



## Population genomics of avian feather mites with contrasting host specificities\*

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Host specificity is a key element to our understanding of symbiont diversification and is driven by multiple macro- and microevolutionary processes. Broad scale (e.g., species-level) studies can uncover relevant processes such as cospeciation and host-switching that shape host-symbiont evolutionary histories. However, these species-level patterns often emerge from processes that occur at finer (e.g., population-level) scales, which are far less studied. Feather mites, despite the obligate and permanent nature of their relationships with avian hosts and typically vertical transmission among host individuals, exhibit variable degrees of cospeciation and host specificity, and little is known about how mite population-level processes differ from or impact species-level patterns. Thus, this system is an ideal model to better understand symbiont-host specificity and to link ecological patterns with evolutionary processes. Here, we studied proctophylloidid mites with contrasting host specificities, *Amerodectes protonotaria* (a specialist found on only one host species) and *A. ischyros* (a generalist found on at least 17 host species). We collected mites from multiple breeding populations of their warbler (Parulidae) hosts. We predicted that the generalist would exhibit less pronounced population genomic structure than the specialist due to higher gene flow between populations (i.e., eroded population structure) and as a result of their apparent ability to disperse among different host species. To facilitate this work, we assembled a draft genome from a single female *A. protonotaria* individual as a reference to detect genetic variants (single nucleotide polymorphisms; SNPs) for use in multiple population genetic analyses. We then used a pooled-sequencing approach and novel workflow to analyze whole-genome data of populations of both mite species. Overall, both species of mite had weak population structure. However, unexpectedly, the generalist mite was more strongly structured than the specialist mites. Thus, our data may indicate that despite their apparent lack of dispersal among host species, specialists disperse more freely across individuals within a single host species while generalists may sort across host species according to geography. Additionally, our results may reflect a previously unexplored period of mite transmission—during the nonbreeding season of migratory hosts—as mite population structure more closely resembles the distribution patterns of these hosts in the nonbreeding period rather than in the breeding season. Our findings challenge assumptions regarding feather mite biology and highlight the potential for further experiments and investigations to better understand the eco-evolutionary factors underlying symbiont diversification at fine versus broad evolutionary scales.

**Keywords:** coevolution, dispersal, gene flow, migration, symbiosis