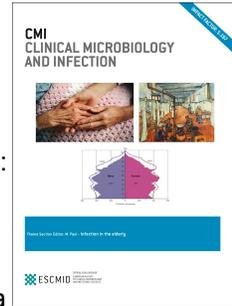


# Journal Pre-proof

Incidence of co-infections and superinfections in hospitalised patients with COVID-19: a retrospective cohort study

Carolina Garcia-Vidal, Gemma Sanjuan, Estela Moreno-García, Pedro Puerta-Alcalde, Nicole Garcia-Pouton, Mariana Chumbita, Mariana Fernandez-Pittol, Cristina Pitart, Alexy Inciarte, Marta Bodro, Laura Morata, Juan Ambrosioni, Ignacio Grafia, Fernanda Meira, Irene Macaya, Celia Cardozo, Climent Casals, Adrian Tellez, Pedro Castro, Francesc Marco, Felipe García, Josep Mensa, José Antonio Martínez, Alex Soriano, COVID19-researchers group



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25 **ABSTRACT**

26 **Objectives:** We aimed to describe the burden, epidemiology and outcomes of co-  
27 infections and superinfections occurring in hospitalised patients with COVID-19.

28 **Methods:** Observational cohort study of all consecutive patients admitted  $\geq 48$  hours  
29 to Hospital Clinic of Barcelona for COVID-19 (February 28<sup>th</sup> - April 22<sup>nd</sup>, 2020) who are  
30 currently discharged or dead. We describe demographic, epidemiologic, laboratory,  
31 and microbiologic results, as well as outcome data retrieved from electronic health  
32 records.

33 **Results:** Of a total of 989 consecutive patients with COVID-19, 72 (7.2%) had 88 other  
34 microbiologically confirmed infections: 74, bacterial; 7, fungal and 7, viral. Community-  
35 acquired co-infection at COVID-19 diagnosis was uncommon (31 out of 989, 3.1%) and  
36 mainly caused by *Streptococcus pneumoniae* and *Staphylococcus aureus*. A total of 51  
37 hospital-acquired bacterial superinfections, mostly caused by *Pseudomonas*  
38 *aeruginosa* and *Escherichia coli*, were diagnosed in 43 (4.7%) patients, with a mean  
39 time from hospital admission to superinfection diagnosis of 10.6 (SD 6.6) days. Overall  
40 mortality was 9.8% (97/989). Patients with community-acquired co-infections and  
41 hospital-acquired superinfections presented with worse outcomes.

42 **Conclusions:** Co-infection at COVID-19 diagnosis is uncommon. Few patients  
43 developed superinfections during hospitalisation. These findings are quite differential  
44 when compared with those of other viral pandemics. As it relates to hospitalised  
45 patients with COVID-19, such findings could prove essential in defining the role of  
46 empiric antimicrobial therapy or stewardship strategies.

47 **INTRODUCTION**

48 The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has  
49 presented a formidable medical challenge before health systems and clinicians [1–4].  
50 With >250,000 cases diagnosed by 9 July, Spain has particularly suffered from this  
51 pandemic [5]. Many decisions have been made with limited clinical experience and  
52 scientific evidence, especially as it concerns treatments for patients hospitalised with  
53 the coronavirus disease 2019 (COVID-19). One such clinical decision is that regarding  
54 the use of antibiotic therapy in patients with COVID-19. Bacterial, especially  
55 *Streptococcus pneumoniae* and *Staphylococcus aureus*, and viral or fungal co-infections  
56 are common complications described as arising in other pandemics caused by  
57 *influenza* viruses [6–9]; however, information concerning incidence of such co-  
58 infections in patients with COVID-19 has been scarce. Similarly, information related to  
59 COVID-19 superinfections is lacking, although it is essential to rational antimicrobial  
60 stewardship.

61 We aimed to describe the burden and epidemiology of community-acquired co-  
62 infections and hospital-acquired superinfections in a large cohort of all consecutive  
63 hospitalised patients admitted with COVID-19 for 48 hours or more in Barcelona, who  
64 are either currently discharged or dead. The impact of co-infections and  
65 superinfections on patient outcomes was also described.

