International Journal of
Health Systems and Medical Sciences

ISSN: 2833-7433
Volume 2 | No 8 | Aug -2023

Indicators for Determining the Degree of Influence of Gene-Modified Shade on the Normative Microflora of the Colon in Laboratory Animals

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Abstract: One such biotope is the Colon, whose regulatory microflora, consisting of indigene and facultative microorganisms, is important for life activity etadi.Ma colon microbiocenosis, consisting of more than 450 microorganisms, is involved in the metabolism of the "master" organism and the formation of colonization resistance in the intestine

Many scientific works have been done on the different effects of gene-modified (GM) products on the human body, and the opinions of experts are different in this regard, in addition to the opinions that there are no negative effects of these products on the human body, works that have been proven to have a negative impact on the body of ham talaygina. Scientific work confirming further views has been proven to have negative effects of GM-product on the immune system in the experiment, liver and pancreas, thymus and spleen, as well as hematological, biochemical changes, mutagenic and reproductive activities, bone marrow cells, which have been shown to have negative effects on ham.

An analysis of many scientific literature shows that there is little work to determine the degree of influence of GM-products on human biotope microbiocenosis, including colon microbiosis, and there is a distribution of raw.

Taking into account the above, the Holda research of GM-shade in the experiment was to determine the degree of influence of white-breed rats on Colon microbiocenosis.

Material and methods. To do this, a total of 90 white non-breeding bats of male sex were involved in the study, which were divided into 3 groups:Group 1 - intact white non-breeding bats (n=30), which were in the standard vivarium ration, GM-li or GM-not soy - fed;group 2-white non-breeding bats (n=30), which were soy - fed to the standard vivarium ration 30).

These groups were representative and differed from each other by only one character. Research has focused on being randomized as well as following the principles of evidence-based medicine. The study strictly followed the ethical principles of working with laboratory animals and the rules of Biological Safety [1.3.5.7.9.11.13].

After the White-breed rats were delivered to the colon mass bacteriological laboratory, the following microorganisms were identified and differentiated according to Bergy's Manual Systematic Bacteriology (1997) using appropriate food environments (Blaurokk, SRM-4 (Mrs-4), Endo,Saburo environments, egg-yellow agar, etc.): Bifidobacterium spp, Lactobacillus spp, Escherichia coli, Enterobacter spp, Proteus SPP, Staphylococcus spp, Streptococcus spp, Candida spp.

Intergenerational and interspecific identification was performed by the firm" HiMedia " (India) using food environments.

Statistical work of the results was carried out using traditional methods of variational statistics, the principles of evidence-based medicine were followed when organizing and conducting research.

Results and their discussion. The results obtained showed that among the groups being compared there were convincing differences in the quantitative indicators under study.

Apparently, in 7 of the 9 studied representatives of the colon microflora (77.78%), convincing changes were detected, it is worth noting that the quantitative indicators of microorganisms have changed in different directions compared to the norm (group 1). Only the indicators associated with Escherichia coli have not changed convincingly in either group. In Endo mukhiti, the quantitative indicators of Escherichia coli (lactozapositive intestinal rod), which form metal-glittering fuchsin-reddish colonies, Cleave GISS-row lactose to acid and gas, pathogenmless Escherichia coli (lactozapositive intestinal rod) and Endo mukhitida, which form dark,light-red(or colorless) colonies, do not have the property of breaking down lactose in the Giss-row, exhibit pathogenicity (R0, 05) were close to one (R0, 05).

The analysis carried out showed that a convincing decrease in quantitative indicators compared to the control group (intakt) in Group 2 (GM-you consumed soy) was observed among representatives of the normative indigene microflora of the colon. Whereas Bifidobacterium srrmicdorium depletion was up to 1.28 times (R0,05), quantitative depletion in Lactobacillus spp was up to 1.53 times (R0,05). It was shown that this condition is the first sign of the onset of processes in the colon of Group 2 laboratory animals that lead to a dysbiotic state.

