ECOLOGICAL GENOMICS

Genomic signals of selection predict climate-driven population declines in a migratory bird

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The ongoing loss of biodiversity caused by rapid climatic shifts requires accurate models for predicting species' responses. Despite evidence that evolutionary adaptation could mitigate climate change impacts, evolution is rarely integrated into predictive models. Integrating population genomics and environmental data, we identified genomic variation associated with climate across the breeding range of the migratory songbird, yellow warbler (*Setophaga petechia*). Populations requiring the greatest shifts in allele frequencies to keep pace with future climate change have experienced the largest population declines, suggesting that failure to adapt may have already negatively affected populations. Broadly, our study suggests that the integration of genomic adaptation can increase the accuracy of future species distribution models and ultimately guide more effective mitigation efforts.

Anthropogenic climate change is having a marked impact on Earth's biodiversity (*1*). Rapid fluctuations in temperature and precipitation can alter the suitability of particular regions and in some cases, exceed the physiological limits of organisms (*2*, *3*). The mismatch between environment and physiology can lead to shifts in species ranges, population declines, or even extinction (*4–6*). The difference between these evolutionary outcomes can in part be determined by the adaptive capacity of a species; those that possess standing genetic variation for climate-related traits are most likely to have the ability to adapt to rapidly changing environments (*7*, *8*). Understanding the effects and distributions of potentially adaptive alleles associated with climate can therefore aid efforts to accurately predict species responses to future conditions (*9*), and aid in mitigation efforts.

Although migratory birds are highly sensitive to climate change (*10–12*), little is understood about how populations differ in adaptive capacity. Breeding ranges of North American migrants have shifted northward (*13*), but microevolutionary responses associated with these shifts remain poorly documented. Although genome-wide associations with climate variables have been shown to affect many groups across the tree of life (*14–16*), in migratory species it is less clear to what extent

genomic variation is shaped by environmental variables. Here, we examined the genomic basis of climate adaptation in a North American migratory bird, the yellow warbler (*Setophaga petechia*). Yellow warblers have a broad breeding range across the United States and Canada and are common throughout their range, though they have experienced local population declines and, in some regions, are listed as a species of concern (*17*). Because of their broad distribution, yellow warblers inhabit a large range of environmental conditions, making them an ideal system for investigating variation in local climate adaptation.

We used restriction site–associated DNA sequencing (RAD-Seq) to test for signals of selection across the breeding range. We examined 104,711 single-nucleotide polymorphisms (SNPs) in 229 individuals from 21 locations (table S1 and fig. S1), using our assembly of the first yellow warbler genome (*18*). Pairwise genetic distance between locations ($F_{ST}/1 - F_{ST}$) was highly correlated with geographic distance, suggesting a strong signal of isolation by distance (Fig. 1A: Mantel's $r = 0.85$, $P = 1 \times 10^{-5}$), consistent with previous findings using microsatellite loci (*19*). Analysis of population structure using ADMIXTURE found little evidence of substructure, consistent with strong isolation by distance (fig. S2). Genetic distance was also significantly associated with environmental distance, based on climate variables, vegetation indices, and elevation, downloaded from public environmental databases (Fig. 1B: Mantel's $r = 0.36$; $P = 0.0006$). In a multiple regression of distance matrices, only geographic distance was significant (MRM: $R^2 = 0.73$; geography $P = 1 \times 10^{-5}$; environment $P = 0.12$), suggesting that isolation by distance is the strongest force structuring genome-wide variation. This result is not unexpected, however, because environmental adaptation likely affects a small fraction of the genome (*9*). We used gradient forest (*20*), a

machine-learning regression tree-based approach, to test whether a subset of genomic variation can be explained by environment and to visualize climate-associated genetic variation across the breeding range (Fig. 1, C and D). Strong differences in environmentally associated genetic variation are apparent across longitude and latitude, and unique genotype-environment associations are present in the Rocky Mountains and Coastal British Columbia. Our results suggest that despite high dispersal capacity and vagility via annual migration, yellow warblers exhibit standing genetic variation associated with the environment among populations and are likely subject to environmentally mediated selection during the breeding season.

