

GEORGIAN MEDICAL NEWS

ISSN 1512-0112

№ 2 (311) Февраль 2021

ТБИЛИСИ - NEW YORK



ЕЖЕМЕСЯЧНЫЙ НАУЧНЫЙ ЖУРНАЛ

Медицинские новости Грузии
საქართველოს სამედიცინო სიახლენი

GEORGIAN MEDICAL NEWS

No 2 (311) 2021

Published in cooperation with and under the patronage
of the Tbilisi State Medical University

Издается в сотрудничестве и под патронажем
Тбилисского государственного медицинского университета

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ЕЖЕМЕСЯЧНЫЙ НАУЧНЫЙ ЖУРНАЛ
ТБИЛИСИ - НЬЮ-ЙОРК

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Версия: печатная. **Цена:** свободная.

Условия подписки: подписка принимается на 6 и 12 месяцев.

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GEORGIAN MEDICAL NEWS

Monthly Georgia-US joint scientific journal published both in electronic and paper formats of the Agency of Medical Information of the Georgian Association of Business Press; International Academy of Sciences, Education, Industry and Arts (USA).
Published since 1994. Distributed in NIS, EU and USA.

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3. Submitted material must include a coverage of a topical subject, research methods, results, and review.

Authors of the scientific-research works must indicate the number of experimental biological species drawn in, list the employed methods of anesthetization and soporific means used during acute tests.

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3. სტატიაში საჭიროა გაშუქდეს: საკითხის აქტუალობა; კვლევის მიზანი; საკვლევი მასალა და გამოყენებული მეთოდები; მიღებული შედეგები და მათი განსჯა. ექსპერიმენტული ხასიათის სტატიების წარმოდგენისას ავტორებმა უნდა მიუთითონ საექსპერიმენტო ცხოველების სახეობა და რაოდენობა; გაუტკივარებისა და დაძინების მეთოდები (მწვავე ცდების პირობებში).

4. სტატიას თან უნდა ახლდეს რეზიუმე ინგლისურ, რუსულ და ქართულ ენებზე არანაკლებ ნახევარი გვერდის მოცულობისა (სათაურის, ავტორების, დაწესებულების მითითებით და უნდა შეიცავდეს შემდეგ განყოფილებებს: მიზანი, მასალა და მეთოდები, შედეგები და დასკვნები; ტექსტუალური ნაწილი არ უნდა იყოს 15 სტრიქონზე ნაკლები) და საკვანძო სიტყვების ჩამონათვალი (key words).

5. ცხრილები საჭიროა წარმოადგინოთ ნაბეჭდი სახით. ყველა ციფრული, შემაჯამებელი და პროცენტული მონაცემები უნდა შეესაბამებოდეს ტექსტში მოყვანილს.

6. ფოტოსურათები უნდა იყოს კონტრასტული; სურათები, ნახაზები, დიაგრამები - დასათაურებული, დანომრილი და სათანადო ადგილას ჩასმული. რენტგენოგრაფიების ფოტოასლები წარმოადგინეთ პოზიტიური გამოსახულებით **tiff** ფორმატში. მიკროფოტოსურათების წარწერებში საჭიროა მიუთითოთ ოკულარის ან ობიექტივის საშუალებით გადიდების ხარისხი, ანათალებების შედეგების ან იმპრეგნაციის მეთოდი და აღნიშნოთ სურათის ზედა და ქვედა ნაწილები.

7. სამამულო ავტორების გვარები სტატიაში აღინიშნება ინიციალების თანდართვით, უცხოურისა – უცხოური ტრანსკრიპციით.

8. სტატიას თან უნდა ახლდეს ავტორის მიერ გამოყენებული სამამულო და უცხოური შრომების ბიბლიოგრაფიული სია (ბოლო 5-8 წლის სიღრმით). ანბანური წყობით წარმოდგენილ ბიბლიოგრაფიულ სიაში მიუთითეთ ჯერ სამამულო, შემდეგ უცხოელი ავტორები (გვარი, ინიციალები, სტატიის სათაური, ჟურნალის დასახელება, გამოცემის ადგილი, წელი, ჟურნალის №, პირველი და ბოლო გვერდები). მონოგრაფიის შემთხვევაში მიუთითეთ გამოცემის წელი, ადგილი და გვერდების საერთო რაოდენობა. ტექსტში კვადრატულ ფხიხლებში უნდა მიუთითოთ ავტორის შესაბამისი N ლიტერატურის სიის მიხედვით. მიზანშეწონილია, რომ ციტირებული წყაროების უმეტესი ნაწილი იყოს 5-6 წლის სიღრმის.