Similar to the above can be observed in the case of Streptococcus spp, another representative of the normative microflora,Ham, whose concentration in the colon was found to have decreased by 1.58 times (R0, 05). This condition has been interpreted as a prelude to ham dysbiotic processes. Assuming that, unlike the control group, there is only one external means of influence (shadow) in Group 2, it was understood that these changes were influenced by it, the decrease in the quantitative parameters of the intestinal indigen microflora was interpreted as a temporary condition, since this is an unfamiliar product for the organism of white-breed rats.

It is worth noting that the quantitative increase in Group parameters fell mainly on Enterobacteria and coagulazamusbat coccus when the control group is compared with the indicators of laboratory animals, considering that their entry into the colon facultative (transistor) microflora, inappropriate the nature of pathogenicity when falling under favorable conditions, it was observed that in this biotope the imbalance of Chunonchi,a quantitative increase in Group 2 was observed in Enterobacter spp and Proteus spp in representatives of the Enterobacteriaceae family – 4.17 times (R0,001) and 6.25 times (R0, 001), respectively. The quantitative increase in these microorganisms was interpreted as the beginning of the processes of dysbiosis in the colon [2.4.6.8.10.12.14.16.18].

In the study of the quantitative indicator Escherichia coli, another representative of the normative microflora of the colon, we witnessed a different picture. It has the ability to break down lactose, while pathogenmas germinated in this Gram-negative bacteria control group at a rate of 5.15±0.2 lg KXQB/ml, the White-breed rats of Group 3 did not germinate from biological material from the large intestine. However, Escherichia coli strains capable of pathogenicity have been recognized in the control group that these strains have not been identified at all, having been germinated at a rate of 5.30±0.3 lg KXQB/ml. This condition is another of the main signs of the dysbiosis process developing in this biotope.

In the quantitative indicators of Enterobacter spp and Proteus spp, other representatives of the Enterobacteriaceae family, changes such as ham lactozanegative Escherichia coli were observed, in other words, their quantitative indicators exceeded the norm limits – 5.45±0.2 lg KXQB/ml and 3.00±0.1 lg KXQB/ml, respectively. These figures were characterized by a convincing abundance of 4.54 and 3.75 times,respectively, from the limits of the norm (R0, 001). Such a condition is caused by the fact that the quantitative decrease in indigenic microorganisms is conditional-an increase in

pathogenic entrobacteria. This pronounced appearance is a sign of the formation of large intestinal dysbiotic processes.

The above drastic changes in Gram-negative bacteria were not observed in Gram-positive cocci, although the quantitative indicators varied between groups, the intensity of the changes was low. If Staphylococcus spp had a convincing increase of 1.50 times compared to Group 1 in Group 3 (4.10±0.1 lg KXQB/ml versus 6.15±0.2 lg kxqb/ml, R0,05, respectively), we witnessed a reverse landscape on Streptococcus spp,i.e. Group 3 recognition rates decreased convincingly by 1.47 times compared to the control group (Group 1) (R0, 05).

According to Candida spp, similar results were obtained to the parameters of facultative microorganisms consisting of ham conditional-pathogenic microorganisms. In the large intestine of white non-breeding rats fed GM-soy, the amount of microorganisms that are part of this generation of yeast fungi has become convincingly higher than the indicators of intact rats that are not fed GM-soy (1.94 times, R0,001).

As a result of GM-soy exposure, when the formation and development of dysbiotic processes in the large intestine of white-breed rats was shown, it became necessary to assess the level of changes in the quantitative indicators of indigene and facultative microflora. To do this, the ratio of the quantitative indicators of the groups being compared to one another was studied.In Group 3 (GM-soy-fed) with a convincing decrease in the quantitative indicator of indigene microorganisms compared to Group 1 (GM-not soy-fed) (R0,001) with a convincing increase in the quantitative parameters of facultative microorganisms (R0,05-R0,001). This condition has been interpreted as another indication that they have developed deep dysbiosis in the colon when exposed to GM-soy.

Although the results of both groups differ from the parameters of intakt laboratory testes, the intensity and depth of the changes were clearly inconsistent in Group 3. So it was important to determine the degree of changes in the GM-free and GM-li shade relative to each other.

