

Katherine Faust Stryjewski

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Education:

Boston University, Biology Department: PhD student in Ecology, Behavior, and Evolution 2008-present
 Louisiana State University: B.S. Biological Sciences, *summa cum laude* 2004-07
 Honors Thesis: Evolution of adaptive plumage coloration in the Variable Antshrike

Publications:

Lance, S.L., C. Hagen, T.C. Glenn, R.T. Brumfield, **K.F. Stryjewski**, and G.R. Graves. 2009. Fifteen polymorphic microsatellite loci from Jamaican Streamertail hummingbirds (*Trochilus*). *Conservation Genetics* 10(4): 1195-1198.
 Duvernell, D.D., J.B. Lindemeier, **K.E. Faust**, and A. Whitehead. 2008. Relative influences of historical and contemporary forces in shaping the distribution of genetic variation in the Atlantic killifish *Fundulus heteroclitus*. *Molecular Ecology* 17(5): 1344-1360.

Awards and Honors:

Sigma Xi Grant-in-Aid of Research 2010
 National Science Foundation Graduate Research Fellowship 2009
 Dean's Fellowship, Boston University 2008
 Phi Kappa Phi Love of Learning Award 2008
 Biological Sciences Undergraduate Research Award, Louisiana State University 2007
 R. Greg Hussey College Achievement Award, Louisiana State University 2007
 Barry M. Goldwater Scholarship 2006
 Tiger Athletic Foundation Undergraduate Honors Thesis Grant, Louisiana State University 2006
 Howard Hughes Medical Association Research Continuation Grant 2005
 Chancellor's Alumni Scholarship, Louisiana State University 2004

Selected Presentations:

Stryjewski, K.F., C.N. Spottiswoode, J.F.R. Colebrook-Robjent, and M.D. Sorenson. 2009
 Divergent, host-specific female lineages within the brood parasitic Greater Honeyguide (poster). Science and Engineering Day, Boston University. *Awarded the Dean's Award for the College of Arts and Sciences.*
Faust, K.E. Hybridization and adaptive variation: Evolutionary insights from the Jamaican Streamertail hummingbird and the Variable Antshrike. Louisiana State University Museum of Natural Science seminar series. 2007
Faust, K.E., G.R. Graves, and R.T. Brumfield. Genetic structure of a hybrid zone between Red-billed and Black-billed Streamertail hummingbirds in Jamaica (poster). North American Ornithological Conference, Veracruz, Mexico. 2006

Field Experience:

Ornithological collecting expedition in Peru with the LSU Museum of Natural Science 2007
 Henslow's Sparrow monitoring in Louisiana with the LSU Dept. of Renewable Natural Resources 2004-05

Research Experience:

Smithsonian National Museum of Natural History Research Training Program 2006
 Howard Hughes Medical Institute Summer Undergraduate Research Program, Louisiana State University 2005
 Chancellor's Future Leaders in Research Program, Louisiana State University 2004-07

Outreach:

Volunteer for BIO BUGS high school science education program, Boston University 2008-09
 President of Tri-Beta Undergraduate Biology Honor Society, Louisiana State University 2006-07

Rapid speciation and diversification in a clade of finches (*Lonchura* spp.)

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Introduction: Speciation is one of the most fundamental yet poorly understood processes in biology. Rapid radiations, in which an ancestral taxon gives rise to a number of new species over a short period of time, are of particular interest to the study of speciation. Rapid diversification is likely to be the result of strong natural and/or sexual selection, allowing for assessment of how populations respond to differing selective forces^{1,2}. This is why adaptive radiations such as Darwin's Finches and African cichlids have been the focus of such extensive research and have provided valuable insight into the complexities of speciation^{3,4}.