9. სტატიას თან უნდა ახლდეს: ა) დაწესებულების ან სამეცნიერო ხელმძღვანელის წარდგინება, დამოწმებული ხელმოწერითა და ბეჭდით; ბ) დარგის სპეციალისტის დამოწმებული რეცენზია, რომელშიც მითითებული იქნება საკითხის აქტუალობა, მასალის საკმაობა, მეთოდის სანდოობა, შედეგების სამეცნიერო-პრაქტიკული მნიშვნელობა.

10. სტატიის ბოლოს საჭიროა ყველა ავტორის ხელმოწერა, რომელთა რაოდენობა არ უნდა აღემატებოდეს 5-ს.

11. რედაქცია იტოვებს უფლებას შეასწოროს სტატია. ტექსტზე მუშაობა და შეჯერება ხდება საავტორო ორიგინალის მიხედვით.

12. დაუშვებელია რედაქციაში ისეთი სტატიის წარდგენა, რომელიც დასაბეჭდად წარდგენილი იყო სხვა რედაქციაში ან გამოქვეყნებული იყო სხვა გამოცემებში.

აღნიშნული წესების დარღვევის შემთხვევაში სტატიები არ განიხილება.

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COMPREHENSIVE BACTERIOLOGICAL STUDY OF THE VAGINAL DISCHARGE DURING BACTERIAL VAGINOSIS

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Despite some progress in the diagnosis and treatment of infectious and inflammatory diseases of the female genitalia system, the prevalence of these diseases is growing steadily and is, according to various authors, from 30% of inpatients to 60-65% of outpatients [4, 6]. Along with sexually transmitted infections, such as syphilis, gonorrhea, trichomoniasis, chlamydia, inguinal lymphogranuloma, herpes and papillomavirus infection, etc., opportunistic pathogens (OP) and microbiota are becoming increasingly clinically important. Optional - and obligate-anaerobic OP, which make up the resident microflora of the urogenital tract, under the conditions of realization of certain exo - and endogenous factors can lead to purulent-inflammatory process of the genitals [2, 10]. The etiological structure of pathogens of infectious processes in the last decade has changed significantly, which is due to the constant evolution of bacteria and involvement of OP in pathological processes [4].

Therefore, the aim of the study was a comprehensive determination of a wide range of OP on the background of normal flora in the vaginal discharge of women of different ages without signs of infectious-inflammatory process but in the presence of nonspecific bacterial vaginosis.

Material and methods. The study was conducted in 298 women aged from 16 to 64 years old. The first group included 53 clinically healthy patients aged from 18 to 52 years old. The laboratory criterion for inclusion in this group was the value of the index of opportunistic pathogenic microflora (IOPM) less than -3 conventional units (c.u.). The second and the third groups also included women aged from 16 to 64 years old with an infectious-inflammatory process in the vagina of varying severity. The criterion for differentiating them by groups was IOPM, which amounted to in the second group from -3 to -1 c.u., and in the third group it was more than -1 c.u. The material for the study was removed by scraping the posterior wall of the vagina with an urogenital probe in a test tube type "Eppendorf". The studies of the biocenosis of the vagina were performed by polymerase chain reaction (PCR) using a set of reagents "Femoflor" (LLC "NVF-DNA Technology") [1]. Nucleic acids were isolated using a set of reagents "Sample-HS"; amplification was performed using DT-Lite (LLC "NVF-DNA Technology"). With the help of special software, the amount (in genome equivalents such as GE/sample) of total bacterial mass (TBM), lactobacilli and each group of OP was calculated. Statistical data processing was performed by methods of variation and correlation analysis using the application package STATISTICA v.10 (StatSoft, Inc.).

