

TITLE: GUT MICROBIOME PROFILES FROM A HUNTER-GATHERER BRAZILIAN GROUP

AUTHORS: CONTEVILLE, L.C. ¹; VICENTE, A.C. ¹

INSTITUTION: 1. OSWALDO CRUZ INSTITUTE, OSWALDO CRUZ FOUNDATION, RIO DE JANEIRO, RJ (AVENIDA BRASIL, 4365, CEP21040-900, MANGUINHOS, RIO DE JANEIRO – RJ)

ABSTRACT:

The advent of urbanization and industrialization brought dramatic changes to the lifestyle and environment, that have been shown to impact the human gut microbiome and human health. The study of groups that still maintain traditional modes of subsistence constitutes an opportunity to reveal the putative gut microbiome profiles previous to the westernized human lifestyle. Here, we generated and analyzed shotgun metagenomes from the gut microbiome of a hunter-gatherer Yanomami group from Brazil. Taxonomic, functional and resistance profiling of the metagenomes were performed using Kraken, SUPER-FOCUS and RGI, respectively. The Yanomami/Brazil gut microbiomes present similarities in taxonomic and functional features with other traditional South American groups, as well as traditional groups from Africa, contrasting with urban-industrialized groups. The taxonomic profile of all traditional groups is characterized by an overall high diversity, the presence of *Treponema* and *Brachyspira* genera, and a high abundance of Firmicutes compared to Bacteroidetes. Considering the microbiome functionality, the main difference between traditional and urban individuals relies on Carbohydrates metabolism: the traditional groups are primarily associated to Central Carbohydrate metabolism, and the urban group are primarily associated to Monosaccharides metabolism, reflecting their distinct diet concerning the types of carbohydrates. Unique features characterize the Yanomami/Brazil: higher abundance of Proteobacteria and *Ralstonia* genus; and the abundance of gene families from Regulation/Cell signaling, Motility/Chemotaxis, and Virulence. Regarding the resistome, most of the resistance genes/mechanisms found in the traditional groups were also identified in the urban group used as control. Of the 624 genes identified, 454 are shared among all groups. Thirty-four genes are shared only among the traditional groups, most of them belong to beta-lactamases class ($n = 11$). Interestingly, some of these beta-lactamases genes (SPG, MSI-OXA, MUS, TUS-1) are chromosomally encoded by soil bacteria, indicating that part of the resistome of these traditional groups resembles soil resistomes, contrasting with the urban group.

Keywords: Gut microbiome, metagenomics, functionality, taxonomy, resistance genes

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