

Many scholars have been intrigued by world's biodiversity since hundreds of years. Why individuals from the same species differ from each other? Why some of them are very similar? What are the factors that influence diversity observed in particular populations? At the beginning, scientists studied features that could be seen with naked-eye or, a bit later, with a microscope and tried to explain phenotypic variation observed among individuals. Groundbreaking discovery that individuals differ also at the level of DNA sequences allowed them to ask the same questions at the molecular level. This began completely new and unexplored era of research. Over many years scientists discovered that differences in DNA sequences observed between individuals can be neutral, with no influence on individual's survival and reproduction, or adaptive, increasing individual's chance to pass on its genes to the next generation. Moreover, scientists understood that DNA sequence variation is affected by demographic factors, such as drastic changes in population size in response to sudden changes in the environment (e.g. during glaciation when many individuals died and those that survived had to flee to refugial areas). Despite decades of research, many questions about factors shaping DNA sequence variation remain unanswered. For example, it is unclear how rapid and recurring changes in population size affect neutral and adaptive variation. Such size fluctuations are observed in pathogens during recurring epidemics or in agriculture pests during outbreak cycles when populations increase in number by orders of magnitude and come back to their endemic size in the end of each outbreak. Understanding genetic consequences of outbreaks is of particular importance if we think about adaptive variation. What happens with genes' variants that are beneficial for particular individual? Does evolution act in a different way in populations that experience rapid and recurrent changes in size and in different way in populations of constant size? I will look for answers to these (and many more) questions using spruce bark beetle as a model system. Spruce bark beetle is one of the most important pests of spruce forests. Under favorable conditions (e.g. storms that destroy trees) population of beetles increases in number and can cause mortality of thousands of trees. In contrast to northern Europe where spruce bark beetle outbreaks are still rare, they happen more and more often in central and southern Europe. During the course of the project I will combine existing knowledge on species biology and ecology with newly generated genomic data. I will analyze whole genome sequences from few hundreds of individuals from several spruce bark beetle populations using classical and novel methods. Results of the project will not only shed light on unknown genetic aspects of population outbreaks but will provide knowledge on population dynamics of spruce bark beetle itself. Genetic information on the species may potentially help to improve management strategies of this important forest pest.