Results and discussion. Qualitative and quantitative composition of the studied microflora in the selected groups is presented in Table 1.

The assessment was performed taking into account the following criteria [6, 9] - with a relative content of lactobacilli more than 90%, and opportunistic aerobes and anaerobes less than 10% of TBM and quantitative content of *Candida spp.*, *Mycoplasma hominis* and *genitalium*, *Ureaplasma urealyticum* and *parvum* less than 10⁴ GE/sample - were considered as normocenosis [3,7]. In the case of a combination of lactobacilli (more than 90%) and fungi or mycoplasmas (more than 10⁴ GE/

sample), the vaginal microflora was regarded as a relative normocenosis. The imbalance of the biocenosis of the I degree was confirmed when the share of lactobacilli decreased from 90% to 20% against the background of increasing the content of aerobes (aerobic imbalance) or anaerobes (anaerobic imbalance), and for the II degree it was below 20% [1,3,5].

Analysis of the obtained data allowed to assess the state of the biocenosis of the vagina in the 1st group as a normocenosis. TBM in these patients ranged from 7.0 to 8.0 lg GE/sample (median 7.7). The content of lactobacilli ranged from 96.3% to 100.0%, the median was 98.7%. The frequency of distribution of facultative anaerobic microorganisms was 0.115 c.u. Out of these, enterobacteria were the most common (98.1%), staphylococci and streptococci were 32.1% and 30.2%, respectively. However, in quantitative terms, their content did not exceed 10^{4.7} (median for enterobacteria was 10^{4.0}; for staphylococci and streptococci median was 0). Out of the obligate anaerobic microorganisms, the more common were *Mobiluncus spp.* + *Corynebacterium spp.* (81.1%) and *Eubacterium spp.* (69.8%). Quantitatively, their content did not reach 10⁴ (median for *Mobiluncus spp.* + *Corynebacterium spp.* was 10^{2.2}; median for *Eubacterium spp.* was 10^{2.3}). The number of *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas* was up to 10^{3.9} (median was 0). Other representatives of OP were found less often. Microorganisms of the genera *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* in patients of the 1st group were not detected. The maximum content of *Ureaplasma urealyticum* + *parvum* was 10^{4.6}; median was 0, while *Mycoplasma hominis* + *genitalium* in patients of the 1st group were absent. Yeast-like fungi were found in relatively small numbers (up to 10^{4.4}, median was 3.2), although it should be noted that in 75% of women of the 1st group their quantity exceeded 10³.

The obtained results do not coincide with the data of other authors [1, 3], namely under the conditions of the normocenosis of the vagina there was revealed a higher content of *Mobiluncus spp.* + *Corynebacterium spp.* (81.1%) and *Eubacterium spp.* (69.8%) in comparison with the data [3], which were 30-38%. In addition, in our studies, the absolute number of OP did not exceed 10^{4.5}, while the findings of other studies stated that there was possible the increase of OP content in the normocenosis up to 10⁵ and above [1, 3]. After conducting a correlation analysis of the content of microorganisms, we, in contrast to other results [1, 3], found positive relationships between TBM and the content of lactobacilli (+0.98; p < 0.05) and enterobacteria (+0.51; p < 0.05). Accordingly, the indicators of lacto- and enterobacteria content had a positive correlation (+0.47; p < 0.05). This, in our opinion, indicated the presence of factors of mutually beneficial coexistence of lacto - and enterobacteria, which provided indicators of bacterial contamination of the vaginal contents.

It is clear from the plethora of combinations and permutations of possible pathogens analyzed that no one organism or cluster of organisms can identify all cases of vaginosis, although many different molecular methods have been used in attempts to provide more definitive diagnostic information about vaginosis [8]. A careful analysis of the organisms identified by molecular

Table 1. Quantitative composition of the biocenosis of vaginal secretions depending on the value of IOPM, lg GE/sample (M±m)