**66 METHODS****67 Study design and patients**

68 This observational cohort study was performed at Hospital Clinic in Barcelona (Spain),  
69 a 700-bed university centre that provides broad and specialised medical, surgical, and  
70 intensive care for an urban population of 500,000 adults (>18 years old). All patients  
71 admitted with COVID-19 for  $\geq 48$  hours between 28 February and 22 April 2020, and  
72 who are currently discharged alive or had died during hospitalisation, were included.  
73 All patients had a diagnosis of COVID-19 confirmed by real-time reverse transcription  
74 polymerase chain reaction (RT-PCR) testing performed on nasopharyngeal throat swab  
75 specimens, and/or by fulfilling clinical diagnostic criteria provided during the  
76 pandemic peak for SARS-CoV-2. These criteria comprised the presence of any of the  
77 following respiratory symptoms, including sore throat, congestion, cough, dyspnoea,  
78 new loss of taste and/or smell, as well as uni- or bilateral interstitial infiltrates in the  
79 chest X-ray. The Institutional Ethics Committee of Hospital Clinic of Barcelona  
80 approved the study and due to the nature of the retrospective data review, waived the  
81 need for informed consent from individual patients (HCB/2020/0273).

82

**83 Data collection and outcomes**

84 For all patients hospitalised with COVID-19, data concerning demographics (age,  
85 gender), epidemiology, comorbidities, laboratory tests, microbiological results (blood  
86 and urine cultures, respiratory samples, urinary antigen tests and antimicrobial  
87 susceptibility), treatment and outcomes (intensive care unit [ICU] admission, length of  
88 hospital stay, and mortality) were collected directly from electronic health records  
89 (EHR) as previously described [10]. The EHR of all patients with positive microbiologic

90 results were reviewed by one of our researchers (CGV, EMG or CC) to assess clinical  
91 significance.

92

### 93 **Procedures**

94 Investigation of bacterial, viral and fungal pathogens in blood, normally sterile fluids,  
95 sputum and other samples was performed with standard microbiologic procedures  
96 upon hospital admission, as requested by the attending physician. Bacterial respiratory  
97 infection was diagnosed in patients with 1 or more positive cultures of respiratory  
98 pathogens obtained from blood, pleural fluids, good-quality sputum (>25  
99 polymorphonuclear leukocytes and <25 epithelial cells) and bronchoalveolar lavage,  
100 and/or a positive urinary antigen test. *S. pneumoniae* antigen in urine was detected  
101 with a rapid STANDARD F *S. pneumoniae* Ag FIA assay (SD Biosensor, Inc. Republic of  
102 Korea). Specific, rapid RT-PCR testing was used for *influenza* A and B viruses, as well as  
103 respiratory syncytial virus (RSV) diagnosis (cobas Liat System, Roche). Multiplex PCR  
104 testing (Flow System, Roche) was also used for *influenza* viruses: A, B and C;  
105 *parainfluenza*: 1,2,3 and 4; and metapneumovirus diagnosis.

106

### 107 **Definitions**

108 Bloodstream infection (BSI) was defined as the growth of a non-skin flora commensal  
109 from  $\geq 1$  blood culture. To define a BSI as that caused by a common skin coloniser such  
110 as coagulase-negative staphylococci or *Corynebacterium*, we required  $\geq 2$  blood  
111 cultures drawn from different sites and a clinical evaluation from one of our  
112 researchers (CGV or EMG). We then considered the clinical significance of such BSI.  
113 Urinary infection was defined as the growth of a bacterium or fungus in a urine culture

114 from a patient with clinical symptoms and/or the consideration of such urinary  
115 infection as clinically significant by one of our researchers (CGV or EMG). *Aspergillus*  
116 tracheobronchitis was defined as the isolation of *Aspergillus* species from  
117 endobronchial specimens of intubated patients with purulent secretions, as well as  
118 clinical validation from one of our researchers (CGV or CC).