Representatives of the intestinal indigen microflora were found to differ between quantitative indicators of Bifidobacterium spp and Lactobacillus spp – a convincing decrease of 1.90 times and up to 2.0 times,respectively (R0, 001).

In 2 of the 9 microorganisms studied (Staphylococcus spp, Candida spp), the intergroup discrepancy was not detected (R>0.05), which became quantitatively close to birbiri. Noteworthy is that 1 of them belongs to the group of facultative microorganisms. There was no known legality in this case. But it was found that indigene microorganisms (Bifidobacterium spp, Lactobacillus spp) decreased even more in Group 3, whereas facultative microorganisms (Enterobacter spp, Staphylococcus spp) increased even more. The results obtained on lactozanegative and lactozapositive Escherichia coli showed a marked difference between these groups. In other words, GM-soy-fed laboratory animals contain all 5 listed elements of dysbiosis, while GM-free soy-consumed rats did not show up vividly.

In order to summarize all the results obtained, we found it necessary to cite all three groups of pointers in a comparative way.

The convincing difference between these groups is obvious, the analyzed figures showed that laboratory animals that are not soy-fed (intact, control) without GM-there are no practical changes in the normative microflora of the colon, no signs of dysbiosis were detected; laboratory animals that consumed GM-soy (group 2) have partially impaired balance between indigene and facultative microorganisms, there are symptoms of dysbiosis, but; In GM-soy-fed hyacinths (group 3), the balance of indigene and facultative microorganisms in relation to one another is disturbed, signs of dysbiosis are clearly observed, all 5 elements of it are identified, colon Total dysbiosis has developed. This condition was interpreted as GM-shade exposure to the organism of white-breed bats. It has been proven that laboratory monsters of GM-soy negatively affect the normative microflora of the colon and call Total dysbiosis [11.13.15.17].

In Level I dysbiosis-changes are observed only among representatives of the indigen group, Bifidobacterium spp and Lactobacillus spp are reduced compared to lactozapositivesshegishia coli, intestinal dysfunction is not manifested.

In Level II dysbiosis - the decrease in indigenic microorganisms is equal, the amount of facultative conditional-pathogenic microorganisms increases, the balance between them is disturbed, the symptoms of intestinal dysfunction are clearly visible.These levels are determined using the dysbacteriosis index (Di:

DII= E.coli KXQB/g / indigene microorganisms, KXQB / g <0.1;

DIII = facultative microorganisms, KXQB/g/ indigene microorganisms, KXQB/g ≤ 0.5.

If DII> 0.1; DIII ≤ 0.5, this is level I of dysbiosis, if Di II > 0.5, Di i is Level II of dysbiosis no matter how many.

The results obtained during our studies were as follows:

Group 1 - 0.31<0.1 (DII); 0.37<0.5 (Di II;

Group 2 - 0.38<0.1 (DII); 0.77<0.5 (Di II;

Group 3 - 1.29<0.1 (DII); 3.56<0.5 (Di II).

The results obtained fully confirmed the above points, that is, there are no signs of dysbiosis in intact laboratory rats (Group 1), in GM-free soy feeders (group 2), the symptoms of dysbiosis are weakly developed (level I), in GM-soy-fed white zotless rats, the symptoms of dysbiosis are clearly manifested (Level II).

Conclusions.

1. GM-free soy-fed white-breed rats were observed in the colon normative microflora on Bifidobacterium spp (1.28 times decrease), Lactobacillus spp (1.53 times decrease), Enterobacter spp and Proteus spp (4.16 and 6.25 times increase). These are the initial signs of dysbiosis and do not indicate the development of complete dysbiosis, as the intergroup discrepancy between Escherichia colilactozanegative and lactosapositive strains has not been detected.

2. No drastic changes in Gram-positive coccus rates were detected in elements 1-3 of colon dysbiosis with the symptoms of this condition evident-while Streptococcus spp had a convincing decrease of 1.47 times compared to intact laboratory rats in the main group, the coagulazapositive Staphylococcus spp had a convincing increase of 1.50 times. This intergroup discrepancy was interpreted as the fourth element of colon dysbiosis.

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