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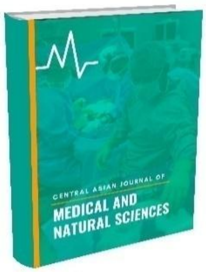

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Microbiological Indicators of Patients with Confirmed Sars-Cov-2 - Infection

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Annotation: 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 COVID-19 coronavirus infection and confirmed SARS-CoV-2 infection (positive real-time RT-PCR, typical for SARS-CoV-2) Results are shown from fecal samples taken from patients Pr. Vulgaris, Pr. Mirobllis, Kl.phevmoniae, Enterobacter hafniae, from sputum samples of St. Pneumoniae, Can. viridans; 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 etiologic agent was SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2). It belongs to the family β of the family Coronaviridae [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 kind of therapy is empirical in nature or 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]. Procalcitonin has been shown to maintain a distinction between bacterial and viral infection and support early discontinuation of antibiotics without affecting patient mortality in 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

3467 patients were diagnosed with COVID-19 coronavirus infection from March 16, 2020 to February 2, 2022. Bacteriological studies were performed on 1169 samples (sputum, feces, blood) taken from them.

Sputum specimens include Sabouraund Dextrose Agar, Endo Agar, Blood Agar, Sari Salt Mannitol Cultures, Salmonella-Shigellez Agar (SS Agar), Bismuth Sulphite Agar, Kligler Medium (Kligler Iron). Agar), nutrient agar (Nutrient Agar). For bacteriological examination of a blood sample, glucose-Sabouraund-Agar (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, and C-reactive protein (CRO) were determined using an automatic biochemical analyzer MINDRAY BS-30 (China).

Results and their 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% of Pr. Vulgaris, 32.6% ida Pr. Mirobllis, Kl.phevmoniae were found in 2.3%, Enterobacter hafniae in 26.8% (Fig. 1).

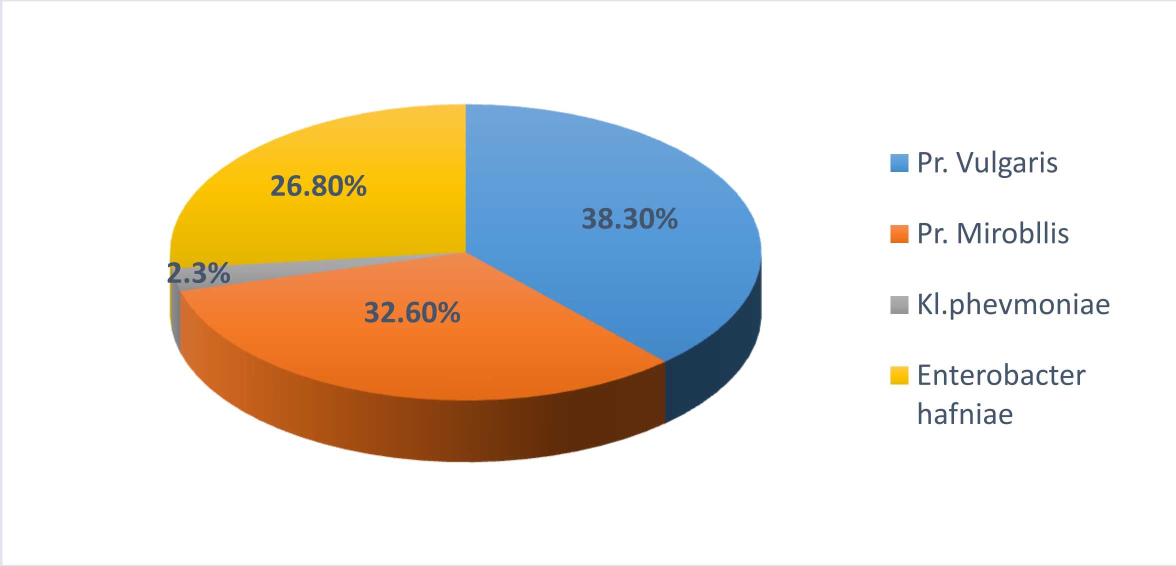

Figure 1. Data of bacteriological inoculation of stool samples

Sputum of 3476 patients was obtained for bacteriological culture, a positive result was obtained in 264 (7.6%). When studying sections of cultures of microorganisms, 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). In 2299 (66.1%) controlled patients, a bacteriological blood test was performed. Microorganisms multiplied in 15.1% of them. The analysis showed that 71.1% of them were S. epidermis and 28.9% S. aureus.

