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Analysis of biocoenosis of oral cavity in children with different degrees of caries activity, who permanently residing in conditions of biogeodeficit of fluorine and iodine.

O.V. Klitynska

*Department of Dentistry of Childhood Age,
State Higher Educational Establishment
"Uzhgorod National University", Uzhgorod,
Ukraine*

Summary: Microbial scenery of the oral cavity plays an important role in the formation and progression of dental disease that is particularly revealing in preschool and early school age. Research microbiota of the oral cavity, species identification and quantitative composition marker is the origin and progression of diseases of the oral cavity as caries, inflammatory and degenerative inflammatory diseases periodontal tissues and lesions of the oral mucosa..

Key words: oral cavity, careis, biogeodeficit , microbiota.

Actuality. Microbial scenery of the oral cavity plays an important role in the formation and progression of dental disease that is particularly revealing in preschool and early school age. According to different authors in the oral cavity occurs more than 100 species of microorganisms, and 1 ml saliva

contains more than 108 microbial cells [6-9]. The prevalence of certain kinds of microorganisms creates conditions for the formation and rapid progression of dental disease [1,5,10,11]. Evaluation of microbial scenery plays an important role in the choice of medical tactics and as a result improve the effectiveness of treatment [2-4,12-14]. For setting the microbial scenery oral saliva sampling was carried out and microbial soft plaque in the cervical area. Hung held the following nutrient medium: - meat peptonny agar to determine TMC (total microbial count) - agar selective for streptococci - selective agar for *Streptococcus mitis* and *S. salivarius*; - semi-selective medium for the isolation of streptococci - semi environment for the allocation of bifidobacteria (environment Blauroka) - Endo environment to check for gram-negative microbiota - bismuth-sulphite agar for the isolation of *Salmonella* and *Shigella* - enterokokovyy agar for the cultivation of species of *Entecococcus* spp.; - laktobak-agar (MRS - Man -Rogosa-Sharpe agar) for the cultivation of lactobacilli in microaerophilic conditions - bifidum, *Bifidobacterium* Agar for cultivation.

For the detection and identification using Gram smears production and further their microscoping, routine biochemical tests. All relevant strains isolated during the experiment strains of microorganisms will be saved.

The study was conducted in 146 children with different degrees of caries activity, aged 3-8 years, who permanently live in conditions of biochemical deficits of different ethnic groups. A survey of children was conducted after informed consent of parents or guardians of LLC "Dental clinic" Dental Faculty SHEI "Uzhhorod National University". Microbiological and immunological studies were conducted in microbiological laboratories Transcarpathian

Ukraine Branch of microbiologists name S.M.Vynohradskoho - TUBM.

Results and discussion. The results of determining microbiota in saliva of inspected children, Roma ethnic group, mixed ethnic groups and the control group presented in Figure 1.

Average value of total microbial number of children in the control group was 4×10^5 , not significantly different rates in children of the Roma ethnic group 6×10^5 ($p > 0.05$)., And the children of mixed ethnic groups was significantly higher and was 6×10^9 ($p < 0.05$).

Among the species belonging were significant differences among children of different groups. So, children of mixed ethnic groups were representatives of normal oral microflora and opportunistic and pathogenic microorganisms.

Normal microflora presented oral *Streptococcus mitis*, *S. salivarius*, *Lactobacillus salivarius*, *Bifidobacterium* spp. - normally found in the mouth, including saliva, plaque, in the mucous membranes of the mouth. Number of microbiota in children of the main group was small: *Streptococcus mitis* - 1×10^4 CFU; *Streptococcus salivarius* - 2×10^4 cfu; *Bifidobacterium* spp - 1×10^4 CFU; *Lactobacillus salivarius* - 8×10^2 CFU; *Lactobacillus acidophilus* - 8×10^1 CFU.

