

# Study of associations between COVID-19 and bacterial infections: a retrospective study

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## Introduction:

The COVID-19 pandemic disease, caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (Sars-CoV-2), has affected millions of people worldwide. Clinical practice highlights that the number of patients with COVID-19 diagnosed with bacterial infections during periods of hospitalization is increasing. Rapid characterization of co-infection is essential in the treatment of most patients with COVID-19, as it can result in failure of antimicrobial therapy. Some studies report the prevalence of variable coinfection among patients with COVID-19, however, it can be up to 50% in patients who did not survive. [1, 2]

The present study aims:

- To assess the occurrence of associations between COVID-19 and bacterial infections in patients hospitalized at Centro Hospitalar Baixo Vouga – Aveiro between April 1, 2020 and December 31, 2021.
- Contribute to the definition of pharmacological therapy strategies in patients with mixed, bacterial and Sars-CoV-2 infections.

## Methods:

A total of 9194 Sars-CoV-2 test results (Abbott molecular) and 3374 clinical isolates (MALDI Biotyper® - Bruker), from various clinical sources, obtained between April 1, 2020 and October 31, 2021 from Centro Hospitalar Baixo Vouga – Aveiro, Portugal, were studied. Bacterial infections on hospitalized patients which had a positive COVID-19 test (n = 183) in a period of in a period of -30 and +30 days, were selected. The most prevalent bacteria in patients COVID-19 positive were determined and associations between occurrence of COVID-19 infection and occurrence of each bacterial infection, analysed. The association strength was evaluated through Odds Ratio (OR) and its 95% confidence interval. The chi-square testing with P values <0.05 were considered as significant association effect. All statistical analyses were performed using R software, using epiR package.

## Results:

We studied 183 hospitalized patients that had positive COVID-19 test and bacterial infections. The percentage of infection was 9,8%. There are several isolates per patient (average 1,7 per patient). The most prevalent bacteria in patients COVID-19 positive are *Escherichia coli* (19,03%), *Klebsiella pneumoniae* (14,84%), *Staphylococcus aureus* (10,65%), *Pseudomonas aeruginosa* (7,42%), *Proteus mirabilis* (7,74%), *Staphylococcus epidermidis* (4,52%), *Candida albicans* (5,16%) and *Enterococcus faecalis* (4,84%). In patients COVID-19 negative (n = 1668) the most prevalent are *Escherichia coli* (21,57%), *Klebsiella pneumoniae* (13,84%), *Enterococcus faecalis* (7,25%), *Staphylococcus aureus* (6,63%), *Staphylococcus epidermidis* (6,49%), *Pseudomonas aeruginosa* (6,20%), *Candida albicans* (5,22%), *Proteus mirabilis* (3,82%). There is a significant association of occurrence between COVID-19 infection and five bacteria (Table 1).

## Discussion:

For five bacteria the OR association strength can be considered moderated. There are differences in bacterial infections between positive and negative COVID-19 patients, mainly in *Staphylococcus aureus*. These results strength the importance to further studies on this association including the evaluation of comorbidities, microbiological distribution, probable increase of nosocomial infection and patient mortality during hospital admission. Agents like *Staphylococcus epidermidis* could be colonisations and is need

### Keywords:

COVID-19, Severe Acute Respiratory Syndrome Coronavirus 2, bacterial infections

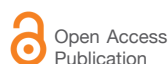
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### Conflict of interest:

The authors declare no conflict of interests.

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careful to understand this data. This analysis may contribute to help in the definition of empirical therapies in patients with mixed COVID-19 and bacterial infections.

**Table 1** - Associations between COVID-19 infection and each bacterial infection.

	COVID + n = 405	COVID - n = 8790	OR	LBCI95%	UBCI95%	p-value*
<i>Escherichia coli</i>	59	661	2.10	1.57	2.79	<0.001
<i>Klebsiella pneumoniae</i>	46	424	2.53	1.83	3.49	<0.001
<i>Staphylococcus aureus</i>	33	203	3.75	2.56	5.50	<0.001
<i>Pseudomonas aeruginosa</i>	23	190	2.73	1.75	4.25	<0.001
<i>Proteus mirabilis</i>	24	117	4.67	2.97	7.33	<0.001
<i>Staphylococcus epidermidis</i>	15	226	1.55	0.89	2.68	0.952
<i>Candida albicans</i>	16	160	2.22	1.31	3.75	0.016
<i>Enterococcus faecalis</i>	15	226	1.55	0.89	2.68	1.000

\* adjusted to simultaneous testing (Bonferroni correction)

#### Ethics committee and informed consent:

The current research was approved by CHBV ethics committee.

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