

Genomics-informed conservation units reveal spatial variation in climate vulnerability in a migratory bird

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Abstract

Identifying genetic conservation units (CUs) in threatened species is critical for the preservation of adaptive capacity and evolutionary potential in the face of climate change. However, delineating CUs in highly mobile species remains a challenge due to high rates of gene flow and genetic signatures of isolation by distance. Even when CUs are delineated in highly mobile species, the CUs often lack key biological information about what populations have the most conservation need to guide management decisions. Here we implement a framework for rigorous CU identification in the Canada Warbler (*Cardellina canadensis*), a highly mobile migratory bird species of conservation concern, and then integrate demographic modeling and genomic offset within a CU framework to guide conservation decisions. We find that whole-genome structure in this highly mobile species is primarily driven by putative adaptive variation. Identification of CUs across the breeding range revealed that Canada Warblers fall into two Evolutionarily Significant Units (ESU), and three putative Adaptive Units (AUs) in the South, East and Northwest. Quantification of genomic offset within each AU reveals significant spatial variation in climate vulnerability, with the Northwestern AU being identified as the most vulnerable to future climate change based on genomic offset predictions. Alternatively, quantification of past population trends within each AU revealed the steepest population declines have occurred within the Eastern AU. Overall, we illustrate that genomics-informed CUs provide a strong foundation for identifying current and potential future regional threats that can be used to manage highly mobile species in a rapidly changing world.

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