

The state of microflora respiratory tract in patients with COVID -19 infection against pneumonium background

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Abstract: Obviously, the role of lung microbiocenosis in the pathology of COVID-19 can have a strong influence on susceptibility to the SARS-CoV-2 virus and on the severity of the disease in general, moreover, the state of lung microbiocenosis plays a leading role in the formation of an immune response against a viral attack, and can influence the outcome of COVID-19 infection and the development of ARDS. In the future, studies of the microbiocenosis of the respiratory tract and lungs in patients with COVID-19 infection (complicated and uncomplicated forms) and comparing them with the severity of this disease will be in demand.

Keywords: SARS-CoV-2, microbiocenosis of the respiratory tract of the respiratory tract, pneumonia.

Environmental change, climate warming, increase in population density High migration activity of the population and other factors provoke the emergence and dissemination of new infections around the world.

The appearance of diseases in December 2019 caused by the new coronavirus ("Coronavirus Disease 2019"), has already entered the history as an emergency situation of international importance. It is known that the most common clinical manifestation of a new infection is pneumonia, as well as a significant part of patients - respiratory distress syndrome [1].

The causative agent of infection - the new Coronavirus SARS-COV-2, which was not previously detected, was identified by Chinese researchers on January 7, 2020 [2]

It is known that the most common clinical manifestation of a new infection is pneumonia, as well as a significant part of patients - respiratory distress syndrome. [one]. In 25% of patients, severe pneumonium develops, which often progresses to respiratory distress syndrome in adults, most often in patients over 50 years old, with the presence of concomitant diseases, such as diabetes, diseases of the cardiovascular system, chronic hepatitis, etc. [3,4].

Many authors note that the microflora of the upper respiratory tract plays an important role in the etiology of complications for influenza and sharp respiratory diseases (ORZ), which are in the first place among all human diseases [5].

Microbiocenosis refers to the microorganisms community, including bacteria, viruses, mushrooms and the simplest, which live in the host body. Microbiocenosis plays a major role in the formation of pulmonary immunity, and healthy lung contains a huge amount of microflora. Microbes increase congenital and adaptive immunity (locally specific in lungs and systemic), the factors that contribute to the respiratory function are released and prevent intrusion into light pathogens [6, 7].

These microorganisms in cases of intense colonization of mucous membranes and / or with a decrease in the resistance of the human body, including under the influence of an acute viral infection, are able to cause the development of bacterial infection of the respiratory tract [8].

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

To date, only very few studies have studied the microbiocenosis of the respiratory tract and the lungs in patients with COVID-19. In patients, both with COVID-19, and with community-hospital pneumonia had many pathogenic and commensary bacteria, which indicated the degree of microbial dysbacteriosis in both painful states. In general, information about the composition of microbiocenosis of the respiratory tract and the lungs in patients with COVID-19 is not sufficiently studied. In order to more accurately find out the composition and role of microbiocenosis of the lungs in the seriousness of SARS-COV-2 infections, further research is needed. [11,12].

The microbiocenosis of the lungs plays a decisive role in heavy patients, since a recent study showed that the lung microflora predicts a clinical outcome and death in these patients [13]. It follows from this that the increased bacterial load in the lungs and enrichment of the lungs in intestinal bacteria is predictors of the adverse effects of the ORDS. Thus, with COVID-19 ORDs, microbiocenosis can play an important role in determining the severity of the disease and ORDS outcomes.

The purpose of the study is to study the composition of microflora of the respiratory tract in patients with COVID -19 infection during the hospitalization period for 2020 .

Material and methods.

When studying microbial peisage, a microbiological study of samples of sputum smears was used. Data processing was performed using a qualitative and quantitative method, which ensures the release of pure cultures of microorganisms and makes it possible to judge more accurately on the etiological significance of isolated microorganisms. A microbiological study of sputum smears of 60 patients over the age

of 30, with a diagnosis of a coronavirus infection (COVID - 19, PCR-positive), in which community-acquired pneumonia has been confirmed clinically and radiologically. The material was obtained on the first day of the flow of deep flipping method. Cytological control of the obtained samples was carried out, taking into account the number of leukocytes and epithelocytes. Samples containing exclusively epithelial cells are excluded from the study. When conducting microbiological studies for accurate accounting of the number of microorganisms, mass breeding of sputum was prepared. For the selection of microorganisms, blood and yolk-salt agar, Endo and Saburo medium were used. The identification of grown by microorganisms in tinnitorial and cultural and biochemical properties was identified.

Results and its discussion.

The risk factor for the development of bacterial pneumonia is a respiratory viral infection. Microbial scenery of pneumonia pathogens in people with COVID -19 against the background of pneumonia The leading position is occupied by representatives of the Bacteria of the genus *Candida* - in 51% of patients. The following positions are divided between the bacteria of the genus *Streptococcus B* in 22% of patients. In a third of cases, *S. pneumoniae* 19 % of patients, *Klebsiella pneumoniae* in 3.1% of patients, *ps. aureogenosa* 1.1%. It has been established that 100% samples of sputum smears contained two microorganism. So, two microbassoassocyant were found in 50% sort of smears and sputum. All 50% dedicated microorganisms were microbassed with *Candida's* shod fungi. Thus, in the overwhelming majority of cases, pneumonia was caused by representatives of the genus *Streptococcus B*, and *S. pneumoniae* microbassoiced with shoal fungi genus *Candida*. *Streptococcus* are isolated enzymes and toxins that determine their ability to cause inflammation. Enzymes ensure the fixation of streptococcus on the epithelium, its introduction into the cell, output to systemic blood flow and distribution throughout the body. The main pathogenic effect of hemolytic streptococcus - destruction of red blood cells. Bacteria distinguish toxins, negatively affecting almost all organs. Hemolytic streptococcus is particularly dangerous for elderly, patients with immunodeficiency, persons who have suffered sharp respiratory viral infections, patients with chronic pathologies in anamnesis. All streptococci with hemolytic activity are divided into two large groups of the method of destruction of red blood cells - with alpha and beta hemolysis. Alpha hemolytic - education on media with blood greenish zone around the colonies due to partial hemolysis. *Pneumococcus* refers to this group and causes inflammation of the lungs. Hemolytic streptococcus lives in a healthy person in minor quantities. Under the influence of negative endogenous and exogenous factors that reduce immunity and overall resistance, the number of bacteria increases sharply, and their pathogenic properties are enhanced. In macroorganism, inflammation develops, the localization of which is determined by the location of the lesion. [fourteen]. At the same time, the

defeat of the interstitial pulmonary tissue with viruses differs from bacterial inflammation and compared to bacterial inflammation requires the appointment of other therapy.

Conclusions. The first positions in the frequency of the selection occupied the bacteria of the genus *Candida* - 51%, the following positions are divided between the bacteria of the *Streptococcus B* (22%), *S. pneumoniae* - 19 %. *Klebsiella Pneumoniae* - accounted for 3.1%, and *ps.aueregonosa* - 1.1%. A significant role is shown in the development of the disease of the microbasscomciation of yeast-like fungi of the genus *Candida* with the dedicated representatives of the microorganisms of the *Streptococcus B* -(22%), *S. pneumoniae* - 19 %.

Thus, during the studies carried out, it was shown that there is a tendency to increase the incidence of non-hospital pneumonia, which can be associated with changes in the etiological structure of causative agents of the disease, as well as the formation of pathosymbiosis of a number of gram-positive microorganisms, which may affect the development and outcome of the disease.

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