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750-1000 Summary 1

Words: 776

*Riverscape genomics of a threatened fish across a hydroclimatically heterogeneous river basin*

Brauer et al 2016

*Adaptation to Climate Across the Arabidopsis thaliana Genome*

Hancock et al 2012

*Bigger Picture*

The Brauer et al 2016 study aimed to use landscape genomics to inform both in situ and ex situ eco-system based management of a threatened southern pygmy perch in Australia. To accomplish this, genotype-environment association analyses (GEA) and FST outlier tests were used to find loci that were either neutral or adaptive. High-resolution environmental data and thousands of SNPs were used to assess population structure and find areas of selection in environments that varied in 40 different ways, including human disturbance, precipitation, and temperature.

The Hancock et al 2012 study did not include a management based broader impact, but similarly focused on finding adaptive loci in the genome. This study focused on the plant species *Arabidopsis thaliana*. In contrast to the Brauer et al 2016 paper, Hancock et al focused on amino-acid changing variants to detect adaptive alleles and the prevalence of selective sweeps. This study compared 107 phenotypes in *A. thaliana* and 13 climate variables using hundreds of thousands of SNPs including non-synonymous, synonymous, and intergenic SNPS.

The Brauer et al 2016 study uses landscape genomics techniques to investigate a threatened species’ potential to act on and adapt using only standing genetic variation. One main goal was to identify and quantify regions that could be under selection, in order to evaluate the resiliency or vulnerability of a species. The main questions addressed included: “Can landscape genomics be used to distinguish signals of selection from other confounding effects (e.g. strong drift) in a threatened, poor dispersive species?”, “Can selection due to human disturbance be distinguished from selection due to natural environmental heterogeneity?”, “Can GEA approaches detect genomic footprints of polygenic adaptation due to hydroclimatic heterogeneity?”.

The Hancock et al 2012 study also investigated the role standing genetic variation in *A. thaliana*, but found that selective sweeps were much more influential in the adaptation of this plant species.

The framework of GEA used in Brauer et al 2016 requires the inclusion of means to rule out the confounding effects of population history and geographic regions, since the perch species can be greatly influenced by physical landscape structure.

*Genomic techniques*

Brauer et al 2016 focused on detecting outlier and neutral loci was done with the Bayesian approach. Remaining neutral SNPs were compared to the Hardy-Weinberg equilibrium. Expected and observed heterozygosity was calculated for both neutral and candidate loci. Effective population size was determined by using the linkage disequilibrium method. Population-specific FST for each site was estimated for both neutral and candidate loci. This study also used a variety of models that assessed the most likely K value (number of populations) from individual genotypes and the probability of that genotype belonging to that population.

The Hancock et al 2012 paper also used a series of model, but instead to predict relative fitness of genotypes grown in a particular climate. This study also focused more on directly testing selective sweeps than Brauer et al 2016.

*Environmental factors*

The Brauer et al 2016 study used principal component analysis (PCA) to analyze the relationship of a subset of 40 candidate variables to allele frequency in order to determine signatures of selection. Then, partial redundancy analysis (RDA) was used to control for spatial genetic structure while comparing environmental factors to genomic diversity patterns.

Hancock identifies 13 environmental variables that could be contributing to adaptive changes in the genome including evidence that aridity, maximum temperature, and precipitation were the most influential.

*Conclusions*

Brauer et al 2016 found that drift was a major evolutionary process that was affecting genetic diversity in this particular system. Temperature and precipitation were the most influential environmental factors found to be a part of a hydroclimatic-driven selection process. Human disturbance effects on loci were much smaller and localized compared to other environmental factors affecting the population regionally.

Hancock et al 2012 concludes that selective sweeps play more of an adaptive role than standing genetic variation. This study suggests that *A. thaliana* may have limitations in their capacity to adapt under rapid climate change due to the species waiting for more mutations in their genome.

Although the Brauer et al 2016 and Hancock et al 2012 papers had similar end goals of determining adaptive loci and comparing environmental factors (temperature and precipitation), the methods and models used in both papers were aimed at answering different bigger picture questions. Brauer focused on detailing landscape genomic methods including calculating FST values and PCA analysis, which were not analysis methods used in Hancock et al 2012. Brauer focuses on neutral and candidate loci compared to Hancock focusing on various kinds of SNPs. However, both papers aim to broadly identify the capacity of their study species to adapt under rapid climate change.