To investigate which populations might be most vulnerable to future climate change, we defined the metric "genomic vulnerability" as the mismatch between current and predicted future genomic variation based on genotype-environment relationships modeled across contemporary populations. We followed the method presented in Fitzpatrick and Keller (*21*) to calculate genomic vulnerability using an extension of the gradient forest analysis. Populations with the greatest mismatch are least likely to adapt quickly enough to track future climate shifts, potentially resulting in population declines or extirpations. Under future climate change scenarios [representative concentration pathways—RCPs—defined by the Intergovernmental Panel on Climate Change (*22*)], the regions with highest genomic vulnerability stretch from the southern Rocky Mountains to Alaska, along with patchy regions in the Eastern United States (Fig. 2A). As expected, genomic vulnerability increases under more severe climate change scenarios; under the most extreme scenario (RCP8.0), nearly the entire range is estimated to have high genomic vulnerability (fig. S4).

If future climate change is correlated with recent shifts (for example, if regional drying over the last century in some regions will continue and become more severe), we expect that recent climate change will have already negatively affected populations with high genomic vulnerability. We tested this idea by comparing genomic vulnerability scores (using 2050 RCP2.6, though the results were robust to different scenarios; fig. S4) to population trends estimated from North American Breeding Bird Surveys (*23*) (Fig. 2B). Regions that had higher genomic vulnerability scores experienced the largest population declines over the past half century [generalized additive model (GAM): adjusted $R^2 = 0.101$; $P < 0.001$; Fig. 2C], showing that populations already in decline are most vulnerable to future climate change and suggesting that a mismatch between genomic variation and climate may have already resulted in negative impacts. We believe that genomic vulnerability can therefore be used alongside other known causes of population decline, such as habitat degradation and avian disease, to understand and predict population dynamics.

Understanding which environmental variables are most closely associated with local adaptation to particular climate conditions and vulnerability

