

The number of emerging alien species is growing worldwide, causing damage in natural and agricultural ecosystems and inflict economic losses. Therefore, a major focus in invasion ecology and management is to identify traits that contribute to invasion success. Invasions, especially of insect species, are often related to multiple introductions, promoting high genetic diversity in the invasive range, and providing source for adaptation in novel habitats. Genomic studies often reveal loci subjected to selection processes, suggesting that adaptation to novel habitats is not hindered. To provide a picture of genomic diversity changes during biological invasions, it is crucial to extend beyond single nucleotide polymorphism (SNP) surveys of genetic variation. Large and medium-size structural variants (SV, larger than 30bp) identified through whole genome sequencing (WGS) can have strong and immediate phenotypic effects and are often related to traits supporting range expansion. Whole genome data allows also to identify evolutionary events such as, gene family expansions or transposable elements (TE) activity that can modulate invasion success.

In the proposed project we will use two hemipteran pest insect species, *Cinara curvipes* and *Leptoglossus occidentalis* invasion models to unravel the genetic mechanisms behind invasion success. **Our aim is to integrate both comprehensive sample collection from native and invasive ranges and WGS data to explain genomic basis of successful invasions driven by the interplay of human-mediated events, demographic mechanisms, local selection, and genome characteristics, of two pest species of conservation and economic concerns.** *Cinara curvipes* and *Leptoglossus occidentalis* represent two hemipteran invaders that have rapidly colonized Europe. While *L. occidentalis* is known to have undergone multiple introductions, resulting in genetically diverse populations, the invasion history of *C. curvipes* remains unresolved. The species differ markedly in their reproductive strategies and dispersal capacities likely contributing differential population structure and genomic diversity. In *C. Curvipes*, potentially lower population genomic variation may be counteracted by genome features such as TE activity and specific gene family expansions. The contrasting life history traits, invasion dynamics, and ecological plasticity of both species offer a unique opportunity for a comparative genomic approach to invasion biology. Together, they serve as complementary model systems to investigate how demographic history, genome architecture, and environmental interactions shape invasion success in forest pest insects. We will combine long and short read NGS sequencing of individual and population pooled samples to obtain a full picture of invasion course, local adaptation and genome characteristics of both species. We will assess adaptation along geographical gradient in the invasive range, evaluate the level of parallel or divergent evolution between native and invasive populations. *L. occidentalis* museum samples will allow time-scale comparisons to investigate whether selection acts on genetic novelty that arose post-invasion or on genetic variation inherited from the native population.