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DYNAMICS OF CHANGES OF THE NUMBER OF LACTOBACILLI AND BIFIDOBACTERIA IN THE GUT OF MICE UNDER THE INFLUENCE OF FAT ENRICHED DIET

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Microecological violations of various organs and body systems are triggers for development of metabolic diseases and related pathological processes, which are based on altered metabolism of lipids. Obesity in adults and children is a global epidemic in most countries of the world, that considered as the main risk factor for non-infectious diseases, such as diabetes, cardiovascular diseases [1-2].

The important role of gut microbiota in the development of metabolic diseases has previously been confirmed in experimental models of obesity in mice. So, colonization of sterile mice by cecal microbiota of mice with obesity resulted in greater weight gain and fat accumulation than the colonization by cecal microbiota of ordinary mice [3]. Gut microbiota can influence on cholesterol metabolism through many mechanisms [4]. Thus, the search for new targets for pharmacological intervention in obesity remains relevant for modern research in this field.

Therefore, the aim of this study was to determine the dynamics of changes in the number of lactobacilli and bifidobacteria in the intestine of mice under the influence of the fat enriched diet.

Experimental studies were conducted on female BALB/c line mice at the age of 6-8 weeks (17-24 g). Animals during the experiment were kept in standard vivarium conditions, in plastic cages in a separate room at a steady temperature (20-22 °C), they were provided with the full mixed feed and had free access to automatic water bowls. The keeping experimental animals was performed in accordance with the requirements of the "European Convention for the Protection of vertebrate animals used for experimental and scientific purposes from 09.20.1985" (Strasbourg, 1986) and in accordance with "General ethical principles of animal experiments".

To simulate obesity, mice during 3 weeks obtained the fat-enriched diet (FED), composed of fats – 60%, proteins – 20% and carbohydrates – 20%. From the next day (1st day of the study), these mice started to receive standard full mixed feed. The dynamic of changes of gut microbiota spectrum was determined during 30 days after FED ended. The number of lactobacilli (on the Man-Rogosa-Sharpe agar medium), bifidobacteria (on the Bifidum-agar medium) and the total number of aerobic and optionally anaerobic microorganisms (on the MPA medium) were defined in the intestine contents (colony forming units (CFU)/mg). Petri dishes with aliquots were cultivated at 37 °C for 48 hours.

In our studies was shown that FED increased the total level of aerobic and optionally anaerobic microorganisms in the gut of mice. On the 4th day after the end of FED, the number of this group of bacteria in the gut was at the level of 4.47 ± 0.07 against 3.11 ± 0.09 Lg(CFU)/mg in intact mice. Total amount of aerobic and optionally anaerobic microorganisms remained at the level that exceeded indicators of intact mice during month of observation (3.98 ± 0.03 Lg(CFU)/mg on the 30th day after mice started to receive standard full-mixed feed again).

We observed decreasing of *Lactobacillus* spp. and *Bifidobacterium* spp amount in the

intestine contents of mice after 3 weeks of FED: the number of lactobacilli in the gut decreased to the level of 0.52 ± 0.06 against 2.68 ± 0.02 Lg(CFU)/mg in intact mice, and the number of bifidobacteria – to the level of 1.44 ± 0.06 against 2.15 ± 0.02 Lg(CFU)/mg in intact mice. It should also be noted that the number of bifidobacteria in the intestine contents of mice that obtained FED recovered during 2 weeks after mice started to receive standard full-mixed feed again, and on the 15^{th} day the level of bifidobacteria in the gut of this group of mice was equal to indicators of intact mice. The number of lactobacilli in the gut of mice that obtained FED remained lower than in intact mice even after 30 days after this mice started to obtain standard feed again.

So, we can make a conclusion that the created by us fat-enriched diet changed gut microbiota of mice. These changes remained significant in comparison with intact mice indicators even after month since mice started to obtain standard diet again.

Given this, further studies of the role of gut microbiota in metabolic disorders, obesity and other metabolic diseases is a perspective direction of their diagnosis and prognosis and developing of new evidence-based treatments of patients with natural and safe biological drugs based on commensal microbiota of human mucous membranes – probiotics, which are proven to normalize intestinal microbiota and affect lipid metabolism, carbohydrate balance, immune response and change the microenvironment within the gut, etc.

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