

Analysis of metagenomic data from howler monkeys feces

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Abstract

There is an increasing use of metagenomic approaches to characterize microbial communities in several environments regarding their structure, function and composition, in particular to access the vast amount of uncultured microorganisms, enabling the understanding of the biological functions that such organisms play in these environments. Here we describe results of a project aiming to sample and analyze the fecal microbiota of captive and non-captive howler monkeys in the São Paulo Zoo. A previous study from our group using 16S rRNA amplicon sequencing has demonstrated differences in the microbiota profile between captive and non-captive individuals. In this project, we performed shotgun sequencing of total DNA obtained from thirteen samples from captive and six from non-captive monkeys, the samples were collected in different seasons. The diet of those groups are different and we have well detailed information about captive diet. Preliminary results show differences between the two groups in terms of taxonomic groups as well as in the function profile. The taxonomic results shows that *Bacteroides*, *Prevotella* and *Parabacteroides* are the most abundant genera in non-captive monkeys and *Prevotella*, *Bacteroides* and *Clostridium* are the most abundant genera in captive monkeys. The taxonomic and functional profiles results suggests that the non-captive monkeys are more susceptible to season changes and captive ones have a more homogeneous microbiota over the year.

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