

ORIGINAL ARTICLE

INTESTINAL MICROFLORA ON THE BACKGROUND OF BACTERIAL VAGINOSIS ON VULVOVAGINAL CANDIDIASIS IN OVERWEIGHT AND OBESE WOMEN

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ABSTRACT

The aim of our work was to study the intestinal microbiome in obese women and further develop differentiated patterns of exposure to the intestinal microbiota to improve metabolism and reduce excess weight.

Materials and methods: Surveyed 120 overweight and obese women. For comparison, 60 women without overweight and obesity were examined. Group I – women with vulvovaginal candidiasis and overweight and obesity (60 women); group II – women with vulvovaginal candidiasis without overweight and obesity (30 women); group III – women with bacterial vaginosis and overweight and obesity (60 women); IV – women with bacterial vaginosis without overweight and obesity (30 women). The study of the intestinal microbiocenosis included the determination of the species and quantitative composition of the microflora. Quantitative indicators of intestinal microflora were studied by seeding 1 ml from each dilution on differential diagnostic media: Endo, Ploskireva, ICA (bismuth – agar sulfide) to detect pathogenic enterobacteria; ZhSA (yellow – salt agar) for determination of staphylococci. To study the hemolytic activity of bacteria was used agar with 5% erythrocyte content of sheep. The presence of *bifidobacteria* in the test material was studied on Blauok medium, and *lactobacilli* – on MRS medium. Statistical analysis of the obtained research results was performed using standard computer packages “Data Analysis” Microsoft Excel for Windows 2002.

Results: Based on the results of studies, we can summarize the nature of changes in the intestinal microbiome on the background of vulvovaginal candidiasis and bacterial vaginosis in women with overweight and obesity. In all women with excess body weight and obesity, intestinal microflora disorders have been registered, which are characterized by the replacing the *lactobacilli* and *bifidum bacteria* to opportunistic pathogens. A significant increase in *Firmicutes* phylum microorganisms and a significant decrease in *Bacteroidetes* phylum were found. The obtained data prove that changes in the species composition of the intestinal microbiota play an important role in the pathogenesis of obesity.

Conclusions: The results indicate the feasibility of monitoring the intestinal microbiota in women with vulvovaginal candidiasis and bacterial vaginosis, especially in the presence of excess body weight and obesity to determine the degree of violations of its components, and timely correction of the detected changes.

KEY WORDS: vulvovaginal candidiasis, bacterial vaginosis, body weight and obesity, intestinal microbiota

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INTRODUCTION

Today, the problem of obesity on our planet affects more than 250 million people, more than 500 million people are overweight. Changes in dietary habits and increased availability of high-calorie food have made overweight and obesity one of the most serious health problems today [1, 2]. In recent years, changes in the human intestinal microbiome has been shown to play an important role in the development of obesity [3, 4]. There are 4 main phylum bacteria (*Bacteroidetes*, *Firmicutes*, *Actinobacteria*, *Proteobacteria*) in the large intestine of healthy people, which are divided into classes, genera and species of microorganisms. The vast majority of microorganisms that inhabit the large intestine are anaerobes. More than 90 % of the microflora of the distal colon in healthy people are microorganisms

of the phylum *Bacteroidetes* and *Firmicutes*. *Firmicutes* include more than 200 species of gram-positive bacteria, in particular, various species of *Clostridium*, *Staphylococcus*, *Streptococcus*, *Enterococcus* [5]. Phylum *Bacteroidetes* is represented by gram-negative bacteria such as *Bacteroides*, *Prevotella*.

Bacteroids play an important role in fat metabolism – provide hepato-intestinal circulation of bile acids and cholesterol catabolism. Normally, deoxycholic and chenodeoxycholic acids with participating the secretory IgA, inhibit the growth of pathogenic and opportunistic pathogens, even in natural for the body concentrations [6].

Proteobacteria include such gram-negative opportunistic enterobacteria as *E. coli*, *Klebsiella spp.*, *Citrobacter spp.*, *Proteus spp.*

Actinobacteria phylum consists of gram-positive bacteria, the most important of which are *Bifidobacterium*. *Bifidobacterium* production of lysozyme, bacteriocins, alcohols and high antagonistic activity against pathogenic bacteria prevent their penetration into the upper gastrointestinal tract [7].

Up to 10% of the total number of intestinal microorganisms are aerobic bacteria – *Escherichia coli*, *streptococci*, *staphylococci*, *enterococci*, various types of opportunistic *enterobacteria*, yeast-like fungi of the genus *Candida*.

In recent years, the development of candidiasis in overweight and obese people is increasingly associated with excessive carbohydrate intake. In addition, chronic inflammation that accompanies obesity affects a person's immune reactivity, increasing the likelihood of developing a fungal infection [8].

Among the fungi of the genus *Candida* which are of major importance as causative agents of candidiasis, are *Candida albicans*, *Candida glabrata*, *Candida tropicalis*, *Candida parapsilosis*, *Candida krusei*. Literature data show that against the background of obesity, *Candida albicans* and *Candida glabrata* are more often isolated from the intestine [9].

The reliability of the intestine ecological barrier is associated with *lactobacilli*. Reducing the number of *lactobacilli* in the intestine leads to the reproduction of pathogenic and opportunistic microorganisms [10].