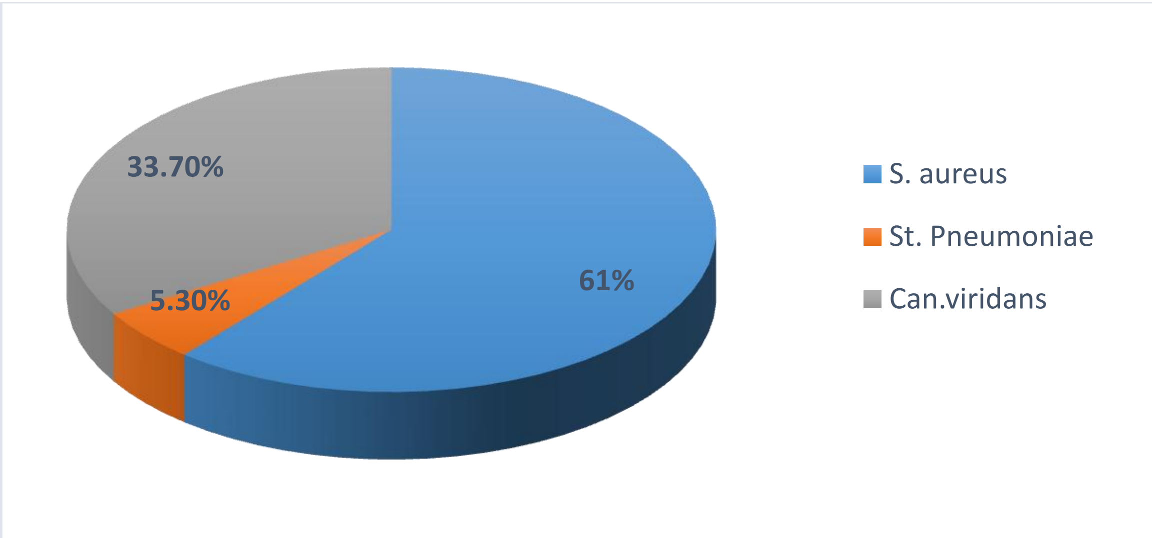

Figure 2. Data of bacteriological inoculation of sputum samples

Of the pathogens identified above, 613 were tested for antibiotic susceptibility. Several antibiotic discs were used to determine the antibiotic susceptibility of the pathogens listed above, 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 the 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).

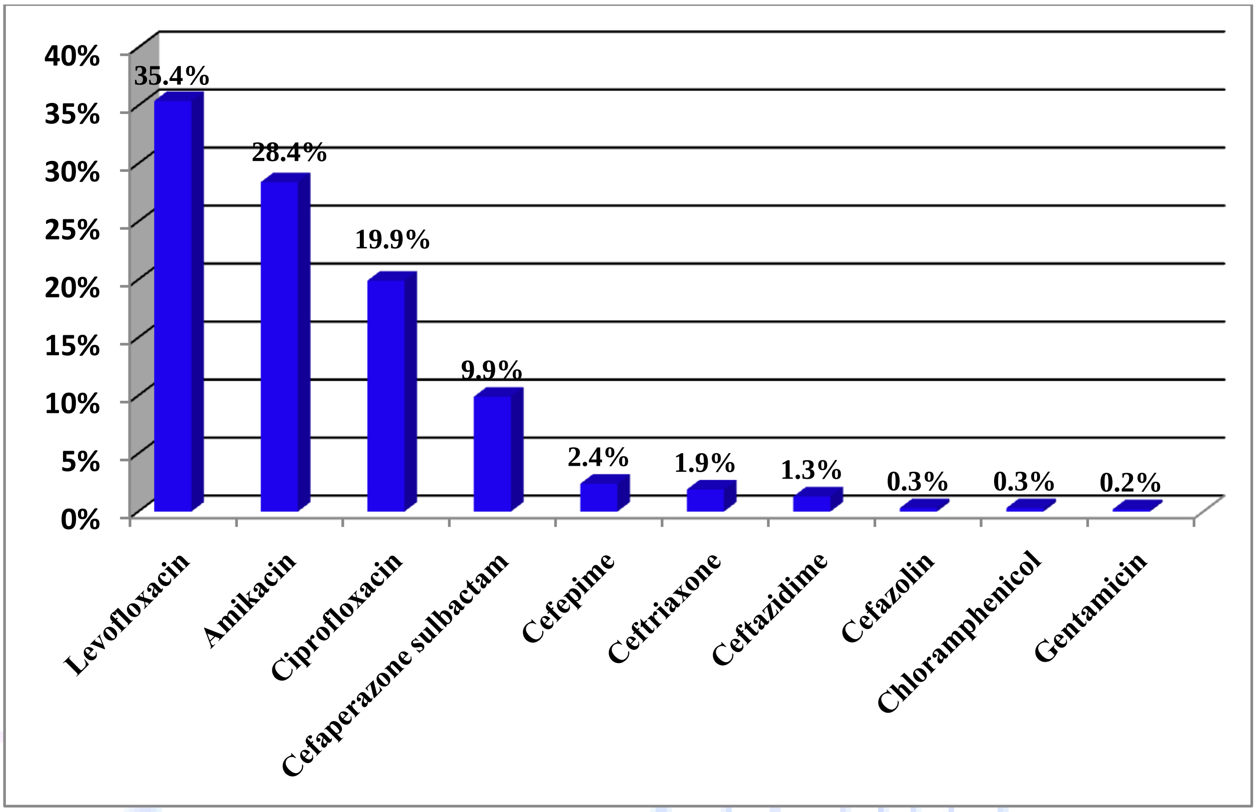

Figure 3. The sensitivity of microorganisms to antibacterial drugs

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. according to the data, the results of 253 sputum samples did not show acute bacterial or fungal infection in 73 (45%) of 165 people, which 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 specimens (10.8% of the total), antimicrobial resistance, mainly Pseudomonas, Enterobacter or Staphylococcus aureus, worsened after intubation [27]. In our study, bacteriological culture analysis of sputum samples from patients showed a positive result in 264 (7.6%), of which 61.0% were found to have S. aureus, St. John's wort. Pneumoniae was found in 5.3% and Can. viridans in 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. The isolation of microorganisms from samples taken from the patient substantiates 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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