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Microbiological Indicators of Patients Infected with Sars-Cov-2

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Abstract

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

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

Relevance of the topic

In December 2019, several cases of severe pneumonia of unknown origin occurred in Wuhan, China [1], later diagnosed as coronavirus 2019 (COVID-19), whose etiological agent was SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2). It belongs to the β family of the Coronaviridae family [2, 3]. On March 11, 2020, the World Health Organization (WHO) declared the disease a pandemic. Bacterial superinfection and mortality from SARS-CoV-2 are significantly higher than from any other common respiratory viral syndrome [5, 6]. As of March 14, 2022, 456,797,217 cases of COVID-19 have been confirmed worldwide, including 6,043,094 deaths. (https://www.who.int/). Superinfection with SARS-CoV-2 by other microorganisms, especially bacteria and fungi, is a critical factor in the development of COVID-19, complicating diagnosis, treatment, and prognosis [7,8]. Bacterial superinfection in inpatients with COVID-19 is associated with disease progression and prognosis. This condition increases hospitalization, antibiotic treatment, and mortality in intensive care units [9,11,12].

In patients with confirmed coronavirus infection, antimicrobial therapy plays an important role in the treatment of suspected or confirmed bacterial respiratory infection. As a rule, this type of therapy is empirical in nature or is intended for the treatment of nosocomial infections acquired during hospitalization in hospitalized patients with pneumonia. Patients may also suffer from secondary infections not related to the respiratory tract, such as urinary tract or bloodstream infections [13,14,15].

It is known that the course of respiratory viral infections is often associated with the addition of severe bacterial and fungal infections [16,17,18]. Many researchers note an increase in the development of secondary bacterial infections caused by Streptococcus pneumonia, Staphylococcus aureus, Haemophilus influenza and Aspergillus sp. However, such data on the prevalence and severity of secondary bacterial infections in hospitalized patients with COVID-19 are currently relatively rare.

One of the possible solutions to justify the prescription of antibacterial drugs for COVID-19 is the use of procalcitonin, a specific biomarker of bacterial infection [6,21]. It has been shown that procalcitonin maintains the distinction between bacterial and viral infection and promotes early antibiotic withdrawal without affecting the mortality of patients with confirmed bacterial infection [22,23]. The use of COVID-19 procalcitonin has been reported and may be an important tool to help reduce the use of antimicrobials [24]. The aim of the study was to determine the microbial landscape and antibiotic susceptibility of the main pathogens isolated from patients with COVID-19.

Materials and methods

For the period from March 16, 2020 to February 2, 2022, 3,467 patients were diagnosed with COVID-19 coronavirus infection. Bacteriological studies were performed on 1169 samples (sputum, feces, blood) taken from them.

Sputum specimens include Saburound dextrose agar, Endo agar, blood agar, cultures with mannitol on sari salt, Salmonella-shigellosis agar (SS agar), bismuth sulfite agar, Kligler's medium (Kligler's iron). agar), nutrient agar (Nutrient Agar). For bacteriological examination of a blood sample, glucose-Sabouraund Dextrose Agar, a blood-agar medium, was used.

All patients with COVID-19 included in this study were diagnosed in accordance with the recommendations for the diagnosis and treatment of pneumonia caused by a new coronavirus infection. All patients had laboratory-confirmed SARS-CoV-2 infection (real-time RT-PCR positive, typical of SARS-CoV-2). Complete blood elements were detected in blood samples by determining the number of leukocytes (WBC), lymphocytes (LYM), mononuclear cells (MONO), neutrophils (NEU). Blood biochemical parameters: aspartate aminotransferase (AST), alanine aminotransferase (ALT), glucose (GLU), urea, creatinine, C-reactive protein (CRO) were determined using an automatic biochemical analyzer MINDRAY BS-30 (China).

Results and discussion

As of March 16, 2020, bacteriological studies in 1169 samples taken from 3467 patients hospitalized with COVID-19 coronavirus infection showed positive results. Bacteriological culture of feces was obtained in 928 patients, while a positive result was obtained in 556 (59.9%) patients. Sectional analysis of isolated microorganisms showed that 38.3% Pr. Vulgaris, 32.6% ida Pr. Mirobllis, Kl.phevmoniae were found in 2.3%, Enterobacter hafniae in 26.8% (Fig. 1).