Many scientists have studied changes in the intestinal microbiota in overweight and obesity. Studies have shown an association between obesity and the composition of the gut microbiome [11].

Thus, a number of studies have found a numerical increase in bacteria of the *Firmicutes* type compared with representatives of the *Bacteroidetes* type and more energy storage from food in overweight people. Some researchers believe that an increase in the microbiome of obese bacteria that ferment polysaccharides with forming the large amounts of short-chain fatty acids (CLA) [12] plays a role in providing an increased energy reserve in the colon and developing the obesity.

Firmicutes, such as those found in large numbers in obese patients, are thought to express genes encoding enzymes that break down undigested polysaccharides. This increases the concentration of KLZHK, providing *colonocytes* with an available source of energy. As a result, the energy value of food increases, which is eventually realized by weight gain [13].

It was found that as the degree of obesity increases, the degree of microecology of the large intestinal cavity increases, which can be explained by the close relationship between the processes of absorption and metabolism in the background of intestinal microecology [14 – 16].

THE AIM

The aim of our work was to study the intestinal microbiome in obese women and further develop differentiated patterns of exposure to the intestinal microbiota to improve metabolism and reduce excess weight.

MATERIALS AND METHODS

In order to solve the tasks set in our work, we surveyed 120 overweight and obese women. For comparison, 60 women without overweight and obesity were examined. All women were divided into groups:

Group I – women with vulvovaginal candidiasis and overweight and obesity (60 women); group II – women with vulvovaginal candidiasis without overweight and obesity (30 women); group III – women with bacterial vaginosis and overweight and obesity (60 women); IV – women with bacterial vaginosis without overweight and obesity (30 women). The data obtained during the examination of 30 healthy women were used as a control.

The study of the intestinal microbiocenosis included the determination of the species and quantitative composition of the microflora. The degree of intestinal biocenosis violations was assessed according to the guidelines by Bondarenko V.M., Matsulevich T.V. "Microbiological diagnosis of intestinal dysbacteriosis" Moscow, 2007.

For quantitative analysis of the intestinal microflora from 1 g of feces delivered without preservatives, a working dilution (1:10) was prepared, from which a number of serial dilutions (10³ – 10¹¹) were made. Quantitative indicators of intestinal microflora were studied by seeding 1 ml from each dilution on differential diagnostic media: *Endo*, *Ploskireva*, *ICA* (bismuth – agar sulfide) to detect pathogenic *enterobacteria*; *ZhSA* (yellow – salt agar) for determination of staphylococci; *Endo* and *Simons citrate* for the determination of *Escherichia coli* and opportunistic *enterobacteria*; *EDDS* medium – for the detection of *enterococci*. To study the hemolytic activity of bacteria was used agar with 5% erythrocyte content of sheep. The presence of *bifidobacteria* in the test material was studied on *Blaurok* medium, and *lactobacilli* – on *MRS* medium. The number of *bifidobacteria* and *lactobacilli* was determined by diluting the material.

Saburo medium was used to identify yeast-like fungi. *MICROLA-TEST* kits "Candida test 21" (Erba Lachema s.r.o. (Czech Republic)) were used for further identification of isolated yeast-like fungi.

The taxonomic position of microorganisms was determined according to the "Determinant of Bergey bacteria". Identification of microorganisms was performed by their cultural and morphological characteristics.

Determination of anaerobic microorganisms was carried out according to the guidelines "Laboratory diagnosis of purulent – inflammatory diseases caused by asporogenic anaerobic microorganisms", Kharkiv, 1985.

Anaerobic intestinal microflora was studied with strict adherence to the technique of anaerobic culture. Solid and liquid nutrient media (thioglycol medium, blood agar with glucose, liver broth, Kitt-Tarozzi medium) were used for the study. The *Anaerocult* system (Merck, Germany) and the *Anaerogas* gas packages were used to create anaerobic conditions. *MICROLA-TEST* kits "Anaero test 23" (Erba Lachema s.r.o. (Czech Republic)) were used for further identification of isolated anaerobic microorganisms.

To assess the degree of intestinal dysbacteriosis, quantitative accounting of colonies grown in dense nutrient media was performed.

The content of UPM in the test material was expressed by the number of colony-forming units in 1 g (CFU / g) of biological material.

Statistical analysis of the obtained research results was performed using standard computer packages "Data Analysis" Microsoft Excel for Windows 2002. The values of the arithmetic mean were calculated – the value (M), the average error of the average value (m), the level of probability of discrepancies (p). The reliability of the obtained data was evaluated by the generally accepted method using the Student's criterion. Reliability was considered established if its probability was at least 95% (0.05).

RESULTS

Intestinal dysbiosis was found in all examined patients with vulvovaginal candidiasis and obesity (group I). II degree of dysbiosis was registered in 41.7% of patients, III degree in 58.3% of women.

When examining women of group I it was found that *E. coli* was detected in the majority of subjects (95 %), but its quantitative level did not reach the indicators in the group of healthy women and was lg 5.8 CFU / g (Fig. 1). *E. coli* with hemolytic properties was sown with a high frequency – 28.3 %, at a concentration of lg 7.2 CFU / g, which significantly exceeded the diagnostic level. Also, among *Proteobacteria* such opportunistic microorganisms as *Serratia spp.* – 31.7 %, *Klebsiella spp.* – 26.7 %, *Enterobacter spp.* – 25 %, *Citrobacter spp.* – 18.3%.

