

Research Project

The genetic and developmental basis of parallel evolution in stickleback foraging morphology

Third-party funded project

Project title The genetic and developmental basis of parallel evolution in stickleback foraging morphology

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and developmental basis of functionally relevant phenotypic variation. This situation has changed with the advent of genomic and developmental tools, making possible integrative research linking molecular variation to fitness-relevant phenotypic variation in some model organisms, including threespine stickleback fish. The aim of the present proposal is to carry out such an integrative study in Swiss populations of stickleback. I will focus on populations that have repeatedly and independently evolved highly divergent foraging morphologies (gill raker apparatus and body shape) in response to contrasting foraging conditions between limnetic and benthic habitats (parallel evolution). These populations will be subject to extensive morphometric analysis, and their natural selective environments will be quantified. This work will be complemented by powerful molecular genetic and developmental experiments, including candidate gene and comparative gene expression analysis, and QTL mapping. These molecular experiments will uncover the genetic architecture of ecologically relevant phenotypic traits, and identify key genes and developmental pathways in their morphogenesis. The synthesis of morphological, ecological, and molecular information will in turn shed light on the mechanisms interacting during parallel evolution. My work will thereby contribute to resolving fundamental issues in evolutionary genetics and understanding biological diversification.

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Published results

382662, Berner, Daniel; Roesti, Marius; Hendry, Andrew P.; Salzburger, Walter, Constrain on speciation suggested by comparing lake-stream stickleback divergence across two continents, 0962-1083, Molecular ecology, Publication: JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

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