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Climate Change

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As the Earth’s climate is rapidly changing, species can respond either through acclimatization, adaptation, migration, or extinction. Adaptation is the process by which natural selection adjusts allele frequencies in a population. The presence of standing genetic variation in populations is important for adaptation as it maintains species’ evolutionary potential. Bay et al. 2018 and Jordan et al. 2017 are two studies that look at a species’ potential to adapt to climate change. Bay examined the genomic basis of climate adaptation in a North American migratory bird, the yellow warbler (*Setophaga petechia*). Jordan used landscape genomics to assess genomic signatures of adaptation to climate in the widespread Australian tree species *Eucalyptus microcarpa.* Both studies take advantage of population and landscape genomics methods to investigate population structure and the potential for adaptation to climate change.

*Study Organism*

While the study organisms in each study are quite different, both species are experiencing population declines, therefore requiring mitigation and restoration efforts. Bay focused on a migratory bird species that can experience a wide variety of climate conditions depending on their breeding site and migratory route. In migratory species it is less clear to what extent genomic variation is shaped by environmental variables. They have experienced local population declines and, in some regions, are listed as a species of concern. Jordan focused on a tree species that has been extensively cleared for agriculture across southeastern Australia, resulting in a highly fragmented distribution. Population fragmentation can reduce gene flow and sharing of adaptive alleles, increasing populations’ risk of maladaptation when the environment changes.

Both studies used a study system with a broad species distribution. With a broad distribution, there is a high potential for populations to adapt to local conditions, therefore, the ability for adaptation is expected to vary across a species’ distribution. This must be taken into consideration when modeling biological responses to climate change, in order to prevent the under- or overestimation of extinction risks or range shifts.

*Population Genomics Techniques*

In both studies, samples were collected at various sites across each species’ distribution capturing the major environmental gradients. To test for signals of selection across the species’ range, Bay used restriction site-associated DNA sequencing (RAD-Seq), while Jordan used DArTseq, a reduced-representation genomic approach. DArTseq selects fractions of the genome that correspond to active genes by using a combination of restriction enzymes which separate low copy sequences from the repetitive fraction of the genome (Sansaloni et al., 2011). Bay and Jordan examined SNPs using the yellow warbler genome and the *Eucalyptus grandis* (closely related species) genome, respectively. SNPs were called and filtered using vcftools.

Both studies performed population structure analyses, first using pairwise FST and Manel tests to test for isolation-by-distance. To assess general population structure, Bay used ADMIXTURE analysis, while Jordan used individual-level PCA. Both studies found low population structure in each species and evidence of isolation by distance.

Jordan then went on to identify putatively adaptive SNPs using four FST outlier detection programs: BAYESCAN, FDIST2, hierarchical FDIST2 and BAYENV. To complement the FST outlier tests, an environmental association analysis was performed in BAYENV2.0 to identify SNPs that were associated with an environmental variable. Bay did not perform any outlier detection programs, but did perform an environmental association analysis using latent factor mixed models (LFMMs) instead of BAYENV2.0. For independent validation of SNPs associated with climate in LFMM analysis, Bay also used Fluidigm assays for targeted genotyping.

Both studies then identified the genomic regions associated with the environmental variables by investigating the distribution of the putatively adaptive SNPs identified in the environmental association analyses. Bay was then able to link some of the strong genotype-environmental associations to genes with known behavioral functions. Because Jordan used the genome of a closely related tree species, there was less certainty in the function of the genes associated with putatively adaptive SNPs. Using only SNPs located within a putative *E. grandis* genic region and Gene Ontology terms for the predicted *E. grandis* genes with associations to the putatively adaptive SNPs, Jordan found that climate adaption may involve a range of biological processes and molecular functions including protein modification and stress response.

*Potential for Adaptation*

Bay and Jordan used different methods to test the potential for genomic adaption to future climate change. Bay used the metric “genomic vulnerability” to investigate which populations might be most

vulnerable to future climate change. They used a regression tree-based approach (gradient forest), to test whether a subset of genomic variation can be explained by environment and to visualize climate-associated genetic variation across the breeding range. They then extended gradient forest to calculate genomic vulnerability as the mismatch between current and predicted future genomic variation based on genotype-environment relationships modeled across current populations. Using a similar idea, but different metric, Jordan compared current allele frequencies of adaptive SNPs to theoretical expected allele frequency changes if populations are to match projected climate change, focusing on mean annual temperature and summer and winter precipitation. They used the proportion of adaptive SNPs currently fixed and the proportion of adaptive SNPs that, under expected allele frequency changes, would lead to fixation or to an allele frequency currently not seen within the sampled distribution as two measures to indicate potential limits to in situ adaptation from current standing genetic variation.

*Conclusions*

Bay found evidence of standing variation for adaptation to different climate regimes and showed that natural selection during breeding months is driving evolutionary shifts in the genome. They also found that populations with high genomic vulnerability had a higher likelihood of population decline, suggesting that yellow warbler populations may have already experienced some negative impacts of climate change.

Jordan also found evidence of standing variation and showed that allele frequency shifts expected to match projected climate change vary between adaptive SNPs and between sites, suggesting that the capacity to adapt in situ may also vary between locations.

Both studies demonstrate the importance of using genomic data to provide a more thorough understanding of future climate change impacts.

**References**

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