Título: Comparing the Gut Microbiota of Two Communities from Amazon Region with the Southeastern in Rio de Janeiro, Brazil

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Resumo:

The human gastrointestinal tract contains all three domains of life, bacteria, archaea, and eukarya. All the bacteria that reside in the human gut achieve cell densities higher than any other ecosystem. The human gut microbiota plays a main role in human health by acting as a barrier against pathogens and exerting important metabolic and immunologic functions. Studies about the human gut microbiota under different dietary habits and sanitary conditions can provide new perspectives. Hence, the aim this present work was to characterize the profile of intestinal biota colonization of individuals belonging to two different communities in the Amazon region, in Brazil and compare that profile with individuals from the southeastern of Brazil and try to correlate any difference found with their food source habits. To achieve these goals, 74 stool samples were collected. Twenty-eight from each community, Puruzinho Lake and Buiuçu, both on the waterfront Madeira River in the neighborhood of Humaita, all located in the Amazon state; and 18 in the Rio de Janeiro state. To perform a comparative analysis of intestinal microbiota, total DNA was isolated using QIAamp DNA Stool Mini kit and amplified by PCR. A pair of primers targeting the 16S rDNA V3 region was used. For all samples, an amplicon corresponding to 236 pb was obtained. To access the intestinal microbiota composition, a denaturing gradient gel electrophoresis (DGGE) was applied. The V4 region of the 16S rRNA gene was sequenced according with Yatsunenko *et al*, 2012. The DGGE revealed a multi-band fingerprinting in all samples analyzed. Moreover, preliminary results revealed DGGE fingerprint homogeneous among individuals from both Amazon communities. However, when compared with samples of individuals from southeastern of Brazil this profile was slightly different. The High-throughput sequencing results showed that the relative abundance of families showed differences between the 3 communities studied and PCoA Weighted Unifrac better explained the results. We were able to conclude that the DGGE statistical results demonstrated significant differences between each location studied; the initial sequencing results showed differences between Amazon and Rio de Janeiro communities. More analyses that are accurate will be made to compare between both Amazon communities. Probably the food habits and type of water used by the Amazon communities are the reasons for bacterial gut differences observed.

Palavras-Chaves: Amazon, Gut Microbiota, High-throughput sequencing

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