Streptococcus sobrinus - typical caries forming species with *Streptococcus mutans* to form a group of similar species *Streptococcus mutans* biochemical properties and effects on the surface of the tooth enamel and tooth tissue destruction. owed by 100% of children of the main group, the average values were *Streptococcus sobrinus* - 4×10^4 CFU.

Other species, including representatives of gram-negative microbiota and species of the genus *Enterococcus* spp. and *Staphylococcus aureus* normally have to be

present among the normal microbiota; Data representatives (*Escherichia coli* - 6×10^6 CFU; *Proteus vulgaris* - 8×10^8 CFU; *Citrobacter freundii* - 2×10^7 cfu; *Pseudomonas aeruginosa* - 1×10^9 CFU; *Enterococcus faecalis* - 1×10^5 CFU; *Enterococcus faecium* - 1×10^3 CFU) is normobiota and opportunistic bacteria by the gastrointestinal tract. A *Staphylococcus aureus* is the causative agent of many infections and diseases causing opportunistic and nosocomial infections in people with lowered immunity sown amount of 1×10^3 CFU.

This oral microbial scenery corresponds to the third degree of dysbiosis V.V.Hazanovoyu for all children of the main group, regardless of the degree of activity of dental caries, and is characterized by the detection of pathogenic monoculture with a sharp decrease in the number or total absence of representatives of normal (physiological) microflora.

The children of the Roma ethnic group frequency of sowing microflora significantly different. So, the average total microbial number was 6×10^5 . Flora represented *Streptococcus mitis* - 9×10^3 CFU; *Streptococcus salivarius* - 1×10^4 CFU; *Bifidobacterium* spp - 2×10^7 cfu; *Lactobacillus salivarius* and *Lactobacillus acidophilus* available.

Among the opportunistic pathogenic *Enterococcus faecalis* - 1×10^5 CFU. All members of the Roma ethnic group were allocated *Streptococcus mutans* in quantities of 1×10^4 CFU and *Streptococcus sobrinus* not sown. Accordingly, in this group of patients diagnosed subcompensated form of dysbiosis, which is characterized by the presence of one or two kinds of opportunistic microorganisms against the background of a reduction in titer lactobacilli.

In the control group inspected flora represented *Streptococcus mitis* - 9×10^3

CFU; Streptococcus salivarius - 1×10^6 CFU; Bifidobacterium spp, Lactobacillus salivarius and Lactobacillus acidophilus available.

Acid-streptokky are Streptococcus sobrinus in number 9×10^3 CFU;

opportunistic presented Enterococcus faecalis - 9×10^3 cfu. The average values of total microbial count was 4×10^5 .