Microorganisms	Clinical diagnosis according to the content of IOPM		
	Normocenosis, n=53, (1 group)	Imbalance of I level, n=128 (2 group)	Imbalance of II level, n=117 (3 group)
	IOPM ≤ -3 (lg GE/sample)	IOPM > -3; ≤ -1 lg GE/sample)	IOPM > -1 lg GE/sample)
Total bacterial mass	7,740±0,037	7,600±0,039 *	6,774±0,076 * #
Normobiota			
<i>Lactobacillus spp.</i>	7,622±0,039	7,009±0,044 *	4,945±0,173 * #
Faculty anaerobic (aerobic) microorganisms			
<i>Enterobacteriaceae spp.</i>	3,777±0,109	5,169±0,068 *	5,179±0,072 *
<i>Streptococcus spp.</i>	0,964±0,205	1,020±0,149	1,753±0,212 * #
<i>Staphylococcus spp.</i>	1,045±0,205	1,316±0,166	1,309±0,169
Obligate anaerobic microorganisms			
<i>Gardnerella vaginalis, Prevotella bivia, Porphyromonas spp.</i>	0,923±0,178	2,190±0,193 *	3,950±0,267 * #
<i>Eubacterium spp.</i>	1,840 ±0,174	3,276±0,165 *	4,150±0,202 * #
<i>Sneathia spp., Leptotrichia spp., Fusobacterium spp.</i>	0,000±0,000	0,465±0,112 *	1,301±0,231 * #
<i>Megasphaera spp., Veilonella spp., Dialister spp.</i>	0,357±0,121	1,038±0,159 *	2,704±0,264 * #
<i>Lachnobacterium spp., Clostridium spp.</i>	0,413±0,138	1,172±0,168 *	1,590±0,201 *
<i>Mobiluncus spp., Corynebacterium spp.</i>	1,951±0,143	3,010±0,106 *	3,085±0,134 *
<i>Peptostreptococcus spp.</i>	0,504±0,130	1,184±0,157 *	1,830±0,223 * #
<i>Atopobium vaginae</i>	0,489±0,123	0,699±0,119	2,356±0,267 * #
Mycoplasmas			
<i>Mycoplasma hominis+genitalium</i>	0,000±0,000	0,023±0,023 *	0,467±0,173 * #
<i>Ureaplasma urealyticum+parvum</i>	1,104±0,228	1,622±0,023 *	2,062±0,223 * #
Yeast-like fungi			
<i>Candida spp.</i>	2,864±0,177	3,197±0,092	2,832±0,137 #

note: * – $p < 0.05$ when comparing the indicators of the 1st group with the 2nd and the 3rd groups;
– $p < 0.05$ when comparing the indicators of the 2nd and the 3rd groups (by t-test)

methods as part of vaginosis may be a self-fulfilling prophesy, because the scoring system was developed to specifically identify women with low numbers of lactobacilli and high numbers of small Gram-variable and anaerobic Gram-negative rods. Therefore, the clinical symptoms associated with vaginosis may occur in the absence of the changes identified by PCR, such as aerobic vaginitis. Subsequently in this scenario, the numbers of lactobacilli are also decreased but are replaced by aerobic organisms such enterobacteria and staphylococci [8, 9].

In patients of the 2nd group IUPM was from 3 to -1 lg GE/sample, which allowed determining of their imbalance of I degree. TBM ranged from 6.0 to 8.0 lg GE/sample (median 7.7). The proportion of lactobacilli ranged from 73.1% to 99.4%, the median was 95.0%. When comparing the mean values, it was found that the value of TBM in the 2nd group was lower than in the 1st by 1.8% ($p < 0.05$). There was shown a decrease in the content of *Lactobacillus spp.* (by 8.0%; $p < 0.05$) with an increase in almost all OP. Accordingly, the rate of normobiota (RNB), which is calculated as the difference between TBM and the number of lactobacilli, was higher in group 2 than in group 1 (0.1 and 0.6 lg GE/sample, respectively).

