**Matias Gomez Words: 833**

Current species or populations distribution may or may not accurately reflect past demographic events that can be linked to climatic oscillations. This is due to the interplay of previous allopatric phases, genetic drift, migration and selection that confound interpretation of contemporary genetic patterns in the organisms under study. For example, secondary contact can wipe out much of the genetic among populations that have come into contact, where levels of gene flow, effective population size and genetic incompatibilities shape complex landscapes of genomic divergence as well as dynamic population histories. Genomic data along with demographic models can unravel past evolutionary events ans allow to understand contemporary distributions. Additionally, as the advent of genome sequencing has allowed to gather data from ancient tissue remains, the possibilities to peer into the recent past of some organisms such as humans, broadens immensely our means to understand and disentangle the evolutionary history of life on earth.

Rougemont and Bernatchez (2018) used a modeling approach based on approximate Bayesian computations, which accounts both for local genomic variation in effective population size and migration rate, to study past and recent factors shaping heterogenous landscapes of divergence in the Atlantic salmon (*Salmo salar*) by comparing alternative scenarios of divergence throughout the North Atlantic, spanning from Eastern North America to Europe. On the other hand, Moreno-Mayar et al. (2018) aimed to understand broad patterns of dispersal, divergence and admixture of the peopling of the Americas by using ancient DNA?. It is to highlight that, since both studies relied on previous genomic data from multiple sources to perform their respective analysis, the authors explicitly stated the need to cross-validate all data to make it comparable and therefore more reliable. A practice that cannot be overlooked when re-analyzing? available genomic data worldwide.

The Atlantic salmon is thought to have diverged between North America and Europe 600,000–700,000 YBP. This species displays anadromous migrations feeding at sea and returning to natal rivers to reproduce, making it prone to local adaptation. Previous studies suggest that rivers in both continents offered refugia to distinct populations and it is therefore likely that population subdivision took place within each continent with subsequent phases of secondary contact between them. To test this hypothesis, four main demographic scenarios of Strict Isolation, Ancient Migration, Isolation with Migration, and Secondary Contact, that included alternatives of population sizes and migration rates within them, were used under an approximate Bayesian computation approach. Demographic inferences supported a model of long periods of geographic isolation with multiple secondary contacts between continents at the end of the last glacial maxima (approximately 10,000-15000 years ago), that could account for the lack of marked differentiation in genetic regions adjacent to highly divergent loci. Isolation patterns within continents showed three main clusters in Europe, but fine-scale explorations of them instead supported a scenario of two ancient refugia with a posterior subdivision of one them into two. Whereas in North America, the two major groups found represent a mixture of multiple European lineages with various phases of secondary contact over time. The heterogenous patterns of genomic divergence in this species may have been caused by those events of introgression among populations, although the authors favored a view of linked selection, while recognized the challenges involved in disentangling such signatures without having recombination rates for the species.

The human colonization of the American continent likely took place ~23 ka ago in Siberia with migrations all the way down to south America. However, how these migrations were shaped by demographic processes is still debated. Moreno-Mayar et al. (2018) sequenced 15 ancient genomes from Alaska to Patagonia and compare them with a set of modern humans to describe how humans populated the continent. Genomic differences among genomes were explored through model-based clustering methods and multidimensional scaling. Posteriorly, demographic inferences were made by evaluating patterns of population size, admixture and linkage disequilibrium. Results confirmed a single and rapid expansion event down to south America followed by multiple populations that extended all over the continent where some social groups maintained highly cohesive patterns concordant with gregarious human behavior, and still reflected in living populations such as those that inhabit the coasts and inland nowadays. Human migration events revealed to be largely complex due to local and long-range movement across the continent where genomic signatures of hitherto unknown population from Australasian origin add to the unsolved fine-scale peopling pattern of the American continent.

Both studies explored wide genome data, in form of SNPs, to resolve different demographic models that help better explain current distributions and genomic signatures in their respective group of study. Although researchers in each study used different methods for the same purpose, this illustrates how wide genomic data can be deeply explored to address complex evolutionary questions that involve almost all evolutionary forces that have shaped contemporary demographic patterns.

References

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