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## The Genetic Basis of Convergent Adaptive Evolution and Ecological Function in Cichlid Fishes

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The genetic basis of adaptive radiations and the mechanisms that influence the rate of convergent evolution have long been debated in the field of evolutionary genetics. The occurrence of high levels of phenotypic convergence in groups of organisms that underwent recent adaptive radiations has led to suggestions that convergence can result from internal factors, such as developmental biases. The fact that natural selection acting on similar organisms is likely to result in outcomes in response to similar pressures does not necessarily explain why some lineages are more prone to converge. However, few convergent phenotypes with proven ecological relevance have been genetically investigated in multiple lineages. Cichlid fishes are the most species-rich family of vertebrates and exhibit an extraordinary level of evolutionary convergence, including a specialized morphology consisting of elongated heads and hypertrophied lips that has evolved several times independently. We used a combination crosses between "lippy" and "non-lippy species", RAD-sequencing and foraging performance assays to a) validate the ecological relevance of the morphological and genetic variation that segregated in our crosses and to; b) map the loci responsible for this variation. The mapped genomic regions show evidence of strong natural selection and affect the individual's foraging performance. The similar phenotypes that evolved in both lineages differ markedly in their genetic architecture. While in the cross between African species the traits have a highly polygenic basis, most of the morphological variation maps to a single locus in the Nicaraguan cichlid cross. The QTL that we detected in both crosses do not overlap, suggesting that repeated evolution in this case was not facilitated by biases in genetic variation. By uniquely combining genetic mapping and foraging performance trials, we uncovered ecologically-meaningful genetic variation and show that convergent evolution can occur through many routes thus not requiring a particular type of genetic architecture.

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