**Hybridization and Speciation**

*Introduction*

It is difficult to experimentally prove speciation, and most analyses involve a combination of different types of analysis.

Lamichhaney et al. (2018) studied speciation in Galapagos finches. Their study focused on a population of *Geospiza fortis* and the effects of one male *G. conirostris* migrant. Their study chiefly focused on the fitness of hybrids, to try to determine if the *G. conirostris* had started a viable and distinct population. In contrast, Kautt et al. (2016) examined sympatric speciation in Nicaraguan cichlids. Instead of the introduction of a new species, they examined evidence for species divergence over time, and identified five genetically distinct species (although they acknowledge that there could be six, which was previously thought to be the number of species in the lake system). Instead of examining a recent event, like Lamichhaney, Kautt and their team investigated a deeper evolutionary event of at least xxxx generations.

*Methods*

Both studies used whole-genome analysis. Kautt began with a PCA, to identify the different genetic groups. Kautt then used RAD-seq analysis, which allows them to randomly sample the entire genome, and examine both neutral and adaptive genomic variation. They specifically used the double digest RAD method, or ddRAD, which uses two enzymes to sample the genome. However, ddRAD is prone to allele dropout, which can cause researchers to underestimate heterozygosity. This wouldn’t necessarily be picked up in their FastQC quality analysis. However, the did not rely solely on ddRAD-seq, and mitigated shortcomings by using other analyses. Lamichhaney’s whole-genome sequencing was able to identify the migrant male conclusively as *G. conirostris,* additionally providing evidence of longer migrations by Galapagos finches. Their analysis found a significant increase in homozygosity in the hybrid bird lineage, indicating increased interbreeding and possible reproductive isolation. Genome-wide average nucleotide diversity declined from 0.17% to about 0.13% over the course of four to six generations, further indicating increased interbreeding in the hybrid population. The decrease in genetic diversity on multiple levels was clear evidence of endogamous breeding.

To complement their whole-genome analysis, both studies paired their results with other methods, including morphological variation. Lamichhaney focus on traits known to be important to finches in choosing a mate. They also chose traits that they already knew were significantly different between *C. fortis* and *C. conirostris*. They focused on body size, bill size, and bill depth. They found strong correlations between bill size and body size, and bill length and bill depth, showing the hybrids as a clear group of “Big Birds” (Lamichhaney Fig. 3). They were also able to identify that the *AXL1* locus on the *B* allele is likely largely responsible for beak depth. Instead of looking at morphological traits, Kautt performed a SNAPP analysis and extensive modeling. They used SNAPP, which is especially useful for analyzing SNP data, to calculate possible phylogenetic trees (Kautt Fig. 3). However, constructing these trees was computationally intense, so they were only able to use three individuals for each species. When modeling the populations, they started with single-populations models and then texted four to six other models. A “bottlegrowth” model fit the data the best, which supported their conclusions from their genomic and phylogenetic analyses.

*Conclusions*

Lamichhaney found significant morphological differences between the hybrid offspring and the G. fortis population. The hybrids had larger beaks, larger body size, and distinctive songs. These traits are all important in choosing a mate, indicating that these two populations could continue to be reproductively isolated. Kautt found evidence for distinct genetic clusters, and ongoing gene flow (Kautt Fig. 2). They also found that speciation occurred very rapidly, and in some cases possibly simultaneously. It appears from their data that the Nicaraguan cichlids provide a clear example of sympatric speciation, as their genetic lineages diverged in the same area without geographic separation. Importantly, the researchers claim that their results are evidence of a multi-species outcome of sympatric speciation.

These studies provide examples that even with whole-genome analysis, it is still difficult to tease apart the exact mechanisms of speciation. Combining genomic analysis with other methods, such as morphological data or modeling, can help create a more complete picture of the speciation process.

*Sources*

Kautt AF, Machado-Schiaffino G, Meyer A. 2016. Multispecies Outcomes of Sympatric Speciation after Admixture with the Source Population in Two Radiations of Nicaraguan Crater Lake Cichlids. *PLoS Genet*. 12:1–33.

Lamichhaney S, Webster MT, Han F, Grant PR, Grant BR, Andersson L. 2017. Rapid hybrid speciation in Darwin’s finches. *Science*. (80- ) 359:224–228.