

The living world is made up of an amazing diversity of organisms that often inhabit changing environments, either fluctuating with seasonal weather changes or reflecting the rapid progress of global climate change. It is easy to imagine that populations inhabiting all sorts of ecological niches must constantly adapt to track changes in their environment. This simple observation raises fundamental questions about whether and how species can adapt to changing environments. Rapid changes in key species traits, observed over the course of a few or several years, have been reported by many scientists. A good example is a classic case of wing colour change in peppered moths in England. Initially, most individuals had white wings, which gave them good camouflage when sitting on the bright bark of trees. However, during the Industrial Revolution, many trees were covered with black soot, causing the dark-winged moths to increase in abundance. Despite numerous examples of rapid phenotypic evolution, identifying its genetic basis has proven much more difficult. Part of the difficulty is that large changes (in colour or behaviour) are often driven by small changes at many genes, making them difficult to detect. However, recent studies indicate that we can overcome this problem by combining novel statistical tools and adequate temporal sampling with whole genome sequencing. These new capabilities allow us to shed new light on long-standing questions about species adaptation and its genetic underpinnings. Can populations continuously adapt to changing environments? What is the genomic architecture of such adaptation? How is genetic variation shaped by fluctuating environmental changes in space and time? How many positions within the genome change, and are there specific positions that facilitate rapid adaptation? The last question is particularly important in the context of recent research suggesting that inversions (mutations that flip large parts of chromosomes) may play a critical role in rapid adaptation. The main aim of the project is to address the above questions using the spruce bark beetle as a model organism. The spruce bark beetle is one of the most destructive insect pests, and many of its characteristics make it a good candidate for studying the genomic basis of rapid adaptation. Spruce bark beetles inhabit large areas of European forests in environments with clear seasons. Global climate change facilitates their massive outbreaks, which are likely to expose the species to strong and changing selection pressures. In addition, my recent study showed that the bark beetle genome contains dozens of polymorphic inversions that may be involved in species adaptation. In addition, by collaborating with scientists who have been monitoring the bark beetle for many years, I have access to a large temporal dataset that allows me to study genetic changes over time. The results of this project will allow us to better understand the phenomenon of rapid adaptation and its genetic underpinnings, as well as will shed light on the spruce bark beetle itself. This could potentially help in the management of this important forest pest.