

knowledge, master practical skills without risk for the patient, to objectively assess the achieved level of skill, to reduce the level of psychological stress during the first manipulations; to approach imitation of activity to reality with a high degree of reliability; hone the clarity, correctness and speed of action that can save the patient's life; analyze and correct mistakes [6-8].

Thus, conducting phantom classes for students allows to study protocols with algorithms for the diagnostic and treatment of simulated situations of personal actions and team interaction in the choice of treatment tactics in different clinical situations and correct most medical errors.

Introduction to the educational process, on all stages of medical education, the using simulation classes will lead to reduce medical errors, reduce complications and increase the quality of diagnostic manipulations and medical care.

**Conclusions.** 1. Use of simulation technologies in preparation future doctors significantly improves both the theoretical level of knowledge and mastering professional and individual competencies, which improves quality training students.

2. It is worth noting that simulation training and skills development on phantoms and models does not replace, but only complements the preparation for the real practical work, and provides control of the teacher over the quality of performance each student action and reduce the time to prepare them.

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## МІКРОБІОЛОГІЧНА ХАРАКТЕРИСТИКА ХВОРИХ НА ГЕНЕРАЛІЗОВАНИЙ КАТАРАЛЬНИЙ ГІНГІВІТ

*Шостенко А.А.*

*Вищий державний навчальний заклад України «Буковинський державний медичний університет» кафедра стоматології дитячого віку, асистент*

## MICROBIOLOGICAL CHARACTERISTICS OF PATIENTS WITH GENERALIZED CATARRHAL GINGIVITIS

*Shostenko A.*

*HSEE "Bukovinian state medical university", department of pediatric dentistry, assistant*

#### Анотація

У статті наведені отримані результати дослідження мікрофлори порожнини рота 82 хворих на генералізований катаральний гінгівіт з хронічним та загостреним перебігом до проведення лікувально-профілактичних заходів. Для ідентифікації основних пародонтопатогенів застосовували полімеразну ланцюгову реакцію з використанням ДНК-зондів із зворотної ДНК-гібридизації. Біохімічну ідентифікацію анаеробних бактерій, стрептококів і грамнегативних бактерій проводили за допомогою тест-системи фірми API (Франція).

**Abstract**

The article presents the results of the study of the oral microflora of 82 patients with generalized catarrhal gingivitis with chronic and exacerbated course before treatment and prevention measures. Polymerase chain reaction using reverse DNA hybridization DNA probes was used to identify the main periodontal pathogens. Biochemical identification of anaerobic bacteria, streptococci and gram-negative bacteria was performed using a test system from ARI (France).

**Ключові слова:** катаральний гінгівіт, пародонт, запалення.

**Keywords:** catarrhal gingivitis, periodontium, inflammation.

The most common periodontal pathology at a young age is catarrhal gingivitis, as evidenced by numerous epidemiological studies by domestic and foreign authors [1, 2, 3, 4]. Of particular concern to the dental community is the tendency of chronic inflammation in the gum tissue to frequent exacerbations, which exacerbate the clinical manifestations of catarrhal gingivitis and require an expansion of the arsenal of medical treatment, which is not always successful.

This problem is due primarily to lack of knowledge of the etiology and pathogenesis of various forms of generalized catarrhal gingivitis,

Their significance to date has not been fully disclosed, despite the large number of studies conducted in this area [2, 3, 5, 6].

It is now believed that the onset of the inflammatory process in the gum tissue is associated with poor oral hygiene and microbial factor of the bacterial dental film. It is believed that the main role in the development of generalized catarrhal gingivitis belongs to opportunistic bacteria. However, it is not established which of them has a dominant role in the formation of different variants of the clinical course, which complicates the choice of antibacterial agents for the treatment of the disease.

**The aim of the study.** To establish the features of changes in the biocenosis of the gingival sulcus in patients with generalized catarrhal gingivitis and to determine the dominant pathogens of chronic and exacerbated inflammatory processes in the tissues of the gums.

**Materials and methods.** There were 82 patients diagnosed with generalized catarrhal gingivitis aged 18 to 30 years, including 38 men (46.3%) and 44 women (53.7%). Depending on the clinical manifestations of the study were divided into two groups: I - 33 patients with chronic generalized catarrhal gingivitis; II - 49 patients with acute disease. The groups were formed identical in age and sex. To analyze the results of clinical and laboratory studies used data obtained for 18 healthy individuals, similar in age and sex to the experimental patients (control group).

For rapid and accurate identification of the main periodontal pathogens, polymerase chain reaction was

used using DNA probes from reverse DNA hybridization (Micro-Dent® test system, Germany) according to standard methods, according to the manufacturer's instructions. Biochemical identification of anaerobic bacteria, streptococci and gram-negative bacteria was performed using a test system from ARI (France).

The obtained data of clinical and laboratory studies were processed by the methods of variation statistics using the software MS Excel 2003 [7].

