

Description of the research topic

General information

Institute: Institute of Nature Conservation, Polish Academy of Sciences.

Research topic: Genome structure of two invasive Hemiptera species, *Cinara curvipes* and *Leptoglossus occidentalis*, and their success outside the natural range.

Scientific discipline: biological sciences.

Name of potential supervisor: dr hab. Aleksandra Biedrzycka.

Background information

PhD Position within the OPUS (2025/57/B/NZ8/01241) project “Invasion success through genomic lens: insights from whole-genome diversity of invasive Hemiptera pests”, funded by the Polish National Science Centre (NCN) OPUS grant nr 2025/57/B/NZ8/01241.

ABOUT THE PROJECT:

The number of emerging alien species is growing worldwide, causing damage to natural ecosystems. A major focus in invasion ecology is to identify traits that contribute to invasion success. Genomic studies can be used to track the invasion process, reveal genomic regions involved in adaptation in the novel range and identify genome characteristics potentially facilitating invasions. In this project, we use two Hemipteran invasive insect species, *Cinara curvipes* and *Leptoglossus occidentalis*, as invasion models to unravel the genetic mechanisms behind invasion success. We will use whole genome data to get insight into population genomic differentiation of single nucleotide polymorphism (SNP), structural variants (SV) that can have strong and immediate phenotypic effects and are often related to traits that support range expansion. We will also identify evolutionary events, such as gene family expansions or transposable element (TE) activity, that can modulate invasion success.

The main question to be addressed in the project

How the structure of the genome may affect the success of invasive species? How invasive insects with different life history traits adapt to novel environments at the genomic level?

What is the role of symbiotic bacteria in the success of invasive insects?

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.

Information on the methods/description of work

The successful candidate will be involved in de novo sequencing, assembly and annotation of *C. curvipes* genome. Further, the genomes of both species will be analysed in terms of structural variation, TE content and expansions of gene families potentially related to survival outside the native range. The presence of facultative bacterial endosymbionts of both species in their native and invasive populations will also be analysed as a potential driver of invasiveness. The research will involve wet-lab work, but will be more skewed towards population genomic analyses.

Additional information

The successful candidate must hold a M.Sc. degree. We seek applicants with:

- a strong interest in evolutionary and population genomics.
- experience or interest in bioinformatic analyses
- good English language, communication and organizational skills.

Place/name of potential collaborators

The PhD student will be supervised by Dr Aleksandra Biedrzycka, an evolutionary, conservation and invasion geneticist, at the Institute of Nature Conservation, Polish Academy of Sciences in Kraków. The candidate will work in collaboration with Dr Pierre Nouhaud, evolutionary geneticist of invasive pest arthropod populations, at INRAE – CBGP Marseilles, France.

References

- Battlay, P., Wilson, J., Bieker, V. C., Lee, C., Prapas, D., Petersen, B., Craig, S., van Boheemen, L., Scalone, R., de Silva, N. P., Sharma, A., Konstantinović, B., Nurkowski, K. A., Rieseberg, L. H., Connallon, T., Martin, M. D., & Hodgins, K. A. (2023). Large haploblocks underlie rapid adaptation in the invasive weed *Ambrosia artemisiifolia*. *Nature Communications*, 14(1), 1717. <https://doi.org/10.1038/s41467-023-37303-4>
- Kołodziejczyk, J., Fijarczyk, A., Porth, I., Robakowski, P., Vella, N., Vella, A., Kloch, A., & Biedrzycka, A. (2025). Genomic investigations of successful invasions: The picture emerging from recent studies. *Biological Reviews of the Cambridge Philosophical Society*. <https://doi.org/10.1111/brv.70005>
- Wellenreuther, M., Mérot, C., Berdan, E., & Bernatchez, L. (2019). Going beyond SNPs: The role of structural genomic variants in adaptive evolution and species diversification. *Molecular Ecology*, 28(6), 1203–1209. <https://doi.org/10.1111/mec.15066>