

# Host avian species and environmental conditions influence the microbial ecology of brood parasitic Brown-headed Cowbird nestlings: What rules the roost?

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September 30, 2023

## Abstract

The role of species interactions, as well as genetic and environmental factors, all likely contribute to the composition and structure of the gut microbiome, however disentangling these independent actors under field conditions represents a challenge for a functional understanding of gut microbial ecology. Avian brood parasites provide unique opportunities to investigate these questions, as brood parasitism results in parasite and host nestlings being raised in the same nest, by the same parents. Here we utilized obligate brood parasite Brown-headed Cowbird nestlings (BHCO; *Molothrus ater*) raised by several different host passerine species to better understand, via 16S rRNA sequencing, the microbial ecology of brood parasitism. First, we compared fecal microbial communities of Prothonotary Warbler nestlings (PROW; *Protonotaria citrea*) that were either parasitized or non-parasitized by BHCO, and communities among BHCO nestlings from PROW nests. We found that parasitism by BHCO significantly altered both the community membership and community structure of the PROW nestling host-associated bacterial microbiome (HABM), perhaps due to the stressful nest environment generated by brood parasitism. In a second dataset, we compared fecal HABMs from BHCO nestlings raised by 6 different host passerines species. Here, we found that the HABM of BHCO nestlings was significantly influenced by the parental host species and the presence of an interspecific nestmate. Thus, early rearing environment is important in determining the HABM of brood parasite nestlings, and their companion nestlings. Future work may aim to understand the functional effects of this HABM variability on nestling performance and fitness.

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