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### Title

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### Authors

Adams, Nicole  
Tell, Lisa A.  
Bandivadekar, Ruta R.  
[et al.](#)

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# Using Genetic Tools to Identify Populations Within Species Could Ease Infrastructure Mitigation

Nicole Adams, Lisa A. Tell, Ruta R. Bandivadekar, and Rachael Bay  
University of California, Davis

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## RESEARCH BRIEF

### Research Question

Recent research suggests that bird populations are declining at alarming rates across the United States. Over the last century, local, national, and international efforts to limit declines in bird populations have resulted in state and federal laws that now protect most of California's 650 bird species. To comply with these protections, transportation infrastructure projects often face strict mitigation requirements, which can be expensive and cause delays. Understanding a project's effects on specific bird populations can refine mitigation requirements and optimize infrastructure planning. For example, whether an individual bird found at a project site is from a stable or declining population could have different implications for the resulting mitigation strategy.

The tools for identifying separate populations within species and understanding protected birds' seasonal movement have been limited until recently. New genetic and genomic tools now provide a method for understanding population differentiation, which is vital to a wide array of conservation goals including estimating population declines, identifying potential for adaptation to stressors, measuring connectivity between populations, and estimating inbreeding. Because infrastructure projects can directly impact genetic diversity and connectivity, a toolkit to assess population structure and the distribution of genetic variation could aid in predicting and mitigating the impacts of such projects. As a test case, researchers at UC Davis sequenced entire genomes for 40 individual Anna's hummingbirds (Calypte anna) from across California (Figure 1) to identify breeding populations and develop a genetic toolkit to assign individuals to those populations (Figure 2). The presence of this species at bridge construction sites has resulted in construction delays in part because little information exists on the status of different populations within the species.

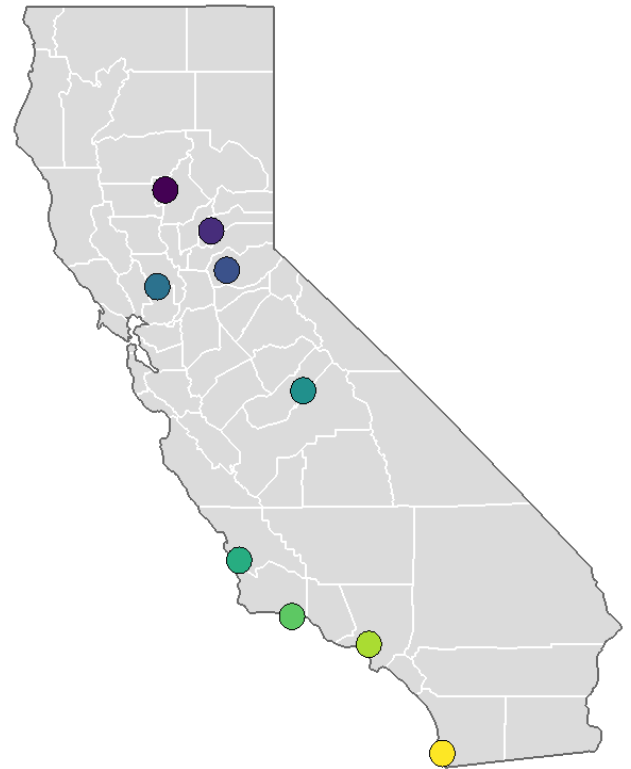


Figure 1. Location of Anna's hummingbird samples collected for genomic analysis

### Key Findings

**Researchers found a weak genetic pattern of geography in Anna's hummingbirds in California.** There was little population differentiation among the 40 individuals sampled across nine locations for this study. This finding suggests that there are no obvious barriers to movement among the sampled populations.

**Despite apparent weak population structure, broad geographical origin can be assigned.** Based on a subset of genetic markers, individual Anna's hummingbirds could be assigned to a breeding region in either Northern or Southern California. Even tests with relatively few genetic markers were able to differentiate the two regions. These findings suggest that a test based on a relatively small set of genetic markers could be used to assign

