

**Hitchhikers' guide to the Galápagos: Population structure and coevolution in lice and mites parasitizing Galápagos mockingbirds**

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We studied the coevolutionary history of multiple ectoparasite lineages parasitizing the endemic mockingbirds of the Galápagos archipelago to examine their mechanisms and modes of speciation. Three parasitic taxa (the amblyceran and ischnoceran louse genera *Myrsidea* and *Brueelia*, and one astigmatid mite species, family Analgidae) were selected as ecological replicates to test the relative contributions of host diversification and geography to patterns of parasite genetic differentiation. Using mtDNA sequences for the cytochrome oxidase I gene (1100 bp) we show that island geography is correlated with the genetic structure of each parasite lineage. Each island or cluster of islands forms a monophyletic group in all three taxa. However, the level of genetic variability differs between the three species. In particular, low levels of inter-island variability are present within *Brueelia*, suggesting occasional migrations between islands or a recent evolutionary origin of island populations. This contrasts with *Myrsidea* and the analgid mites, which show deep genetic splits, especially in the mites. Patterns of diversification are topologically congruent in *Myrsidea*, Analgidae and their mockingbird hosts. However, a few discrepancies are observed suggesting occasional differences in evolutionary trajectories of the three organisms. This system, when supplemented with additional genetic data, will provide a detailed opportunity to untangle the correlates of parasite diversification, their mode of speciation and the evolution of host specialization in parasitic lice and mites.

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