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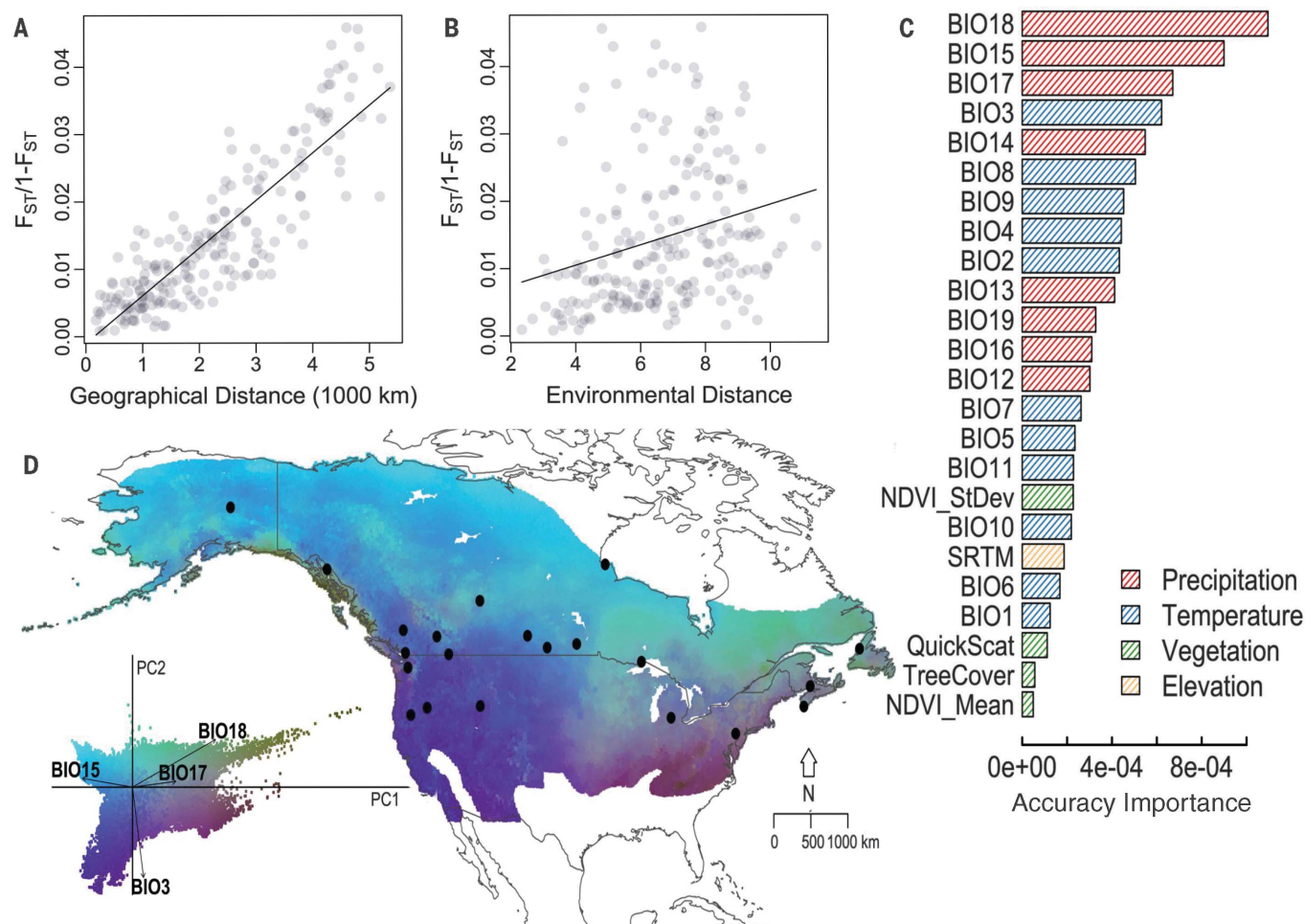*Corresponding author. Email: rachaelbay@gmail.com

Fig. 1. Geography and environment explain genomic variation in yellow warblers. (**A**) Pairwise genetic distance ($F_{ST}/1 − F_{ST}$) is associated with geographical distance and (**B**) environmental distance. (**C**) Ranked importance of environmental variables based on gradient forest analysis shows that climate, especially precipitation, strongly explains genomic variation.

(**D**) Gradient forest-transformed climate variables show climate adaptation across the breeding range. Colors are based on principal components analysis (PCA) of transformed climate variables [(D) inset: loadings of all variables are shown in fig. S3]. Points on map reflect sampled locations, and arrows on PCA show the loadings of top climate variables on PCA.

can prove useful in determining the biological mechanisms involved in population declines. Climate variables, especially precipitation measures, were most strongly associated with genomic variation across the breeding range of yellow warblers (Fig. 1C). Of the 25 environmental variables tested in the gradient forest analysis, the top three explanatory variables were precipitation related: (i) precipitation of the warmest quarter (BIO18), (ii) seasonality of precipitation (BIO15), and (iii) precipitation of the driest quarter (BIO17). Overall, precipitation variables were most important, followed by temperature variables and to a lesser extent, vegetation and elevation variables, suggesting that adaptation to precipitation is important on the breeding grounds.

To investigate the genomic basis of adaptation across contemporary climate gradients, we identified genomic regions associated with the top precipitation-related variables using latent factor mixed models (LFMMs) (24), which test for associations between genotypes and environments

while accounting for background population structure (Fig. 3A and fig. S5). We found 85, 67, and 35 SNPs associated with climate variables BIO18, BIO15, and BIO17 (described above), respectively [false discovery rate (FDR)–corrected $P < 0.05$]. These SNPs were broadly distributed across the genome, on 27 chromosomes (table S2). For the 13 SNPs associated with all three variables, we identified 12 adjacent genes with a range of functions including zinc finger genes (ZNF397 and ZKscan1), peptide secretion (SCT and MUC4), and transmembrane proteins (CDHR5, SLC25A33, and TEMEM201). Targeted genotyping using Fluidigm assays for 17 SNPs associated with climate in the LFMM analysis in an additional 309 birds at 29 locations independently validated climate associations in 8 out of 17 SNPs (FDR-corrected $P < 0.05$; table S3) with marginal associations in an additional two SNPs (FDR-corrected $P < 0.1$).

