**Matías Gómez Words: 785**

Despite speciation being a main driver of biological diversity, the origin of species remains a central question in evolutionary biology. Only since the emergence of modern genetics the underlying mechanisms of species separation have become tractable. When species form, there must be a substantial reduction in their shared genetic material to the point where those groups cease to be genetically compatible. Therefore, barriers to gene flow lie at the heart of the appearance of new species from ancestral ones. Whether physical isolation is indispensable to initiate genetic incompatibilities, or these can arise during ongoing geneflow, is still a contentious issue in evolutionary biology. Furthermore, the role of hybridization in reestablishing gene flow between incipient species, or contrarily, acting as a seed for new ones, has just begun to be addressed in modern biology.

Kautt et al. (2016) provided evidence for an empirical example of fast (~1000 generations) multispecies outcomes of sympatric speciation in lake cichlids in Nicaragua, relying on genomic data along morphology and biogeographical distribution of fish in four lakes. Lamichhaney et al. (2018), on the other hand, reported a rare and single founder effect on Darwin`s finches that gave rise to a population of incipient hybrid species under only three generations. Besides genomic and morphological variation, researchers identified song patterns as a signature of a premating barrier that prevented inter-specific breeding. Since the onset of reproductive isolations marks the start of a new species, the overall aims in both studies gravitated around reconstructing or tracking the steps that led to lineage divergece.

When studying speciation one must to recognize and tell apart the evolutionary units under study. To better assess the species identity of your group one can resort in morphology, geographical origin, behavioral or ecological patterns, genomic data, be it in form of SNPs or whole-genomes, if available. Initially, Lamichhaney et al. (2018) identified a male founder finch as *Geospiza fortis* based on morphological resemblance, but its larger size and different song cast doubts. A phylogenetic tree inferred from whole-genomes revealed the individual to belong to the *G. conirostris* species. Likewise, Kautt et al. (2016) found equivocal correspondence between morphological and genomic data (SNPs) for some benthic fish species and opted for recoding those difficult individuals according to their genetic signature. Once species identities have been settled, the evolutionary scenarios and trajectories of species can be addressed.

By following the breeding of a finch immigrant (*G. conirostris*) with a resident *G. fortis* female and its descendants for six generations over three decades on an Island, Lamichhaney et al. (2018) witnessed the emergence of a lineage of viable, fertile and highly inbred hybrids as evidenced by an increase in homozygosity, decrease in nucleotide diversity and extensive linkage disequilibrium across genomes over five generations. The large bill and body size of the offspring as compared with that of the original parentals, were favorable and allowed them to colonize a new niche previously unexploited by coexisting species. By contrast, to distinguish sympatric from secondary contact events of speciation in already divergent lineages of fish, Kautt et al. (2016) used SNPs to infer demographic and evolutionary history of current sympatric groups. Since genetic clustering methods do not consider demographic patterns, the authors started by assessing possible past admixture scenarios with a test (f3-statistics) that compares a population against two reference ones to look for signatures of introgression. Yet, if an admixture event happened before sympatric species diverged, the reference populations would share equal proportions of admixed genotypes. Alternatively, by incorporating migration in phylogenetic trees to evaluate if they improve the fit of the tree, but if all migration edges have a small increase in the tree’s fit they do not offer much information either. A third option is to execute coalescent simulations under well-defined models and compared them to the site frequency spectrum that captures the distribution of allele frequencies of the whole population. This last method showed the strongest support for a model of admixture from the source population into new lakes prior to sympatric speciation.

Overall, both studies show how the advent of genomics has revolutionized the study of speciation by making previously intractable issues approachable and testable and thereby illuminating the biological diversification process. Still, it remains difficult to distinguish pure sympatric speciation from secondary contact as discriminating between the causes of shared polymorphisms remains inherently challenging.

**References**

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