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Clinical and microbiological features of pathology of the nose and paranasal sinuses in patients with community-acquired pneumonia

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Abstract: This article presents the results of a comprehensive otolaryngological and microbiological study of diseases of the nose and paranasal sinuses in patients with community-acquired pneumonia. These diseases are closely interconnected, since the upper and lower respiratory tract are a single whole, have structures and functions and mechanisms for the development of pathological conditions. The etiopathogenesis of bacterial inflammatory diseases of the upper and lower respiratory tract is based on the disruption of the integrity of epithelial cells under the influence of respiratory viruses. Under the influence of the general toxic effect of the virus, phagocytosis is inhibited, immunological protection is disrupted, resulting in favorable conditions for microbial colonization in the nasopharynx and further spread of infections to the paranasal sinuses and lower respiratory tract. As a result of the clinical and microbiological study, it was revealed that inflammatory diseases of the nose and paranasal sinuses such as acute and chronic rhinosinusitis, allergic and vasomotor rhinitis, and deviated nasal septum were often encountered in community-acquired pneumonia. To determine the nature of the microbial landscape of the upper and lower respiratory tract, a comparative microbiological analysis of the nose and sputum was carried out. The analyzes showed that no significant difference in pathogenic microflora was detected between the upper and lower respiratory tract. The main pathogen in both diseases was Streptococcus pneumoniae. The correspondence of the pathogenic microflora of the nasal cavity and lower respiratory tract when detecting rhinosinusitis in patients with community-acquired pneumonia confirms the pathogenetic relationship of inflammatory processes in these organs, as well as the need for parallel diagnostics, treatment, and prevention.

Keywords: Upper and lower respiratory tract, rhinosinusitis, community-acquired pneumonia, microbiological analysis, Streptococcus pneumoniae.

Introduction: The results of medical statistics convincingly indicate an increase in the number of diseases of the nose, paranasal sinuses (PNS) [1,2] and bronchopulmonary pathology [3]. Close anatomical and physiological connections between the upper and lower respiratory tract are the reason that the increase in the number of rhinosinusitis keeps pace with the increase in the number of pulmonary diseases [4] and, in particular, community-acquired pneumonia (CAP). The incidence of pneumonia in Europe and North America is 5-10 cases per 1,000 population. Mortality from severe pneumonia reaches 10% and continues to grow [3; 5]. Most often, pneumonia occurs in children, the elderly and in chronic diseases of the respiratory system. Acute respiratory viral infections (ARVI) are undoubtedly the main risk factor for community-acquired pneumonia, acute rhinosinusitis (ARS) and chronic rhinosinusitis (CRS). They develop at any stage of the disease if bacterial flora (streptococci, staphylococci, etc.) joins in. It is known that some viruses (influenza, parainfluenza, adenovirus, respiratory syncytial virus, coronavirus, etc.) simultaneously affect the epithelial cells of the upper and lower respiratory tract [13]. The etiology of community-acquired pneumonia is directly related to the opportunistic microflora colonizing the upper respiratory tract. Of the numerous microorganisms, only a few with increased virulence are capable of causing an inflammatory reaction when they enter the lower respiratory tract. Pneumococcus should be considered one of these pathogens. Since S. pneumoniae has more than 90 serotypes with different antigenic properties, this microorganism can be present in the nasopharynx for years and can cause the development of CAP, ARS and otitis media at any time [3,9]. For some microorganisms, the development of bronchopulmonary inflammation is not typical [3]. Their isolation from sputum most likely indicates contamination of the material with the flora of the upper respiratory tract, and not the etiologic significance of these microbes. Such microorganisms include Streptococcus viridans, Staphylococcus epidermidis, Enterococcus spp., Neisseria spp., Candida spp.

It is believed that with almost any ARVI, the paranasal sinuses are involved in the process to one degree or another [10,12]. Acute rhinosinusitis is caused by viruses in 95% of cases; a bacterial process develops 5-7 days after the onset of ARVI [6,7]. Under the influence of the virus on the ciliated epithelium of the nasal cavity and paranasal sinuses, the epithelial cells lose cilia, the epithelium becomes loose, and mucosal edema develops. As a result of these processes, as well as the active release of proinflammatory mediators, an inflammatory reaction develops. The consequence of this is a violation of sinus aeration, inactivation of mucociliary clearance, and accumulation of serous exudate in the lumen of the sinuses. A decrease in the rate of mucociliary transport allows for an extension of the contact time of pathogenic bacteria with the mucous membrane and promotes bacterial infection [8,12,13].

METHODS

A total of 80 patients with community-acquired pneumonia who were hospitalized in the pulmonology department of the multidisciplinary clinic of the Tashkent Medical Academy were examined. Among the examined were 32 men and 48 women aged 18 to 65 years (the average age in the group was 45.6 ± 8.75 years). All patients had their complaints and history of the disease studied in detail, and their general condition was examined.