A nearly complete molecular phylogeny of the finch family Estrildidae has recently revealed a remarkable example of rapid radiation in the genus *Lonchura* (Sorenson et al., in prep). Twelve of the roughly 28 recognized species of *Lonchura* munias, occurring in Australia, New Guinea, or nearby islands, form a well-supported clade. Preliminary analyses based on sequence data for the mitochondrial ND2 gene indicate that the diversification of these 12 species is recent, with an average of only 1.2% sequence divergence across the basal node in the phylogeny (Figure 1). Based on a survey of the literature, this appears to be one of the fastest and most recent avian radiations with a comparable number of species. Even Darwin's finches, the most famous example of rapid radiation in birds, display a higher level of genetic divergence and presumably longer evolutionary history than the *Lonchura* clade⁵. These munias are also distinguished by a wide diversity of plumage coloration and patterning, far exceeding that observed in other recent avian radiations, and have an unusual distribution for recently evolved species: two overlapping groups of four allopatric species inhabit corresponding areas of Papua New Guinea (Figure 2)⁶. While this pattern is consistent with initial divergence in allopatry, the sympatry of two or three closely related species in each of these areas indicates that non-neutral processes such as sexual selection may be responsible for morphological diversification in *Lonchura*. This unique distribution allows for comparisons among closely related sympatric and allopatric species pairs, making it an ideal system for investigating processes such as reinforcement of reproductive isolation.

Objectives: The primary objective of this project is to investigate the history of speciation and patterns of genomic differentiation in the *Lonchura* radiation. Using multi-locus genomic data and morphological measurements, I will ask: (1) What are the evolutionary relationships among the 12 species in this clade? (2) Are closely related forms generally allopatric, indicating that initial divergence of species in this group began with geographic isolation? (3) How prevalent is

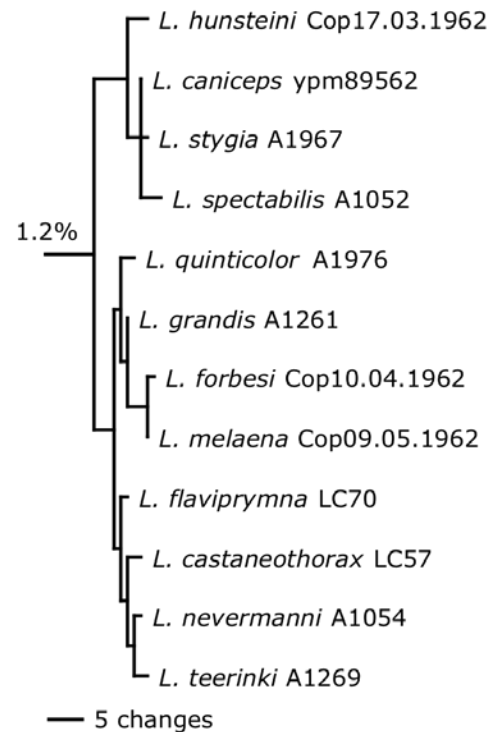


Figure 1. Maximum parsimony tree based on complete ND2 sequences. Tree rooted using *Lonchura monitcola* and *L. montana* as outgroups (not shown). Tree length = 66 steps, CI = 0.83. The average genetic distance across the basal node in the phylogeny is 1.2%. This analysis includes only one sample per species; based on limited additional sampling, at least some of these species are not monophyletic for mtDNA.

hybridization? Is there a genomic signal of reticulation for taxa that have come back into sympatry? (4) What are the patterns of plumage and genetic diversification in allopatry versus sympatry? Is there evidence of reinforcement of reproductive isolation, such that sympatric taxa are more divergent in plumage than allopatric taxa? A massive, multi-locus dataset will be used to reconstruct the history of speciation in this group and will also provide an opportunity to look for genomic “islands” of stronger than expected differentiation between species, providing evidence of a role for natural selection in the morphological and/or ecological differentiation among sympatric species.

