Invasive Alien Species (IAS) are animals and plants that are introduced accidentally or deliberately into a natural environment where they are not normally found, with serious negative consequences for their new environment. Human-mediated biological invasions are a component of global change, and their impact on the communities and ecosystems they invade is substantial and complex. Understanding ecological and evolutionary processes that promote invasion is a key first step in developing long-term approaches to prevent future invasions and to manage existing ones. Genetic studies of expanding populations demonstrate that adaptation to novel environments can occur within 20 generations or less, indicating that evolutionary processes can influence invasiveness. There is growing research effort to understand the role of selection in determining rapid micro-evolutionary processes over contemporary timescales. Still, it remains largely unknown how local environments shape genomes and population genetic structure of invasive species that successfully colonise a wide range of habitats. The ecological factor that is believed to affect invasion success profoundly is the pathogen pressure. According to the enemy release hypothesis, an alien species introduced to a new region will experience reduced impacts from natural enemies resulting in a competitive advantage over resident species.

In the proposed project, we are going to use native and invasive populations of common raccoon *Procyon lotor* to determine the genetic factors responsible for the spectacular success of the invasion of this species in Europe. We will compare genomic diversity of populations in the native and invasive range of the species to determine the mechanisms responsible for rapid local adaptation, that enables functional responses to environmental change and determines the success of the invasive species. We are going to investigate "genetic paradox" of invasive species. Bottlenecks that occur during establishment in the new environment should theoretically reduce fitness and evolutionary potential of populations, yet introduced species often become invasive. Due to relatively large and diverse founder populations and multiple introduction events the genetic variation within invasive populations is often retained at levels similar to, or even higher than, native populations. Using a number of single nucleotide polymorphisms located both in the functional and noncoding regions of the raccoon genome and analysing populations from native and invasive raccoon range we are going to search for footprints of selection and determine the genomic regions that undergone selection as a result of the invasion process. To get a comprehensive insight into the factors playing a role in successful invasion, we will use DNA metabarcoding approach to assess and compare the composition of raccoon pathogenic fauna between native and invasive populations. According to the enemy release hypothesis, raccoon pathogens from introduced populations should present lover diversity and prevalence, which facilitates the success of invader. The results from our project will give insight into the genomic basis of adaptation in successful invasive species.