

Summary

In the era of intensive human movements across and between countries and continents, numerous species are intentionally and unintentionally transferred out of their native ranges. However, only a fraction of those species establish successful populations outside their native ranges, causing serious ecological and economic damage. Invasive alien species are one of the most serious concerns to modern nature conservation; therefore, a major focus is placed on identifying the traits that contribute to invasion success.

My PhD thesis aimed to investigate a group of mechanisms that drive successful adaptation and facilitate invasion. I focused on assessing mechanisms shaping genetic diversity and selection pressure, and the role of the gut microbiome in promoting local adaptations. Recent studies highlight the role of genomic data in providing a complex understanding of mechanisms underlying invasive species success. The complementation of the genomic findings with investigating the gut microbiomes offers an additional dimension to understanding factors facilitating invasions.

In the first part of my thesis, I conducted a systematic review of studies that employed genomic data to analyze the influence of demographic mechanisms shaping the genetic diversity and natural selection during invasions. I identified a clear pattern indicating that primary reductions of diversity caused by genetic drift and bottlenecks during establishment in the new range are frequent; however, they do not result in a permanent reduction of genomic diversity. The diversity is usually restored by admixture of individuals from separate introductions and/or introgression of advantageous genetic variants. Moreover, selection footprints are often detected in genomic regions related to specific biological functions, putatively facilitating invasion, such as temperature tolerance, immunity, metabolic pathways, and insecticide resistance. The systematic review of articles allowed for the detection of knowledge gaps and proposed directions for future research.

The pattern that I have identified by analysing published articles was confirmed by examining the genetic structure and adaptive changes related to the spread of the raccoon *Procyon lotor*, which is one of the most rapidly expanding invasive mammals in Europe. I detected the reduction of genetic diversity in the invasive range and admixture between invasive populations. The footprints of parallel selection between invasive populations and one from the native range, inhabiting similar environmental conditions, suggest habitat-specific local adaptations. The results highlight the importance of habitat matching between native and invasive ranges not only by environmental, but also by genetic data. Selection footprints were detected in regions of the genome related to reproduction, hormonal pathways, neurological processes, cognitive functions, locomotor system, and biochemical

processes associated with environmental changes. Selection footprints in those particular groups of genes suggest that local adaptations may play a role in outcompeting native species.

In the final part of my dissertation, I analyzed the differences in composition and functional profiles of raccoons' populations' gut microbiomes, as a non-genetic factor potentially influencing invasion. The microbiome composition of both ranges was differentiated, which may either reflect diverse diet sources or the loss and gain of microbial taxa during the invasion process. Invasive populations exhibited higher levels of inter-population microbiome diversity than the studied native populations. The high intra-population diversity did not confirm the influence of the population bottleneck on the level of microbiome diversity in invasive populations. Native populations, however, had a less diverse microbiome, similar between geographically distant locations, suggesting microbiome stability, indicating its resilience, but also possibly related to a more simplified, anthropogenic diet. Despite the differences in microbiome composition between ranges, the functional profiles of gut microbiomes from invasive and native populations overlapped, suggesting functional redundancy, i.e., the same functions are provided by different bacterial groups. In raccoons' invasive populations, the high level of differentiation and undisturbed functional profiles may be another factor facilitating invasion.

The management of invasive species is most effective during the initial stages of invasion, when actions to prevent the migrations and the establishment of new populations should be undertaken. Results of both systematic review and raccoons' invasion studies indicate that admixture of genetically divergent populations facilitates invasion. Therefore, during later invasion stages, countermeasures are less effective, as restoring the genetic diversity may drive local adaptations and invasion. Using the information on the genetic variation, I showed that habitat-matching between native and invasive range further facilitates success in the new range. Thus, climatic and environmental conditions should be considered while predicting vulnerability to invasion, even in such a cosmopolitan species as the raccoon. Genomic data may improve invasive species management, not only by reconstructing the invasion history, but also by estimating the adaptive potential. As a result, it will be possible to plan effective management actions tailored to particular species.