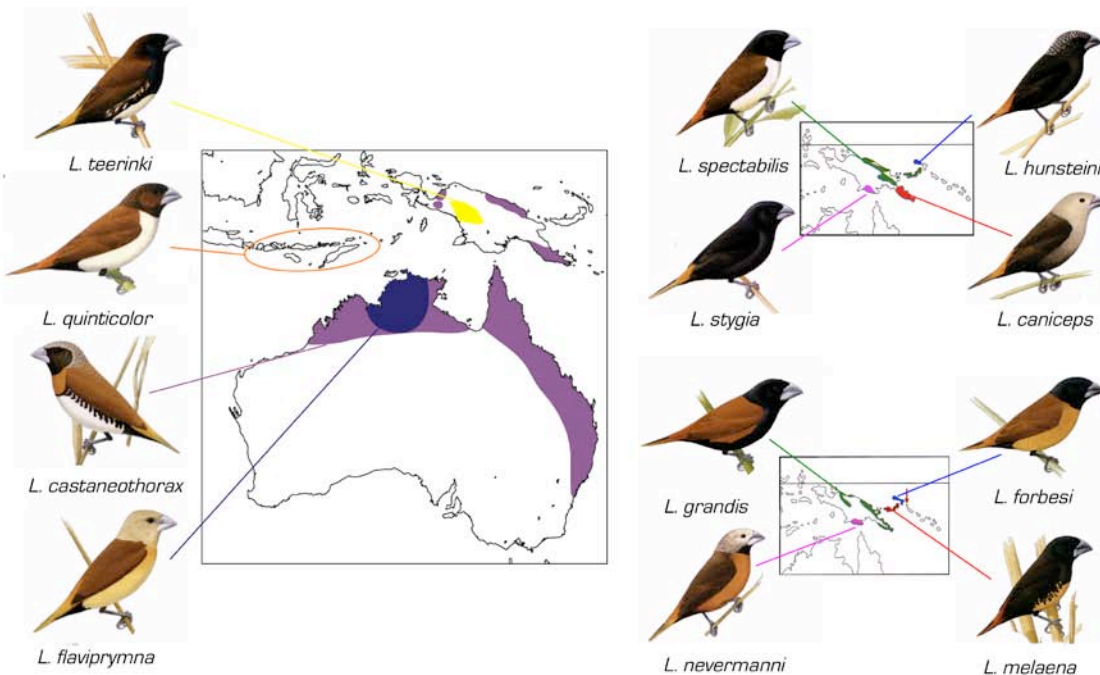


Figure 2. Distributions of the 12 species in the *Lonchura* radiation⁶.

Methods and Experimental Design: Fieldwork for this project will be carried out in Papua New Guinea and Australia. The primary objective will be to collect specimens and tissue samples for genetic and morphological analysis. I will also observe foraging behavior, record vocalizations and, if possible, observe mating and nesting behavior. As little is known about the biology of most of these species, initial observations will necessarily be exploratory, but as details of their ecology, mating behavior, and interactions with each other in sympatry are uncovered, behavioral experiments may be developed to test hypotheses related to ecological diversification and sexual selection. The occurrence and frequency of hybrid individuals will be of particular interest.

To quantify patterns of diversity in coloration, I will use a spectrophotometer to quantify plumage coloration in specimens of each species. To examine evolutionary relationships and measure the level of introgression between sympatric species, I will sequence restriction-site associated DNA (RAD tags)⁷. Briefly, genomic DNA is cut using a restriction enzyme, and an adaptor with a sample-specific barcode and sequencing primer is ligated onto the cut ends. These fragments are then sequenced on an Illumina Genome Analyzer, producing thousands of short, ~70 bp sequence fragments. Using this method, a single flow cell lane can generate sequence

data from thousands of loci scattered throughout the genome for up to 20 or more individual samples (DaCosta and Sorenson, in prep). Given the recency of the *Lonchura* radiation, it is likely that incomplete lineage sorting will result in substantial paraphyly at individual genetic loci, such that this type of multi-locus genomic data will be necessary to reconstruct the relationships among these species. Computational methods for calculating species-level relationships from multiple independently segregating loci are becoming increasingly available and are continually improving⁸. In addition, our lab at Boston University has already completed preliminary work using RAD tags in other birds.

