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BACKGROUND

Coronavirus disease 2019 (COVID-19), caused by the SARS-



CoV-2 virus, is affected by a variety of factors. Evidence suggests a relationship between COVID-19 and the nasopharyngeal microbiota. This study compares the diversity and taxonomic composition of the nasopharyngeal microbiota with clinical outcomes of COVID-19.

METHODS

A descriptive and comparative study was performed on patients classified into four groups according to their disease severity. For each study group, 26 patients were recruited: patients hospitalized in the intensive care unit (G1), hospitalized in regular hospitalization wards (G2), those without hospitalization and with mild or no symptoms with SARS-CoV-2 (G3), and healthy patients (G4). SARS-CoV-2 was tested on all patients using RT-PCR. The nasopharyngeal microbiota was characterized by PCR, targeting 13 genera of bacteria.

RESULTS

Group 1 (N=26) 80 Group 2 (N=26) Group 3 (N=26) Group 4 (N=26) Frequency (%) 60 40 20 0 Proteobacteria division Others Firmicutes Lactobacillus spp. Eubacterium spp. Veillonella spp. Clostridium spp. Enterococcus spp. Others Bacteroidete **Firmicutes** Actinobacteria **Bacteroidetes** division division division

Figure 1. Frequency nasopharyngeal microbiota



Some bacteria were significantly more frequent in hospitalized patients (G1, G2) compared to the nonhospitalized patients (G3 y G4). This is the case with *Lactobacillus* (G1=96.2% of cases, G2=92.3%, G3=23.1%, G4=15.4%). Similarly, *Prevotella* (G1=96.2%, G2=80.8%, G3=3.8%, G4=23.1%). In the same way, *Veillonella* (G1=92.3%, G2=96.2%, G3=7.7%, G4=11.5%) presented a similar distribution. However, some bacteria were detected more frequently in healthy and asymptomatic subjects, such as Others Bacteroidetes (OB) and Others Firmicutes (OF). Similarly, relative abundance shows similar results to percentage frequency.

Table 1. Demographic and clinical characteristics of the study groups

	SARS-CoV-2 positive			SARS-CoV-2 negative
	ICU	Hospitalized	Mild/Asymptomatic	Negative
CHARACTERISTICS	N (%)	N (%)	N (%)	N (%)

Figure 2. . Frequency nasopharyngeal microbiota

CONCLUSION

There are several alterations in the nasopharyngeal microbiome associated with SARS-CoV-2 infection status and disease severity, reported in this study. The presence of *Lactobacillus, Prevotella, Veillonella,* and the Proteobacteria division were higher in critical and hospitalized patients, compared to asymptomatic and healthy subjects. On the other hand, others Bacteroidetes and species of *Firmicutes* were predominant in the groups of asymptomatic and healthy subjects. The nasopharyngeal microbiota should be studied in the future as a therapeutic, diagnostic, and prognostic tool in COVID-19.

Gender						
Male	20 (76.92)	21 (80.77)	14 (53.85)	11 (42.31)		
Female	6 (23.08)	5 (19.23)	12 (46.15)	15 (57.69)		
Age (Me/SD)	54.04 ± 13.08	57.85 ± 12.80	54.54 ± 12.43	51.73 ± 14.73		
Clinical symptoms						
Cough	18 (69.23)	18 (69.23)	2 (7.69)	1 (3.85)		
Expectoration	3 (11.54)	3 (11.54)	0 (0.00)	0 (0.00)		
Fever	21 (80.77)	12 (46.15)	3 (11.54)	1 (3.85)		
Dyspnea	26 (100.00)	22 (84.62)	0 (0.00)	0 (0.00)		
Fatigue	11 (42.31)	12 (46.15)	0 (0.00)	0 (0.00)		

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