Table 1

		<i>Streptococcus mitis</i>	<i>Streptococcus sobrinus</i>	<i>Pseudomonas aeruginosa</i>	<i>Enterococcus faecalis</i>	<i>Enterococcus faecium</i>	<i>Proteus vulgaris</i>	<i>Lactobacillus salivarius</i>	<i>Lactobacillus acidophilus</i>	<i>Staphylococcus aureus</i>	<i>Bifidobacterium</i>	<i>Citrobacter freundii</i>	<i>Escherichia coli</i>
<i>Streptococcus mitis</i>	r	1	-0.03632	-0.07963	-0.02141	-0.04393	0.02341	0.21537	0.46036	-0.07302	0.77805	-0.07387	-0.07985
<i>Streptococcus mitis</i>	σ	--	8.36E-01	6.49E-01	9.03E-01	8.05E-01	8.94E-01	0.21404	5.39E-03	6.77E-01	3.78E-08	6.73E-01	0.6484
<i>Streptococcus sobrinus</i>	r	-0.03632	1	-0.04681	-0.07599	0.99134	-0.03547	-0.04883	-0.00636	0.23332	-0.02791	-0.02339	-0.0419
<i>Streptococcus sobrinus</i>	σ	8.36E-01	--	7.89E-01	6.64E-01	0	8.40E-01	0.78057	9.71E-01	0.17737	8.74E-01	8.94E-01	0.8111
<i>Pseudomonas aeruginosa</i>	r	-0.07963	-0.04681	1	-0.03722	-0.03155	-0.06418	0.92528	-0.05538	-0.12008	-0.04147	-0.0485	-0.03102
<i>Pseudomonas aeruginosa</i>	σ	6.49E-01	7.89E-01	--	8.32E-01	8.59E-01	7.14E-01	2E-15	7.52E-01	4.92E-01	8.13E-01	7.82E-01	8.60E-01
<i>Enterococcus faecalis</i>	r	-0.02141	-0.07599	-0.03722	1	-0.0605	-0.1068	-0.04136	-0.05318	0.22091	-0.02369	-0.03769	0.97643
<i>Enterococcus faecalis</i>	σ	9.03E-01	6.64E-01	8.32E-01	--	0.73396	5.41E-01	0.81351	7.62E-01	2.02E-01	8.93E-01	8.30E-01	0
<i>Enterococcus faecium</i>	r	-0.04393	0.99134	-0.03155	-0.0605	1	-0.03461	-0.04216	-0.05415	0.2357	-0.04585	-0.03992	-0.0303
<i>Enterococcus faecium</i>	σ	8.05E-01	0	8.59E-01	0.73396	--	8.46E-01	0.81288	0.76099	1.80E-01	7.97E-01	0.82264	8.65E-01
<i>Proteus vulgaris</i>	r	0.02341	-0.03547	-0.06418	-0.1068	-0.03461	1	-0.08462	-0.10864	0.36465	-0.08301	0.15265	-0.06085
<i>Proteus vulgaris</i>	σ	8.94E-01	8.40E-01	7.14E-01	5.41E-01	8.46E-01	--	6.29E-01	5.34E-01	3.13E-02	6.35E-01	3.81E-01	0.7284
<i>Lactobacillus salivarius</i>	r	0.21537	-0.04883	0.92528	-0.04136	-0.04216	-0.08462	1	0.186	-0.17998	0.33466	-0.0766	-0.03123
<i>Lactobacillus salivarius</i>	σ	0.21404	0.78057	2E-15	0.81351	0.81288	6.29E-01	--	0.28471	0.30085	4.94E-02	6.62E-01	0.85867
<i>Lactobacillus acidophilus</i>	r	0.46036	-0.00636	-0.05538	-0.05318	-0.05415	-0.10864	0.186	1	-0.23537	0.5945	-0.09864	-0.05251
<i>Lactobacillus acidophilus</i>	σ	5.39E-03	9.71E-01	7.52E-01	7.62E-01	0.76099	5.34E-01	0.28471	--	1.73E-01	1.66E-04	5.73E-01	7.65E-01
<i>Staphylococcus aureus</i>	r	-0.07302	0.23332	-0.12008	0.22091	0.2357	0.36465	-0.17998	-0.23537	1	-0.18186	0.41907	0.2231
<i>Staphylococcus aureus</i>	σ	6.77E-01	0.17737	4.92E-01	2.02E-01	1.80E-01	3.13E-02	0.30085	1.73E-01	--	2.96E-01	1.22E-02	1.98E-01
<i>Bifidobacterium</i>	r	0.77805	-0.02791	-0.04147	-0.02369	-0.04585	-0.08301	0.33466	0.5945	-0.18186	1	-0.07844	-0.03421
<i>Bifidobacterium</i>	σ	3.78E-08	8.74E-01	8.13E-01	8.93E-01	7.97E-01	6.35E-01	4.94E-02	1.66E-04	2.96E-01	--	6.54E-01	8.45E-01
<i>Citrobacter freundii</i>	r	-0.07387	-0.02339	-0.0485	-0.03769	-0.03992	0.15265	-0.0766	-0.09864	0.41907	-0.07844	1	-0.03126
<i>Citrobacter freundii</i>	σ	6.73E-01	8.94E-01	7.82E-01	8.30E-01	0.82264	3.81E-01	6.62E-01	5.73E-01	1.22E-02	6.54E-01	--	0.85853
<i>Escherichia coli</i>	r	-0.07985	-0.0419	-0.03102	0.97643	-0.0303	-0.06085	-0.03123	-0.05251	0.2231	-0.03421	-0.03126	1
<i>Escherichia coli</i>	σ	0.6484	0.8111	8.60E-01	0	8.65E-01	0.7284	0.85867	7.65E-01	1.98E-01	8.45E-01	0.85853	--

