Pioneering Insights into the Cross Kingdom Effect: First Study of Gut Microbiome Shifts in Zoo-Housed Hamadryas Baboons

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Introduction

Whipworm infection is caused by a parasitic eukaryotic nematode belonging to the genus *Trichuris*. Infections range from subclinical disease to more severe clinical signs, including frequent and painful defecation, bloody diarrhea, and vomiting. Due to the long-life cycle of this parasite, treatments must extend over many months and, thus, re-infections are common. There are several species within the genus, *Trichuris* with a broad host range, capable of infecting a variety of domestic and exotic animals. Notably, the species *Trichuris trichiurais* zoonotic, infecting both human and non-human primates. Despite their importance, there is limited knowledge about the effects of *T. trichiura* infection and whipworm treatment on the microbiome of infected baboons.

Understanding the gut microbiome of zoo-housed primates is critical due to their close contact with humans and potential exposure to antimicrobial treatments. While wild Hamadryas baboons have been studied for age and seasonal microbiome changes, no comprehensive analysis has explored the entire gut microbiome, including bacteria, fungi, protists, and viruses, in captive individuals.

Purpose

This study analyzed the effects of Cephalexin and albendazole treatment on the entire fecal microbiome of a population of 14 captive Hyamadras baboons (including bacteria, fungi, parasites, and phages).

Methods

31 fecal samples were collected over four months from a population of 14 Hamadryas baboons at the Oakland Zoo. All baboons received albendazole treatment for *Trichuris trichiura* on January 7, 2025, prior to sample collection and monthly Cephalexin. Samples were analyzed using community-wide metagenomic sequencing to track temporal shifts across microbial taxa over the four-month sampling period. Reads were classified by aligning against a comprehensive decontaminated database containing Bacteria, Parasite, Fungal, and Viral taxa. *T. trichiura* was identified in the sample using 18S sequencing.



Results

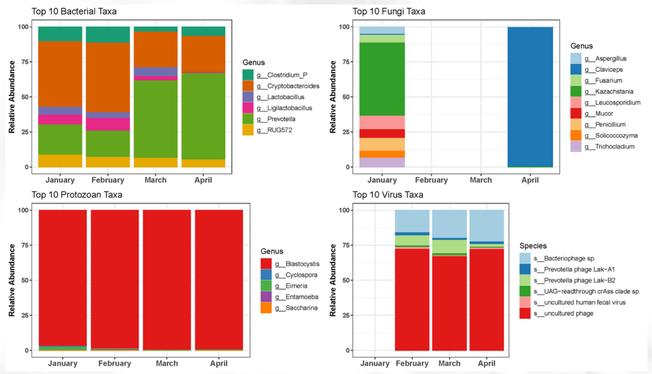


Figure 1): Species bar plots depicting the percent abundances of Bacteria **(A)**, Fungi **(B)**, Protozoa **(C)**, and Phages **(D)**. Abundances for each group are calculated using exact sequence matches of taxa-specific short DNA fragments.

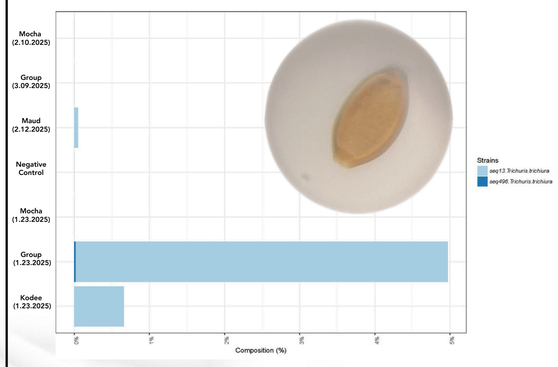


Figure 2): Detection of *T. trichiura* in baboons using 18S amplification and sequencing. The x-axis indicates the relative abundance of *T. trichiura* compared to other Eukaryotes.