In group 2 as well as in group 1, enterobacteria (98.4%), staphylococci, and streptococci were most common in 34.4%

and 28.1% of cases, respectively. The number of enterobacteria was significantly higher (36.9%; $p < 0.05$) than in group 1. At the same time, in all patients their absolute number was more than 104 (median for enterobacteria 5.2 lg GE/sample). In the 2nd group, as well as in the 1st, the more commonly met microorganisms were *Mobiluncus spp.* + *Corynebacterium spp.* (87.5%) and *Eubacterium spp.* (79.7%); in quantitative terms, their content was higher than in the 1st group (respectively, 54.3% and 78.0%; $p < 0.05$ in both cases). The median for *Mobiluncus spp.* + *Corynebacterium spp.* amounted to $10^{3.3}$; for *Eubacterium spp.* it was $10^{3.5}$. Contents of *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas spp.* exceeded 10^4 in 22.7% of women. The number of *Atopobium vaginalis* and *Peptostreptococcus spp.* increased, especially the latter (by 134.9%; $p < 0.05$). Also, there was found more often the combination of *Megasphaera spp.* + *Veilonella spp.* + *Dialister spp.* and *Lachnobacterium spp.* + *Clostridium spp.* respectively, up to 26.6% and 29.7% of cases, which was statistically significant comparing to the 1st group (76.1% and 96.7%, respectively; $p < 0.05$ for both cases). In contrast to the 1st group, in the 2nd there were microorganisms of *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* The indicators of mycoplasmas and yeast-like fungi did not differ significantly from the 1st group, which however does not coincide with the literature [1,3,4,6].

Thus, such features as a decrease in TBM, the number of lactobacilli and the appearance of representatives of *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* and *Mycoplasma hominis* + *genitalium* appeared to be characteristic for the 2nd group of patients. Our analysis showed a weakening of the positive correlation between SBM and lactobacilli content (+0.62; $p < 0.05$) and the disappearance of the relationship between SBM and enterobacterial content. At the same time, there were revealed numerous positive connections of medium strength between indicators of facultative and obligate anaerobes. This, in turn, indicates the appearance in the 2nd group of factors that contribute to the growth of these microorganisms. No correlations between mycoplasmas and fungi, as in the first group of patients, were found.

The changes that were characteristic for the 2nd group were much more pronounced in the 3rd group. IOPM was more, namely 1 lg GE/sample, which allowed diagnosing of imbalance of II degree. There was a significant decrease in TBM, which was less than in the 1st group by 12.5% and less than in the 2nd by 10.9% ($p < 0.05$ in both cases). The content of lactobacilli was sharply reduced, the share of which ranged from 0 to 98.6%. The value of TBM ranged from 4.5 to 8.0 lg GE/sample (median 7.5). PNB was 1.8 lg GE/sample (exceeded the same value in the 1st group by 15.5 times and in the 2nd group by 3.1 times; $p < 0.05$ in both cases). The absolute number of enterobacteria compared to group 2 did not change. It was noted that in most patients (95.7%) their content exceeded 10^4 (median for enterobacteria 5.1 lg GE/sample). In the 3rd group, a significant number of streptococci was diagnosed, it appeared to be in 81.8% and 71.8% ($p < 0.05$ in both cases) more than in the 1st and 2nd groups, respectively.

It should be noted that the amount of *Eubacterium spp.* exceeded not only in the 1st group, but also in the 2nd (by 26.7%; $p < 0.05$), and the median for *Mobiluncus spp.* + *Corynebacterium spp.* amounted to $10^{3.2}$; for *Eubacterium spp.* it was $10^{3.5}$. The less frequency was indicated for *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas spp.*, it appeared to be 69.2%. The content of *Atopobium vaginalis* and *Peptostreptococcus spp.* exceeded the indicators of the 1st group by 4.8 times and 3.6 times, respectively ($p < 0.05$). *Megasphaera spp.* + *Veilonella spp.* + *Dialister spp.* and *Lachnobacterium spp.* + *Clostridium spp.* were diagnosed in 51.3% and 37.6% of patients, which exceeded the content of this microflora not only in the 1st but also in the 2nd group (2.6 times; $p < 0.05$). In 39.3% of women, their absolute content was greater than 10^4 . *Ureaplasma urealyticum* + *parvum* were detected in 45.3% of cases. The appearance of *Mycoplasma hominis* + *genitalium* in the 3rd group was noted in 11.1% of cases, and their content above 10^4 was recorded in 6.8% of women. Yeast-like fungi occurred with the same frequency as in other groups (80.3% of cases).

