

Research Project

Genomic rearrangements and the origin of species

Third-party funded project

Project title Genomic rearrangements and the origin of species

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Organisation / Research unit

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Background: As we witness the sixth mass extinction, it is increasingly pressing to understand the mechanisms that underlie the emergence and maintenance of species. The evolution of reproductive isolation is the foremost requirement for speciation, and barriers that reduce interspecific gene flow are key to maintain species boundaries. Large-scale rearrangements through chromosomal fusion and fission have been suggested to represent such barriers. However, their importance and impact on the rate of speciation are not understood. This project sets to unravel the role of chromosomal fusion and fission during the process of speciation both on a micro- and macroevolutionary level within a single genus. Combining phylogenomic and population genomic approaches, my project will provide an unprecedented picture on the impact of large-scale chromosomal rearrangements for the emergence and maintenance of biodiversity, advancing the field of speciation research.

Hypotheses: My project addresses three key hypotheses that have not been empirically tested in an integrative manner: i) Chromosomal fusion and fission accelerate the rate of speciation. ii) Large-scale chromosomal changes through fusion and fission between sister species represent intrinsic barriers, i.e. constrain interspecific gene flow and hybridization. iii) Reinforcement maintains species boundaries in the absence of genomic rearrangements.

Procedure: The study system is *Erebia* – the most species rich Palearctic butterfly genus – whose cold-adapted species are yet threatened by climate change. Its recent radiation across Europe has been attributed to rapid changes in chromosome numbers but not formally tested. Using genome-based data and phylogenetic comparative methods, I will first assess the macroevolutionary impact of differing chromosome numbers as a result of fusion and fission on the rate of speciation. I will then identify the microevolutionary processes at play between three sister species of the recently evolved *Erebia tyndarus* species complex, where species differ in their number of chromosomes or not. Based on population genomic data from within and outside the known contact zones, I will assess the levels and locations of interspecific gene flow along the genome as well as the genomic footprint of intrinsic barriers as represented by differing chromosome numbers. Finally, I will evaluate the role of reinforcement driving interspecific differentiation and gene flow, combining genomic with phenotypic and ecological cline analyses. Many hundred specimens were already collected and are available for immediate analysis, and interspecific contact zones have been identified.

Importance: Integrating micro- and macroevolution, this project provides unparalleled insights into the genomic mechanisms that promote speciation and therefore the emergence and maintenance of biodiversity. The results will resolve the role of large-scale genomic architectural changes acting as intrinsic barriers to gene flow and significantly advance the recently emerged field of speciation genomics. Being adapted to high elevation environments, *Erebia* will face severe ecological alterations in the near future

as a result of climate change. This work will thus give novel insights into the evolutionary mechanisms at play in a species group that is threatened by climate change, making *Erebia* a model system for many similarly threatened species in the Alps. The results allow establishing a general evolutionary framework, enabling to predict the genomic fate of Alpine species and thus provide a basis for future policy implementations of national and international stakeholders.

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