

Abstract title – 255 characters

Diversity of Strongylid Nematode Communities in Wild Western Lowland Gorillas

Authors – maximum 14

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There is growing concern that changes in parasite communities can significantly affect the survival of fragile wildlife host populations. Western lowland gorillas (*Gorilla gorilla gorilla*) are among the most critically endangered mammalian species. They are phylogenetically closely related to humans (*Homo sapiens*) and, as large terrestrial herbivores, are keystone species for their ecosystems. As such, it is of mounting importance to understand their ecology and conservation threats, including those encompassed by parasitic diseases. Current understanding of wildlife helminths is scarce compared to knowledge on human and livestock helminths, including application of epidemiological modelling.

Gastrointestinal parasite infections are typically asymptomatic in primates, but alterations to transmission mechanisms or host susceptibility can exacerbate the clinical implications of infection. Ongoing habitat disturbance or reduction, changing climate and shifts in group dynamics may all influence the impact of parasite infections on the western lowland gorilla. While *Gorilla* host a broad spectrum of parasites, strongylid nematodes are particularly prevalent, occurring in complex communities within host individuals, as is typical for large terrestrial herbivores. However, little is known on the diversity or epidemiology of these strongylid communities in non-human primates, with traditional coproscopic methods unable to distinguish strongylid nematodes to the species-, or even genus-, level due to indistinguishability of eggs. Modern advances in high-throughput sequencing (HTS) techniques allow analysis of these complex strongylid communities, including identification of both dominant and rare species. We employed an HTS-methodology, utilising ITS-2 metabarcoding within the MiSeq Illumina platform, for strain-level identification of strongylid communities. We successfully applied this approach, previously optimised by our team, to describe the genetic diversity

of gastrointestinal strongylid communities in 208 faecal samples from western lowland gorillas, spanning four countries within the Congo basin. Alongside, we also employed 16S rDNA sequencing to describe the gut bacterial community, allowing us to investigate interactions between the two communities within the gastrointestinal system.

We established baseline data of strongylid nematodes infections in wild western lowland gorillas, identifying 134 strongylid haplotypes, comprising six genera. We found that *Necator* and *Oesophagostomum* were dominant genera across localities, with alpha diversity consistent across all localities except one. Though, greater variations were seen in beta diversity between localities, when concerning strongylid community compositions. We also identified interactions between certain strongylid species and gut bacterial genera. Our presented work provides the framework for ongoing research on the comparison of strongylid nematode diversity across all four *Gorilla* subspecies, hoped to provide insight into strongylid epidemiology in the context of host ecology and phylogeny.