

### **How Removing a "soulless" Invasive Shrub Affects the Community Structure of Songbirds**

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Amur honeysuckle (*Lonicera maackii*) is a highly invasive shrub that threatens ecosystems throughout the Eastern USA. Regarding birds, the shrub represents an ecological trap and affects avian species composition. Due to its detrimental effects on ecosystems, managers have invested substantial effort towards removing the shrub. Although many have explored the impact that Amur honeysuckle has on birds, few have examined how birds might be impacted by its removal. We investigated how the community composition of avian species in rural riparian forests is impacted by the removal of Amur honeysuckle. To accomplish this, we identified plots within rural riparian forest in southwestern Ohio that are invaded by or removed of the shrub. At these plots, during the 2019 peak breeding season, we performed avian point counts and collected vegetation data to capture differences in the avian community and habitat respectively among plots. We found that the avian community differed between plots invaded by vs. removed of Amur honeysuckle, with species overall more abundant in plots removed of the shrub. While removed plots had higher abundances of woodpeckers, species that prefer open woodland habitat, and the Acadian flycatcher, the abundance of other species, e.g., Northern cardinals, did not differ between plot types. A better understanding of how Amur honeysuckle removal impacts birds will help optimize management strategies and mitigate impacts to avian species.

### **Mito-Nuclear Incompatibilities Between *Rhegmatorhina hoffmannsi* and *Berlepschi* Across an Amazonian River**

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Investigating genomes of birds in hybrids zones provides a good opportunity to assess the reproductive isolating mechanisms responsible for speciation. *Rhegmatorhina hoffmannsi* and *berlepschi* are sister species that have divergent mitochondrial haplotypes across the Aripuan River, but the centers of the plumage and nuclear transitions are located 180 km to the north of the mitochondrial break. Because the mitochondrial haplotypes do not cross the river barrier, we hypothesize that cytonuclear incompatibilities could be respon-

sible. To test this hypothesis, we sequenced a reference whole-genome (N50=10.8Mb) for *hoffmannsi*, and resequenced nuclear and mitochondrial genomes (11X) for 67 individuals spanning the hybrid zone. We compared genomes using *Fst* outlier analysis, and conducted haplotype analysis for candidate genes. We found evidence for mito-nuclear incompatibilities between populations inhabiting different banks of the Aripuan River. However, according to haplotype frequencies, males that are heterozygous for the nuclear incompatibility genes, but which have *berlepschi* mitochondria, are still viable and/or fertile. We suggest that these males are enabling the asymmetric movement of *hoffmannsi* nuclear genes over *berlepschi* populations on the right bank of the Aripuan River. We also found that genes responsible for differences in plumage color between the two species are not physically linked to the genes responsible for the mito-nuclear incompatibilities. Such lack of linkage between speciation genes and plumage color genes suggest that the *hoffmannsi* plumage color alleles will keep moving northward, which could eventually result in extinction of the *berlepschi* phenotype.

### **Integrating Abundance and Tracking Data to Identify Important Places for a Boreal-Breeding Migratory Songbird**

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Conservation planning for animals that migrate at hemispheric scales is notoriously challenging. The advancement of eBird-derived abundance estimates throughout the annual cycle provides an exciting step toward identifying critical locations for conservation. Additionally, advances in tracking technology for small migratory birds have resulted in a wealth of data that can contribute unique information to guide conservation decisions. We used light-level geolocation data from ten breeding sites across the boreal forest for >50 black-poll warblers (*Setophaga striata*) and eBird Status and Trends weekly abundance data to identify key locations for the species during pre and post breeding migration. We used a novel approach to explore eBird abundance data during the migratory periods by applying a temporally dynamic least cost paths analysis to identify spatial concentrations during migration. We then integrated individual-level tracking data and used the integrated spatial surface to identify locations of conservation importance and compare them to locations identified using only the weekly eBird abundance data. The integration of dynamic abundance data with