119 All of these clinically-indicated infections were categorised as co-infections or  
120 superinfections. If diagnosis was at onset or within the first 24h of COVID-19 hospital  
121 admission, these infections were defined as community-acquired co-infections. If  
122 diagnosis occurred  $\geq 48$ h of admission for COVID-19, these infections were defined as  
123 hospital-acquired superinfections.

124

#### 125 **Statistical analysis**

126 For the purpose of the present study, a descriptive analysis of clinical and laboratory  
127 tests was performed. Continuous and categorical variables were presented as median  
128 (interquartile range [IQR]) and absolute number (percentage), respectively. We used  
129 the Mann-Whitney U-test,  $\chi^2$  test and Fisher's exact test to compare differences  
130 between patients who had other infections and those who did not. Significance was a  
131 p-value  $< 0.05$ . Statistical analyses were performed with Microsoft SPSS-PC+, version  
132 22.0 (SPSS, Chicago, IL, USA).

133 **RESULTS**

134 We assessed 989 consecutive adults with COVID-19 at our hospital who had either  
135 been discharged or had died during the study period. Of these, 552 (55.8%) were male  
136 and the median age was 62 (IQR 48-74) years. Main patient characteristics by groups  
137 are shown in Table 1. Table 2 details the number of microbiology tests requested by  
138 attending physicians and positive results with clinical significance. A total of 88 non-  
139 COVID-19 infections were documented in 72 (7.3%) patients: 74, bacterial; 7, fungal;  
140 and 7, viral. A total of 74 bacterial infections were diagnosed in 61 of 88 patients (3  
141 infections in one patient, 2 in 12 individual patients and 1 in every remaining patient).  
142 The most common bacteria isolated were *S. pneumoniae* (12 cases); *S. aureus*, 12;  
143 *Pseudomonas aeruginosa*, 10; *Escherichia coli*, 7; and *Klebsiella pneumoniae*, 6.

144

145 **Community-acquired co-infections**

146 Overall, 31 of 989 (3.1%) patients had 37 community-acquired co-infections. Thirty  
147 community-acquired bacterial co-infections were documented in 25 (2.5%) patients.  
148 Specifically, bacterial pneumonia co-infection was documented in 21 (2.1%) patients at  
149 COVID-19 diagnosis. Two of these co-infections were with different bacteria. *S.*  
150 *pneumoniae* (one patient had a *Moraxella catarrhalis* co-infection) and *S. aureus* (one  
151 patient had a *Haemophilus influenzae* co-infection) were the most common bacteria in  
152 this scenario. Two patients had infections caused by methicillin-resistant *S. aureus*.  
153 Diagnosis of community-acquired bacterial co-infection was performed with one or  
154 more of the following tests: urinary antigen test in 12 cases; good quality sputum, 2  
155 and blood cultures, 1.

156 Viral community-acquired co-infection was detected in 7 of 989 (0.6%) patients, of  
157 whom one presented with bacterial co-infection as well: 4 cases of *influenza A* virus  
158 co-infection; 1, *influenza B* virus; 1, respiratory syncytial virus and 1, herpetic disease.  
159 Two of these 7 (28.6%) patients, with *influenza A* and *influenza B* virus co-infections,  
160 respectively, died.

161

### 162 **Hospital-acquired superinfections**

163 A total of 51 hospital-acquired superinfections were documented in 43 patients. Of  
164 these, 44 were bacterial and diagnosed in 38 (3.8%) patients. The mean time from  
165 hospital admission to superinfection diagnosis was 10.6 (SD 6.6) days. Of these 44  
166 superinfections, 25 (56.8%) occurred in patients admitted to the ICU. The most  
167 frequently isolated microorganisms were *P. aeruginosa* (8 cases); *E. coli*, 6; *Klebsiella*  
168 spp., 5 and *S. aureus*, 5. The most common hospital-acquired superinfections were  
169 those of the respiratory tract and bacteremia. Multidrug-resistant Gram-negative  
170 bacteria (MDR-GNB) were isolated in 7 patients: 3, MDR-*P. aeruginosa* infection; 2,  
171 Extended-Spectrum  $\beta$ -Lactamase (ESBL)-*E. coli*; and 2, ESBL-*K. pneumoniae*. Table 3  
172 details epidemiology of all bacterial co-infections and superinfections.