One of the strongest associations between genotype and climate was upstream of genes with known function in avian behavior and migration. A SNP on chromosome 5 was very strongly

associated with all three top environmental variables (LFMM $P < 0.001$; Fig. 3), and these associations were validated with Fluidigm assays ($P < 0.001$; Fig. 3, C and D). The highest allele frequencies at this SNP occurred in the Maritime provinces of Canada (Nova Scotia and Newfoundland), areas of high rainfall and low seasonality. This SNP is upstream of two genes, DRD4 and DEAF1 (Fig. 3B), that have known associations with migration in birds (25, 26). The DRD4 gene in particular, a dopamine receptor, has been extensively studied for its involvement in novelty-seeking behavior in primates, fish, and birds (26). Polymorphisms in this gene are linked to novelty-seeking or exploratory behavior in a number of bird species (27, 28), and linkage blocks extend into the neighboring DEAF1 gene, a transcription factor involved in serotonergic signaling. The exploratory phenotype has been linked to dispersal, which is thought to allow species to occupy new environments (25), but experimental studies linking behavior, genotype, and environment are needed to fully understand how these variants might
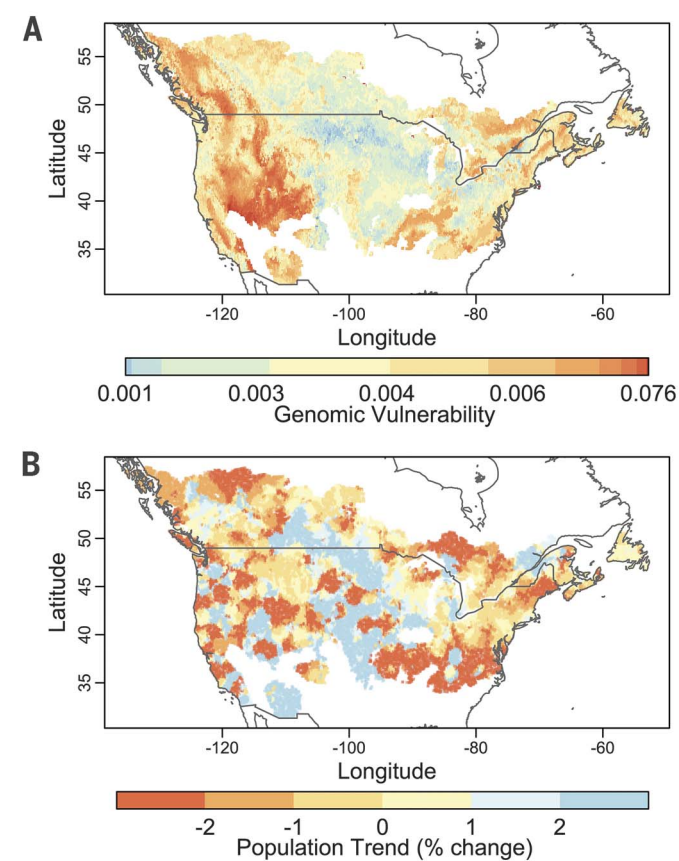
Fig. 2. Genomic vulnerability to future climate change is associated with a higher probability of population decline. (**A**) Genomic vulnerability based on 2050 RCP2.6 projections. (**B**) Population trend estimates (percent change per year) for yellow warblers based on North American Breeding Bird Survey analysis (*23*). (**C**) Generalized additive model (GAM) showing the relationship between population trend and predicted genomic vulnerability. The black line represents the model fit, and the shaded area is the 95% confidence interval.
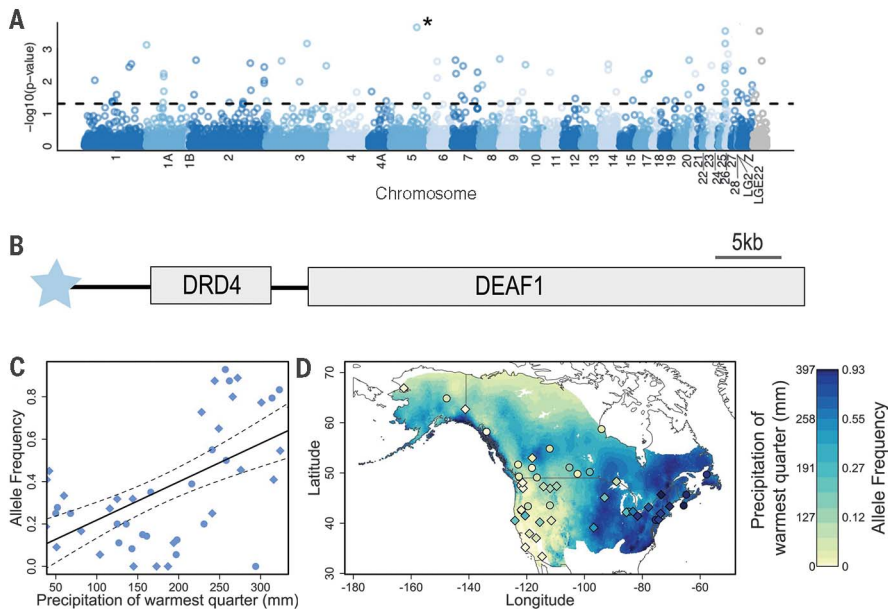
Fig. 3. Genome-wide variation associated with climate variables. (**A**) Manhattan plots show the significance level (FDR-corrected) for SNP associations with precipitation of the warmest month (BIO18). Dashed line represents $P = 0.05$. Colors distinguish different chromosomes, and gray points are SNPs on scaffolds not anchored to a chromosome. (**B**) The most significant SNP association, marked with an asterisk (*) in (A), is upstream from the *DRD4* and *DEAF1* genes. (**C** and **D**) Correlations between allele frequency and BIO18 for this SNP. Samples genotyped by RAD-Seq are represented as circles, and samples genotyped with Fluidigm assays are shown as diamonds.

