

TITLE: Phylogenetic history, host-specificity, and genetic structure in Spinturnicidae bat mites from the Baja California peninsula

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ABSTRACT: Parasites represent a large part of Earth's biodiversity. They play many essential ecological roles, notably in regulating food webs and driving species richness, and characterizing parasite communities is essential to studies of host-parasites interactions, evolution, and conservation. Bats carry numerous parasites with different levels of host-specificity and adaptations, but these parasitic communities remain poorly understood in many ecosystems. In this study, Spinturnicidae wing mites collected from bats along the Baja California peninsula and in northwestern Mexico were studied. Their mitochondrial COI and 16S gene and nuclear 18S gene were sequenced and Maximum-likelihood and Bayesian phylogenetic analysis were carried out to characterize species diversity. Host-specificity and phylogenetic congruency were measured for each mite species and median-joining haplotype networks were computed to investigate within-species structure. Here we show that phylogenetic trees mostly support previously described morpho-species of Spinturnicidae mites. However, our phylogenetic analyses cluster *S. americanus* and *S. carloshoffmani* into a single monophyletic clade, indicating that they are more closely related than previously thought. Overall, Spinturnicidae mites were highly host-specific and had significant phylogenetic congruency with their bat hosts. However, species-level haplotype networks showed low differentiation between sampling sites and between hosts. This study is the first molecular characterization of North American Spinturnicidae mites, and it supports similar studies reporting high host-specificity in European Spinturnicidae. However, further work is needed to disentangle species-specific patterns of genetic structure and their causes.