

ment tendency to the right that is characteristic for stress reactions which is accompanied by the increase of hepatocytes. In a liver of the experimental rats the karyogram had a more smoothed character, with 2 peaks being distinguished without any doubt. In a whole, the karyogram was displaced to the left. It is necessary to mention also that the karyogram for both groups which were under the conditions of a chronic stress was displaced to the left as compared to the immobilized rats' karyogram.

The spirit extract produced from dead bees stimulates the process of regeneration of hepatocytes population by means of a mitosis under both chronic and sharp stresses. In addition, AI in liver of the rats that were given the dead bees extract proves to be higher alongside a better pathomorphological result. This can be explained by the fact that under some stressful factors hepatocytes originally perish due to apoptosis, and only after that one can see both monocellular and local necrosis in the organ[8]. Taking into account the above, we can come to the following conclusion that the spirit extract produced from dead bees possesses a certain activity stimulating stress adaptation processes in the liver.

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THE PRACTICALLY HEALTHY PEOPLE'S LARGE INTESTINE MICROBIAL FLORA COMPOSITION

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At present, the normal microflora is, practically, being considered, as the owner's human organism integral part, the original and the peculiar extracorporeal human organ, having involved just into the proper and also the allogenic and the foreign substances, just into the structure, which the first is, practically, being involved just into the absorption, and, through which the translocation is being proceeded on, as the useful, well as the potentially harmful agents, including the microbial origin [3].

The practically healthy people's at the age in the range from 3 up to 45 years microbial flora has been studied and thoroughly investigated by us. The microscopic and the culture methods use have been shown, that the protozoa infection has been made up 2,73 % (e.g. 3 persons) just in this group, and this, moreover, is, considerably, being lowered the people's with the gastrointestinal tract pathologies analogous index. So, in all these cases, the protozoa finding has been accompanied with the bowels microflora disbiotic changes, having, at the same time, the various degree of the manifestation.

The «normal» microflora notion has already been defined, as the large intestine bacterial dissemination average physiological value, having taken into consideration the received final results' oscillations.

All these investigations have been carried out, having defined the qualitative and the quantitative compositions of the bacterial communities with the following space structure identification and also the ecological groups' hierarchy.

The received final data analysis has been permitted to be identified the 390 microorganisms strain and also to be related them to the 11 deliveries.

The bowels microflora composition study and the thoroughly investigation had already been shown, that its composition was enough diverse and suffice various (table 1). The obligate – anaerobic flora analysis was been shown, that the bowels' colonization density by the obligate – anaerobic bacteria had been presented by the representatives' high level concentrations, having been studied and thoroughly investigated taxa. So, the bacteroides' values oscillations have been from 10^8 up to 10^{10} QEU/gr. The clostridia's dissemination lower bound has not been exceeded 10^5 QEU/gr. Thus, the healthy man's average colonization density by the obligate – anaerobic microorganisms has been defined, as $10,3 \pm 0,7$ QEU/gr.

Table 1. The Large Intestine's Microflora Main Representatives

Microorganisms	Abs.	%	1gr. QEU/gr., M□m
Lactobacteria	80	100,0	8,8□0,6
Bifidus bacteria	80	100,0	9,3□0,1
Escherichia	80	100,0	7,4□0,3
Bacteroides	52	65,0	10,3□0,1
Enterococcus	14	17,5	4,7□0,2
Enterobacteria (totally)	17	21,3	3,7□0,2
Protei	8	10,0	3,5□0,1
Клебсиеллы	6	7,5	3,4□0,7
Enterobacter	3	3,7	3,1□0,5
Staphylococci	16	20,0	4,1□0,4
Candida Fungi	22	27,5	3,3□0,1
Clostridia	5	6,2	6,0□0,8

So, the singled out microorganisms identification was shown, that the bacteroides were being occupied the dominating situation among the anaerobic flora, which were being made up the most numerous bacteria group, as by the character frequency, well as by their colonization density. Thus, the healthy people's average bacteroides' content just in the bowels has been equaled to 10,3□0,1 QEU/gr., and they have been discovered at the 65,0 % examined persons. The bacteroides – are the Gram – positive anaerobic bacilli, which are not being formed the spores; they give the following growth, just in the form of the whitish or the grayish colonies with the smooth edges, having had the 3 – 6 mm [1] just on the solid and nutrient medium.

By the authors' majority data, the clostridia are the Gram – positive, spore – forming, frequently movable, bacilliform bacteria, and the obligate anaerobes [4]. They are being related to the bowels' normal microflora optional part. But they are being found seldom, and, moreover, their quantity will not have to be exceeded 10⁷ QEU/gr. just in the normal biocoenosis [2,5]. The clostridia have been found just at 5 persons, that has been made up 6,25 % in the carried out studies and thoroughly investigations, for all this, the dissemination density has been varied in the range from 10⁵ up to 10⁷ microbial bodies, having had the average value, which is equal to lgr. 6,0 □ 0,8 QEU/gr.

The aerobic microflora analysis has been shown, that the microorganisms' abundance is being dominated just in the healthy people's bowels. The biocoenosis' constant representatives have been the lactobacteria (e.g. 100,0 %), for all this, all these microbes have been found just in the titres in the range of 10⁷ – 10¹⁰ QEU/gr. at the examined majority.

The bifidus bacteria have also, frequently, been discovered just in the microflora (e.g. 100,0 %), for all this, the dissemination average arithmetic value has been rather considerable (e.g. lgr. 9,3□0,1 QEU/gr.).

