



Host specificity varies widely in dispersal-limited symbionts*

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A fundamental aspect of symbiotic relationships is host specificity, ranging from extreme specialists associated with only a single host species to generalists associated with many different species. Although symbionts with limited dispersal abilities are typically host specialists, some are known to associate with multiple hosts, but our understanding of the causes and consequences of this variation is limited. Understanding the micro- and macroevolutionary causes of variations in host specificity is often hindered by sampling biases and the limited power of traditional evolutionary markers. Here, we studied dispersal-limited feather mites to address the barriers associated with estimates of host specificity for dispersal-limited symbionts. We sampled mites (Proctophyllodidae: *Amerodectes*, *Proctophyllodes*, and *Tyrannidectes*; Trouessartidae: *Trouessartia*) from 92% of warbler (Parulidae) species that breed in the United States and Canada (45/49 species across 13 genera and 2 hybrids) to study mite phylogenetic relationships and host-symbiont coevolution. For parulid mites of the genera *Amerodectes* and *Tyrannidectes*, we used pooled-sequencing (Pool-Seq) and short-read Illumina technology to interpret results derived from a traditional barcoding gene (cytochrome c oxidase subunit 1) versus 11 protein-coding mitochondrial genes using concatenated and multispecies coalescent approaches. Mite-host specificity varies widely despite the statistically significant congruence between mite and host phylogenies, and host-switching is identified regularly regardless of the genetic marker resolution (i.e., barcode versus multilocus). However, the multilocus approach was more effective than the single barcode in detecting the presence of a heterogeneous Pool-Seq sample. These results suggest that presumed symbiont dispersal abilities are not always strong indicators of host specificity or of historical host-symbiont coevolutionary events. Comprehensive sampling at fine phylogenetic scales may help to better elucidate the microevolutionary filters that impact macroevolutionary processes regulating symbioses, particularly for dispersal-limited symbionts.

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