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**THE TAXONOMICAL COMPOSITION AND SENSIBILITY  
TO ANTIBIOTICS OF BACTERIA – CAUSATIVE AGENTS OF  
INFECTIONS OF THE UPPER RESPIRATORY TRACT**

**Abstract**

The purpose of this work was to identify, study the biological features, identify and determine the sensitivity of antibiotics actions of dominant microorganisms isolated in patients with inflammatory diseases of the upper respiratory tract.

Key words: inflammatory diseases of upper respiratory tract, *Staphylococcus*, *Streptococcus*, mono infections, mixed infections, sensitivity to antibiotics

**Introduction**

Upper respiratory tract occupy one of the leading inflammatory diseases [2]. Often acute process becomes chronic, there is a significant percentage of severe disease, there is a high mortality

In this regard, the need to constantly improve specific prevention study pathogens circulation upper respiratory tract infections in the population in terms of mass immunization [1].

The constant increase in bacterial resistance to antibiotics complicates the process of effective treatment of patients with inflammatory diseases of the upper respiratory tract bacterial etiology [2]. At the same time knowledge of the etiology of inflammation and sensitivity to antibiotics of infectious agents facilitates adequate therapy improves prognosis and reduces the risk of a sharp transition process in chronic[5].

**Materials and methods**

The material for the study of the allocation of the throat, nose and phlegm. All tests were performed according to [3]. In 2016 - 2017 years as a result of bacteriological examination of sputum, secretions of the nose and throat, in 897 patients with upper respiratory tract infection - residents.



The experimental part of the work was performed in the clinical diagnostic laboratory of the State Scientific and Technical Engineering Center for Problems of Water Purification and Water Conservation of the STI «Vodooobrobka» Physico-Chemical Institute. A. V. Bogatsky National Academy of Sciences of Ukraine.

From sputum, secretions from the nose and throat was isolated 1490 strains of microorganisms patients with abnormalities of ENT organs.

Material collected in compliance with the rules of aseptic. From collecting dry sterile cotton swab is introduced into the interior cavity of the nose, throat phlegm . Morning phlegm that stand out in the attack of coughing, collected in a sterile bank. .In this research Drill test material using the following nutrient media: Yolk-salt agar, Endo Agar, Saburo Agar, Blood agar..

Determination of the sensitivity of microorganisms to antibiotics was carried disco diffusion method according to [4]. Research on sensitivity to antibiotic drugs subject pure cultures of microorganisms or colony isolated from dense nutrient mediums initial seeding of clinical material. Disks with antibiotics used to determine antibiotic susceptibility of infectious agents isolated from patients with pathological material

### Results and discussions

Isolated strains were identified as the bacterium of 11 genera *Staphylococcus*, *Streptococcus*, *Klebsiella*, *Escherichia*, *Enterobacter*, *Proteus*, *Pseudomonas*, *Candida*, *Bacillus*, representing 12 species dominated by representatives of the genera *Staphylococcus* and *Streptococcus*( Fig. 1).

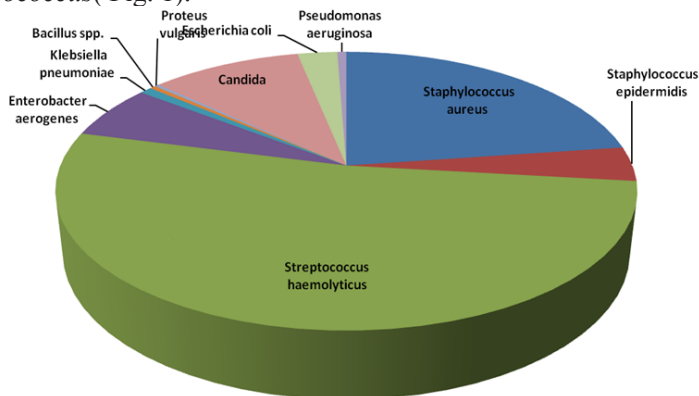


Fig. 1 Frequency allocation microorganisms of different taxonomic groups of patients with inflammatory diseases of the upper respiratory tract.



In patients with inflammatory diseases of the upper respiratory tract, infections were more often caused by a mono-infections. (Fig.2)

The amount of examined	mono- infection		mixed infection	
	abs.	%	abs.	%
897	522	58,2	375	41,8

**Fig.2 The frequency of mono- and mixed infections in the patients with inflammatory diseases of the upper respiratory tract**

The most common mixed infection is caused by *Staphylococcus aureus* and *Streptococcus haemolyticus*, which is found in 39.2 % of patients.

A study of the sensitivity of isolated strains to antibiotics showed that the bacteria of the genera *Staphylococcus* and *Streptococcus* were resistant to the action of amoxicillin and doxycycline, and are sensitive to ofloxacin, gatifloxacin, ceftriaxone, cefoperazone. The bacteria of the *Enterobacteriaceae* family were most sensitive to ofloxacin, cefoperazone, gatifloxacin. And resistant to doxycycline, cefazolin, amoxicillin.

### Conclusions

Our data indicate that in recent years has been an increasing resistance of microorganisms, including bacteria genera *Staphylococcus* and *Streptococcus* to antibacterial drugs used in clinical practice.

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