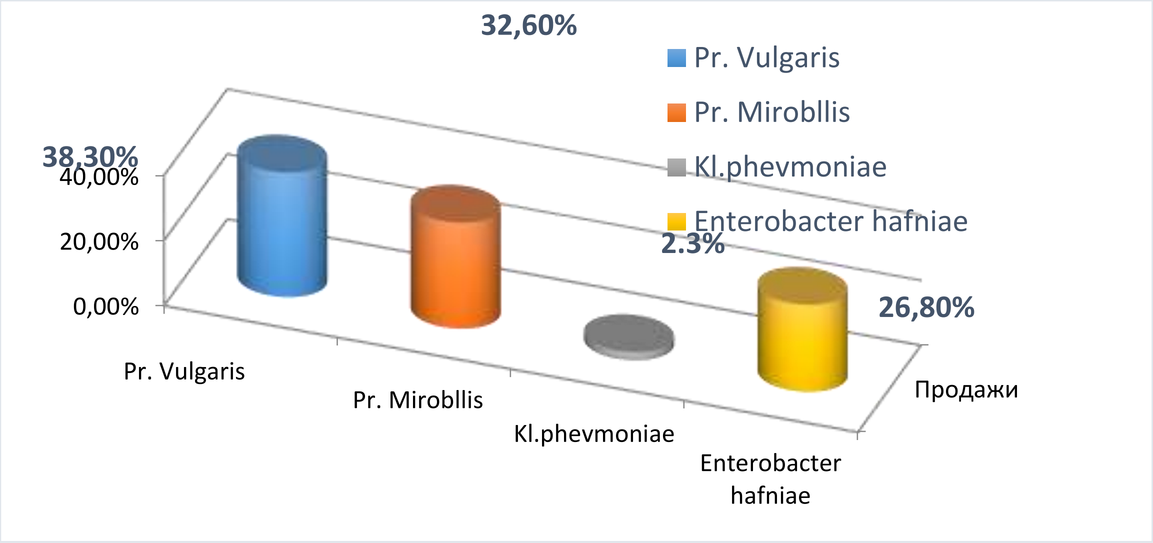

Figure 1. Data of bacteriological culture of stool samples

Sputum of 3476 patients was obtained for bacteriological culture, a positive result was obtained in 264 (7.6%). When studying microorganism culture sections, 61.0% were infected with S. aureus, St. John's wort. Pneumoniae was found in 5.3% and Can. viridans in 33.7% (Fig. 2). Bacteriological examination of blood was performed in 2299 (66.1%) controlled patients. Microorganisms multiplied in 15.1% of them. The analysis showed that 71.1% of them were S. epidermis and 28.9% S.aureus.

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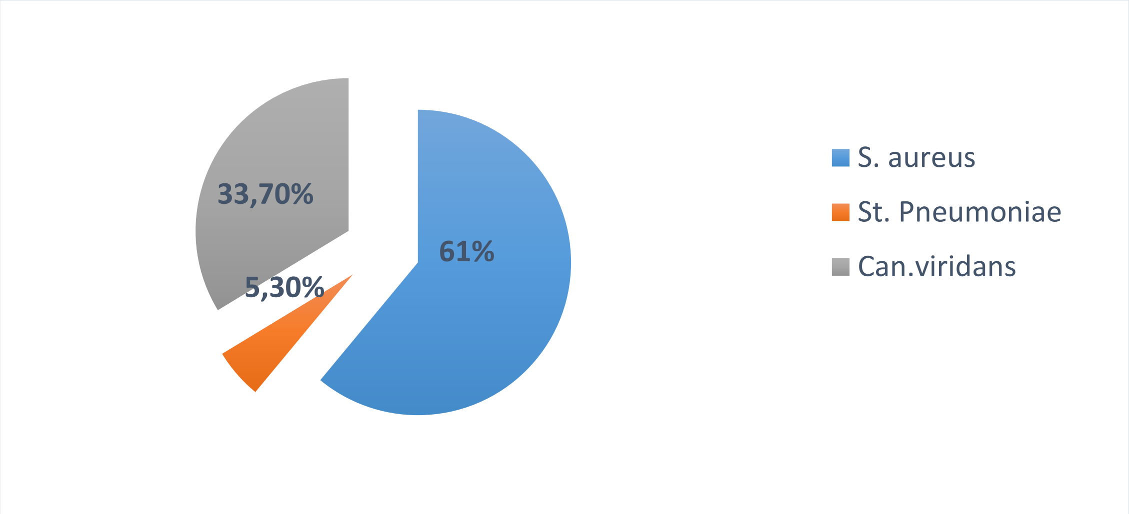

Figure 2. Culture data from sputum samples

Of the pathogens identified above, 613 were tested for antibiotic susceptibility. Several antibiotic disks were used to determine the antibiotic susceptibility of the above pathogens, and the number and percentage of the most susceptible to antibiotics during the study were as follows. 217 (35.4%) isolated microorganisms were susceptible to levofloxacin, 174 (28.4%) to amikacin, 122 (19.9%) to ciprofloxacin, 61 (9.9%) to cefaperazone sulbactam, 14 (2.4%) %)%) to cefepime and 12 (2.4%) %) to cefepime. 12 (1.9%) to ceftriaxone. Low sensitivity to cefazidin, cefazidime, gentamicin, chloramphenicol was noted. Sensitivity to semi-synthetic penicillins (benzylpenicillin, ampicillin) has not been identified.

Thus, only 35.5% of biological extracts obtained for the purpose of basic treatment with antibacterial drugs were microorganisms. Most of them were hypersensitive to levofloxacin, amikacin, ciprofloxacin (Fig. 3). The microorganisms found in our study were in some respects similar to other published data [25], differing from similar data from studies in China in that pneumococci and Haemophilus influenza were the main pathogens [26].

Liu H. H. et al. Based on the data obtained, the results of 253 sputum samples did not reveal an acute bacterial or fungal infection in 73 (45%) of 165 people, who were usually collected within 24 hours after intubation. The number of potential pathogens increased 1 week or less after intubation in 72 (64.9%) of 111 cases, indicating late pneumonia in 70.8% and colonization in 29.2%. In 12 of these evening samples (10.8% of the total), antimicrobial resistance, mainly Pseudomonas, Enterobacter or Staphylococcus aureus, worsened after intubation [27]. In our study, bacteriological cultural analysis of sputum samples from patients showed a positive result in 264 (7.6%), of which S. aureus, St. John's wort was detected in 61.0%. Pneumoniae was found in 5.3% and Can. viridans at 33.7%. Most of the isolated microorganisms were sensitive to levofloxacin, amikacin, ciprofloxacin and cefoperazone sulbactam.

Conclusion:

1. Most hospitalized patients have co- or COVID-19. advanced forms of superinfection.
2. All patients diagnosed with can. viridans received one or another antibacterial drug on an outpatient basis.
3. Isolation of microorganisms from samples taken from a patient allows substantiating the forms of the disease (pneumonia, gastrointestinal, septic).
4. Most of the isolated microorganisms were sensitive to antibacterial drugs such as levofloxacin, amikacin, ciprofloxacin, cefaperazone, sulbactam.

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