**Research results and their discussion.**

Conducted microbiological studies of the contents of the gingival sulcus showed that chronic and exacerbated generalized catarrhal gingivitis have differences in the etiological structure of possible pathogens of the above pathological processes.

Positive cultures of material taken from patients with chronic generalized catarrhal gingivitis mainly showed aerobic microflora, among which priority was given to opportunistic pathogens, the frequency of detection of which in the gingival sulcus increased sharply: Str. Salivarius to 69.9% of cases, Str. sanqvius up to 75.8% of cases, Str. Epidermidis up to 60.6% of cases, Str. Haemoliticus up to 57.5% of cases, Peptostreptococcus up to 51.5% of cases (table 1). These bacteria are most often found in 2-3 component associations.

Thus, the peculiarity of changes in the microbiocenosis of the gingival sulcus in patients with chronic generalized catarrhal gingivitis is the increase in this category Str. Salivarius, Str. sanqvius, peptostreptococci, hemolytic streptococci and, to a lesser extent, certain conditions, obviously, and trigger the development of chronic inflammation in the tissues of the gums. Against this background, which is especially important, the frequency of sowing of such aggressive forms of bacteria as Stf. Aureus, a fungus of the genus Candida, fusobacteria in patients with chronic generalized catarrhal gingivitis is not significant (from 6.1% to 3.05% of cases). It was found that the main microbial factor of chronic generalized catarrhal gingivitis is not one single microorganism, but the association of many of these.

Table 1.

Microbiocenosis of toothed furrow in patients with generalized catarrhal gingivitis with different clinical course

Type of microorganisms	Groups of respondents					
	I group (n=33)		II group (n=49)		Healthy patients (n=18)	
	Abs.	%	Abs.	%	Abs.	%
Lactobacillus spp.	27	81,8	26	53,1	17	94,4
Str. salivarius	23	69,9	35	71,4	6	33,3
Str. veridans	17	51,5	24	48,5	12	66,6
Str. sangvius	25	75,8	24	48,5	2	11,1
Str. haemoliticus	19	57,5	32	65,3	1	5,6
Stf. epidermidis	20	60,6	27	55,0	0	0
Peptostreptococcus	17	51,5	14	28,0	1	5,6
Stf. aureus	2	6,1	27	55,0	1	5,6
Enterobacter	0	0	5	10,2	0	0
Bacteroides spp.	1	3,0	8	16,3	0	0
Fusobacteria spp.	1	3,0	14	28,6	0	0
Candida albicans	1	3,0	23	46,5	0	0

In patients with generalized catarrhal gingivitis with an acute course, the microbial spectrum expanded due to the appearance in the tissues of the gums, in a larger number of subjects, staphylococci and fungi of the genus *Candida* and other aggressive bacterial species (see Table 1).

Серед виділених збудників запального процесу в тканинах ясен переважали *Stf. Aureus* (у 55%), *str. Epidermidis* (у 55%), *Candida Albicans* (у 46,5%) і *str. Hemoliticus* (у 65,3%), нерідко *Fusobacteria* (28,5%) та не властиві здоровому пародонту *Enterobacter* (10,2%) і *Bacteroides spp.* (28,6%).

Among the isolated pathogens of the inflammatory process in the gum tissues was dominated by *Stf. Aureus* (55%), *p. Epidermidis* (55%), *Candida Albicans* (46.5%) and *str. Hemoliticus* (65.3%), often *Fusobacteria* (28.5%) and not characteristic of healthy periodontium *Enterobacter* (10.2%) and *Bacteroides spp.* (28.6%).

Thus, during the analysis of the results of microbiological research in patients with generalized catarrhal gingivitis with an acute course revealed a significant increase in the incidence of *Stf. Aureus*, *Stf. Epidermidis*, *Candida albicans*, *Fusobacteria spp.*, *Enterobacter*, *Bacteroides spp.* These microorganisms occupy a leading place in the development of exacerbations of chronic inflammation in the tissues of the gums.

Analysis of the species composition of the gingival microflora in patients with acute generalized catarrhal gingivitis also showed a decrease in the incidence of gingival tissue lactobacilli by 41.3% of cases, and found that the most common association is a combination of epidermal and *Staphylococcus aureus* and *Staphylococcus aureus* and hemolytic streptococcus. This, in turn, proves the polymorphism of bacteria detected during the examination of patients with generalized catarrhal gingivitis with an exacerbated inflammatory process in the gum tissue.

Thus, based on these results, we can conclude that the biocenosis of the gingival sulcus in patients with chronic generalized catarrhal gingivitis is characterized by a wide range of aerobic opportunistic bacteria. The

leading role is played by the obligate microaerophilic microflora, which is in the associative relationship. Central to the development of exacerbations belongs to staphylococci and fungi of the genus *Candida*. There is a partial displacement of bacteria that stabilize normobiosis (*Lactobacillus spp.*, *Str. Sangvius*), probably due to increased reproduction of *Candida* fungi, anaerobic staphylococci and streptococci, as well as uncharacteristic for healthy microbiocenosis healthy gum tissue bacteriobacteria and fusobacteria.

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