

TITLE: Assessment of fecal microbiome differences in captive and non-captive howler monkeys: implications for conservation planning and management

AUTHORS: Riyuzo, R.¹; Fernandes, G.R.¹; Pereira, I.S.¹; Moura, L.M.S.¹; Amgarten, D.¹; Martins, L.F.¹; Cruz, J.B.³; de Oliveira, J.C.F.²; Setubal, J.C.¹; da Silva, A.M.¹.

INSTITUTIONS: 1. INSTITUTO DE QUÍMICA, UNIVERSIDADE DE SÃO PAULO, SÃO PAULO, SP (Av. Prof. Lineu Prestes, 748, Butantan - São Paulo); 2. UNIVERSIDADE FEDERAL DE SÃO PAULO, CAMPUS DIADEMA, DIADEMA, SP (Rua São Nicolau, 210, Centro - Diadema); 3. FUNDAÇÃO PARQUE ZOOLOGICO DE SÃO PAULO, SÃO PAULO, SP (Av. Miguel Estéfano, 4241 - Vila Santo Estéfano - São Paulo).

ABSTRACT:

Howler monkeys (*Alouatta spp*) are endemic of South American tropical forests and are highly susceptible to the yellow fever virus, thus playing an important role as sentinels of outbreaks. Brazil is experiencing its worst yellow fever outbreak in decades, which is wiping out some wild howler monkey populations. One strategy to regrow endangered populations is the introduction in the wild of captive-bred animals. Due to the significance of the gut microbiome in animal health, understanding its composition and function may help conservation planning and management of these species. The present study aims to compare the gut microbiomes of captive and non-captive howler monkeys. Fecal samples from Sao Paulo (Brazil) Zoo Park captive animals and non-captive animals that live in the park's Atlantic rain forest patch were obtained in two different seasons in two consecutive years, followed by 16S amplicon and shotgun sequencing. Data analysis revealed differences in the microbial community structure, diversity, and function between the two populations, with non-captive individuals showing higher phylogenetic diversity indices and enrichment of specific metabolic functions. The microbiome of non-captive monkeys appears to be more susceptible to seasonal changes than the microbiomes of captive individuals, perhaps due to seasonal changes in food availability. In the microbiota of captive animals we did not identify members of the genus *Faecalibacterium*, which was identified in the non-captive samples, and which is an abundant genus in the healthy human gut microbiome. Several novel bacterial and viral genomes were recovered from the shotgun sequences.

Keywords: Howler monkey, fecal microbiome, *Faecalibacterium*, shotgun metagenomics

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