Lower Respiratory Tract Microbiocenosis in Patients with Covid -19 Infection

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Abstract Microbiocoenosis refers to the community of microorganisms, including bacteria, viruses, fungi and protozoa, that live in the host . Microbiocenosis plays a major role in the formation of lung immunity, and a healthy lung contains a huge amount of microflora. Microbes enhance innate and adaptive immunity (locally specific in the lungs and systemically), release factors that contribute to respiratory function and prevent pathogens from invading the lungs.

Keywords: Microbiocenosis, new coronavirus SARS-CoV-2, respiratory tract.

Environmental change, warming climate, increasing population density high migration activity and other factors are triggering the emergence and spread of new infections around the world.

The emergence in December 2019 of diseases caused by a new coronavirus ("coronavirus disease 2019") has already gone down in history as an international emergency. It is known that the most common clinical manifestation of the new infection is pneumonia and, in a large proportion of patients, respiratory distress syndrome [1].

The causative agent, a new coronavirus SARS-CoV-2, which has not been identified before, was identified by Chinese researchers on January 7, 2020[2].

25% of patients develop severe pneumonia, which often progresses to respiratory distress syndrome in adults, most commonly in patients over 50 years of age, with comorbidities such as diabetes, cardiovascular disease, chronic hepatitis, etc. [3,4].

Many authors have noted that the upper respiratory tract microflora plays an important role in the etiology of complications of influenza and acute respiratory diseases (ARIs), which are at the top of all human diseases in terms of prevalence [5].

These microorganisms in cases of intensive colonization of mucous membranes and/or when human body resistance decreases, including under the influence of acute viral infection, can cause the development of bacterial infection of the respiratory tract [8].

Modern classifications of pneumonias provide for mandatory establishment of etiology, as etiological diagnosis largely determines the course of the disease and the most rational type of its treatment [9, 10].

To date, very few studies have investigated respiratory tract and lung microbiocenosis in patients with COVID-19. Patients with both COVID-19 and community-acquired pneumonia had many pathogenic and commensal bacteria, indicating a degree of microbial dysbiosis in both disease states .

In general, information on the composition of the respiratory tract and lung microbiome in patients with COVID-19 is poorly understood. Further research is needed to better understand the composition and role of the lung microbiome in the severity of SARS-CoV-2 infections. [11,12].

Lung microbiocenosis plays a crucial role in critically ill patients, as a recent study showed that lung microflora predict clinical outcome and death in these patients [13].

It follows that an increased bacterial load in the lungs and enrichment of the lungs with intestinal bacteria are predictors of adverse outcomes in ARDS. Thus, in COVID-19 ARDS, the microbiocenosis may play an important role in determining the severity of the disease and the outcomes of ARDS[6,7].

The aim of this study was to characterise the microbiocenosis of the respiratory tract in patients with COVID-19 infection during hospital admission for the year 2020.

Material and methods.

Microbiological examination of sputum smear samples was used to study microbial paisage. Data processing was carried out by qualitative and quantitative method, that provides isolation of pure cultures of microorganisms and allows to judge more precisely about etiological significance of isolated microorganisms. Microbiological examination of sputum smears from 60 patients over 30 years old diagnosed with Covid 19, PCR-positive, in whom community-acquired pneumonia was confirmed clinically and radiographically was carried out. The material was obtained on the first day of admission from sputum by deep coughing. The samples were cytologically checked for leucocyte and epithelial cell counts. Samples containing only epithelial cells were excluded. For microbiological examination a serial dilution of sputum was prepared to accurately count the number of microorganisms. Microorganisms were isolated using blood and egg yolk-salt agar, Endo and Saburo media. The grown microorganisms were identified by tinctorial and cultural and biochemical properties. The number of microorganisms was expressed as the decimal logarithm of CFU/ml.

Results and discussion.

Respiratory viral infection is a risk factor for bacterial pneumonia. Microbial landscape of causative agents of pneumonia in Covid -19 subjects with background pneumonias is led by representatives of Candida genus bacteria >1x103 CFU/ml - in 51 % of patients. The next positions are divided between bacteria of the genus Streptococcus B >1x109 CFU/ml in 42% of patients. S.aureus bacteria >1x109 CFU/ml were detected in 28% of patients. In 12% of patients S. Pneumoniae >1x109 CFU/ml, Klebsiella pneumoniae >1x102 CFU/ml in 3.1% of patients, ps.auereogenosa >1x102 CFU/ml in 1.1%. It was found that 100% of the sputum smear samples contained two microorganisms. Thus, two microbacilli were detected in 50% of smear and sputum samples. All 50% of the micro-organisms isolated were associated with Candida yeast fungi. Thus, in the vast majority of cases pneumonia was caused by representatives of Streptococcus genus B, and S. S.aureus microassociated with yeast fungi of the genus Candida. Streptococci secrete enzymes and toxins that account for their ability to cause inflammation. The enzymes ensure that the streptococcus fixates on the epithelium, enters the cell, enters the systemic bloodstream and spreads throughout the body. The main pathogenic effect of haemolytic streptococci is the destruction of red blood cells. The bacteria release toxins that affect virtually all organs. Haemolytic streptococcus is especially

dangerous for the elderly, immunodeficient patients, those who have had acute respiratory viral infections, patients with a history of chronic pathologies. All streptococci with haemolytic activity are divided into two large groups according to the way the red blood cells are destroyed - with alpha- and beta-haemolysis. Alpha-haemolytic is the formation of a greenish zone around the colonies on media with blood, due to partial haemolysis. Pneumococcus belongs to this group and causes pneumonia. Haemolytic streptococcus occurs in a healthy person in low numbers. Under the influence of negative endogenous and exogenous factors that reduce immunity and general resistance, the number of bacteria increases dramatically and their pathogenic properties increase. Inflammation develops in the macroorganism, the localization of which is determined by the location of the lesion. [14]. At the same time, lesions of the interstitial lung tissue by viruses are different from bacterial inflammation and require different therapy compared to bacterial inflammation.

Conclusions. Candida bacteria ranked first, with 51%, followed by Streptococcus bacteria B (42%) and S.aureus bacteria >1x109 CFU/ml in 28% of cases. In 12% of cases S. Pneumoniae >1x109 CFU/ml, Klebsiella pneumoniae >1x102 CFU/ml in 3.1% of the patients, ps.auereogenosa >1x102 CFU/ml in 1.1% of the patients. The significant role of yeast-like fungi of the genus Candida in the development of the disease with the isolated representatives of microorganisms of the genus Streptococcus B and S. aureus has been shown.

Thus, in the course of the carried out researches it has been shown, that the tendency of increase of morbidity of community-acquired pneumonia is observed, that can be connected with changes in etiological structure of causative agents, as well as with formation of pathosymbiosis of some gram-positive microorganisms, that can influence on development and outcome of the disease.

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