

ABSTRACT for DEB-2040883

Interspecific interference, character displacement and range expansion

Why are some species so widespread while others are restricted to small geographic areas? Negative interactions between closely species, such as aggression and reproductive interference, could prevent species from expanding their range. If so, traits that enable species to avoid negative interactions with close relatives should be associated with range expansion events. This prediction will be tested, for the first time, using a widespread species of dragonfly that shows extraordinary variation in wing coloration – so much so that it was once thought to be multiple species. Dark-winged (melanic) individuals experience much lower levels of interference from closely related species than do light-winged (non-melanic) individuals. This system provides an unparalleled opportunity to advance understanding of how negative interactions between species affect species distributions. As species' ranges shift in response to climate change, some species will interact with close relatives that they have not encountered previously. The results of this project should help predict the outcome of those interactions and, therefore, species distributions in the future. The project includes collaborations with researchers in Latin America and will provide field, lab and computational research training for students in the U.S., U.K, and Costa Rica. A Spanish-language version of an existing citizen science initiative will be launched to expand engagement with the public. Results of the project will be disseminated in both languages through multiple venues.

Building on well over a decade of research on the evolutionary causes and consequences of reproductive and aggressive interference in rubyspot damselflies (*Hetaerina* spp.), this project tackles the question of how adaptations that reduce interspecific interference affect range expansion. The focal species, *H. titia*, varies in wing coloration both seasonally and geographically. To understand why this species' wing coloration changes seasonally, a series of field experiments will be carried out to distinguish among alternative evolutionary trade-off hypotheses. To distinguish among alternative scenarios for the origin and loss of the seasonal color change, phylogenetic relationships among populations throughout the species' range will be reconstructed using whole-genome data. To further clarify how the seasonal color change evolved, multivariate phylogenetic trait evolution models will be fit to a range-wide phenotypic dataset. Finally, to test the range expansion prediction, coalescence models will be used to compare rates of diversification and historical demography among *H. titia* populations and between *H. titia* and four congeners. This project will also produce the first range-wide intraspecific phylogenetic analysis of the evolution of a polyphenic trait, and new genomic resources for rubyspot damselflies.