Ketterson / Nolan Research Group Collection

This document is part of a collection that serves two purposes. First it is a public archive for data and documents resulting from evolutionary, ecological, and behavioral research conducted by the Ketterson-Nolan research group. The focus of the research is an abundant North American songbird, the dark-eyed junco, *Junco hyemalis*, and the primary sources of support have been the National Science Foundation and Indiana University. The research was conducted in collaboration with numerous colleagues and students, and the objective of this site is to preserve not only the published products of the research, but also to document the organization and people that led to the published findings. Second it is a repository for the works of Val Nolan Jr., who studied songbirds in addition to the junco: in particular the prairie warbler, *Dendroica discolor*. This site was originally compiled and organized by Eric Snajdr, Nicole Gerlach, and Ellen Ketterson.

Context Statement
This document was generated as part of a long-term biological research project on a songbird, the dark-eyed junco, conducted by the Ketterson/Nolan research group at Indiana University. For more information, please see IUScholarWorks (https://scholarworks.iu.edu/dspace/handle/2022/7911).

License/Disclaimer Statement
By downloading this document or using any information contained therein, you agree to the license terms outlined at https://scholarworks.iu.edu/dspace/handle/2022/15256, which explain terms governing use, creation of derivative research, and requirements for citing the document.

For additional information, visit the Ketterson/Nolan Lab community on the IUScholarWorks repository.
Tandem Use our recently completed junco
Most population show TR variation, but
Variation in TR length of
A All populations show TR variation in
Another candidate gene, Funding for this
No consistent pattern of distribution of

• aspects associated with migration. We are examining DNA from 6 sub
approaches to problems in conservation. A recent study by Mueller, mammals in the genus Junco
variable migratory behavior of the North American
factor involved in circadian rhythm regulation) is
help to explain the highly

QUESTIONS
• Do frequencies of ADCYAP1 or CLOK TR polymorphisms co-vary with population migratory phenotype?
• Do ADCYAP1 or CLOK TR polymorphisms correlate with individual migratory restlessness?

EXPERIMENTAL DESIGN
• DNA collected from 8 populations with variable migratory behavior (Table 1).
• Birds from two recently diverged populations were raised in a common garden and tested for migratory restlessness.
• Amplicon length measured with ABI 3730 and Peak Scanner in multiplex PCR.

RESULTS
ADCYAP
• All populations show TR variation in ADCYAP gene (Figure 2a).
• No consistent pattern of distribution of ADCYAP allele frequencies between populations with similar migratory phenotypes (Figure 2a).
• Mean individual allele length positively correlated (r²=0.15, p=0.11) with migratory restlessness in the migratory population tested (Figure 3).

CLOK
• Most population show TR variation, but one allele dominant in all populations (Figure 2b).
• No consistent difference in CLOK allele frequencies between populations with different migratory phenotypes.
• Individuals heterozygous for short CLOK allele tend to have lower migratory restlessness in both populations (Mt. Laguna p=0.58, UCSD p=0.28).

CONCLUSION
Variation in ADCYAP and CLOK do not appear to explain polymorphic differences in migratory phenotype, but may contribute to population-specific individual variation in migratory restlessness.

FUTURE DIRECTIONS
• Test more individuals for migratory restlessness.
• Test more populations with different migratory phenotypes.
• Use our recently completed junco transcriptome to search for other candidate genes.

FUNDING
• Funding for this project was provided by a NSF grant to EDK.

LITERATURE CITED