

TITLE: COMPOSITIONAL ANALYSIS OF THE FECAL MICROBIOTA OF PATIENTS WITH COVID-19

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ABSTRACT:

The Sars-CoV-2 virus, which causes the disease COVID-19, is responsible for the pandemic that has spread around the world since the end of 2019. The viral RNA of the new coronavirus was found in the intestinal microbiota of infected patients and studies have already demonstrated the correlation between the severity of Sars-CoV-2 infection and the composition of the fecal microbiota of infected patients. In this context, the present research aimed to evaluate the effects of COVID-19 on the fecal microbiota of 3 patients, one patient with mild symptoms (P1), one with severe symptoms (P2) and one without COVID-19 (P3), through metabarcoding analyses. Total DNA from stool samples was extracted using the DNeasy® PowerSoil® kit (QIAGEN), followed by amplification of the 16S rRNA gene and sequencing on an Illumina MiSeq Platform. Sample P2 revealed a community of archaea, totaling 4.8% belonging to the phylum Euryarchaeota in relation to the total number of prokaryotes in the sample. The most abundant genera were Methanobrevibacter and Methanosphaera, which contain species associated with the regulation of hydrogen levels in the intestine and play an important role in metabolic health. This same phylum showed values lower than 1% in P1 and P3. In P2 patient, the phylum Bacteroidota was responsible for 0.3% of the total number of prokaryotes, while in P1 and P3 this phylum was responsible for 28.8% and 10.8% respectively. The amount of Bacteroides found in the patient with severe symptoms (P2) was equivalent to 0.5% of the amount detected in the patient with mild symptoms (P1). The reduced abundance of these bacteria in the feces microbiota has been reported as indicative of inflammatory diseases. Finally, P2 presented a value of 16.1% of Actinobacteria, while P1 and P3 presented values lower than 5% of the total bacteria in the samples of these patients. The Actinobacteria genera Bifidobacterium and Collinsella, found in greater quantities in patient P2, indicate an immune response to SARS-CoV-2, and both are reported to be highly effective against infection by the virus. The analysis revealed differences among the compositions of the fecal microbiota of the patients and show that microorganisms may be involved in the modulation of the hosts inflammatory responses during infection by Sars-CoV-2.

Keywords: COVID-19, gut bacteria, metabarcoding, Sars-CoV-2

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