173 Seven of 989 (0.7%) patients had fungal hospital-acquired superinfections: 3 cases  
174 caused by *Aspergillus fumigatus* and 4, *Candida albicans*. Two patients were diagnosed  
175 with bacterial and fungal superinfections. All three patients with tracheobronchitis  
176 caused by *A. fumigatus* had prior lung disease and a median age of 75 (IQR 70-75)  
177 years. These patients were also critically ill and received mechanical ventilation  
178 support and high corticosteroid dosage. In this series of patients, only one died.

179 Patients with *C. albicans* superinfection had the following clinical syndromes: two

180 cases of candidemia in an ICU setting; one case of a nosocomial urinary tract infection  
181 related to a urinary catheter and one case of a complicated intra-abdominal infection.  
182 Two patients died.

### 183 **Outcomes**

184 Overall mortality for patients hospitalised with COVID-19 for 48 hours or more was  
185 9.8% (97 of 989 patients). Table 1 details the most important outcomes in hospitalised  
186 patients with COVID-19 who present without infection, those with community-  
187 acquired co-infection and those with hospital-acquired superinfection. Remarkably,  
188 patients with community-acquired co-infections were admitted to the ICU more  
189 frequently. In comparison to those without infection, patients with hospital-acquired  
190 superinfections had prolonged length of hospital stay and higher mortality.

191 **DISCUSSION**

192 We present a large series of patients from a Spanish region dramatically affected by  
193 the COVID-19 pandemic, focusing on describing community-acquired co-infections and  
194 hospital-acquired superinfections in these patients. Remarkably, bacterial pneumonia  
195 co-infection in patients hospitalised for COVID-19 was lower when compared with co-  
196 infections occurring in patients suffering from other respiratory virus infections such as  
197 *influenza* H1N1 or *influenza* H3N2 [6,8,11,12]. A minority of patients had bacterial or  
198 fungal superinfections and co-infections caused by other viruses.

199 Our results are concordant with a recent review that summarised nine studies  
200 reporting data concerning co-infections in patients with COVID-19. An 8% rate for  
201 bacterial and fungal co-infections was described [13]. In a recent letter, Kim et al  
202 reported relatively low rates (ranging from 0% for most pathogens to 12% in  
203 rhinovirus/enterovirus) of co-infections between SARS-CoV-2 and other respiratory  
204 pathogens [14]. Bacterial community-acquired pneumonia co-infections documented  
205 in our cohort have been especially low. Considering the high number and severity of  
206 bacterial co-infections previously reported in patients with *influenza* H1N1 and H3N2  
207 [6–9], upon arrival of the COVID-19 pandemic, our hospital protocol recommended the  
208 initiation of antibiotic therapy for all hospitalised patients with COVID-19. Experience  
209 acquired within the first, few weeks led us to reconsider this approach, so as to  
210 administer empiric antibiotic therapy solely to patients admitted for COVID-19 and  
211 who present with a chest x-ray suggestive of bacterial infection, need for direct ICU  
212 admission or severe immunocompromised condition. Our results support the  
213 avoidance of antibiotic therapy in most patients hospitalised for COVID-19. The reason

214 for which bacterial co-infections are quite low in patients with COVID-19 is unknown; it  
215 is tempting to speculate that some immunological facts like macrophage  
216 hyperactivation play a role. Nonetheless, when bacterial co-infection is suspected, we  
217 recommend an antibiotic approach with optimal *S. aureus* coverage such as ceftaroline  
218 or ceftriaxone/cefazolin plus levofloxacin in areas with low MRSA prevalence.

219 Frequency of hospital-acquired superinfections remained low despite the fact that  
220 many patients were undergoing severe immunosuppressant treatments. Some factors  
221 may provide an explanation for that observation, including empiric antibiotic use,  
222 isolation measures or host macrophage activation. Further, the lack of additional  
223 microbiologic tests after SARS-CoV-2 was detected may have also contributed. Further  
224 studies will be needed to elucidate the role of each measure in decreasing  
225 superinfections. Superinfections have been mainly related with ICU admission,  
226 especially with the use of mechanical ventilation and catheters; expected  
227 epidemiology linked closely with predominant hospital flora. In our study, the rate of  
228 MDR infections was relatively low due to the possible impact of COVID-19 isolation  
229 measures precluding horizontal transmission among patients.

