



Universität
Basel

Research Project

DIFFER

Third-party funded project

Project title DIFFER

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Organisation / Research unit

Departement Umweltwissenschaften / Evolutionary Biology (Salzburger)

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Genetic diversity – that is, the genomic variation among individuals of a given species – is pivotal for adaptation to environmental alterations and an important factor for ecosystem resilience. Yet, the determinants of genetic diversity remain poorly understood. Population size is often used as a proxy for genetic diversity, but the amount of genetic variation within populations is not always reflected by their population size. Instead, factors such as linked selection, the recombination-, mutation-, and speciation rate, or life history and ecological traits may be more strongly connected to genetic diversity. So far, the interplay of all these parameters has not been empirically investigated, so that their relative contributions to genetic diversity are unknown. In DIFFER!, I propose to thoroughly examine the role of all these potential determinants of genetic diversity by means of combining cutting-edge genomic techniques with a highly suitable model system: the more than 200 endemic cichlid fish species of the East African Lake Tanganyika. Owing to their great morphological and behavioral variation, contrasting speciation rates, and their recent radiation, these fishes offer an ideal framework for comparative analyses. Availability of long-read reference assemblies, recombination maps, a massive dataset of underwater photographs for estimating census population sizes, together with population sequencing of selected species and family-based 'trio' sequencing will enable me to investigate specifically the interplay between genetic diversity and (i) life history and ecological traits, (ii) speciation and hybridization rates, and (iii) mutation rates, while at the same time controlling for variation in population size, selection, and recombination. The results of this project will contribute towards the understanding of organismal evolution and provide a new basis for the evaluation of genetic diversity in ecosystem management.

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