

Diversity analysis of Howler monkey (*Alouatta spp.*) fecal microbiota

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Howler monkeys (*Alouatta spp.*) are endemic species from the Atlantic Forest biome that can be found in primary and secondary forests and even in small forest fragments. Their diet is based on tree leaves and fruits, depending on the season. This study aims to investigate the diversity of gastrointestinal bacterial community of howler monkeys that inhabit São Paulo Zoo Park, both in captivity and non-captivity, to correlate possible differences between their respective microbiotas and diets. We have collected a total of 25 fecal samples from captive and non-captive individuals at different seasons in 2013-2015. Total DNA extracted from the samples were then analyzed by 16S rRNA gene V3-V4 amplicon sequencing using the MiSeq-Illumina platform. The obtained sequences were used for alpha- and beta-diversity estimates as well as for phylogenetic profiling using mostly the QIIME package. Our initial results point to differences both in the microbial community profile and diversity between the two groups. The phyla Spirochaetes and Elusimicrobia were detected only in captive animals while Tenericutes and Melainabacteria were present only in the microbiota of non-captive individuals. Nevertheless, Bacteroidetes and Firmicutes showed high abundance (~60-70%) in both groups. The microbiota of the non-captive group was richer than the captive one, and presents a large fraction (~70%) of OTUs that were unclassified at the genus level. Among the identified genera, we observed an abundance of *Bacteroides* and *Prevotella* in the microbiota of captive animals. In humans, these two genera have been related to diets high in fat/protein and carbohydrates/fiber, respectively.

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