**Matías Gómez Words: 756**

The genetic basis of adaptation is a central goal in functional and evolutionary biology as it provides insight into how organisms interact and respond to their environments. To pinpoint a gene or set of them that are responsible for any given traits in a live system, not only provides a mechanistic understanding of life functioning, but it also widens the possibilities to predict future organismal responses to rapidly changing environments, such as those faced under a climate change scenario. Moreover, identification of genomic patterns of potentially adaptive variation in wild populations is central to inform and guide conservation efforts. The capacity of species to adapt to changing conditions is determined by their existing genetic variation and phenotypic plasticity potential. However, to distinguish true cause and effect signals in live systems is a daunting task due their inherent complexity as well as that of the environment in which they occur. To bridge this gap, the emerging field of Landscape Genomics seeks to undercover potential adaptive genetic variation by combining extensive environmental datasets with high quality genomic resources.

Hancock et al. (2011) conducted a genome-wide scan in the widely distributed plant *Arabidopsis thaliana*  to detect putatively adaptive loci to climatic conditions. Species with a wide distributional range represent great models to examine genetic basis and modes of adaptation as they inhabit regions with extensive climatic variation. They evaluated correlations of 13 climate variables with genetic regions that exhibited enrichment of likely functional (non-synonymous substitutions ) variants against putative neutral (synonymous substitutions) genetic and intergenic variants. By comparing these two types of variants, researchers increase their confidence of actually picking up a genetic signal that affects phenotypic expression such as that of a change in the translation of nucleotides into amino acids that in turn impacts protein composition and function. Similarly, Brauer et al. (2016) aimed to detect selection across a hydroclimatically heterogeneous river basin on a fish (*Nannoperca australis*) with a confined geographical distribution in Australia. In this case they also relied on a set of composite environmental and geospatial variables to examine correlations with putatively adaptive genomic regions but performed *F*st outlier test to tell apart adaptive loci from neutral ones.

Although on both studies SNPs variants were used for their wide-genome scans, the approach to validate the detected putatively adaptive loci differed. Hancock et al. (2011) found climatic correlations associated to enriched genetic regions involved in photosynthesis, auxin biosynthesis, gravitropism and energy metabolism. If these loci had a real adaptive basis, they should be able to predict relative fitness of genotypes in plants from a particular climate. Their experimental designed to test this hypothesis consisted of selecting the SNPs in the 0.01 % tail of correlations with climatic variables and keeping those alleles that were more common in climatic conditions similar to those where they planted 147 *A. thaliana* plants. A strong correlation between reproductive success and allele count emerged with their estimation of relative fitness, derived from total silique (seed capsules) length, and the allele null distribution created from resampled sets of SNPs. This confirmed that the identified loci indeed played a role on relative fitness. Conversely, Brauer et al. (2016) found that temperature and precipitation were the environmental parameter that mostly influenced the allele frequencies of 216 candidate adaptive loci detected by two software (BAYESCAN and FDIST ). These correlations were found by using a spatially generalized linear mixed-model (*gINLAnd*) approach and a partial redundancy analysis.

Additionally, both studies assessed the geographical/spatial distributions of adaptive SNPs. Hancock et al. (2011) found SNPs correlated with humidity were widespread, while those correlated with daylength tended to be confined. Localized SNPs can be related to “hard selective sweeps”, new advantageous mutations that rapidly reach fixation. To test for this selection signature a pairwise haplotype homozygosity (PHS) analysis, that accounts for loss of genetic variation in neighboring selected SNPs, was performed. The results showed that SNPs with smallest geographic extent have higher enrichment variants, implying that selective sweeps are an important mode of adaptation in *A. thaliana.*  On the contrary, in *N. australis*  the distribution of outlier loci around a mean of 0.6, that is not close to 1 or fixation, seemed to correspond to polygenic “soft sweeps” where small changes of allele frequencies in standing genetic variation are responsible for the adaptive trait.

Overall, these two studies illustrate the power of Landscape Genomics and the achievable set of analysis when studying a model species (*A. thaliana*  ) or a non-model one (*N. australis*), and the implications this field of research can have under a scenario of climate change.

**References**

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