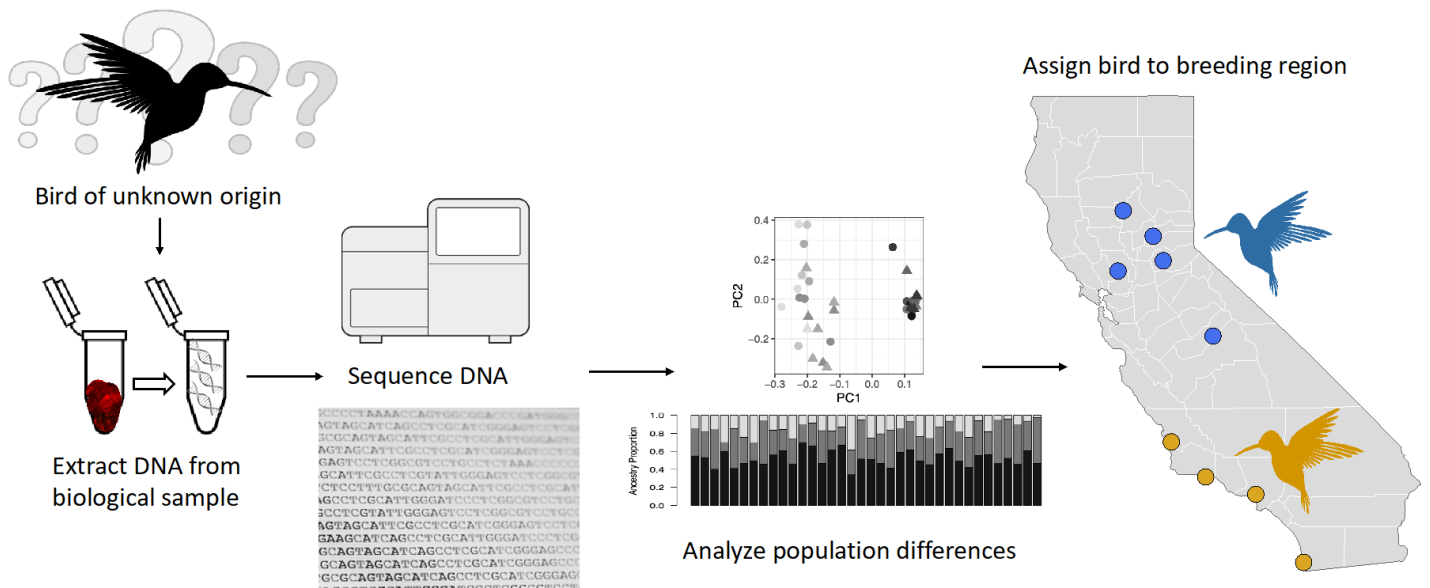


Figure 2. Flow chart depicting the process of assigning a breeding region to a bird of unknown origin using genomic tools

broad-scale geographic origin despite a lack of overall differentiation among locations across California.

**These broad geographical regions of well-mixed populations may be due to Anna’s hummingbird’s changing population dynamics.** Anna’s hummingbird’s northern range limit has expanded over the last century from the Sacramento Valley to as far north as southwestern Alaska. Winter population sizes in central California have remained constant over the last half century and populations in northern California are increasing.

## Research Implications

This is one of the first studies looking at genetic variation and population structure in Anna’s hummingbird, and the first to leverage the power of whole genomes. While the UC Davis findings suggest that little population differentiation exists, a more complete view of distinct breeding populations of Anna’s hummingbird in California would be facilitated by more extensive geographic sampling. Currently, data from more locations are being sequenced to increase the resolution of the population structure analysis. Results should lead to a more high-resolution definition of populations across the California range of Anna’s hummingbird and a more precise assay.

This research also has implications for other avian species, especially those with declining habitats and population sizes, that could be highly differentiated and potentially more affected by infrastructure construction. Use of a genetic toolkit developed from this type of analysis could provide a better understanding of population-specific effects on these species. This information could be critical for minimizing impacts on birds during infrastructure projects, especially bridge construction.

## More Information

This research brief is drawn from “Genetic Toolkit for Assessment and Prediction of Population-Level Impacts of Bridge Construction on Birds,” a report from the National Center for Sustainable Transportation, authored by Rachael Bay, Lisa Tell, Nicole Adams, and Ruta Bandivadekar of the University of California, Davis. The full report can be found on the NCST website at <https://ncst.ucdavis.edu/project/genetic-toolkit-assessment-and-prediction-population-level-impacts-bridge-construction>.

For more information about the findings presented in this brief, please contact Dr. Rachael Bay at [rbay@ucdavis.edu](mailto:rbay@ucdavis.edu).

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