230 Aspergillosis complicating COVID-19 was clinically quite different and not as frequent  
231 as that observed in patients with *influenza* [12,13]. In patients with COVID-19,  
232 aspergillosis usually manifested as tracheobronchitis, especially in association with  
233 patients with prior lung disease, prolonged mechanical ventilation and high  
234 immunosuppressor dosage. In the opinion of this study's authors, this fact may also be  
235 in part related to the different immunologic dysfunction in influenza and COVID-19  
236 infections [11,13,15]. Macrophages are the key host cell in fighting *Aspergillus* spp. due

237 to their involvement in *Aspergillus* spores recognition [16]. Patients admitted with  
238 COVID-19 also had *Candida* spp. superinfections mainly related with parenteral  
239 nutrition and urinary catheters.

240 Anecdotal cases of co-infections during SARS-CoV-2 and other virus infections have  
241 been previously reported [16–19]. Our results support that respiratory virus  
242 community-acquired co-infection is relatively uncommon in hospitalised patients with  
243 COVID-19. However, viral co-infections could lead to severe diseases, and this study  
244 was conducted in a mostly non-*influenza* season (incidence could vary in fall/winter).

245 Overall mortality in the cohort of patients hospitalised  $\geq 48$  hours was 9.8%. We found  
246 that patients with other infections had worse outcomes, prolonged length of hospital  
247 stay, higher rates of ICU admission and increased mortality. These findings are in  
248 agreement with previous studies, which documented an association between co-  
249 infection in respiratory virus pandemics and poor prognosis [6–8]. However, this is  
250 unadjusted to baseline patients' characteristics and cannot be completely attributed to  
251 co-infection and/or superinfections.

252 The strengths of this study comprise the large number of patients included, as well as  
253 the clear, complete collection of clinical and microbiologic data. However, our study  
254 does have some major limitations that should be acknowledged. First, this is a  
255 retrospective study reporting clinically significant, microbiologically documented  
256 infections. However, no systematic testing for co-infections was performed, and it is  
257 possible that either some attending physicians did not order microbiologic tests for  
258 their patients or some patients may have had co-infections or superinfections not  
259 documented by performed microbiologic tests. A concern held among our team is

260 whether initial challenges arising during the management of patients with COVID-19  
261 potentially decreased the number of requests for microbiologic tests to rule out other  
262 infections. Notwithstanding, infection rates reported in our study remained low, even  
263 in patients in whom urinary antigen testing or other types of test had been performed.  
264 Second, we described a cohort of patients currently discharged or dead. Some patients  
265 with severe COVID-19 infection that required ICU admission, mechanical ventilation  
266 and prolonged length of hospital stay remain hospitalised. It is conceptually easy to  
267 believe that superinfection is higher in this population. Third, respiratory RT-PCR  
268 techniques used were limited to the virus. PCR testing for the detection of atypical  
269 pathogens was not performed in our patients. Additionally, and as mentioned prior,  
270 we initially treated all hospitalised patients with antibiotics within the first, few weeks,  
271 for which the impact of such practice in preventing superinfections remains unknown.  
272 That stated, the first four limitations might underestimate the frequency of co-  
273 infections or superinfections in patients with COVID-19. Lastly, as this study was  
274 conducted at a single centre, there may have been influence when describing  
275 nosocomial infections. Frequency and microbiologic epidemiology may also vary  
276 significantly according to different geographical contexts.

277 In conclusion, bacterial, fungal and viral co-infections and superinfections in  
278 hospitalised patients with COVID-19 are low; however, when present, they may cause  
279 severe diseases with worse outcomes. *S. pneumoniae* and *S. aureus* are the most  
280 common pathogens to cause community-acquired pneumonia co-infections. In our  
281 area, *P. aeruginosa* and *E. coli* were frequent bacteria that caused hospital-acquired  
282 superinfections. Our findings are important when defining the role of empiric  
283 antimicrobial therapy or stewardship strategies in hospitalised patients with COVID-19.

