

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

“Nobody is perfect” – probably this applies to every living organism on Earth. Through a variety of processes, organisms’ genomes accumulate mutations. Some mutations will benefit the individuals that carry them, but many others will cause harm. Understanding how harmful mutations accumulate, and how beneficial mutations spread, is thus a cornerstone topic in the study of evolution.

Evolutionary mathematical models suggest that populations undergoing rapid spatial expansion can accumulate deleterious mutations much more readily than under more stable conditions. It is because natural selection is less efficient in expanding than in stable population. In humans, such a spatial expansion took place around 70,000 years ago, when our ancestors left Africa and quickly spread across most of Eurasia. According to mathematical theory, then, Europeans should harbor more deleterious mutations than Africans. Empirical data, however, has produced results that contradict these predictions.

In the proposed project, I plan to investigate the accumulation of deleterious mutations in an expanding population. To study this process in real time, I will use the wild ancestors of the popular aquarium fish, the guppy (*Poecilia reticulata*). Guppies are widespread in their native range in Trinidad, but humans have artificially introduced them into a number of previously guppy-free rivers over the last few decades. My study will focus on such a population, established approx. 60 years ago. Since introduction, this population has rapidly expanded, spreading to lower parts of the river and forming an excellent system to study genetic consequences of spatial expansion. By utilizing some of the latest techniques for sequencing and analyzing whole genomes, I aim to assess whether expanding populations do indeed accumulate deleterious mutations in the manner predicted by mathematical theory.

My second aim is to explore the potential to acquire beneficial mutations from interbreeding between closely related species. This process also features prominently in human evolutionary history, again during that rapid out-of-Africa expansion phase. When they entered Eurasia, *Homo sapiens* encountered *Homo neanderthalensis* – Neanderthals. We know from genetic analyses that these species can, and did, interbreed, and that some Neanderthal genes entered the *Homo sapiens* gene pool and have remained there to this day. It is likely that these genes were beneficial for our ancestors, and that this is why these genes have been preserved into the present.

My target guppy population is also a good model for studying this process. As the introduced guppy population expanded its range downstream, it entered the range of a closely related species (*Poecilia obscura*). These species can interbreed and produce viable offspring, but the question remains as to whether there is free gene flow between the species, and how that gene flow might be related to beneficial mutations. By studying the genomes of these fish in this river, I hope to help answer this.