The research methods used included endoscopic examination of the ENT organs, with all formations in the nasal cavity being carefully examined. To determine the prevalence of the inflammatory process, all patients underwent 3D radiography and computed tomography of the ENT. Particular attention was paid to changes in the ENT organs and, if necessary, consultation with other specialists was carried out.

The microbiological characteristics of the upper and lower respiratory tract in patients with community-acquired pneumonia were studied using bacteriological methods. Sterile applicators were inserted into the middle nasal passage and smears were taken to determine the pathogenic microflora of the nose and the UR. Sputum was collected with a spatula in a sterile container. Analysis of pathological discharge from the middle nasal passage and sputum was carried out in the bacteriological laboratory of the multidisciplinary clinic of the Tashkent Medical Academy. Bacteriological culture was performed on enriched selective nutrient media from the company "bio Merieux" (France).

DISCUSSION OF THE RESULTS

3D radiography and computed tomography of the paranasal sinuses were performed in all 80 patients. Radiological changes in the paranasal sinuses were recorded with a thickening of the mucous membrane of more than 6 mm. Radiological changes were detected in 25 (31.25%) patients. Three patients showed a total decrease in pneumatization of all paranasal sinuses: two had right-sided hemisinusitis, 11 had right-sided maxillary ethmoiditis, and 15 had left-sided maxillary ethmoiditis.

As a result of the study of smears taken from the nasal cavity, microflora was obtained from the 46th (100%) patient. A total of 71 microorganisms were identified. Mixed flora was obtained from 22 (47.8%) of 46 patients, the maximum number of pathogens in the association was 3. Gram-positive facultative anaerobes were identified in 46 (64.7%) strains from among bacteria, the majority were microorganisms of the genus Streptococcus and Staphylococcus. 17 (22.0%) gram-negative facultative anaerobes. Gram-negative aerobes were identified in the amount of 2 (2.5%) strains (Neisseria spp.). Fungal flora was isolated from 6 (7.8%) patients, more often isolated in association with bacterial pathogens.

Microorganisms isolated from patients with rhinosinusitis (n=54)

Microorganisms	Upper respiratory tract		Lower respiratory tract	
	number	%	number	%
Streptococcus pneumoniae	18	39,1	20	43,5
Haemophilus influenza	9	19,5	6	13,0
Staphylococcus aureus	7	15,2	6	13,0
Streptococcus viridans	7	15,2	3	0
Streptococcus pyogenes	5	10,8	7	15,2
Staphylococcus haemolyticus	5	10,8	3	5,5
Staphylococcus epidermidis	4	8,7	2	4,3
Klebsiella pneumonia	4	8,7	6	13,0
Candida spp.	6	11,1	2	4,2
Neisseria spp.	2	4,3	-	0
Proteus mirabilis	1	2,1	-	0
Escherichia coli	2	4,3	2	4,3
Entorococcus faecalis	1	2,1	**2**	4,3
Total:	71	-	59	-

Bacteriological examination of sputum collected from 46 patients revealed 59 strains of microorganisms. The results of microbiological examination of sputum culture are presented in Table 3. The growth of microorganisms in sputum culture was noted in 36 (78.2%) patients, in 10 (21.7%) patients microorganisms were not detected. Mixed microflora was detected in 6 (13.0%) patients, the maximum number of pathogens in the association was 2. Gram-positive facultative anaerobes were detected in 41 (69.5%) strains of bacteria, the majority, as in the results of culture from the middle nasal passage, were microorganisms of the genus Staphylococcus and Streptococcus. The growth of 11 (18.6%) gram-negative facultative anaerobes was obtained. Gram-negative aerobes were detected in the amount of 2 (3.0%) strains (Moraxella catarrhalis). Fungal flora was isolated from 5 (7.7%) patients, most often isolated in association with bacterial pathogens.

CONCLUSIONS

Having examined 80 patients with CAP, it is worth noting a fairly high prevalence of complaints and symptoms characteristic of inflammatory diseases of the nasal mucosa, in particular rhinosinusitis. In our study, 46 (67.5%) patients were found to have symptoms of ARS and CRS. Radiological changes were detected in 25 (31.25%) patients.

In many ways, the etiopathogenesis of rhinosinusitis is similar to CAP. The microflora obtained from sputum and the middle nasal passage in patients with CP is almost identical. As a result of the study of smears taken from the nasal cavity, microflora was obtained in 46 (67.5%) patients, growth was noted in all patients. A total of 71 microorganisms were identified. During bacteriological examination of sputum taken from patients, 59 microorganisms were detected, no growth was noted in 10 (21.7%) patients. The main pathogen in acute and chronic rhinosinusitis in patients with CAP was Streptococcus pneumoniae (39.1% and 43.5%, respectively).

Thus, based on the data obtained, it can be concluded that inflammatory diseases of the nose and PNS are interrelated with CAP. Early diagnosis and parallel treatment of rhinosinusitis with CAP gives us a quick and complete recovery of patients and reduces the development of complications. Timely and effective treatment of inflammatory diseases of the upper respiratory tract after an acute respiratory viral infection is considered one of the preventive measures for CAP.

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