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750-1000 summary

Understanding the mechanisms behind evolutionary adaption is crucial in order to understand how species have survived despite the ever-shifting environmental conditions they face. While many studies have identified genes under selection, using population genomic analyses, these results are rarely paired with detailed ecological and behavioral data (Bosse *et al*, 2016). In addition, while there are a number of field studies that have documented the action of natural selection on traits, few have examined the underlying molecular mechanisms (Barret *et* al, 2018). As a result, developing a comprehensive understanding of the evolutionary adaption of a population by combining phenotype, genotype, and fitness, has remained a challenge. However, using species that are well studied both genetically and ecologically, scientists such as Nadeau *et al*., Bosse *et al*., and Barret *et al*., have a platform from which they can begin to construct the phenotype-genotype-fitness continuum.

Nadeau *et al* (2016) focused on the relationship between genotypic and phenotypic variance in the coloration and patterning of three *Heliconius* butterfly species. Focusing on previous mapped locus *Yb* and using population genomics, they identified SNPs that were strongly associated with the phenotypic variation in the 1 – Mb interval (which is shared by the three *Heliconius* species: *H. erato*, *H. melpomene*, and *H. numata*). They found that the majority of the SNP’s were found in the introns of the *cortex* gene for all three species. Since *cortex* was the only gene in the candidate region (1-Mb interval) that was consistently expressed across all three species with varying wing color and pattern, they concluded that *cortex* is a major regulator of wing color and pattern. Although they cannot confirm that *cortex* is not influenced by other genes in the region. In addition to their current analysis, they found that *cortex* falls into a family of cell-cycle regulators, which lead to the conclusion that *cortex* controls pigmentation by controlling scale cell development.

Bosse *et al* (2016) also mostly focused on the relationship genotypic and phenotypic variation for bill length in the bird species *Parus major* using data from three long term study populations (2 from the Netherlands and 1 from the UK). They first identified the loci under selection by running a PCA with phenotype as the first Eigenvector, choosing the outlier regions that were also supported by fixation index analyses. They fitted all the SNP’s in a mixture model analysis and found that bill length was highly polygenic and has been under divergent selection. They found that the SNP’s from *COL4A5* had the strongest associations to bill length and narrowed their study to focus on that locus. They compared the variation of the *COL4A5* locus to the reproductive success to determine how natural selection has affected the variation. They found that the UK population had a positive correlation with fledglings whereas the dutch populations had a negative, but not significant, correlation. This relationship led them to conclude that there was a fitness advantage for having longer bills in the UK population. Over the past 26 years there has been an increase in bill length in the UK. While this change is usually associated with a change in diet, as demonstrated in Darwin’s finch studies, there was no change in the natural diet for the Netherlands or the UK. Instead, this trait was being selected as a result of human interference: bird feeders. They found that those with longer bills (the *COL4A5* homozygotes) were more likely to use the feeders than their shorter-billed counterparts. Unlike Nadeau *et al* (2016), they didn’t examine the mechanisms that contributed to this selection. However, this study is particularly interesting because it not only an excellent example of natural selection in a wild population, it also is an excellent example of how our presence is affecting trait selection.

Unlike the previous two studies, Barret *et al* (2018) focused more on the fitness of their study species, focusing on the changes in fur coloration in wild mice in Nebraska. They collected 481 mice from both dark and light regions and released them into enclosures that was open to avian but not terrestrial predators. Using mark and recapture, they tracked the survival of the individuals every two weeks for 14 months. They found that the mice with coloration that correlated with the background habitat (i.e. light fur in light sand, dark fur in dark sand) had a higher survival rate in comparison to the introduced individuals. After sequencing all the individuals, they determined which SNP’s are associated with the dorsal brightness and compared them to the genotype frequencies under a model with and without selection. From there they were able to distinguish seven SNP’s, six in or near regulatory regions of the gene *Agouti*, and one deletion of serine. To further examine the affects of the deletion of serine, they created two matching lines of lab mice, one with and one without the deletion. They then compared the coats under a spectrophotometer and found that the mice with the deletion had significantly lighter coats. They further examined the underlying mechanisms and found that the deletion of serine decreases the strength of the interactions with attractin, which reduces pheomelanin production, creating the lighter coat.

Although each of the three studies used different analyses and had different focuses, all three integrated either phenotype and genotype or phenotype-genotype-fitness. This interdisciplinary examination not only helps us to determine what has changed, but it can help us to understand why and how it has changed. Understanding how different environmental, either biotic or abiotic, factors shape the genetics of an organism can help us to predict how species are going to adapt (if they can keep up) to the imminent threat of climate change.