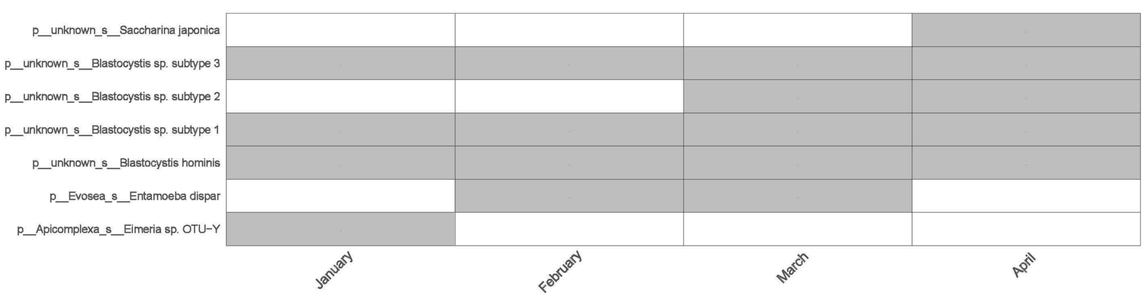


Figure 3): The detection of seven protozoan parasites in the baboons over the four-month sampling period using metagenomic sequencing. Shading of the table indicates the parasites presence (gray) or absence (white). A parasite strain determine to be present if it was identified in at least 5% of baboons in each monthly sample set.



Conclusion

This is the first study to analyze the entire microbiome and parasite composition of zoo-housed Hamadryas baboons. An intense temporal shift in the baboon fecal microbiome was observed between January and April. Bacterial taxa from the *Prevotella* genus dominated the microbiota in March and April, possibly a result of the monthly Cephalexin treatment. *Prevotella* have been previously described with widespread resistance to cephalosporin antibiotics including Cephalexin[1,2]. The expansion of *Prevotella* species in the baboon feces correlated with a greater abundance of *Prevotella* phages, viruses that infect these bacteria.

The fungal component of the microbiome was diverse in January; however, diversity decreased dramatically through the rest of the study. The most abundant protozoa in the study were *Blastocystis*, a genus of human and hominid protozoan parasites[3,4]. Four strains or subtypes of *Blastocystis* were detected in the baboons at varying abundance with B. hominis and subtypes 3 and 1 being conserved across all timepoints while subtype2 only appeared in fecal samples from March and April. Due to the resilience of *T. trichiura* eggs and their low-abundance in the sample (1-3 eggs/fecal gram) the whipworm parasite was detected separately via enhanced lysis and 18S marker gene amplification. *T. trichiura* abundance was evaluated at 0.2-5% abundance in infected baboons in relation to other eukaryotes (Fungi and protozoa).

The results of this study demonstrates the utility of metagenomic sequencing as an unbiased, all-in-one test to detect all pathogens and parasites including bacteria, fungi, intestinal worm parasites, protozoa, and viruses. This technology allows for more encompassing diagnostics and for assessing microbial cross-kingdom effects in complex samples.

References

1. Castillo, Y., Delgadillo, N. A., Neuta, Y., Hernández, A., Acevedo, T., Cárdenas, E., & Castillo, D. M. (2022). Antibiotic susceptibility and resistance genes in oral clinical isolates of Prevotella intermedia, Prevotella nigrescens, and Prevotella melaninogenica. Antibiotics, 11(7), 888.
2. Sharma, G., Garg, N., Hasan, S., & Shirodkar, S. (2022). Prevotella: An insight into its characteristics and associated virulence factors. Microbial pathogenesis, 169, 105673.
3. Stensvold, C. R., Tan, K. S., & Clark, C. G. (2020). Blastocystis. Trends in parasitology, 36(3), 315-316.
4. Alfellani, M. A., Jacob, A. S., Perea, N. O., Krecek, R. C., Taner-Mulla, D., Verweij, J. J., ... & Stensvold, C. R. (2013). Diversity and distribution of Blastocystis sp. subtypes in non-human primates. Parasitology, 140(8), 966-971.

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