be involved in climate adaptation. However, this SNP represents a single locus with significant associations between genotype and environment, but many other highly significant candidates exist (table S2), highlighting the complex and polygenic nature of climate adaptation.

Expected patterns of environmentally mediated evolution in migratory animals are complex but could drastically alter predictions of species response to climate change. We showed that standing variation for adaptation to different climate regimes exists and that natural selection during breeding months is driving evolutionary shifts in the genome. High genomic vulnerability, or mismatch between current allelic variation and future environmental conditions, was correlated with a higher likelihood of population decline, suggesting that yellow warbler populations may have already experienced some negative impacts of climate change over the past 50 years.

Our results show how the integration of genomic, environmental, and demographic data can provide a more thorough understanding of future climate change impacts on a migratory bird species. More broadly, we illustrate a new approach for understanding climate-associated causes of current and future declines and an important tool for making more-informed conservation decisions.

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Yellow warblers already in decline

As the climate changes, species' ability to adapt to changing conditions may relate directly to their future persistence. Determining whether and when this will happen is challenging, however, because it is difficult to tease apart the causes of decline or maintenance. Bay *et al.* looked at the relationship between genomic variation and the environment in North American populations of the yellow warbler (see the Perspective by Fitzpatrick and Edelsparre). Genes linked to exploratory and migratory behavior were important for successful climate adaptation. Furthermore, populations identified as ''genetically vulnerable'' because of limited climate-associated genomic variation were already declining.

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