

MICROBIOLOGICAL INDICATORS OF PATIENTS WITH CONFIRMED SARS-COV-2 INFECTION

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Abstract

The article presents a bacteriological analysis of patients admitted to the Bukhara Regional Infectious Diseases Hospital on March 16, 2020 to February 02, 2022 with a diagnosis of COVID-19 coronavirus infection and confirmed SARS-CoV-2 infection (a positive result of real time PCR, typical for SARS-CoV-2). The results are presented from stool samples taken from patients of Pr. Vulgaris, Pr. Mirobllis, Kl. phevmoniae, Enterobacter hafniae,, from sputum samples of St. pneumoniae, Can.viridans; St. epidermis, St. aureus were isolated from the blood sample. Most of the isolated microorganisms were sensitive to levofloxacin, amikacin, ciprofloxacin and cefaperazone sulbactam.

Keywords: Antibiotic resistance; COVID-19; pneumonia; SARS-CoV-2; sputum culture; blood culture.

INTRODUCTION

In December 2019, several cases of severe pneumonia of unknown origin emerged in Wuhan, China [1], which was later diagnosed as Coronavirus Disease 2019 (COVID-19), with its etiologic agent identified as SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2), belonging to the β genus of the Coronaviridae family [2, 3]. On March 11, 2020, the World Health Organization (WHO) declared this disease a pandemic [4]. The bacterial superinfection and mortality rate due to SARS-CoV-2 is significantly higher than that of any other widespread respiratory viral syndrome [5, 6]. As of now, more than 437 million confirmed cases of COVID-19 have been recorded worldwide, including nearly 6 million deaths (<https://www.who.int/>).

Superinfection by other microorganisms, especially bacteria and fungi, in SARS-CoV-2 patients plays a crucial role in the evolution of COVID-19, increasing the challenges of diagnosis, treatment, and prognosis [7, 8]. Bacterial superinfection in hospitalized COVID-19 patients is associated with disease progression and prognosis. This condition increases the need for intensive care unit (ICU) admission, antibiotic treatment, and mortality rates [9, 10].

Antimicrobial therapy plays an essential role in treating suspected or confirmed bacterial respiratory infections in patients diagnosed with coronavirus infection. Typically, such therapy is





empirical or aimed at treating nosocomial infections acquired during hospitalization for pneumonia. Patients may also suffer from secondary infections unrelated to the respiratory tract, such as urinary tract infections or bloodstream infections [11, 12].

It is well known that respiratory viral infections are often accompanied by severe bacterial and fungal infections [13, 14]. Many researchers have noted an increase in secondary bacterial infections caused by *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Haemophilus influenzae*, and *Aspergillus* sp. [15, 16]. However, data on the prevalence and severity of secondary bacterial infections in hospitalized COVID-19 patients remain relatively scarce.

One of the solutions that may justify prescribing antibacterial drugs in COVID-19 is the use of specific biomarkers of bacterial infection, such as procalcitonin [6, 17]. Procalcitonin has been shown to support the differentiation between bacterial and viral infections and facilitate the early discontinuation of antibiotics in confirmed bacterial infections without affecting patient mortality [18-22]. Reports suggest that procalcitonin may serve as a significant tool in reducing antimicrobial use in COVID-19 cases [23-26].

Objective of the Study The objective of this study is to determine the microbial landscape and antibiotic susceptibility of major pathogens isolated from patients infected with COVID-19.

Materials and Methods

Between March 16, 2020, and February 2, 2022, a total of 3,467 patients diagnosed with "Coronavirus Infection COVID-19" were hospitalized and treated. A total of 1,169 samples (sputum, stool, and blood) from these patients underwent bacteriological examinations.

Sputum samples were cultured on Sabouraud agar, Endo agar, neutral agar, blood agar, and mannitol salt agar. Stool samples were cultured on Salmonella-Shigella agar (USA), bismuth sulfite agar, blood agar, and mannitol salt agar. Blood samples for bacteriological examination were cultured using neutral agar, Endo agar, bismuth sulfite agar, blood agar, and mannitol salt agar.

All COVID-19 patients included in this study were diagnosed and treated in accordance with guidelines for diagnosing and managing pneumonia caused by the novel coronavirus infection. All patients had laboratory-confirmed SARS-CoV-2 infection (positive real-time RT-PCR for SARS-CoV-2). Complete blood count analyses included measurements of white blood cells (WBC), lymphocytes (LYM), mononuclear cells (MONO), and neutrophils (NEU). Blood biochemical parameters such as aspartate aminotransferase (AST), alanine aminotransferase (ALT), glucose (GLU), urea, creatinine, and C-reactive protein (CRP) were measured using a MINDRAY BS-30 (China) automatic biochemical analyzer.

Results and Discussion

Bacteriological examinations yielded positive results in 1,169 samples collected from 3,467 hospitalized COVID-19 patients. A total of 928 stool samples were analyzed, and 556 (59.9%) tested positive for bacterial growth. The distribution of isolated microorganisms showed that *Proteus vulgaris* was found in 38.3% of cases, *Proteus mirabilis* in 32.6%, *Klebsiella pneumoniae* in 2.5%, and *Enterobacter hafniae* in 26.8% of cases.





A total of 3,476 sputum samples were analyzed for bacteriological culture, and 264 (7.6%) yielded positive results. The distribution of isolated microorganisms was as follows: *Staphylococcus aureus* (61.0%), *Streptococcus pneumoniae* (5.3%), and *Candida viridans* (33.7%).

Blood samples from 2,299 patients (66.1%) were tested for bacterial growth, and 15.1% were positive. Analysis showed that 71.1% of cases involved *Staphylococcus epidermidis* and 28.9% involved *Staphylococcus aureus*.

A total of 613 isolated pathogens were tested for antibiotic susceptibility. The best antibiotic sensitivity rates were observed for levofloxacin (35.4%), amikacin (28.4%), ciprofloxacin (19.9%), cefoperazone-sulbactam (9.9%), cefepime (2.4%), and ceftriaxone (1.9%). Sensitivity to cephazolin, ceftazidime, gentamicin, and chloramphenicol was found to be low. No sensitivity was observed to semi-synthetic penicillins (benzylpenicillin, ampicillin).

Thus, among the biological isolates obtained for rational antibacterial treatment, microorganisms were identified in only 35.5% of cases. Most of these were highly sensitive to levofloxacin, amikacin, and ciprofloxacin.

Our findings share some similarities with previously published data [27-29]. However, they differ from similar studies conducted in China, where pneumococci and *Haemophilus influenzae* were the predominant pathogens [30-34].

According to Liu HH et al., among 253 sputum samples collected within 24 hours after intubation from 165 patients, 73 cases (45%) did not show acute bacterial or fungal infections. Potential pathogens were isolated in 72 out of 111 cases (64.9%) after ≥ 1 week of intubation, with 70.8% indicating late pneumonia and 29.2% indicating colonization. In 12 cases (10.8%), worsening resistance to antimicrobial agents was observed, primarily involving *Pseudomonas*, *Enterobacter*, or *Staphylococcus aureus* [35-39]. In our study, bacteriological sputum cultures yielded positive results in 264 cases (7.6%), with *Staphylococcus aureus* (61.0%), *Streptococcus pneumoniae* (5.3%), and *Candida viridans* (33.7%) being the most frequently isolated microorganisms.

Conclusion

Thus, among the biological isolates obtained for rational antibacterial treatment, microorganisms were identified in only 35.5% of cases. Most of these were highly sensitive to levofloxacin, amikacin, and ciprofloxacin.

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