

Title: AN EXPLORATORY STUDY OF THE BRAZILIAN GUT MICROBIOME

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Abstract:

Our knowledge about human gut microbiota, its resident species and their functional interaction capacity with its host is rapidly growing in recent years. These studies have provided important information with respect to what constitutes a 'healthy gut microbiota' while furthering our understanding of the role of gut microbes in intestinal and metabolic diseases. Little is known about how the gut microbiota varies across different countries. However, some evidence suggests strong differences that may be associated with the level of industrialization of that society. In this scenario, Brazil presents a unique combination of large demographic distribution and nutrition transition. The aim of this work was to evaluate the intestinal microbiota of healthy Brazilian volunteers and its relation with other populations. Microbiome profiling, blood biochemical data (lipid profile), 24-h dietary recall and gastrointestinal functioning questionnaires were performed in 54 healthy volunteers. Stool samples were collected, DNA was extracted and the bacterial 16S rDNA was sequenced using Illumina's MiSeq Platform. Sequences were processed using Qiime and analyzed using the R environment for statistical computing. Appropriate data was collected from the published literature and used in the analysis. Two clusters of individuals were detected in the intestinal microbiome of Brazilians, one more *Prevotella* prevalent (Cluster A) and other more *Bacteroides* prevalent (Cluster B), containing 45% and 55% of subjects, respectively. Brazilian subjects from Cluster A segregated with Malawi/Venezuela Amerindians subjects. Cluster B subjects segregated with USA subjects, a heavily industrialized population. Diet parameters assessed with 24-h Recall for Brazilian subjects resembled those observed in an industrialized USA population. Host metabolic parameters evaluated in these subjects, such as HDL cholesterol and triacylglycerol, were distinct between Brazilian clusters A and B, although all within normality. The Brazilian gut microbiome shows a more even distribution of enterotypes than previously seen in samples either from industrialized countries or from agrarian societies.

Key words: microbiome, diet, clustering, 16rDNA, sequencing.

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