In earlier works by using culture methods, *M. hominis* was detected in 24 to 75% of vaginosis cases and in 13 to 22% of women without vaginosis. Finding of *M. hominis* using PCR yielded similar results. There was reported a 53% carriage rate of *M. hominis* in women with vaginosis and zero detection in health women. In the same manner, it was reported that *M. hominis* was present in low numbers in the healthy vagina but that the concentration of *M. hominis* was increased by a factor of 10,000 in women with vaginosis. Moreover, studies using quantitative PCR have shown that women with vaginosis have larger quantities of *M. hominis* and that these levels correlate with Gram stain criteria for vaginosis [8].

Thus, for the 3rd group it was characteristic even more decrease in TBP, the number of lactobacilli with an increase in staphylococci and streptococci, and obligate anaerobes than in other groups of women. It should be noted that there appeared a positive correlation between TBM and the content of lactobacilli (+0.67; $p < 0.05$) and between the content of facultative and obligate anaerobes, which indicated the inhibition of the growth effect on the biocenosis of the vagina. This fact, in turn, was confirmed by the numerous positive links of mycoplasmas with anaerobes. Correlation analysis data showed that with the deepening of the degree of dysbiosis there had increased the number and strength of positive links of OP. It was possible to assume that at a bacterial vaginosis the studied microflora acquired properties of self-support and progressive self-stimulation. The *Candida* family did not form correlations in all three studied groups of women.

Conclusions. Under the condition of normocenosis, enterobacteria predominated among the facultative-anaerobic flora of the vagina, and among the obligate-anaerobic flora of the vagina there predominated *Mobiluncus spp.* + *Corynebacterium spp.* and *Eubacterium spp.* Representatives of the species *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* and *Mycoplasma hominis* + *genitalium* were absent in the normocenosis.

The dysbiosis of the I degree was characterized by a decrease in TBM and the number of lactobacilli on the background of increasing of the content of anaerobes, including *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* and *Mycoplasma hominis* + *genitalium*.

In the conditions of the dysbiosis of II degree there were observed the lowest indicators of TBM and lactobacilli with a significant increase of the absolute number of streptococci and obligate anaerobes. According to the correlation analysis, it was found that with the deepening of the degree of the dysbiosis the direct dependence of TBM and the number of lactobacilli decreased with increasing of the number and strength of positive links of OP (but not yeast-like fungi), which indicated self-support and self-stimulation in bacterial vaginosis.

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SUMMARY

COMPREHENSIVE BACTERIOLOGICAL STUDY OF THE VAGINAL DISCHARGE DURING BACTERIAL VAGINOSIS

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Along with sexually transmitted infections opportunistic pathogens and normal microbiota are becoming increasingly clinically important. Opportunistic pathogens can lead to purulent-inflammatory process of the genitals. The aim of the current work was to detect qualitative and quantitative composition of vagina contents in non-specific bacterial vaginosis.

Vaginal microbiota of 298 women aged from 16 to 64 years old was analyzed. Examination was provided by polymerase chain reaction.

In normocenosis with domination of enterobacteria the prevalence index of conditionally-pathogenic microflora wasn't more than 3 lg GE/sample. With absence of mycoplasmas the quantity of conditionally-pathogenic microorganisms

wasn't more than 104,5. At same time in patients with dysbiosis of I and II levels index of conditionally-pathogenic microflora was from 3 to 1 and less than 1 lg GE/sample accordingly; there was diagnosed a significant decrease of the total bacterial mass. Simultaneously, decreasing of *Lactobacillus* quantity (more expressed in dysbiosis-II) meanwhile appearance of mycoplasmas and utmost constant quantity of *Candida* was revealed.

A comprehensive determination of a wide range of opportunistic pathogens on the background of normal flora in the vaginal discharge of women of different ages had been studied.

Keywords: bacterial vaginosis, polymerase chain reaction, dysbiosis, normocenosis.