The quantitative indicators of registering the citrate-stimulating bacteria exceeded the norm and were within lg 6.2 CFU/g–lg 7.5 CFU/g.

When examining patients of group I was revealed an increase in qualitative and quantitative indicators of staphylococci seeding, streptococci belonging to *Firmicutes*. The seeding frequency of *S. faecalis* reached 70 %, *S. aureus* – 48.3 %, *S. epidermidis* with hemolytic properties – 46.7 %.

A high level of intestinal contamination with gram-positive cocci with pathogenic properties was registered: lg 5.4 CFU/g – lg 5.6 CFU/g. The amount of *S. faecalis* (lg 7.3 CFU/g) also exceeded the diagnostic level.

Fungi of the genus *Candida* were found in the intestine in 100 % of women with vulvovaginal candidiasis at a concentration of lg 6.5 CFU/g. *Candida albicans*–71.7 %, *Candida glabrata* –20.0% were most often sown from the intestines of patients of group I. Other species of fungi were isolated with insignificant frequency (Fig. 2).

Therefore, it can be assumed that the source of highly virulent strains of fungi that infect the mucous membranes of the genitals is the intestine, and without inhibiting the growth of fungi in it, any therapy aimed at treating genital candidiasis is usually unsuccessful and subsequently leads to recurrence of the disease.

The analysis of seeding indicators of indigenous intestinal microflora made it possible to state a significant decrease in its number – *Lactobacillus spp.* was sown in 73.3 % of women at a concentration of lg 5.2 CFU/g, and *Bifidobacterium spp.* in 68.3 % of subjects at a concentration of lg 6.2 CFU/g.

Among the representatives of the anaerobic microflora a significant proportion were bacteria of the phylum *Firmicutes*: *Peptostreptococcus spp.* was detected in 53.3% of patients, *Blautia spp.* in 75%, *Clostridium spp.* in 51.7%, *Eubacterium spp.* in 63.3%. The quantitative level of seeding these microorganisms in women with vulvovaginal candidiasis increased by almost two orders of magnitude compared to normal (Fig. 1).

Among other members of the obligate anaerobic microflora, there was a significant decrease in the qualitative and quantitative level of seeding from the intestine of *Bacteroides spp.* (38.3 %, lg 6.7 CFU/g) and *Prevotella spp.* (13.3 %, lg 6.0 CFU/g).

In 73.3 % of the examined patients of group I, associative forms of bacterial intestinal contamination were revealed. Mostly three – four component associations of staphylococci with opportunistic enterobacteria and fungi of the genus *Candida* were registered.

For comparison, the second group of women with vulvovaginal candidiasis without overweight and obesity was examined. The frequency of registration of grade III dysbacteriosis in patients with vulvovaginal candidiasis without overweight and obesity was 36.7 %, grade II–63.3 %. Intestinal microecology disorders in patients of group II were manifested in an increase in the frequency of seeding the lactose-negative *E. coli* – 16.7 %, *E. coli* (heme +) – 20 %, and certain species of enterobacteria (*Klebsiella spp.* – 23.3 %). Gram-positive cocci contaminated the intestines of women with vulvovaginal candidiasis without excess body weight and obesity with a much lower frequency than in women of group I. *S. aureus* was sown in 23.3% of women, *S. epidermidis* with hemolytic properties in 13.3 %. Quantitative seeding rates of opportunistic pathogens were also lower, compared with women of group I, but exceeded the rates of intestinal contamination in the group of healthy women.

Increased intestinal contamination with gram-negative rods and gram-positive cocci was accompanied by a deficiency of *Lactobacillus spp.* in 90% of subjects and *Bifidobacterium spp.* in 83.3% of group II women. Absence of *Lactobacillus spp.* found in 10% of patients with *Bifidobacterium spp.* in 16.7%. Fungi of *Candida* in the II group of examined patients were sown with a lower frequency (93.3%) than in patients of the first group. Quantitative indicators of *Candida* fungi (lg 5.3 CFU / g) also significantly exceeded the diagnostic level. *C. albicans* was found in 56.7% of cases in the species composition of *Candida* fungi. Among *Candida* non-albicans fungi, *C. glabrata* was most often registered in 23.3%, *C. parapsilosis* in 6.7% (Fig. 2).

As in the previous group of patients, the intestinal microflora was in 3–4 component associations. Associations of opportunistic pathogens were found in 66.7% of women in group II.

