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VAGINARY MICROFLORA SPECTRUM AT BACTERIAL VAGINOSIS OF DIFFERENT DEGREE

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Summary

The prevalence of sexually transmitted diseases in recent years has been steadily increasing and is up to 60-65% among outpatient gynecological patients. At the same time, resident microbiota of the urogenital tract - conditionally pathogenic microorganisms, which include facultative anaerobic and obligate anaerobic opportunistic microorganisms. Aim - to study the etiological structure of pathogens of infectious processes of the urogenital tract. The study involved 298 women aged 16 to 64 years who turned to a gynecologist for a preventive examination or for pregravid preparation.

The results obtained are generally comparable with the data of other authors. The difference was more frequent detection in our studies with normozinoz *Mobiluncus spp.* + *Corynebacterium spp.* (81.1%) and *Eubacterium spp.* (69.8%) compared with the data of [2] - 30-38%. In addition, in our studies, the absolute number of conditionally pathogenic microorganisms did not exceed $10^{4.5}$, while a possible increase in their content was noted at normocenosis up to 10^5 and higher.

Key words: bacterial vaginosis, hormonal regulation, dysbiosis

СПЕКТР ВАГІНАЛЬНОЇ МІКРОФЛОРИ ПРИ БАКТЕРІАЛЬНОМУ ВАГІНОЗІ РІЗНОГО СТУПЕНЯ

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Резюме

Розповсюдженість венеричних захворювань в останні роки невідмінно зростає і становить до 60-65% серед амбулаторних гінекологічних хворих. У той же час резидентна мікробіота мочеполової системи - умовно-патогенні мікроорганізми, що складаються з факультативно-анаеробних і облигаційних анаеробних умовно-патогенних мікроорганізмів. Мета роботи - вивчити етіологічну структуру збудників інфекційних процесів. У дослідженні прийняли участь 298 жінок у віці від 16 до 64 років, які звернулися до гінеколога для профілактичного огляду або прегравідарної підготовки.

Результати дослідження в цілому співвідносяться з даними інших авторів. Різниця полягає в більш частому виявленні в наших дослідженнях нормозиноза *Mobiluncus spp.* + *Corynebacterium spp.* (81,1%) і *Eubacterium spp.* (69,8%) у порівнянні з даними [2] - 30-38%. Крім того, в наших дослідженнях абсолютна кількість умовно-патогенних мікроорганізмів не перевищує 10^{4,5}, в той час як можливе збільшення їх вмісту відзначається при нормоценозах до 10⁵ і вище.

Ключові слова: бактеріальний вагіноз, гормональна регуляція, дисбіоз

СПЕКТР ВАГИНАЛЬНОЙ МИКРОФЛОРЫ ПРИ БАКТЕРИАЛЬНОМ ВАГИНОЗЕ РАЗЛИЧНОЙ СТЕПЕНИ

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Резюме

Распространенность венерических заболеваний в последние годы неуклонно растет и составляет до 60-65% среди амбулаторных гинекологических больных. В то же время резидентная микробиота мочеполовой системы - условно-патогенные микроорганизмы, в состав которых входят факультативно-анаэробные и облигатные анаэробные условно-

патогенные микроорганизмы. Цель работы - изучить этиологическую структуру возбудителей инфекционных процессов мочеполового тракта. В исследовании приняли участие 298 женщин в возрасте от 16 до 64 лет, которые обратились к гинекологу для профилактического осмотра или прегравидарной подготовки.

Полученные результаты в целом сопоставимы с данными других авторов. Разница заключалась в более частом выявлении в наших исследованиях нормозиноза *Mobiluncus* spp. + *Corynebacterium* spp. (81,1%) и *Eubacterium* spp. (69,8%) по сравнению с данными [2] - 30-38%. Кроме того, в наших исследованиях абсолютное количество условно-патогенных микроорганизмов не превышало 104,5, в то время как возможное увеличение их содержания отмечалось при нормоценозах до 10⁵ и выше.

Ключевые слова: бактериальный вагиноз, гормональная регуляция, дисбиоз

Topicality

The prevalence of sexually transmitted diseases in recent years has been steadily increasing and is up to 60-65% among outpatient gynecological patients [1]. At the same time, resident microbiota of the urogenital tract - conditionally pathogenic microorganisms, which include facultative anaerobic and obligate anaerobic opportunistic microorganisms [1-3]. At the same time, data on the etiological structure of pathogens of infectious processes have not been finally established, which requires a comprehensive definition of the qualitative and quantitative spectrum of conditionally pathogenic microorganisms, as well as representatives of the normal flora in the vagina in women of reproductive age.