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311

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313 *Writing – Review & Editing:* all authors; *Conceptualization:* C.G-V.; *Investigation:* C.G-  
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**Table 1. Main characteristic of patients hospitalized for COVID-19 more than 48 hours in our hospital.**

Cohort characteristics	Patients without infection n=917	Patients with community-acquired co-infection n=31	Patients with hospital-acquired superinfection n= 43		
			p*	p**	
Median age, years (IQR)	61 (48-74)	63 (54.5-74)	0.671	67 (55.75-74.25)	0.006
Male sex (%)	510 (55.6)	18 (58.1)	0.956	26 (60.5)	0.822
<b>Comorbidities</b>					
Hypertension (%)	167 (18.2)	7 (22.6)	0.537	7 (16.3)	0.748
Diabetes mellitus (%)	89 (9.7)	7 (22.6)	0.019	7 (16.3)	0.160
Chronic heart disease (%)	122 (13.3)	9 (29)	0.013	7 (16.3)	0.576
Chronic lung disease (%)	95 (10.4)	6 (19.4)	0.110	7 (16.3)	0.218
Chronic renal disease (%)	47 (5.1)	8 (25.8)	<0.001	6 (14)	0.013
Cancer (%)	77 (8.4)	1 (3.2)	0.259	8 (18.6)	0.021
<b>Inflammatory markers at onset</b>					
Median C-reactive protein (IQR)	7.06 (3.31-13.29)	6.76 (3.20-9.79)	0.714	11.78 (5.55-17.87)	0.012
Median ferritin (IQR)	544 (249.5-1100)	208 (154-431.5)	0.042	797 (296-1743)	0.575
Median lymphocyte count (IQR)	0.9 (0.6-1.2)	0.8 (0.6-1.1)	0.892	0.783 (0.5-1.1)	0.088

<b>Median lactate dehydrogenase (IQR)</b>	287 (233-372)	264 (221-377.5)	0.477	311.5 (247.5-471-8)	0.193
<b>Treatment at onset</b>					
<b>Lopinavir-ritonavir (%)</b>	732 (79.8)	27 (87.1)	0.227	35 (81.4)	0.802
<b>Hydroxychloroquine (%)</b>	799 (87.1)	29 (93.5)	0.225	40 (93)	0.186
<b>Azythromycin (%)</b>	751 (81.9)	26 (83.9)	0.779	36 (83.7)	0.761
<b>Remdesivir (%)</b>	39 (4.3)	0 (0)	0.226	2 (4.7)	0.559
<b>Ceftriaxone (%)</b>	528 (57.6)	24 (77.4)	0.028	32 (74.4)	0.029
<b>Ceftaroline (%)</b>	26 (2.8)	2 (6.5)	0.232	5 (11.6)	0.001
<b>Immunomodulatory treatment</b>					
<b>Tocilizumab (%)</b>	200 (21.8)	5 (16.1)	0.450	16 (37.2)	0.018
<b>Methylprednisolone (%)</b>	238 (26)	9 (29)	0.701	25 (58.1)	<0.001
<b>Dexamethasone (%)</b>	23 (2.5)	4 (12.9)	0.01	8 (18.6)	<0.001
<b>Median length of hospital stay (IQR)</b>	9 (5-15)	8 (4.5-11.5)	0.565	20 (11-27.75)	<0.001
<b>Intensive Care Unit (ICU) admission (%)</b>	109 (11.9)	8 (25.8)	0.02	29 (67.4)	<0.001
<b>Median Length of ICU admission (IQR)</b>	3 (1-10)	3 (0-9)	0.888	5 (0.5-20)	0.095
<b>Death (%)</b>	86 (9.4)	5 (16.1)	0.21	8 (18.6)	0.047

Two patients with community-acquired co-infection developed hospital-acquired superinfections.

\*Comparison of patients without infection versus patients with community-acquired co-infection.

