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Analysis of spectrum and determination of antibiotic sensitivity of causative agents of upper respiratory tract infections

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Abstract

In order to study spectrum of causative agents of upper respiratory tract diseases in patients of different age categories, a total of 1646 clinical samples have been investigated. It was determined that in all age categories gram-positive cocci were most commonly found. Changes in the species and genus composition of the coccal microflora were noted. Study of the contamination of the throat determined that leading causative agents were microbes of genus *Streptococcus*, while on the nasal mucosa dominated bacteria's were from genus *Staphylococcus*. Determination of the sensitivity of *Staphylococcus* strains towards antibiotics showed resistance against macrolides and group of penicillin of the beta-lactam antibiotics. As for *Streptococcus* strains, aminoglycosides and macrolides exhibited the least activity. Thus, the identification of the microbial spectrum of pathogens of upper respiratory tract infections and their sensitivity to antibiotics contributes to differentiated antibiotic therapy in children and adults with upper respiratory tract infections.

Keywords: monoinfection, mixed infection, antibiotic sensitivity

1. Introduction

Upper respiratory tract infections is a group of acute infectious inflammatory diseases of the upper respiratory tract of various localization and etiology. These infections are a group of the most common acute diseases which are observed on an outpatient basis. Since they are characterized by a high frequency of occurrence, lead to disability, are a frequent cause of hospitalization and the occurrence of chronic inflammatory diseases, they are important not only in the medical, but also in the socio-economic aspect. [1]

The etiology of community-acquired respiratory infections is usually caused by normal microflora of the upper respiratory tract - oral cavity, nose, mouth and nasopharynx. Normal microflora plays an important role in protecting the body from pathogenic microbes, at the same time it can cause the development of various infectious diseases. Important conditions for this is multiplicity infection and disorder of the body immune system. The more manifestation of these disorders, the wider the range of microorganisms that can cause infectious complications.

The microflora of the upper respiratory tract are presented by microorganisms of different genus. Mostly are found *Streptococcus*, *Neisseria*, *Staphylococcus*, also observed presence of *Diphtheroids*, *Mycoplasma*, *Bacteroides*, *Hemophilic bacteria*, *Pneumococci*. [1, 2]

Various microorganisms are recognized as important etiological agents of pharyngitis, tonsillitis, otitis, and sinusitis. It has been reported that *S. pneumoniae*, *H. influenzae*, group A streptococci and *S. aureus* are often isolated microorganisms from the cases of sinusitis, while *S. pyogenes*, is certainly the most clinically important etiological agent of bacterial tonsillopharyngitis. [1, 3, 4, 5]

An important task for a non-hospital infection is a rational choice of antibiotics, since this leads to a decrease in the frequency of prescribing antibacterial drugs, a more complete clinical and bacteriological treatment of the patient, and ultimately - limiting the growth of

antibiotic resistance in the microbial population. [6]

The priority in choosing antimicrobial therapy for infectious inflammation belongs to identifying the pathogen and determining its sensitivity to antibacterial drugs. Unfortunately, outpatient doctor more often have to start treating patients without further verification of the etiological agent, because of the different problems connecting with bacteriological investigations - the result of analyses is ready after several days; to take sample may be related with serious manipulations and etc. The effectiveness of the choice of starting antibiotic therapy in this case depends on the doctor's knowledge of the epidemiological situation and the potential pathogens that most often cause infectious processes of various localization. Knowledge and understanding of these points allows increasing the effectiveness of starting therapy. Empirical consideration of the above components allows conducting targeted antibiotic therapy at the first, starting stage of patient treatment. However, in case of choosing an adequate antibiotic therapy should be guided by regional data on resistance of microorganisms. [7,8]

Based on the above mentioned, the purpose of our investigation was to study the spectrum of the most common causative agents of the upper respiratory tract diseases and determination of the sensitivity /resistance of the selected microflora to antibacterial drugs.

Material and method

Bacteriological examination of 1646 clinical materials (samples from throat-1278 and nose-368) isolated from patient was made according to methodological recommendations. Morphological and biochemical properties of strains were studied by standard methods using different selected media (1,5% Nutrient agar, Nutrient broth, 5% Blood agar, Manitol-salt agar, Saburo agar and etc.) and API-test systems. Antibiotic sensitivity was determined by Kirby Bayer's method. 21 standard antibiotic discs form 6 different groups - β -lactam antibiotics, aminoglycosides, macrolides, tetracyclines, quinolones and rifamycins - were used. [9, 10]

Result and Discussion

Total of 1646 clinical material were examined during 2016-2017. Patient were divided in different age categories: I - under 6 years (230), II - from 7 up to 13 years (171), III - from 14 up to 18 years (101), IV - from 19 up to 60 years (817), V - 60 years up (327). The largest number of received samples was from throat, which in separate age categories was varied from 74% to 87%.

In the study of contamination of the upper respiratory tract, it was found that the microflora of the nasal mucosa in 81% of cases is represented by monocultures and in 19% by different bacterial associations. The leading role belonged to gram-positive cocci, with a clear predominance of *Staphylococcus* microorganisms.

