The impact of nutrition and anthelminthic treatment on the gut microbiome in a lab-to-wild model

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The mammalian gastrointestinal tract is a rich ecosystem and focal-point for a wealth of interactions; it is the largest site of the host immune system and diet-derived nutrient absorption, whilst also a preferential niche for helminth parasites and host to the community of microorganisms known as the gut microbiota. Whilst host-nutrition is a key source of intestinal microbiota it also plays a fundamental role in the development of an effective immune response, highlighted by immunodeficiency and increased susceptibility to infection in the malnourished. Moreover, intestinal helminth infections can impair nutrient absorption and compromised immunity can lead to reduced anthelmintic efficacy. To date, the relationship between nutrition, helminth immunity and the gut microbiome has been studied in controlled laboratory models focusing on alterations of specific macro- or micro-nutrients. However, these are unlikely to truly represent findings in natural populations where there is more genetic, ecological, and behavioural variation that can determine exposure and susceptibility to infection, as well as the occurrence of co-infections alongside fluctuations in resource availability due to seasonal shifts which can impact the gut microbiome composition and diversity. We used a high-quality, nutrient-rich diet to experimentally supplement both wild and wild-derived, lab-reared wood mice (*Apodemus sylvaticus)* and measured anthelmintic treatment efficacy and resistance to infection with the gastrointestinal nematode *Heligmosomoides polygyrus.* Previously, we have shown that in both settings, wood mice given this supplemented diet, were more resistant to *H. polygyrus* infection, cleared adult worms more efficiently after treatment and had higher general and parasite-specific immune responses. Here, we expand upon these findings with gut microbiome data from the same study, where we highlight key differences in the diversity and composition of the microbiome between the lab and wild, during infection and determine how supplemented nutrition impacts this – beginning to unravel the mechanisms driving nutrition-induced *H. polygyrus* resistance.