Table 1 (abstract FC-046) Outcomes parameters

Table 1: Outcome parameters

	Total (N=237)	Unvaccinated (N=126)	1 dose (N=33)	2 doses (N=63)	>=3doses (N=15)	p
Severe/Critical ARDS	114(48)	77 (61)	9 (27)	24 (38)	4 (26)	$<10^{-3}$
HFNC	132(56)	97(77)	12(36)	19(30)	4(27)	$<10^{-3}$
NIV	118(50)	82(65)	14(43)	20(32)	2(13)	$<10^{-3}$
Cannula/Mask	80(34)	16(13)	15(45)	37(59)	12(80)	$<10^{-3}$
MV	96 (40)	64 (51)	12 (36)	18(28)	2 (13)	0.003
Mortality	117(49)	72(57)	14 (42)	27 (42)	4(26)	0.04

ARDS: Acute Respiratory Distress Syndrome, HFNC: High Flow Nasal Cannula , NIV: Non Invasive Ventilation, MV: Mechanical Ventilation

FC-047

Microbiological profiles of severe pneumopathies during the COVID-19 pandemic: interest of multiplex PCR screening

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Rationale: The clinical presentation during respiratory infection with SARS-CoV-2 is similar to the infection with other respiratory pathogens; however, the management and prognosis are different. The search for these agents has been reduced during the covid pandemic but does not prevent their co-existence with SARS-CoV-2. The objectives of this study were to identify the bacteria and viruses responsible for respiratory infections using the multiplex PCR diagnostic test and characterize clinical profiles during the COVID-19 pandemic.
Patients and methods/materials and methods: An observational study was performed between January 2020 and September 2022, in the Intensive Care Unit (Monastir, Tunisia), including patients admitted with hypoxemic respiratory failure. Respiratory samples were analyzed using a qualitative multiplex PCR technique (RespiFinder). Diagnosis of Covid-19 infection was based on COVID PCR test or chest CT scan.
Results: During the study period, 352 COVID-19 patients with hypoxemic respiratory failure were admitted to our ICU. PCR multiplex was made in 60 patients given the unavailability of this technique during the COVID-19 pandemic. The median age of these patients was 50 years [IQR: 41–70] and the median SAPS II score was 31 [IQR: 20–39]. The main clinical signs presented by the patients were dyspnea and cough. The multiplex PCR was positive in 45% of cases. When the PCR panel was performed, 86% of patients were receiving antibiotic treatment. All germs identified were viruses and no bacterial infection was detected in our study: 14 cases of Influenza A (H1N1), 3 cases of VRS B, 3 cases of coronavirus 229E, 1 case of coronavirus HKU1, 3 cases of coinfection Rhinovirus/Enterovirus, 1 case of coinfection coronavirus NL63/HKU1, 1 case of coinfection coronavirus 229E/VRS B and 1 case of coinfection Influenza B/Adenovirus. The diagnosis of SARS-Cov2 infection was observed in 28.3% of cases, 23.5% of them were coinfections (4 cases). During hospitalization, 69% of these patients required invasive mechanical ventilation.
Conclusion: Pathogenic microorganisms with respiratory tropism still exist during.
The COVID-19 pandemic and may be responsible for severe respiratory infections. Their research must be performed simultaneously with the SARS-CoV-2 diagnostic test to adapt the therapeutic management of patients.
Compliance with ethics regulations: Yes in clinical research.

FC-048

Oropharyngeal bacterial microbiota analysis at hospital admission: a comparison of COVID-19 and cerebral vascular disease patients

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Rationale: Alterations in oropharyngeal (OP) microbiota have been associated with viral infections, with potential bi-directional interactions. In published studies, the OP of COVID-19 patients was mostly compared to healthy patients, with inconsistent observations. The aim of this monocenter prospective study was to compare the OP bacterial microbiota profile in patients admitted to the hospital for COVID-19 and for stroke.
Patients and methods/materials and methods: Patients admitted in our tertiary hospital either for COVID-19 pneumonia diagnosed with a positive polymerase chain reaction (PCR) for SARS-CoV-2 in nasal swab or for an ischemic or hemorrhagic stroke (with negative SARS-CoV-2 PCR) were enrolled respectively during the second and third waves of the pandemic, and between September and December 2021. COVID-19 patients were admitted to general wards or directly to the intensive care unit (ICU). Exclusion criteria were antibiotic exposure during the past 15 days, coagulopathy, endotracheal intubation and pregnancy. OP swabs were taken from the hard palate within the first 24 h after admission and used for a 16S rRNA gene-targeted metagenomic analysis. Demographic data, medical history, and in-hospital deaths were recorded.
Results: A total of 135 swabs were taken, and 83 were analyzed: 55 in the COVID group (65 [64–69] years, 22 women), including 16 patients in an ICU subgroup, and 28 in the stroke group (72 [64–80] years, 11 women). The multivariate analysis showed that the reason for admission significantly influenced the beta diversity ($p < 0.001$). The beta diversity in the two subgroups of COVID patients was similar. The beta diversity was not influenced by age, smoking habits, or proton pump inhibitor treatment and was not associated with in-hospital mortality. Alpha diversity in COVID patients (population richness and population diversity) and the stroke group was not significantly different. At the genus level, 38 genera were identified with significant relative abundance differences between COVID and stroke groups. Among them, 34 taxa, including the genus *Veillonella* and family *Prevotellaceae* were significantly increased in COVID patients, while 4 taxa, including the genus *Streptococcus* were significantly depleted. The microbiota was dominated by taxa belonging to 4 phyla: Firmicutes (*Streptococcus, Veillonella, Gemella*), Bacteroidota (*Prevotella*, *Prophyromonas*), Fusobacteriota (*Fusobacterium, Leptotrichia*) and Proteobacteria (*Neisseria*).
Conclusion: In this study, a significant difference in OP bacterial microbiota was observed in COVID-19 patients, including more pro-inflammatory genera, compared to other newly admitted patients for a stroke. It can be assumed that this dysbiosis occurred earlier during viral infection. Moreover, this dysbiosis was not associated with respiratory failure severity.
Compliance with ethics regulations: Yes in clinical research.

FC-049

Lung microbiota compositions differ between influenza, COVID-19 and bacteria-related acute respiratory distress syndromes

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