**Landscape Genomics: Detecting Adaptive Selection**

In the last decade, genomic techniques have become more powerful and increasingly popular when investigating a variety of scientific problems. Landscape genomics in particular has recently been applied to issues of climate change. Various analysis techniques can be used to identify adaptations in a species that may be correlated with environmental changes. However, it is difficult to determine if results show true signals of adaptation, or just random variation. Both Hancock et al. (2011) and Brauer et al. (2016) investigated how different populations may be adapting to climate change, but they used different strategies to determine if their analyses found true adaptive signals.

Hancock’s team studied the effects of climate change on ﻿*Arabidopsis thaliana*, a plant species frequently used by botanists as a model organism. In their approach, researchers used both genomic methods and field transplants to investigate the effects of changing environmental conditions on plant fitness. First, they used a pairwise Pearson correlation to choose 13 key climate variables. They enriched different SNPs and then, using a partial Mantel test, they calculated correlations between climate variables and the different phenotypes. They found strong correlations between day length and development time, temperature and leaf yellowing, and temperature/moisture and dormancy-related traits. This implies a genetic basis for climate adaptations. They also found significant enrichment of the amino acid changing SNPs, although this was accompanied by evidence of contributions of linkage disequilibrium. By looking for cases of extended pairwise haplotype homozygosity, they were able to find evidence of hard selective sweeps, further implying an adaptive response to climate change.

However, they had not conclusively determined if they had picked up true signals of adaptation, or perhaps had their results skewed by correlations between the climate variables themselves. They surmised that if their models were accurate, they would be able to predict which plants would survive better in a transplant experiment. After transplanting individuals from a wide geographic range to a narrow area (Lille, France), they found that they had accurately predicted which plants would have a higher fitness. They found a strong correlation between their chosen fitness index and the selected alleles. These results, combined with their previous evidence of hard selective sweeps, is strong evidence that some *A. thaliana* are adapting to climate change.

In contrast, Brauer’s team focused solely on modeling to determine if southern pigmy perch were showing adaptive responses to climate change. Gene flow among the different populations is restricted, so researchers applied a kind of “riverscape genomics” to separate possible signs of selection from shared population history. They performed FST outlier tests using BayeScan to identify outlier loci. To determine if they had detected true signals of adaptation, Brauer used a second GEA model (a kind of mixed model) to test if the FST outliers correlated with their chosen environmental factors. Researchers identified that temperature and precipitation were the most important environmental factors, but that differences between locations were responsible for the most variation. It appears that genetic drift remains a major factor behind the genetic diversity of these fish populations. They also found that as populations are fragmented smaller, they face greater heterogeneous selection pressure. However, environmental factors were responsible for some variation. The correlation shown by the GEA model implies that there is adaptive selection occurring in southern pigmy fish. Brauer found that multiple processes were influencing genetic variability in southern pigmy perch, perhaps making them more able to adapt to a changing climate in the future.

Both of these studies faced the same central issue: when you detect outlier alleles, how do you determine if they are the result of adaptive selection or just random chance? Both examined the effects of environmental factors on populations across a variety of areas, and how these factors may influence adaptation. They both tried pare down an initial list of many climate variables to only those most relevant to the study. Brauer’s multi-step technique seemed more robust, and they checked their results with a PCA. Hancock relied more on human judgement, picking which variable was more ecologically relevant when their model showed that two were correlated. When it came to determining if their model had accurately detected adaptive selection, Hancock chose another simple solution: they tested it in the field. This method is beneficial in that it provides clear, practical evidence of fitness. Researchers are as sure as they can be that they successfully identified adaptive SNPs. Brauer, on the other hand, focused on pairing different modeling techniques together to construct a complete picture. The GEA model was able to find that some loci responded to the same environmental factors across locations, showing some evidence for adaptive selection. Both methods showed evidence of adaptive selection, but their goals were slightly different. Hancock was looking for evidence of adaptive selection specifically, while Brauer was interested in general genomic trends throughout the landscape. Both studies illustrate the importance of tailoring your analysis methods to the question you are asking.

**Sources:**

﻿Brauer CJ, Hammer MP, Beheregaray LB. 2016. Riverscape genomics of a threatened fish across a hydroclimatically heterogeneous river basin. *Mol Ecol.* 61:5093–5113.

Hancock AM, Brachi B, Faure N, Horton MW, Jarymowycz LB, Sperone FG, Toomajian C, Roux F, Bergelson J. 2011. Adaptation to Climate Across the *Arabidopsis thaliana* Genome. *Science.* 334:83–87.