

Ecological factors affecting microbiomes in Verreaux's sifakas (*Propithecus verreauxi*) and Ring-tailed lemurs (*Lemur catta*) at Beza Mahafaly Special Reserve

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This past summer, I was awarded the Natural History Collections Summer Research Scholarship to conduct a pilot study in southwestern Madagascar exploring the effects of habitat type on lemur microbiomes. All animals have a microbiome (the microbial communities living on and in an organism), and the relationship between an organism and its microbiome is a rapidly growing research topic¹. Comparative studies of the primate microbiome have found that closely related species have similar gut and skin microbiota, and that this similarity decreases between more distantly related taxa². Climate, habitat type, degree of habitat degradation and fragmentation, and available food resources have also been supported as factors influencing the gut microbiome of primates⁴. Environmental changes that affect a primate's microbiome may affect their health and susceptibility to disease^{3,4}. Despite the importance of the microbiome for primate hosts, most research on microbiome diversity in primates has been limited to the gut microbiome, leaving the hair, oral, and genital microbiomes relatively unexplored.

For these reasons, I chose to examine the hair, oral, genital, and gut microbiomes of Verreaux's sifaka (*Propithecus verreauxi*), as well as the gut microbiome of ring-tailed lemurs (*Lemur catta*), in Beza Mahafaly Special Reserve in Southwestern Madagascar. There is a habitat gradient from moist riverine forest to dry deciduous forest within the Reserve⁵, allowing me to assess the relationship between habitat type and lemur microbiome diversity. Additionally, the two lemur species included in this study vary in their habitat use, group structures, and diets^{6,7}. I hypothesized that microbiome composition and diversity will vary between individuals living in different habitat types for both species. I also hypothesized that the aforementioned species-specific host evolutionary history and traits will create observable species-level differences in microbiome diversity. Lastly, I hypothesized that microbiomes from different body regions will be uniquely affected by habitat type, with some body region microbiota being more variable than others.

Over the course of three weeks, I was able to collect 102 samples from fifteen *P. verreauxi* individuals and twelve *L. catta* individuals. For the sifaka, I collaborated with an existing research team who conduct annual capture and release of juveniles. We went out into the Reserve every day and attempted to track 2-4 groups with unmarked yearlings, then would sedate the juveniles and bring them back to camp to collect samples. These samples included swabs of their oral, genital, and fecal microbiomes and plucked hair tufts from their head, chest, and rump. For the ring-tailed lemurs, I took fecal samples opportunistically while following groups in the Reserve on a daily basis.



Since returning from the field, I have been extracting the microbial DNA from all of my samples using specialized microbiome protocols. Once I have finished this step, I will assess the quality of the extractions by quantifying their DNA concentration. I will then amplify the 16S rRNA bacterial gene—a highly conserved gene used to identify different bacterial taxa—in all of my samples. Sequencing will be carried out through the UMass Genomics Resource Laboratory on Illumina platforms. Using existing 16S rRNA databases, I will classify the bacterial taxa in my samples and calculate the diversity within and between samples. Lastly, I will conduct statistical analyses to explore the relationship between microbiomes and host species, and the effect of habitat type and species on measures of microbiome diversity. I hope to use the results of this pilot study to inform my dissertation research, which will more specifically examine the effects of ecological fluctuations and anthropogenic disturbance on lemurs in the Reserve over three field seasons.

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