

Institute: Institute of Nature Conservation, Polish Academy of Sciences

Title: A role of genomic diversity and pathogen pressure in the invasion success – a case study of natural and invasive populations of common raccoon.

Name of potential (lead/principal) supervisor: dr hab. Aleksandra Biedrzycka, prof. IOP PAN

Background information:

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. 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.

The main question to be addressed in the project:

We 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. Comparing genomic diversity of populations in the native and invasive range of the species we determine the mechanisms responsible for rapid local adaptation that determines the success of the invasive species. Using a number of single nucleotide polymorphisms located both in the functional and noncoding regions of the raccoon genome 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 lower 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.

Information on the methods/description of work:

The PhD student will be involved in a project described above, her/his specific responsibilities will be

1. Fieldwork – The coordination of sample collection and collaboration with hunters in Poland, Czech Republic and Germany.
2. Lab work
 - DNA extraction from various sample types (tissue, smears) for genomic analysis and metabarcoding
 - Preparation of genomic libraries for RAD-seq experiment, sequencing of libraries
 - Preparation of amplicon libraries for pathogen metabarcoding and library sequencing.
3. Data analysis (using R and Linux/Unix environment)

- Participation in sequencing data filtering and SNP calling and analysis of SNP diversity. Comparing genomic diversity of native and invasive raccoon populations and searching for genomic signatures of selection and population structure. The aim of this task is to characterise variation in a large number of SNPs randomly scattered through the genome. Rad-seq methods have the ability to detect loci under selection in genome scans, given the density of markers and the extent of linkage disequilibrium (LD). Random location of Rad-seq SNPs both in coding and noncoding regions will also enable understanding of population structure and demography, assessing population subdivision, migration rates and routes or population size changes through time.
- Metabarcoding data analysis. Comparing the pathogen pressure between the invasive and native populations. We will test for bacterial, micro-eukaryotic and helminth composition.

Additional information (e.g., special requirements from the candidate):

A background in ecology, evolution, genetics and/or bioinformatics will be a plus. Familiarity with R, Linux/Unix, computing clusters, and the use of bioinformatic tools would be advantageous. Most important is to be an independent learner.

Place/name of potential collaborator:

The PhD fellowship and all the research that will be performed as the PhD project are the part of the National Science Centre in Poland project no. 2020/37/B/NZ8/03801, awarded to dr hab. Aleksandra Biedrzycka. Bioinformatics analysis will be performed with help of dr Maciej Konopiński. Laboratory work will be performed in the Laboratory of Genetic Diversity in the Institute of Nature Conservation, PAS and in the Laboratory of Molecular Ecology, Institute of Environmental Sciences, Jagiellonian University.

References:

Biedrzycka A., Konopiński M., Hoffman E., Trujillo A., Zalewski A. 2019. Comparing raccoon major histocompatibility complex diversity in native and introduced ranges: Evidence for the importance of functional immune diversity for adaptation and survival in novel environments. *Evolutionary Applications* 00: 1-16, DOI: 10.1111/eva.12898.

Biedrzycka A., Popiolek M., Zalewski A. 2020. Host-parasite interactions in non-native invasive species are dependent on the levels of standing genetic variation at the immune locus. *BMC Evolutionary Biology* 20: 43.

Bock DG, Caseys C, Cousens RD, Hahn MA, Heredia SM, Hübner S, Turner KG, Whitney KD, Rieseberg LH. 2015. What we still don't know about invasion genetics. *Mol Ecol.* 24(9):2277-97. doi: 10.1111/mec.13032.