In women of this group, changes in the anaerobic component of the intestinal microbiocenosis differed from those obtained in patients of group I. In contrast to the results obtained in group I patients, no significant differences were found from the rate of seeding of *Bacteroidetes* phylum bacteria. Frequency and quantitative indicators of

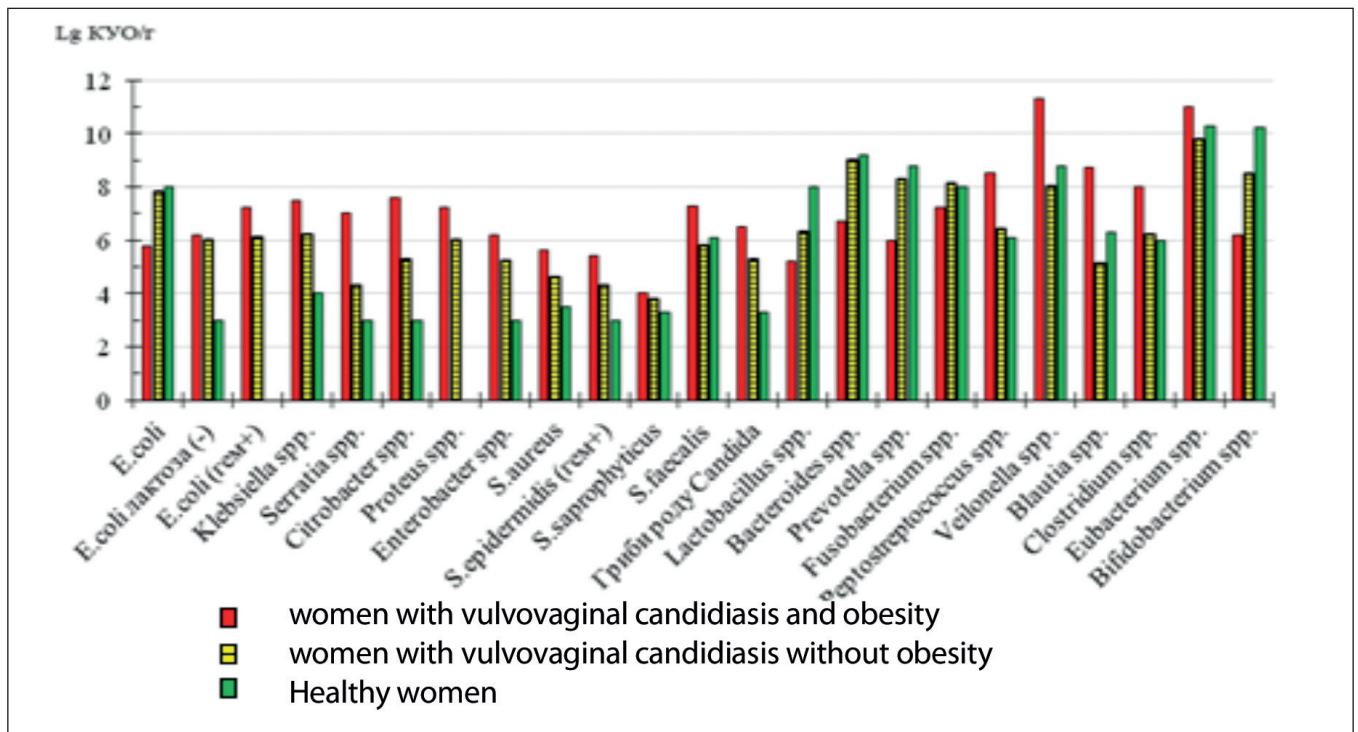


Fig.1. The composition of facultative and obligate anaerobic intestinal bacteria in women with vulvovaginal candidiasis and obesity

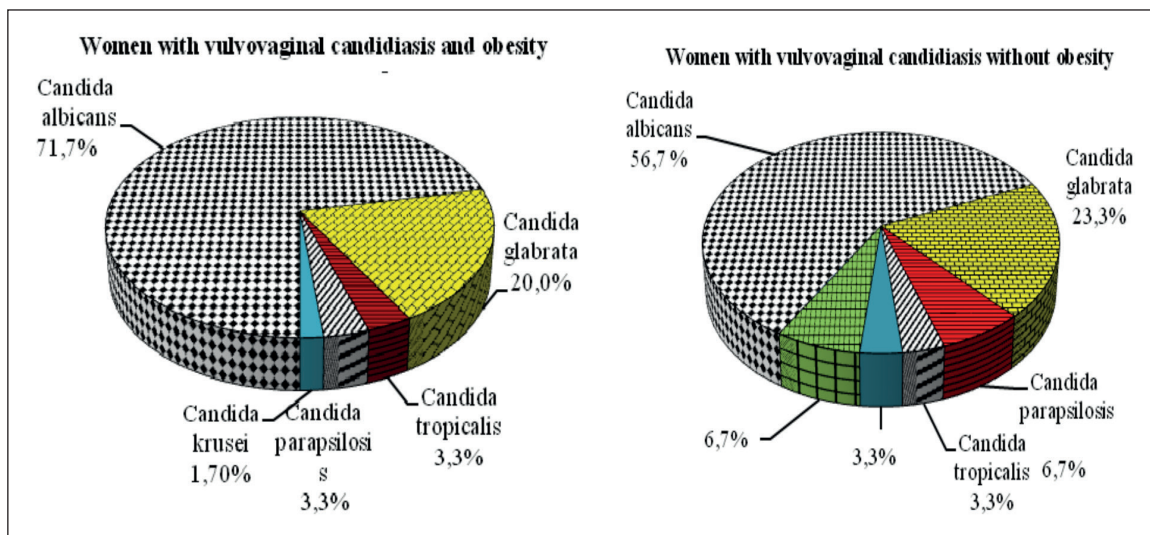


Fig.2. Species composition of genus *Candida* fungi isolated from the intestine in women with vulvovaginal candidiasis with obesity and without obesity.

seeding *Bacteroides* spp. were in 73.3% (lg 9.0 CFU / g) and *Prevotella* spp. in 30.0% (lg 8.3 CFU / g).