РЕЗЮМЕ

РЕЗУЛЬТАТЫ КОМПЛЕКСНОГО БАКТЕРИОЛОГИЧЕСКОГО ИССЛЕДОВАНИЯ СОДЕРЖИМОГО ВЛАГАЛИЩА ПРИ БАКТЕРИАЛЬНОМ ВАГИНОЗЕ

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При инфекциях, передаваемых половым путем, все большее клиническое значение приобретают условно-патогенные микроорганизмы и нормальная микробиота.

Целью исследования явилось определение качественного и количественного состава содержимого влагалища при неспецифическом бактериальном вагинозе у женщин разных возрастных групп.

Проанализирована микробиота влагалища у 298 женщин в возрасте от 16 до 64 лет. Исследование проводилось методом полимеразной цепной реакции. При нормоценозе с преобладанием энтеробактерий, показатель

распространенности условно-патогенной микрофлоры не превышал 3 lg GE/образец. При отсутствии микоплазм количество условно-патогенных микроорганизмов было не более 104,5. У пациентов с дисбактериозом I и II степени индекс условно-патогенной микрофлоры составил от 3 до 1 и менее 1 lg GE/образец, соответственно. Установлено значительное уменьшение общей бактериальной массы. Выявлено уменьшение количества *Lactobacillus spp.* (более выраженное при дисбактериозе-II), появление микоплазм, и максимально постоянного количества *Candida spp.*

რეზიუმე

საშოს შიგთავსის კომპლექსური ბაქტერიოლოგიური გამოკვლევის შედეგები ბაქტერიული ვაგინოზის დროს

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სქესობრივი გზით გადამცემი ინფექციების დროს სულ უფრო დიდ კლინიკურ მნიშვნელობას იძენს პირობით-პათოგენური მიკროორგანიზმები და ნორმული მიკრობიოტა.

კვლევის მიზანს წარმოადგენდა სხვადასხვა ასაკობრივი ჯგუფის ქალებში ბაქტერიული ვაგინოზის დროს საშოს შიგთავსის სახეობრივი და რაოდენობრივი შემადგენლობის შესწავლა.

ნორმოცენოზის პირობებში ენტერობაქტერიების დომინირებით პირობით-პათოგენური მიკროფლორის გავრცელების მანველებელი არ აღემატებოდა 3 ლგ GE/ნიმუშში. მიკოპლაზმების არ არსებობის დროს პირობით-პათოგენური მიკროორგანიზმების რაოდენობა იყო არაუმეტეს 10⁴,5-სა. I და II ხარისხის დისბაქტერიოზით პაციენტებში პირობით-პათოგენური მიკროფლორის ინდექსი შეადგენდა, შესაბამისად, 3-დან 1-მდე და უფრო ნაკლებს 1 ლგ GE/ნიმუშში. გამოვლენილია ბაქტერიული მასის მნიშვნელოვანი შემცირება, *Lactobacillus* spp. რაოდენობის შემცირება (უპირატესად II ხარისხის დისბაქტერიოზის დროს), ამავდროულად გამოვლინდა მიკოპლაზმები და სოკო კანდიდას მაქსიმალურად მუდმივი რაოდენობა.

ნური მიკროფლორის ინდექსი შეადგენდა, შესაბამისად, 3-დან 1-მდე და უფრო ნაკლებს 1 ლგ GE/ნიმუშში. გამოვლენილია ბაქტერიული მასის მნიშვნელოვანი შემცირება, *Lactobacillus* spp. რაოდენობის შემცირება (უპირატესად II ხარისხის დისბაქტერიოზის დროს), ამავდროულად გამოვლინდა მიკოპლაზმები და სოკო კანდიდას მაქსიმალურად მუდმივი რაოდენობა.

MORPHOLOGICAL CHANGES IN PERIODONTAL TISSUE DURING PERIODONTITIS

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Periodontitis is a dental polymicrobial, chronic inflammatory condition, which begins with a simple inflammation of the gums and characterized by the loss of alveolar bone, supporting structures of teeth and periodontal complex, forming abnormal periodontal pockets and finally by loss of teeth [5,7,15,16,23,28].

An important factor in the development and progression of periodontitis is the symbiotic-antagonistic relationship between oral bacteria and the host [11,28].