The considerable physiological role is being belonged to the bacteria bowels' group among the large intestine aerobic flora. The study and the thoroughly escherichia qualitative and the quantitative compositions investigation are being presented the quite reasonable ones for us. It has, moreover, been shown in this work, that the *E. coli* have been found at all the examined ones (e.g. 100 %) with the values fluctuations just in the range of from the 200 mln. up to 1 bln. microbial bodies in 1 gr. faeces, for all this, the dissemination value was equal to lg 7,4□0,3 QEU/gr.

The opportunistic pathogen enterobacteria (e.g. 21,25 %) have been sowed, quite often, just from the healthy people's faeces. The high microbial number has been fixed just for the protei – lgr. 3,5□0,1 QEU/gr. and also the клебсиелл – lgr. 3,4□0,7 QEU/gr., the enterobacteria (lgr. 3,1□0,5 QEU/gr.) have been discovered the less dissemination.

The staphylococci and the fungi sort of *Candida* have been met, enough frequently, among the opportunistic pathogen microorganisms. The representatives sort of *Staphylococcus* have been found at the 20,0 % persons, for all this the *S. epidermidis* (e.g. 15,0 %) has been sowed much more frequently, the *S. aureus* (e.g. 3,75 %) – considerably much infrequent, and 1,25 % has been fallen for the part of the rest sorts and types.

The yeast – like fungi sort of *Candida* (e.g. 27,5 %) have been registered, fairly often, at the healthy people's microflora. However, the dissemination has been rather insignificant by all these microorganisms, and the average arithmetic value has been made up lgr. 3,3□0,1 QEU/gr..

Thus, all these carried out studies and thoroughly investigations have been shown, that the healthy people's large intestine microflora is usually being characterized by the aerobic microorganisms' dominance. It should be noted, that this microorganism is quite able to be used, as the indicator one, at the microflora carried out study and thoroughly investiga-

tion, which is, as in the quite norm, well as at the pathology.

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BLOOD ERYTHROCYTE LIPIDS IN CONDITIONS OF ADAPTATION TO ALIMENTARY STRESS-FACTORS OF RATS

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Erythrocyte phospholipids (PL) and lipid fatty acids (FA) composition was investigated at different stages of exposure to high-caloric diet in male Wistar rats. Fat diet mainly included 2% of cholesterol and 19% of tallow of the total allowance. The animals were divided into 4 groups, 10 rats in each: control group comprising intact rats kept on the vivarium standard allowance; and groups comprising animals kept on experimental diet (30 days – group 1; 90 days – group 2; and 180 days – group 3). Lipids were extracted from erythrocytes by Bligh and Dyer method (1959). Quantitative analysis of certain phospholipids classes after thin layer chromatography was made according to V.E. Vaskovsky et al method (1972, 1975). FA methyl ethers were received by Carreau and Duback method (1978), analyzed on Shimadzu GC17A gas-liquid chromatographer equipped. Results were represented in relative percentage of total FA.

Separation of erythrocyte PL mixture of rats identified six components including phosphatidylcho-

line (PC), phosphatidylethanolamine (PE), phosphatidylserine (PS), sphingomyelin (SM), phosphatidylinositol (PI). Rats of group 1 demonstrated PL redistribution towards PS and PE accumulation and PI and PC share reduction. Onset of the deficit PI and PC, the PL which form outer monolayer of membrane lipid frame, indicate activation of specific phospholipases and intensification of lipoperoxidation processes contributing to plasma membrane destruction. Changes in erythrocyte membrane at PS, PC and PE level in rats kept on high-caloric diet for 90 days was of the same direction as in rats of test group 1. PC deficiency in outer layer of erythrocyte membranes was compensated by SM maintenance within the range pertinent to control group animals. Such condition can be described as a compensatory response of cell to long-term exposure to stress factors of alimentary nature. Moreover, due to the high saturation with PE cholesterol is hardly built into the inner monolayer. This helps to preserve hydrophil surrounding of cell membrane integral proteins and, therefore, their function. Depletion of erythrocyte PC which forms outer shell of cell lipid matrix was evidenced at a longer exposure to high-caloric diet (180 days) as well. PC reduction in group 3 was accompanied by reliable increase in PS and SM level as compared to control group, meaning that erythrocytic cell was structurally and functionally inadequate. Due to high saturation with SM, the clusters forming phospholipid in a membrane receive large quantity of cholesterol, and this results in lower permeability of cell membrane and interference in active metabolic processes. Thus, on the 180th day of the experiment cell membrane became unable to resist the continuous flow of alimentary stress factors, and the stage of cell compensatory protection depletion occurred that had been formed by the 90th day of high-caloric diet.

Analysis of the qualitative composition of FA of erythrocyte lipids showed that rats with dyslipidemia have considerable changes in FA composition as compared to control group. 14:0, 18:0, 17:0 FA share was observed to increase in group 1. Unsaturated FA demonstrated minor increase in relative level of 18:1n9, reliable accumulation of some n6 – 20:4n6, 22:4n6, 22:5n6 family FA and drop in 18:2n6. Share of polyunsaturated fatty acids (PUFA) of n3 family slightly reduced due to the identified decrease in 20:5 and 22:6. FA saturation index in rats of group 1 was low. Growing share of 22:4n6 and 22:5n6 in erythrocyte lipids can be deemed a compensatory response to the deficiency of 22:6n3. Blood erythrocytes of group 2 showed reduction of 12:0 and 15:0 share and increase in 16:0 and 18:0. On the contrary, rats of group 3 demonstrated growth of 12:0 level. Accumulation of saturated 14:0, 16:0 and 18:0 FA in erythrocyte lipids was more evident than in rats of group 2. Modification of n6 composition in PUFA was distinguished by reducing 18:2n6 share, reliable figures being obtained from rats of group 3; and growth of relative 20:2n6,