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Phylogeography of the *Habronattus amicus* species complex (Araneae: Salticidae) of western North America, with evidence for localized asymmetrical mitochondrial introgression

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Abstract

The frequency and significance of hybridization and gene introgression in spiders (Araneae) is unclear, largely because few studies have combined multiple lines of evidence in the study of systems where introgression is likely. Here we consider multiple types of data to gauge the prevalence and importance of mitochondrial introgression for three species of the *Habronattus amicus* species complex distributed in western North America. A comprehensive phylogeographic sample recovers some geographically-coherent mitochondrial clades, but conspicuously fails to resolve nominal species as monophyletic. This pattern of discordance between molecules and morphological taxonomy is studied in more detail for two species, *H. amicus* (Peckham and Peckham) and *H. ustulatus* (Griswold), found in syntopy on three dune systems in south-central Oregon. Here, multivariate morphological analyses clearly distinguish these two species, but also reveal a narrow window of size overlap between small *H. amicus* females and large *H. ustulatus* males. A quantitative assessment of microhabitat use shows that these species occupy different microhabitats at two of three dune systems, but that this difference breaks down at a single site (Summer Lake). Consistent with the size overlap and ecological data, mitochondrial data suggest interspecific gene flow at Summer Lake, which is apparently asymmetric from *H. amicus* into *H. ustulatus*. The introgression dynamics revealed in south-central Oregon impact our interpretation of mitochondrial gene trees for the entire species complex, and provide important insight into how hybridization may be influencing evolution in this diverse spider genus.

Key words: hybridization, incomplete lineage sorting, morphometrics, habitat selection, gene tree incongruence

Introduction

It is well-established that mitochondrial lineage histories, as estimated by reconstructed gene trees, sometimes differ from actual population or species histories. This gene tree-species tree incongruence has many causes (e.g., Pamilo & Nei 1988; Maddison 1997; Degnan & Rosenberg 2009), and has been a motivation for the "mitochondrial to multigenic" transition in animal evolutionary genetics (e.g., Brito & Edwards 2008). However, even when mitochondrial lineage histories differ from taxic histories, study of these particular organellar histories can still tell us much about evolutionary dynamics. For example, "misleading" gene trees resulting from mitochondrial gene flow across species boundaries (introgression) provide biologically significant information, if other lines of evidence allow researchers to pinpoint introgression as a cause of observed mitochondrial gene tree patterns. This additional evidence might come from studies of morphology, ecology, or other independently-evolving nuclear gene data (e.g., Croucher *et al.* 2007; McGuire *et al.* 2007; Good *et al.* 2008; Bossu & Near 2009).

Many different biological inferences are possible if mitochondrial introgression can be established. At the very least, such patterns tell us that heterospecifics are interacting sexually, either at present or historically.

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