Title: STUDY OF MICROBIOMA OF PACIENTS WITH CHAGAS DISEASE

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Abstract

Recent studies suggest that the composition of the microbiota can impact susceptibility to disease mediated by the immune system. The pathogenesis of Chagas cardiomyopathy is not well established, inflammation in the myocardium is large relative to the number of parasites presents suggesting an inappropriate immune response to the parasite. This study aimed to describe the intestinal microbiota according to clinical form of Chagas disease (Ch) by amplifying the gene 16s ribosomal RNA gene. It was selected 88 stool samples of patients with Chagas disease: 29 with the cardiac form (CC), 28 with the indeterminate form (CI) and 31 negative controls (NC). The characterization of the microbiological conditions of these patients was performed by amplification of the V4 domain segment bacterial 16S ribosomal RNA using the primers F515 (5'-CACGGTCGKCGGCGCCATT-3 ') and R806 (5'-GGACTACHVGGGTWTCTAAT-3'), in the next generation sequencing platform Ion PGM Torrent. The generated sequences were analyzed using the QIIME software and statistical analysis was performed using the nonparametric Kruskal-Wallis test. The principal coordinates analysis (PCoA) unweighted and weighted showed no difference between CC and CI. Statistical analysis of phylum, genus, family and class among patients with CC *vs* CI did not find any significant result. However, when compared patients with Chagas disease (Ch) *vs* NC, the following differences were found: in the class *Betaproteobacteria* Ch (1.30%) *vs* NC (2.10%) (p = 0.003), in the families *Bacteroidaceae* Ch (15.43%) *vs* NC (25.72%) (p = 0.014), *Rikenellaceae* Ch (0.23%) *vs* NC (0.35%) (p = 0.005), *Alcaligenaceae* Ch (1.29%) *vs* NC (2.08%) (p = 0.004) and in the genus *Bacteroides* Ch (15.43%) *vs* NC (25.72%) (p = 0.014), *Blautia* Ch (1.62%) *vs* NC (2, 22%) (p = 0.044) and *Dialister* Ch (0.93%) *vs* NC (2.06%) (p = 0.004). Our data suggest that patients with Chagas disease may have a different microbiota of healthy controls. Apparently, the microbiome is not related to pathogenesis of Chagas cardiomyopathy since the bacteria population was similar in patients with indeterminate and cardiac form.

Keywords: Chagas disease, gut microbiota, next generation sequencing.