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HBV-Mediated Innate Immune Evasion Increases the Risk

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Description

Over the past four decades, molecular population genetics has proven to be a fruitful field in addressing fundamental questions regarding the population biology of helminth parasites. Although its implementation by parasitologists initially lagged behind those in other fields, molecular population genetic methodologies have since been used to help elucidate the ecology, epidemiology/epizoology and evolution for a number of parasitic helminths. Moreover, the field has been integral in overcoming inherent challenges by allowing indirect inferences on population biology. By sequencing one or a few targeted loci, parasitologists could begin to elucidate previously unknown or inaccessible helminth population dynamics. For example, molecular markers have proven essential in parasite studies on cryptic, mating systems contemporary or historical effective population sizes, phylogeography, local scale transmission.

Helminth species do not exist in isolation within a host; rather, a host is a microcosm of an ecosystem for which there may be a community of microbes (bacteria and viruses), protozoans, or helminths concurrently infecting a host. It is recognized that the makeup of a microbial community can impact both the host and the 'ecosystem' which the host. Likewise, infection by multiple helminths and/or protozoan parasites is a major concern in livestock and wildlife given that co-infections have the potential to exacerbate morbidity or mortality of the host. Thus, knowing the helminth and protozoan parasite community composition in a host (what we describe as the parabiome) is critical given the potential for the community composition to influence the host immune response, other organisms residing in the host (e.g., dysbiosis), as well as the variable pathogenicity of parasites. Moreover, characterization of a parabiome is useful in understanding broader community ecology questions concerning species interactions, diversity and abundance. We note that the term parabiome represents a subset (*i.e.* helminths and protozoans of a host) of the term holobiont, which is defined as a metazoan organism with all associated microorganisms living on or in it.

With regard to helminths, parabiome work has largely centred on nematodes. Prior to the use of molecular markers, morphological analysis of third larval stage (L3) larvae was used for livestock nematode identification, which was largely limited to the genus level. Taking advantage of the ability of NGS to generate large amounts of sequence data, conducted a proof-of-concept study to determine if deep amplicon sequencing, that is, metabarcoding, of nematode ITS-2 (Internal Transcribed Spacer unit 2 of the rDNA complex) could be used to identify L3 larvae to species as well as ascertain species composition in a host. Using eight laboratory-reared species of nematodes, they found that ITS-2 reliably differentiated species. However, when pooling L3 larvae of different species, sequencing produced species-specific amplification biases. Applying a correction factor to account for the biased amplification, their method was able to detect species at low frequencies within samples and access species proportions. In addition, their method identified species that were difficult to identify morphologically. For example, the sequence data revealed L3 *Haemonchus contortus*, whereas morphological identifications only reported *Haemonchus placei*.

Other parabiome studies have focused on foundational parasite biodiversity and community ecology questions. For ecample they used a 18s rDNA region to provide family-level identification of helminth, fungi and protozoan parasites across 11 non-human primate species. They found previously unreported families from some primates and that closely related primate species had greater parabiome similarity.

Titcomb a scientist tested for associations between the nemabiome and host traits or phylogenetic relatedness across 17 species of sympatric mammalian herbivores in Kenya as well as assessed parasite-sharing networks among hosts. Key findings included 53% of the nemabiome dissimilarity among faecal samples explained by host species, significant congruence between host and parasite phylogenies, and that host gut morphology predicted nematode community composition.

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