Representatives of anaerobic gram-positive microflora belonging to the *Firmicutes* type, contaminated the intestines of group II patients also with a lower frequency than in patients of group I.

From our studies it can be concluded that in patients of group II the imbalance between bacteroids and representatives of the microflora type *Firmicutes* was less significant than in women of group I.

Thus, the obtained data indicate that the most significant dysbiotic intestinal disorders were registered in the group of patients with vulvovaginal candidiasis in combination

with overweight and obesity. Detection of pathological changes in the intestinal microbiocenosis in these patients indicates the need to develop preventive and curative measures aimed at eliminating from the microbial associations of potentially pathogenic microflora and fungi of *Candida*, as well as normalizing the relationship between *Firmicutes* and *Bacteroidetes* towards the latter.

The task also included the study of intestinal microbiome in women with bacterial vaginosis and obesity. The majority of women in group III registered the formation of intestinal dysbiosis, mainly II-III degree (II degree-31.7%, III degree – 68.3%). The amount of *E. coli* in patients of group III did not reach the level of healthy women. In the

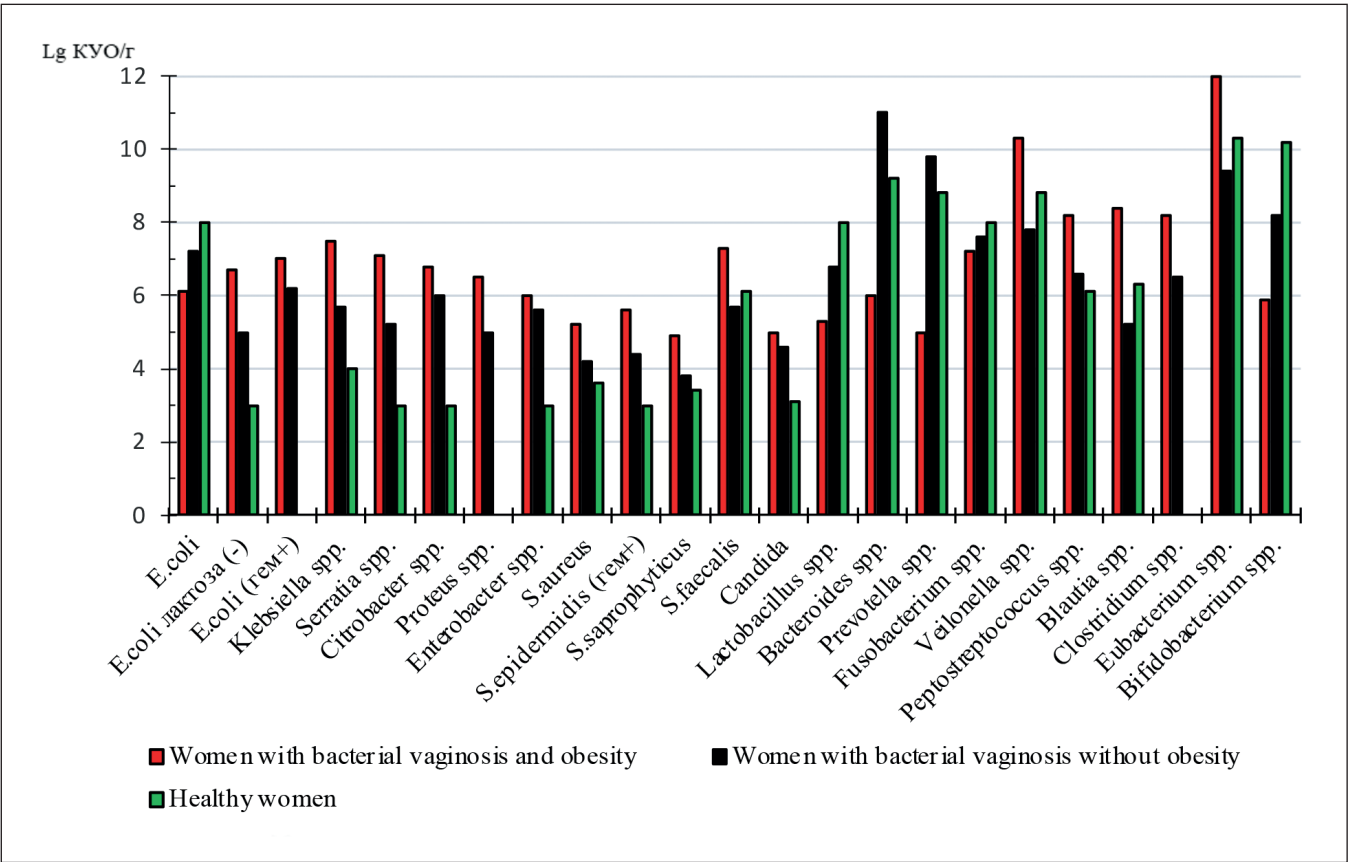


Fig. 3. The composition of facultative and obligate anaerobic intestinal bacteria in women with bacterial vaginosis and obesity