\*\*Comparison of patients without infection versus patients with hospital-acquired superinfection.

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**Table 2. Number of microbiology tests ordered and positive results with clinical significance in patients with COVID-19.**

Test	Number of patients with positive results/total patients	Number of patients with positive results/ tested patients	Number of tests with positive results/total tests
Blood cultures	16/989 (1.6%)	16/267 (5.9%)	37/680 (5.5%)
Urine cultures	19/989 (1.9%)	19/337 (5.6%)	19/717 (2.6%)
Respiratory samples (non-COVID)	25/989 (2.5%)	25/252 (9.9%)	23/845 (2.7%)
Pneumococcal urinary antigen	12/989 (1.2%)	12/230 (5.2%)	12/234 (5.1%)
<i>Influenza A</i> PCR	4/989 (0.4%)	4/248 (1.6%)	5/252 (1.9%)
<i>Influenza B</i> PCR	2/989 (0.2%)	2/250 (0.8%)	2/255 (0.8%)
Respiratory syncytial virus PCR	1/989 (0.1%)	1/251 (0.4%)	1/256 (3.9%)
Other respiratory virus PCR*	0/989	0/5	0/16

\*5 patients underwent PCR testing for *Influenza C*, human *Metapneumovirus* and *Parainfluenza* 1, 2, 3 and 4. All were negative.

**Table 3. Detailed epidemiology of microbiological documented bacterial infections in patients hospitalized with COVID-19.**

Bacterial co-infection*	N=74 (%)
Infections at COVID-19 diagnosis	30/74 (40.5)
Community-acquired pneumonia co-infections	21/30 (70)
<i>S. pneumoniae</i>	12/21 (57.1)
<i>S. aureus</i>	6/21 (28.6)
<i>H. influenzae</i>	2/21 (9.5)
<i>M. catarrhalis</i>	1/21 (4.8)
Lower respiratory co-infection in patients with bronchiectasis	2/30 (6.6)
<i>P. aeruginosa</i>	2/2 (100)
Concurrent urinary tract infection	7/30 (23.3)
<i>E. coli</i>	1/7 (14.2)
<i>K. pneumoniae</i>	1/7 (14.2)
<i>E. faecium</i>	1/7 (14.2)
<i>P. mirabilis</i>	1/7 (14.2)
<i>C. koseri</i>	1/7 (14.2)
<i>S. aureus</i>	1/7 (14.2)
Hospital-acquired superinfections complicating patients admitted for COVID-19	44/74 (59.5)
Ventilator-associated pneumonia	11/44 (25)
<i>S. aureus</i>	4/11 (36.4)
<i>P. aeruginosa</i>	3/11 (27.3)
<i>S. maltophilia</i>	2/11 (18.2)
<i>K. pneumoniae</i>	1/11 (9)
<i>S. marcescens</i>	1/11 (9)
Hospital-acquired pneumonia	4/44 (9)
<i>S. aureus</i>	1/4 (25)
<i>P. aeruginosa</i>	1/4 (25)
<i>S. maltophilia</i>	1/4 (25)
<i>K. pneumoniae</i>	1/4 (25)

<b>Bacteremia</b>	16/44 (36.3)
<b>Coagulase-negative staphylococci</b>	7/16 (43.7)
<i>P. aeruginosa</i>	3/16 (18.7)
<i>E. faecium</i>	3/16 (18.7)
<i>E. coli</i>	2/16 (12.5)
<i>S. anginosus</i>	1/16 (6.2)
<b>Urinary tract infection</b>	12/44 (27.3)
<i>E. coli</i>	4/12 (33.5)
<i>K. pneumoniae</i>	3/12 (25)
<i>E. faecalis</i>	2/12 (16.7)
<i>E. faecium</i>	1/12 (8.3)
<i>P. aeruginosa</i>	1/12 (8.3)
<i>S. marcescens</i>	1/12 (8.3)
<b>Polymicrobial intra-abdominal infection (<i>E. coli</i>, <i>E. faecium</i>, <i>E. faecalis</i>)</b>	1/44 (2.3)

\*Some patients had more than one bacterial infection.