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PROJECT TITLE: Genomic consequences of artificial introduction, expansion and population replacement in the Trinidadian guppy

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1. Research project objectives/research project hypothesis

A major aim in evolutionary biology is to quantify the effects that demographic history has had and can have on the patterns and dynamics of deleterious and adaptive variation. The project aims to validate theoretical predictions recently developed in this field. In particular, I aim to answer the following questions:
1. Is population expansion associated with accumulation of deleterious mutations at the expansion front?
2. How deleterious mutations affect gene flow between populations in secondary contact zones?
3. Do fast-evolving genes invade local populations more rapidly than other parts of the genome?
To address these questions, I will investigate the genomic consequences of a recent introduction of the Trinidadian guppy *Poecillia reticuata* into a previously guppy-free area inhabited by its sister species. *P. obscura*. An auxiliary aim, necessary to parametrize the genomic analyses required to achieve aims 1-3, is to assess mutation rate in the guppy genome. As a consequence, this study will provide one of the few assessments of genome-wide mutation rate in vertebrates.

2. Research project methodology

In the project I will sample guppy fish from the Turure River, where man-made introgression event began approximately 60 years ago. Since that time, *P. reticulata* has spread down the river and has likely replaced *P. obscura* in most of the sites it's invaded. Additionally, I will sample several rivers connected to the Turure River. In these sites *P. obscura* populations might have experienced rapid adaptive introgression of *P. reticulata* genes. Whole genome resequencing will be performed on approx. 100 individuals of both species and data will be analyzed using the publicly available guppy reference genome together with multispecies whole genome alignments. The resulting dataset will be used to identify deleterious variants segregating in populations, and to estimate genetic admixture across the genomes in both species. Using a mixture of bioinformatics and statistical methods I will then investigate mutation load in the expanding *P. reticulata* population, strength and patterns of gene flow between *P. retulculata* and *P. obscura*, and associations between deleterious mutation load and gene flow.
In addition, I will resequence two laboratory-derived parent-offspring families to estimate mutation rate in the guppy. These parameters will be used for computer simulations, and for inferring population history, effective population size, divergence time, and rate of gene flow between species.

3. Expected impact of the research project on the development of science

Questions around how changes in population size affect deleterious mutation loads, and how deleterious variation shapes the genomic landscape of introgression, is a heavily debated subject, with implications for understanding present-day distributions of genetic variation and for assessing the impacts of anthropogenic-induced changes to species' distributions. Empirical evidence for accumulation of deleterious variants in expanding populations is often contradictory, while the impact of deleterious variation on hybridization dynamics has received little attention. This process might be however crucial for general evolutionary mechanisms. Therefore expected results of the project might have direct and indirect impact on such fields as medicine, human genetics and conservation biology.