Microbiota. Internal correlation

Pearson correlation coefficients "r" and the level of reliability "σ" for different pairs of microorganisms

All patients with decompensated caries had established the presence of oral

dysbiosis 3-4 degrees. These figures correspond dysbiotic change of 1 degree.

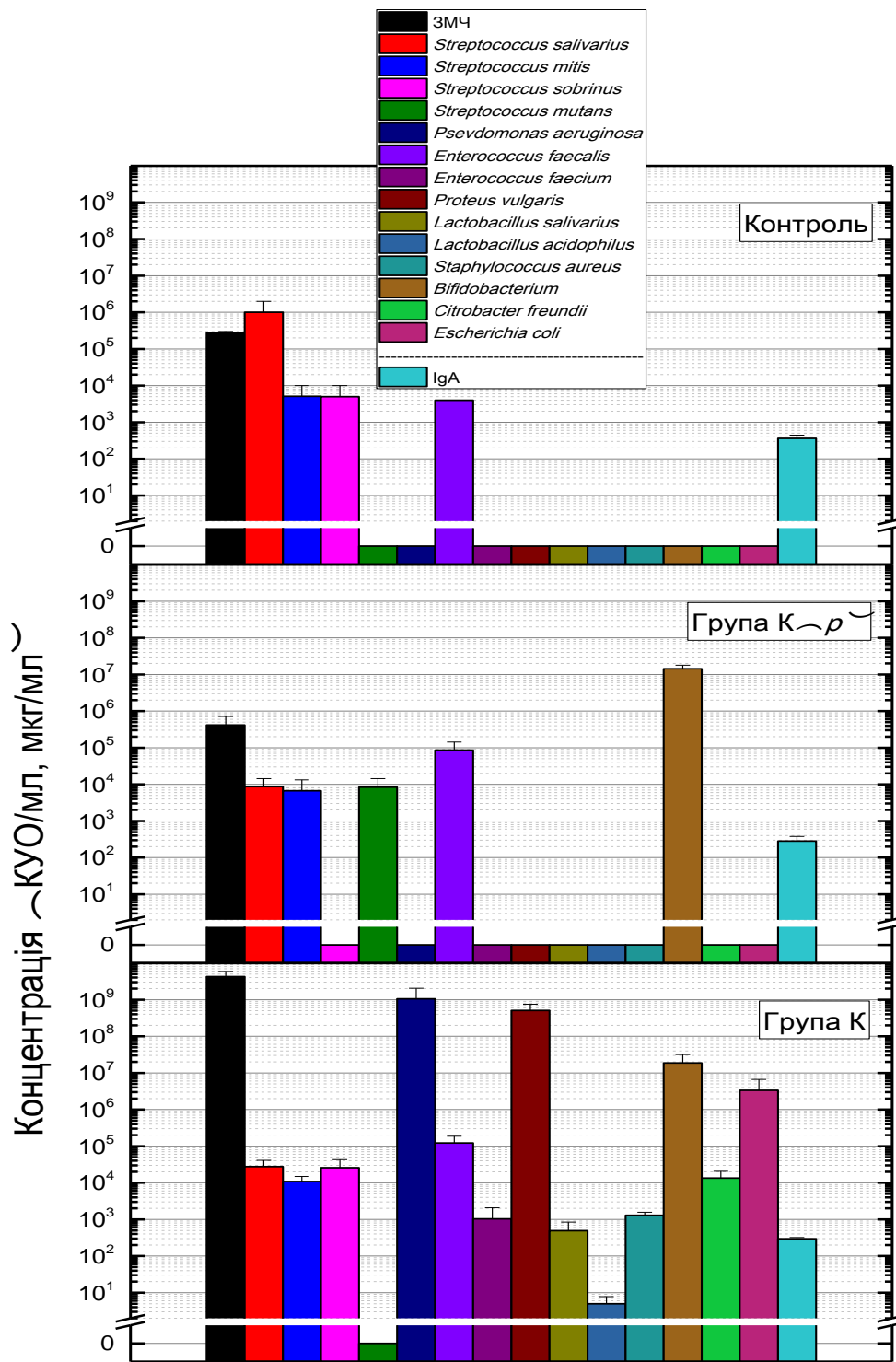


Figure1. Determination of various types of microorganisms and secretory immunoglobulin A in saliva inspected depending on the ethnic group.

Were the following bacteria: Streptococcus sobrinus - 100%; Streptococcus mitis - in 88.3%; Streptococcus salivarius - at 82.4%; Escherichia coli - 5.9%; Proteus vulgaris - at 47.1%; Citrobacter freundii - at 53.1%; Pseudomonas aeruginosa in 47.1%; Lactobacillus salivarius - at 11, 8% of cases (there are doubts about the plant species, 97% accuracy, using biochemical test Erba-Lachema, needs clarification on MALDI); Staphylococcus aureus - at 76.5%; Enterococcus faecalis - in 88.3%; Enterococcus faecium - 5.9%; Bifidobacterium spp.- in 53.0% (giving

Streptococcus sobrinus - typical cavities forming species with Streptococcus mutans to form a group of similar species Streptococcus mutans biochemical properties and effects on the surface of the tooth enamel and tooth tissue destruction. One of the most important factors of virulence is its acid stability. In the analysis of the mechanism kyslotostiykosti streptokoiv and adaptation to the acidic environment found that Streptococcus sobrinus can continue its growth and reproduction in acidity pH 5.0, in such circumstances it continues to ferment carbohydrates through glycolysis and continues to acidification of the environment around them, with specific enzyme System Streptococcus sobrinus (including fosfottransferazna system) in a state of higher activity at pH 5.0 than in a neutral