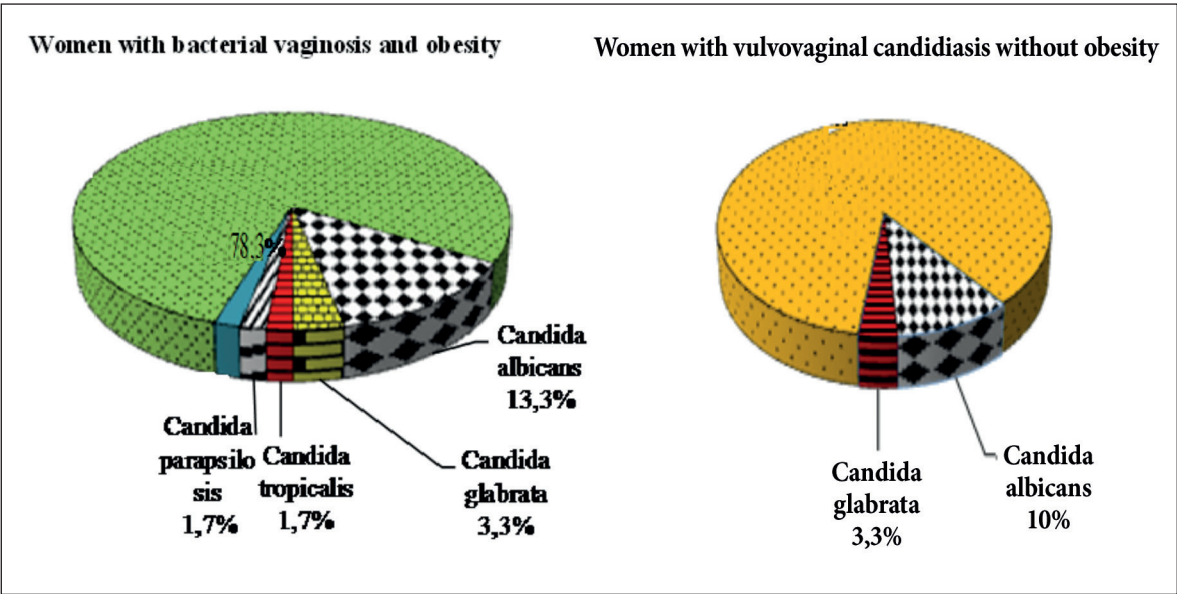


Fig. 4. Species composition of fungi of the genus *Candida* isolated from the intestines of women, with bacterial vaginosis and obesity and without obesity

spectrum of *Escherichia coli* there is an increase in the frequency of detection and concentration of *E. coli* with hemolytic properties – 25% (lg 6.7 CFU / g) (Fig. 3). Qualitative indicators of intestinal contamination of women with bacterial vaginosis and obesity (group III) indicate a high frequency of seeding the opportunistic enterobacteria: *Enterobacter* spp.-21.7%, *Proteus* spp. in

16.7%, *Citrobacter* spp. in 28.3%, *Klebsiella* spp. in 23.3%, *Serratia* spp. in 48.3%, in concentrations exceeding the diagnostic level > lg 6.0 CFU / g and data obtained from the examination of healthy women. Examination of women with bacterial vaginosis and obesity revealed an increase in the qualitative and quantitative indicators of staphylococci seeding, streptococci belonging to *Firmicutes*.

The seeding frequency of *S. aureus* reached 36.7%, *S. epidermidis* (heme +) – 38.3%, *S. saprophyticus* – 41.7%, *S. faecalis* – 76, %. Quantitative indicators of seeding the coccal microflora also reached a significant level: lg 5.2 CFU / g – lg 7.3 CFU / g.

The frequency of detecting the genus *Candida* fungi in female patients of this group was not very high and was 21.7%. *Candida albicans* was found with the highest frequency – 13.3%. Other species of fungi were isolated with insignificant frequency (Fig. 4).

Quantitative indicators of intestinal contamination in women of group III by the genus *Candida* fungi were – lg 5.0 CFU / g and exceeded the diagnostic level (> lg 4.0 CFU / g). Also, in patients of group III there is a significant decrease in the frequency of excretion and the quantitative level of seeding the protective intestinal microflora: *Lactobacillus spp.* – 63% (lg 5.3 CFU / g), *Bifidobacterium spp.* – 73.3% (lg 5.9 CFU/g).

Studying the intestinal biocenosis in women with bacterial vaginosis and obesity, it was found that the lactobacilli and bifidum bacteria, which are normally dominant in the intestinal microflora, are replaced by opportunistic aerobic microorganisms and obligate anaerobes. Thus, among gram-positive obligate anaerobes, *Peptostreptococcus spp.* – 56.7%, *Clostridium spp.* – 56.7%, *Eubacterium spp.* – 68.3%, *Blautia spp.* – 61.7 %. Quantitative indicators of these microorganisms significantly exceeded the diagnostic level and seeding rates of microorganisms in the group of healthy women and was in the range of lg 8.2 CFU / g – lg 12.0 CFU/g.