In the case of mono-infections, *S. aureus* and *S. epidermidis* were the most common etiological agents and their isolation frequency was 48% by separately. It should be mentioned that the highest incidence of *S. aureus* 56% was in the first age category. The prevalence of *S. pyogenes* and streptococci of the viridians group were less common and it was noticed in 2% of cases for each. As for mixed infections, the leading positions were taken by different associations: *S. aureus* + *E. coli* - 24%, *S. aureus* +

Klebsiella spp.-18%, *S. epidermidis* + *E. coli* - 18%, *S. epidermidis* + *S. pyogenes* - 12% and etc. *Candida albicans* was met only in microbial associations and the frequency of isolation was 4%. The highest rate of mixed infections 27% of cases was detected in first age category. Thus, based on our investigations we can notify that the most numerous group of microorganisms that cause diseases of the nasal mucosa and paranasal sinuses are microorganisms of genus *Staphylococcus*.

In the following studies of the upper respiratory tract, it was found that the microflora of the throat mucosa in 42% of cases is represented by monocultures and in 58% were accounted by mixed infections. The leading role also belonged to gram-positive cocci, with a clear predominance of *Streptococcus* microorganisms.

In the contamination of the throat mono-infections in all age groups microbes of the genus *Streptococcus* were dominated. *S. pyogenes* was in leading position with isolation rate 80%, as for streptococcus group of viridans, *S. aureus* and hemolytic *Enterococcus spp.* isolation frequency was less - 18%, 1.4% and 0.6% respectively. Mixed infections accounted for 58%. The highest rate of them 67% was in the fifth age category. Among the microbial associations combinations of *S. pyogenes* + *Candida albicans* and *S. pyogenes* + *S. aureus* were the leaders - 32% and 25% respectively. The less frequency of isolation was determined for streptococci of viridians group + *Candida albicans* - 9% and different associations with gram negative microorganisms of the genera *Escherichia*, *Klebsiella*, *Pseudomonas* and *Proteus* - *S. pyogenes* + *E. coli* - 5%, *S. pyogenes* + *Klebsiella spp.* - 3.4%, *S. pyogenes* + *Proteus spp.*- 2.7%, *S. pyogenes* + *P.aeruginosa* - 2.3% and etc. In all age categories the throat mixed infections were characterized with 37% of isolation of *Candida albicans*. The highest incidence of *Candida albicans* 53% was observed in the fifth age category. Thus, depend on our studies we can mention that in the throat infections the leading role belonged to gram-positive cocci with a clear predominance of genus *Streptococcus*.

Considering results of the sensitivity of the most common pathogens to antibacterial drugs, it was found out that avelox showed the highest 100% activity towards to *S. aureus* strains. Different rate of susceptibility against *Staphylococcus* strains was noticed for antibiotics used in our studies: mefloclid - 94.5%, floxan - 93%, ciprofloxacin - 92%, rifampicin - 80%, dalacin - 68%, zinnat - 65.5%, claforan - 62.5%, triaxone - 57.5%, doxycycline - 36%, amibac - 33.5 %, gentamicin - 28%. The sensitivity of beta-lactam antibiotics of group penicillin ranged from 14.5% - 25.5% and group of macrolides - 9-25.5%. There were no major differences in antibiotic sensitivity between *S. aureus* and *S. epidermidis*.

As for the *S. pyogenes* strains the following susceptibility pattern against antimicrobial agents was shown: the highest activity was shown for mefloclid - 97.8%, avelox - 97.6%, floxan - 96% and ciprofloxacin - 94.6%. They are followed by triaxone and zinnat - 74% for each. The activities of other antibiotics were in following order: dalacin - 71.2%, amoxicillin - 69%, ampicillin - 59%, doxycycline - 54.5%, clarithromycin - 52%. The lowest activity towards *S. pyogenes* strains was determined for antibiotics: gentamicin, abimac, sumamed and erythromycin - 39.5%, 32.3%, 22%, 17.7% respectively.

Conclusions

As a result of our work it was found that Gram-positive cocci are most commonly found microorganisms in infections of the upper respiratory tract. Investigations also determined the changes in the species and genus composition of the coccal microflora. The dominated microorganisms of the nasal mucosa were *Staphylococcus*, while on the mucous membrane of the throat *Streptococcus* were more often allocated. As causative agents of diseases of the upper respiratory tract among *Staphylococcus* are found both *S. aureus* and *S. epidermidis* and among *Streptococcus* isolates were prevailed strains of *S. pyogenes*.

In the etiological structure of throat diseases, the high prevalence belongs to the fungal flora. *Candida albicans* was isolated in 37% of cases, whereas in diseases of the nose, fungi were determined only in 4%.

Study of the sensitivity of isolated strains to antibacterial drugs showed that *Staphylococcus* strains were resistant against macrolides and beta-lactam antibiotics of group penicillin. As for *Streptococcus* strains, aminoglycosides and macrolides exhibited the least activity against them.

Thus, the identification of the microbial spectrum of pathogens of upper respiratory tract infections and their sensitivity to antibiotics contributes to differentiated antibiotic therapy in children and adults with upper respiratory tract infections.

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