

16S rRNA GENE-BASED PROFILING OF HOWLER MONKEY FECAL MICROBIOTA

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Abstract

Howler monkeys (*Alouatta* spp.) are endemic animals 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 from captive and non-captive howler monkeys that inhabit São Paulo Zoo Park 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. In addition, a 16S amplicon sequence dataset of fecal samples from Mexican black howler monkeys was incorporated in the analyses. The 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 captive and non-captive groups. When the microbial composition present in fecal samples of Brazilian monkeys were compared with Mexican monkeys, we observed that the microbial community of Brazilian captive individuals are very different from the other groups. Among the identified genera, we observed higher 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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