Dominant in the intestines of a healthy person *Bacteroides spp.* were sown only in 41.7 % of surveyed women of group III at a concentration of lg 6.0 CFU/g, and *Prevotella spp.* in 15% at a concentration of lg 5.0 CFU/g.

In 68.3 % of women with bacterial vaginosis and obesity, opportunistic intestinal microflora was in multicomponent associations. The associations included hemolytic species of gram-negative *enterobacteria*, *Candida fungi* and *Firmicutes* phylum microorganisms in various combinations.

The results obtained in our study indicate an increase in the relative number of *Firmicutes* against the background of a decrease in the number of *Bacteroidetes* in patients with bacterial vaginosis in combination with obesity. Changes in the *Firmicutes* / *Bacteroidetes* ratio suggest that there is a relationship between the microflora and the formation of excess body weight and obesity.

Examination of women with bacterial vaginosis without obesity (group IV) also revealed differences in the composition of the intestinal microflora.

In the examined group IV dysbacteriosis of the II degree was found in 56.7 % of cases, dysbacteriosis of the III degree is in 43.3 % of cases.

In patients with bacterial vaginosis without obesity, a lower frequency of intestinal contamination with staphylococci with pathogenic properties (*S. aureus* – 20 %, *S. epidermidis* (heme +) – 16.7 %) was registered.

Among *enterobacteria*, *E. coli* (heme +) was sown with a lower frequency – 16.7 %, *Klebsiella spp.* – 20 %, *Citrobacter spp.* – 16.7 %, compared with data obtained from patients of group III.

The study of quantitative indicators of intestinal biocenosis in patients with bacterial vaginosis without obesity showed that in this group there are lower concentrations of opportunistic *enterobacteria* (lg 5,2 KUO/g – lg 5,7 KUO/g) and *staphylococci* with pathogenic properties (lg 4, 2 CU/g – lg 4.4 CFU/g), but these indicators exceeded the data obtained in the control group.

Negative changes in the indicators of intestinal microecology in patients of group IV were mainly manifested by low quantitative indicators of normal microflora (*Lactobacillus spp.* – lg 6.8 CFU / g and *Bifidobacterium spp.* – lg 8.2 CFU / g). *Lactobacillus* deficiency was registered in 63.3 % of group IV patients, and their absence in 16.7 % of subjects. Decreased seeding levels of *Bifidobacterium spp.* were found in 56.7 % of group IV patients, in 13.3 % of patients *Bifidobacterium spp.* were not sown.

The frequency of seeding the *Candida* fungi in patients of group IV was 13.3 %. Among them, fungi of *C. albicans* were found in 10 % of cases, *C. glabrata* in 3.3 % (Fig. 4).

Among the obligate anaerobic microflora in women with bacterial vaginosis without obesity with high frequency and in large numbers sown *Bacteroides spp.* in 83 % (lg 11.0 CFU/g), *Prevotella spp.* in 36.7 % (lg 9.8 CFU/g). *Peptostreptococcus spp.* was found in 43.3 % (lg 6.6 CFU/g), *Clostridium spp.* in 40 % (lg 6.5 CFU/g).

In 43.3 % of the IV group women patients the sowing of opportunistic pathogenic microflora in 2 – 3 species associations were recorded.

Therefore, it can be concluded that there are differences between the indicators of intestinal biocenosis in groups of women with bacterial vaginosis and obesity, as well as with bacterial vaginosis and without obesity, which consist in a violation of the ratio of *Bacteroidetes* / *Firmicutes* towards a significant increase in bacteria *Philou Firmicutes*, a significant increase conditionally – pathogenic *Enterobacteriaceae*, significant intestinal contamination with genus of *Candida* fungi, the formation of multicomponent associations of conditionally pathogenic microorganisms against the background of a significant decrease or absence of normal intestinal microflora.

Based on the results of studies, we can summarize the nature of changes in the intestinal microbiome on the background of vulvovaginal candidiasis and bacterial vaginosis in women with overweight and obesity.

In all women with excess body weight and obesity, intestinal microflora disorders have been registered, which are characterized by the replacing the *lactobacilli* and *bifidum bacteria* to opportunistic pathogens. A significant increase in *Firmicutes* phylum microorganisms and a significant decrease in *Bacteroidetes* phylum were found. The obtained data prove that changes in the species composition of the intestinal microbiota play an important role in the pathogenesis of obesity [17].

Detection of pathological changes in the microbiocenosis indicates that the intestinal microflora may play an important role in the occurrence of disorders in the biocenosis of the vagina in women, as well as be of great importance in the pathogenesis of obesity. Considering all this, it becomes necessary to develop preventive and therapeutic measures aimed

at eliminating from the microbial associations of potentially pathogenic microflora and restoring the level of bifido – and lactoflora in the intestines of patients. The most severe dysbiotic processes develop in patients with vulvovaginal candidiasis and overweight and obesity (group I), as well as with bacterial vaginosis and overweight and obesity (group III) due to increased concentrations of hemolyzing, lactose-negative *Escherichia coli*, pathogenic properties, and *Candida* fungi.

