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Landscape Genomics Summary

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As climate change is a persistent problem, it is important to understand how natural selection creates and maintains adaptive genetic diversity in heterogenous environments. Brauer et al. (2016) and Hancock et al. (2011) are two studies that assessed the correlation between adaptive loci and environmental factors in two different study systems. The methodology used to identify these candidate adaptive loci differed between both studies as did the approaches that were used to account for neutral effects such as populations structure and history. It is important that landscape genomics studies account for these neutral effects because they can result in false signals of selection of adaptation.

*Study systems*

Brauer and colleagues completed their riverscape genomic analysis in the threatened southern pygmy perch (*Nannoperca australis*), which is an ecological specialist with low dispersal potential. As a threatened species, the pygmy perch is likely to have small effective population sizes, experience population isolation as well as repeated local extinction-recolonization cycles and inbreeding. These characteristics could make it difficult to differentiate between signals of neutral processes (i.e., genetic drift) and signals of selection. In this study, they do confirm that drift is a major evolutionary process shaping genetic diversity in the river system of the pygmy perch.

Hancock et al. (2011) conducted their genome-wide scan to identify climate-adaptive loci in the plant *Arabidopsis thaliana*, a non-threatened species with larger dispersal potential ([Falahati‐Anbaran](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Falahati-Anbaran%2C+Mohsen), Lundemo, & [Stenøien](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Sten%C3%B8ien%2C+Hans+K), 2014). The populations of *A. thaliana* are less likely to exhibit signals of neutral processes, as they will have larger effective population size and will not likely experience population isolation and repeated local extinction-recolonization cycles. While both studies should account for the effects of neutral processes, these confounding effects are likely to be more evident in the smaller pygmy perch population in the Brauer study.

*Landscape Genomics approaches*

Brauer used a Bayesian approach with Bayescan to detect outlier loci that are potentially under selection (not conforming to neutral expectations). The remaining neutral loci were tested against Hardy-Weinburg equilibrium. To test for associations between allele frequencies and environmental variables, Brauer used genotype-environment association (GEA) methods. They used a linear mixed-model approach to create two different models for each locus. The first model includes the environmental variable as the fixed effect, which influences the allele frequencies whereas in the other model, the environmental variable has no effect. Using GEA methods allows for the model to account for neutral genetic structure. The combination of outlier tests and GEA increases the detection of true positives, where signals of selection are not confused with signals from other confounding effects.

The Hancock study does not take advantage of the outlier tests but does use GEA methods. To test for correlations between genetic variants or phenotypes and environmental variables, they used a partial Mantel test, which generated a Spearman correlation value. To control for population structure, they used a kinship matrix. From these analyses, they found strong correlations between various environmental factors and phenotypes. Using a common garden experiment, they then tested whether a set of alleles with the strongest climate correlations could predict variation in fitness of genotypes grown in a particular climate. If they could predict the relative fitness of the genotypes, then this would confirm that they are observing true signals of potential selection.

*Environmental Variables*

Both studies began with 40 environmental variables that had to be narrowed down to a select few for their models. In the Brauer study, they took 40 environmental variables and divided them into five categories. Within each category, they used variance inflation factor (VIF) analysis to exclude highly correlated variables until all remaining variables were under a VIF threshold of 10. Principal components analyses were then performed for the remaining variables in each category to retain a few principal components, which were then used as synthetic environmental variables in the GEA analyses. In the Hancock study, they “pruned” their environmental variables down based on the pairwise Pearson correlations of the variables. In cases where variables were strongly correlated with each other, the variable with the most obvious link to the ecology of *A. thaliana* was selected.

*Conclusions*

Both studies used landscape genomics techniques to investigate the role of standing genetic variation in their specific study system.

As stated earlier, Brauer found that drift is a major evolutionary process shaping genetic diversity in the river system of the pygmy perch. They also found evidence of environmentally-driven selection as well, with temperature and precipitation acting as important environmental factors influencing allele frequencies. They included a conservation component, by testing the effects of human disturbances on adaptive variation. From this analysis, they found that human disturbances only effect loci on a local scale.

Hancock found that selection on standing genetic variation plays a role in *A. thaliana* populations but determined that selective sweeps are likely an important mode of adaptation in *A. thaliana*. The fixation of a new mutation that occurs in selective sweeps may pose problems for future adaptation capabilities of *A. thaliana* populations. The fixation of a certain allele may be advantageous for the population under the current environmental pressures, but as environmental conditions change, it will be difficult for the population to adapt. This is due to the long generational time required for a new mutation to appear and reach fixation. Selection on standing variation is likely important for adaptation as standing variation has the potential to be selected for under future environmental pressures.

**Literature Cited**

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