Comparative Analysis of Gut Microbiota Composition and Diversity in Wild Mammals from the Kruger National Park, South Africa

Sheylle Green 1, Talhah Loonat 1, Maclean Bassett 2, Massimiliano Tagliamonte 3, Lucious Chabuka 1, Lavanya Singh 1, Marco Salemi 2, Tulio de Oliveira 1,5, Michele Miller 6, Peter Buss 4, Eduan Wilkinson 1, Carla Mavian 1,2

1: Centre for Epidemic Response and Innovation (CERI), School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa

2: Emerging Pathogens Institute and Department of Pathology, College of Medicine, University of Florida, Gainesville, Florida, United States of America

3: University of Florida, Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, Florida, United States of America

4: Veterinary Wildlife Services, Kruger National Park, SANParks, Skukuza, South Africa

5: KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), University of KwaZulu-Natal, Durban, South Africa

6: South African Medical Research Council Centre for Tuberculosis Research, Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Tygerberg, Cape Town, South Africa.

Abstract

Background:

The gut microbiome plays a critical role in host health, and the microbial community composition is heavily influenced by the prevailing conditions in the gut environment. Studies on the gut microbiota of large African wild mammals remain underrepresented. We investigated how distinct dietary groups (carnivores, non-ruminant, and ruminant herbivores) influence gut microbiota composition and diversity in coexisting wild mammals from the Kruger National Park.

Methods:

The V3–V4 region of the 16S rRNA gene was sequenced from 94 faecal samples from nine mammal species using Illumina MiSeq. We analysed diversity and composition using the QIIME 2 pipeline. Rarefaction confirmed adequate sequencing depth. Alpha diversity was assessed using Shannon index and Faith's phylogenetic diversity (PD), while beta-diversity was evaluated using weighted and unweighted UniFrac distances. Group differences were tested using PERMANOVA and Kruskal–Wallis tests.

Results:

After filtering, 89 samples (carnivores: $n = 31$; non-ruminants: $n = 37$; ruminants: $n = 21$) were included. Beta diversity analyses showed distinct clustering of dietary groups (weighted: pseudo-F = 27.76, $p= 0.001$), but no significant differences among host species within each group. Alpha diversity was highest in non-ruminants (Shannon: 6.79 ± 0.47; Faith’s PD: 17.44 ± 3.34), followed by ruminants and carnivores (both $p < 0.001$).

Taxonomic profiling revealed group-specific signatures. Carnivores were dominated by *Fusobacteriaceae*, *Clostridiaceae* and *Peptostreptococcaceae*. Both ruminants and non-ruminants both showed high levels of fibre-degrading bacteria, such as *Rikenellaceae* and *Oscillospiraceae*, while non-ruminants were additionally enriched in *Spirochaetaceae* and p-251-o5, reflecting hindgut fermentation strategies.

At the species level, lions had higher *Peptostreptococcaceae*, hyaenas uniquely showed *Clostridia_UCG-014*, and warthogs were enriched in p-251-o5. Elephants and rhinoceroses shared core fermentative taxa, while buffalo and impala exhibited similar profiles with subtle differences, highlighting additional host-specific influences.

Conclusions:

Dietary classification strongly influenced gut microbiota composition and diversity, with herbivores exhibiting richer, more complex communities compared to carnivores. Among herbivores, non-ruminants harboured higher diversity than ruminants, likely due to their diverse, less specialized hindgut fermentation. Our findings help deepen our understanding of wildlife microbiomes and support future conservation and health monitoring work in African ecosystems.