CONCLUSIONS

1. In patients with vulvovaginal candidiasis and bacterial vaginosis and overweight and obesity, there is a decrease in the content of *Bacteroidetes* phylum bacteria and a deficiency of protective microflora (*Lactobacilli*, *Bifidum bacteria*), gram-positive anaerobic microorganisms *Phylo Firmicutes* and fungi of the genus *Candida*.
2. In groups of patients with vulvovaginal candidiasis, the frequency of intestinal contamination with fungi of the genus *Candida*, including *Candida non-albicans* was 100 % in women of group I and 93.3 % of women in comparison group (group II) in high concentrations that significantly exceeded the diagnostic level $> \lg 4.0$ CFU/g. The spectrum of fungi most often included *Candida albicans*. Other species of *Candida non albicans* were less common.
4. The results indicate the feasibility of monitoring the intestinal microbiota in women with vulvovaginal candidiasis and bacterial vaginosis, especially in the presence of excess body weight and obesity to determine the degree of violations of its components, and timely correction of the detected changes.

REFERENCES

1. V0Z. Izbytochny ves i ozhirenie. http://www.who.int/gho/ncd/risk_factors/overweight/en/
2. Gregg E.W., Shaw J.E. Global health effects of overweight and obesity. *N. Engl. J. Med.* 2017; 377 (1): 80–81. doi: 10.1056/NEJMe1706095.
3. Castaner O., Goday A., Park, Y.M., Lee, S.H., Magkos, F., Shiow, S.T.E., Schröder H. The Gut Microbiome Profile in Obesity: A Systematic Review. *Int. J. Endocrinol.* 2018, 4095789.
4. Bell, C.G. The Epigenomic Analysis of Human Obesity. *Obesity* 2017; 25: 1471–1481.
5. Samojlova Ju.G., Olejnik O.A., Sagan E.V., Vorozhova I.N., Filippova T.A., Denisov N.S., D'jakov D.A. Sostav i metabolicheskaja aktivnost' mikrobyoty pishhevaritel'noj sistemy u detej i podrostkov s ozhireniem. *Sibirskij zhurnal klinicheskoy i jeksperimental'noj medicyny.* 2020;35(3):38–46. doi:10.29001/2073-8552-2020-35-3-38-46.
6. Barczyńska R., Litwin M., Sliżewska K., Szalecki M., Berdowska A., Bandurska K. et al. Bacterial microbiota and fatty acids in the faeces of overweight and obese children. *Pol. J. Microbiol.* 2018;67(3):339–345. doi: 10.21307/pjm-2018-041.
7. Milani C., Duranti S., Bottacini F., Casey E., Turroni F., Mahony J. et al. The first microbial colonizers of the human gut: composition, activities, and health implications of the infant gut microbiota. *Microbiol Mol Biol Rev.* 2017; 81 (4).
8. Friedman D.Z.P., Schwartz I.S. Emerging fungal infections: New patients, new patterns, and new pathogens. *J. Fungi* 2019; 5: 67.
9. Surain P., Aggarwal N.K. *Candida*, a human pathogen and major types of candidiasis. *Int J Pharm Sci & Res* 2019; 11(1): 41–67. doi: 10.13040/IJPSR.0975-8232.11(1).41-67.
10. Matthew H. Foley, Sarah O'Flaherty, Garrison Allen, Alissa J. Rivera et al. *Lactobacillus bile salt hydrolase substrate specificity governs bacterial fitness and host colonization.* *Proceedings of the National Academy of Sciences.* 2021; 118 (6): e2017709118 doi: 10.1073/pnas.2017709118.
11. Volkova N. I., Ganenko L. A., Golovin S. N. Rol' mikrobioti kishhechnika v razvitii ozhireniya i ego metabolicheskogo profilja (chast' II). *Medicinskij vestnik -Severnogo Kavkaza.* 2019;14(2). 391396. doi: <http://dx.doi.org/10.14300/mnnc.2019.14098>
12. Ley RE, Turnbaugh PJ, Klein S, Gordon JL. Microbial ecology: human gut microbes associated with obesity. *Nature.* 2006;444(7122):1022–3. doi:10.1038/4441022a.
13. Blüher M. Metabolically Healthy Obesity. *Endocr Rev.* 2020; 41(3):405–420. doi:10.1210/endrev/bnaa004.
14. Muscogiuri, G. et al. Gut microbiota: a new path to treat obesity. *Int. J. Obes. Suppl.* 2019; 9: 10–19. doi: 10.1038/s41367-019-0011-7.
15. Wang, S.-Z.; Yu, Y.; Adeli, K. Role of Gut Microbiota in Neuroendocrine Regulation of Carbohydrate and Lipid Metabolism via the Microbiota-Gut-Brain-Liver Axis. *Microorganisms* 2020; 8: 527.
16. Crovesy, L.; Masterson, D.; Rosado, E.L. Profile of the gut microbiota of adults with obesity: A systematic review. *Eur. J. Clin. Nutr.* 2020; 74: 1251–1262.
17. Magne F, Gotteland M, Gauthier L, Zazueta A et al. The Firmicutes/Bacteroidetes Ratio: A Relevant Marker of Gut Dysbiosis in Obese Patients? *Nutrients.* 2020 May 19; 12(5):1474. doi: 10.3390/nu12051474.

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The Authors declare no conflict of interest.

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