interestingly, there is a difference in the frequency of outbreaks between populations from the southern and northern part of the species range. Southern populations tend to regularly outbreak, while northern do not. Due to the economic importance of the spruce trees, ecology and biology of the spruce bark beetle is well-studied. Additionally, genomic sequence of the spruce bark beetle is known and several ongoing studies investigate genome-wide variation across species range. The availability of genomic resources makes spruce bark beetles a great model to study effects of population size changes on species evolution. In particular, main areas of research that we can shed light on while looking at the genome level include: evolutionary history of the species or neutral and adaptive evolution (the process describing the change in the frequency of genetic variants that have, or do not have the effect on the individual's survival or reproduction) . However, to be able to take full advantage of the available genomic dataset, we have to estimate the rate at which new genetic variants (new mutations) appear in the genome.

The main goal of this project is to estimate how often new mutations occur in the spruce bark beetle genome and to directly use this information to deepen our understanding of its evolutionary history and evolution of its genome. Since such estimation can be done by counting new mutations that occur during one breeding cycle, I am going to breed several spruce bark beetle families, sequence genomes of the parents and their offspring and search for new mutations within the obtained genome sequences. Finally, from the number of observed new mutations I will calculate mutation rate.

The rate at which mutations occur is a key parameter in population genetics that helps to estimate the time of divergence of the species and parts of its genome. For example, having in hand mutation rate estimate, an accurate prediction of the recent expansion of a species is possible. Namely, mutation rate estimate allows us to make predictions of time in years and of changes in population size in the number of individuals, while inferring demographic history of a species and making it much easier to interpret. As a result, the picture of the spruce bark beetle evolutionary history will be more detailed, clear and hence more informative. Additionally, mutation rate will be used to date large chromosomal mutations (chromosomal aberrations) recently discovered within the spruce bark beetle genome. Particularly, there are several inversions (parts of the genome that rotated by 180 degrees) and now we find both inverted and non-inverted fragments across the species range. It is known that such polymorphic inversions may play an important role in species adaptation (e.g. they may lock together genetic variants that "work" particularly well with each other increasing survival and reproduction of individuals) but their role in the spruce bark beetle genome remains unknown. The first step towards understanding the potential function of inversions would be knowing their age. Did they occur before or after the last expansion of the bark beetle (after Last Glaciation)? Or maybe they are even older?

The detailed demographic history of a spruce bark beetle and the knowledge about the age of inversions will lay the foundation to understand how exactly changes in population size can affect species genetic variation and will allow us to shed light on adaptation processes within a spruce bark beetle.