The oral bacteria have the ability to retain plaque and create biofilms on the cervical surfaces of the teeth. The colonization and continued presence of bacteria in the subgingival area leads to the progression of the gingivitis, formation of the pocket and bone loss [19,26].

According to electron microscopic studies, the presence of fusiform, coccobacilli as well as spirochetes was demonstrated in the gingival oral epithelium, adjacent connective tissue and capillaries. The above-mentioned periodontopathic bacteria have the ability to colonize between gingival and subgingival tissue and damage the gingival epithelial and blood-dendritic cells [4,19,23].

As a result of the influence of the microorganisms on the periodontal attachment, the progression of the disease divides into the following steps: 1) colonization near the gum line, - 2) integration and survival in the biofilm milieu, - 3) migration below the gum and, - 4) suppression of the host mucosal defense [10].

There are up to 700 species of microorganisms in the oral cavity, including periodontopathogens [8,13,28], which cause the development of periodontitis [28]. According to certain authors, there are bacteria of red complexion that are most associated with the development of severe periodontitis, namely: *Porphyromonas gingivalis*, *Tannerella forsythia*, *Aggregatibacter actinomycetemcomitans* and *Treponema denticola* [3,11,15,28].

Women and men have an equal periodontal pathogen colonization. However, the women have a higher risk of periodontitis onsets and the most prevalent causative agent is *P. Gingivalis*, whilst the most prevalent causative agents of the periodontitis in men are *P. Gingivalis*, *P. Intermedia*, *T. Forsythensis* and *T. Denticola*. However, most frequently *T. Forsythensis* is observed [28].

Aggressive periodontitis usually affects people under the age of 30 and is characterized by the rapid development of destructive changes. The family cases are rare. Morphologically it is characterized by the plasmacytic inflammatory infiltration, the domination of neutrophils in the connective tissue and the presence of the fibrin-coated plaque [28].

There are many etiological factors causing periodontal disease, one of which is poor oral hygiene. Poor oral hygiene increases chances of the development of periodontal disease by two to five times [17].

According to epidemiological studies periodontitis is highly prevalent globally [25]. The data of studies held at Harvard School of Dental Medicine show that overall periodontitis prevalence is 55.5% ($\pm 1.4\%$), from which 20.7% ($\pm 1.2\%$) is moderate and, 2.8% ($\pm 0.5\%$) is severe [5,14]. Approximately half of the adult USA population has periodontitis [16].

According to the analysis of the studies conducted by sex, age and countries from 1990 to 2017, 796 million people had severe periodontitis on a global scale [12].

Studies show that the prevalence of severe periodontitis varies throughout the world. The highest prevalence rates were reported in Africa (4.2%, 95% CI 2.0-7.1) and South America (4.0%, 95% CI 0.9-9.1) compared to Europe (0.1%, 95% CI 0.1-0.2). However, the lowest prevalence was found in Asia (1.2%, 95% CI 0.5-2.2) and North America (0.8%, 95% CI 0.4-1.4) [5]. In Georgia unhealthy periodontal tissues were found in 66.9 % of men and 57.5 % of women [2].

Periodontal pathogens are harmful not only to the oral cavity but also affect the development of the fetus and our body as a whole. There is also a link between periodontitis and general somatic diseases (Kvaratskhelia et al., 2020). Laboratory studies have established the presence of periodontopathogens in saliva, subgingival plaque and placenta [27].

Based on one of the systematic reviews, there is a connection between periodontitis and cancer [9]. In particular, patients diagnosed with periodontitis have a higher risk of developing mouth cancer, also lungs, and pancreatic cancer [22]. Women with periodontitis are two to three times more likely to develop breast cancer [24].

Due to above mentioned, histomorphological examination in patients with periodontitis is becoming more important, that is not well introduced in dental practice. The results of such studies may play an additional role in detecting the precancerous lesions oral cavity cancer and planning preventive measures for oral cancers [19].

The aim of our study was a morphological study of periodontal tissues in patients with severe generalized periodontitis in Georgia in order to detect signs of the possible precancerous lesions.

Material and methods. 59 patients with the severe periodontitis were studied. The patients were selected for the 3069 per-