Significance: The process of speciation is fundamental to every aspect of biology. Major advances toward a better understanding of the genetics of reproductive isolation have come from model organisms in the laboratory⁹, but how speciation typically proceeds in nature remains an intriguing and difficult question. The bulk of what we know comes from a small number of tractable natural systems in which it has been possible to ascertain the causes of speciation and how it has progressed^{3, 10-12}. Rapid radiations such as this one in *Lonchura* provide a prime opportunity to study this process in nature. Due to its rapid rate of speciation and the diverse plumage morphologies of its species, the *Lonchura* radiation has potential to vastly improve our understanding speciation, sexual selection, and the development of reproductive isolation, all central concepts of evolutionary biology.

Schedule: I am currently in the second year of my doctoral studies at Boston University. I have already obtained tissue samples from museum collections to provide proof of concept for RAD tag sequencing in *Lonchura*. I will begin fieldwork for this project in September 2010 with a trip to northern Australia to collect and observe *L. castaneothorax* and *L. flaviprymna*. An expedition to Alotau, Milne Bay Province, in Papua New Guinea is planned for spring 2011 for *L. castaneothorax*, *L. grandis*, and *L. caniceps*. Additional fieldwork will take place during 2012, and genetic data collection, analysis, and writing will be completed by spring of 2014, my estimated date of graduation. Smaller-scale studies will be completed and published as the project progresses. For example, an initial paper focusing on genetic introgression between the two Australian species would be relevant to conservation of *L. flaviprymna*, which may be in danger of genetic swamping by *L. castaneothorax*^{13, 14}.

Works Cited

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2. M. R. Orr, T. B. Smith, *Trends Ecol. Evol.* **13**, 502 (1998).
3. T. D. Kocher, *Nature Reviews Genetics* **5**, 288 (2004).
4. P. R. Grant, B. R. Grant, *Science* **296**, 707 (2002).
5. K. Petren, P. R. Grant, B. R. Grant, L. F. Keller, *Molecular Ecology* **14**, 2943 (2005).
6. P. Clement, *Finches and Sparrows*. (Princeton University Press, Princeton, 1999).
7. N. A. Baird *et al.*, *PLoS One* **3**, e3376 (2008).
8. S. V. Edwards, *Evolution* **63**, 1 (2009).
9. D. C. Presgraves, *Nature Reviews Genetics* **11**, 175.
10. B. R. Grant, *Zoology* **106**, 255 (2003).
11. M. D. Sorenson, K. M. Sefc, R. B. Payne, *Nature* **424**, 928 (2003).
12. J. S. McKinnon *et al.*, *Nature* **429**, 294 (2004).
13. K. Immelmann, *J Ornithol* **103**, 344 (1962).
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Budget and Justification

<u>Item</u>	<u>Amount</u>
Airfare from Boston, MA to Port Moresby, Papua New Guinea (requested from the American Ornithologists' Union, grant pending)	\$2,500
Airfare from Port Moresby to Alotau, Papua New Guinea	\$250
Food and subsistence for one month in Alotau	\$1000
Supplies and equipment for collecting birds, preparing specimens, and preserving tissues (mist nets, skinning kits, bird bags, spring scales, tissue storage buffer, etc.) to supplement what is already owned by our lab	\$250
<u>Total:</u>	<u>\$4000</u>
Total Requested:	\$1500

The above items will enable me to travel to Alotau, Milne Bay Province, Papua New Guinea in the spring of 2011 to collect specimens and tissue samples of three of my 12 species of interest: *Lonchura castaneothorax*, *L. grandis*, and *L. caniceps*, as well as observe their behavior and interactions in sympatry. The cost of airfare from Boston to Port Moresby has already been requested from another funding source, as noted. Funding for additional fieldwork and expenses has been sought from the Explorer's Club and the American Philosophical Society, and funding from the Systematic Research Fund has been requested for RAD tag library preparation and sequencing of the samples collected in Australia. We anticipate requesting further funding from the National Geographic Society and the National Science Foundation for future field expeditions to Papua New Guinea and the remainder of the genomic sequencing.