Conclusions. Research microbiota of the oral cavity, species identification and quantitative composition marker is the origin and progression of diseases of the oral cavity as caries, inflammatory and degenerative inflammatory diseases periodontal tissues and lesions of the oral mucosa. In particular, Streptococcus sobrinus, which was allocated 100% of the surveyed children aged 4-6 years

questionable results (65%) using biochemical anaerotestu Erba-Lachema, needs clarification on MALDI).

Streptococcus mitis, S. salivarius, Lactobacillus salivarius, Bifidobacterium spp. - Normally found in the oral cavity, including saliva, plaque, in the mucous membranes of the oral cavity.

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environment, creating conditions for the emergence of enamel demineralization, especially deciduous teeth in children [7, 12-14].

Other species, including representatives of gram-negative microbiota and species of the genus Enterococcus spp. and Staphylococcus aureus normally have to be present among the normal microbiota; Representatives of data (Escherichia coli, Proteus vulgaris, Citrobacter freundii, Pseudomonas aeruginosa, Enterococcus faecalis, E. faecium) is normobiotoyu and opportunistic bacteria by the gastrointestinal tract. A Staphylococcus aureus is the causative agent of many infections and diseases causing opportunistic and nosocomial infections in people with reduced immunity.

residing near biogeochemical fluorine and iodine deficiency, considered the most acidophilus bacteria that persist in the mouth of man because of bacteria colonies in rN5, 0 still active synthetic processes, they lack the shock and stress protein that has been proven to hemostatniy culture, DNA, RNA analysis and Western blotting.

Their timely identification and efficient removal of toxic effects by reducing their

number will reduce the risk of diseases of the oral cavity and create conditions for proper formation of all the structures of the oral cavity in children.

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