Aim - to study the etiological structure of pathogens of infectious processes of the urogenital tract. **Materials and methods.** The study involved 298 women aged 16 to 64 years. The 1st group consisted of 53 women aged from 18 to 52 years old who turned to a gynecologist for a preventive examination or for pregravid preparation. Clinical complaints, the patient data did not show, upon examination, pathological changes were not detected. The laboratory criterion for inclusion in this group was the value of the index of conditionally pathogenic microflora (ICPM) less than -3 cu. The 2nd and 3rd groups were women aged from 16 to 64 years old who turned to a gynecologist for the presence of an infectious-inflammatory process in the vagina of varying severity. The criterion for differentiating them into groups was ICPM, which was in the 2nd group from -3 to -1 u.e., and in the 3rd group - more than -1 in.e. The exclusion criterion was the detection in the vaginal discharge at least one of the unconditionally pathogenic microorganisms - *Trichomonas vaginalis*, *Neisseria gonorrhoeae*, *Chlamydia trachomatis*, as well as the causative agents of herpes and syphilis. The study of the vaginal biocenosis was performed by the method of polymerase chain reaction (PCR) in real time using the Femoflor reagent kit and the DT-Lite detection amplifier

(NPF-DNA-Technology LLC) [2]. Material for the study was taken by scraping from the posterior side wall of the vagina. Quantitative results were expressed in genome equivalents per sample (GE / sample), the total bacterial mass (MBP), the number of lactobacilli and each group of opportunistic microorganisms were calculated. Statistical data processing was performed by methods of variation and correlation analyzes using the software package STATISTICA v.10, (StatSoft, Inc.).

Research results

The analysis of the obtained data allowed us to estimate the spectrum of the vaginal biocenosis in the 1st group as normocenosis. The MBP in these patients ranged from 7.0 to 8.0 lg GE / sample (median 7.7). The share of lactobacilli ranged from 96.3% to 100.0%, the median - 98.7%. Of the optional anaerobic microorganisms, enterobacteria were found with a maximum frequency (98.1%), staphylo- and streptococci - 32.1% and 30.2% of cases, respectively. However, in quantitative terms, their content did not exceed $10^{4.7}$ (the median for enterobacteria is $10^{4.0}$; for staphylo and streptococci it is 0).

From obligate anaerobic microorganisms, *Mobiluncus spp.* prevailed + *Corynebacterium spp.* (81.1%) and *Eubacterium spp.* (69.8%). In quantitative terms, their content did not exceed 10^4 (the median for *Mobiluncus spp.* + *Corynebacterium spp.* $10^{2.2}$; for *Eubacterium spp.* - $10^{2.3}$). *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas spp.* - 35.8%; in quantitative terms, their content did not exceed $10^{3.9}$ (median - 0). *Atopobium vaginalis* (28.3%) and *Peptostreptococcus spp.* were less common. (22.6%), even more rarely - *Megasphaera spp.* + *Veillonella spp.* + *Dialister spp.* and *Lachnobacterium spp.* + *Clostridium spp.* - 15.1% of cases, respectively. The content of all these microorganisms did not exceed $10^{3.6}$, the median - 0. Microorganisms of the species *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* in patients of the 1st group did not occur.

Ureaplasma urealyticum + *parvum* was found in 37.7% of cases (maximum content $10^{4.6}$; median - 0), while *Mycoplasma hominis* + *genitalium* did not occur in patients of the 1st group. Yeast-like fungi were encountered quite often - in 84.9% of cases and also in relatively small amounts (up to $10^{4.4}$, median - 3.2), although it should be noted that 75% of women in the 1st group had more than 10^3 .

The results obtained are generally comparable with the data of other authors. [2]. The difference was more frequent detection in our studies with normocenosis *Mobiluncus spp.* + *Corynebacterium spp.* (81.1%) and *Eubacterium spp.* (69.8%) compared with the data of [2] - 30-38%. In addition, in our studies, the absolute number of conditionally pathogenic microorganisms did not exceed $10^{4.5}$, while a possible increase in their content was noted at normocenosis up to 10^5 and higher. [2].

In patients of the 2nd group ICPM was in the range from -3 to -1 lg GE / sample, which allowed them to determine the I degree imbalance. MBP ranged from 6.0 to 8.0 lg GE / sample (median 7.7). The share of lactobacilli ranged from 73.1% to 99.4%, the median - 95.0%. MBP in the 2nd group was 1.8% lower than in the 1st group ($p < 0.05$). In quantitative terms, the amount of *Lactobacillus spp.* (8.0%; $p < 0.05$) with an increase in almost all conditionally pathogenic microorganisms. Accordingly, the rate of normobiota (RNB), which is calculated as the difference in MBP and the number of lactobacilli, was higher in the 2nd group than in the 1st group (respectively, 0.1 and 0.6 lg GE / sample). Among the optional anaerobic microorganisms, enterobacteria were found with a maximum frequency (98.4%), staphylo- and streptococci - in 34.4% and 28.1% of cases, respectively. The number of enterobacteria was significantly higher (by 36.9%; $p < 0.05$) than in the 1-1 group. At the same time, in all cases their absolute amount was greater than 10^4 (the median for enterobacteria was 5.2 lg GE / sample). From obligate anaerobic microorganisms, as well as in the 1st group, *Mobiluncus spp.* + *Corynebacterium spp.* (87.5%) and *Eubacterium spp.* (79.7%); in quantitative terms, their content was higher than in the 1st group (by 54.3% and 78.0%, respectively; $p < 0.05$ in both cases). Median for *Mobiluncus spp.* + *Corynebacterium spp.* amounted to $10^{3.3}$; for *Eubacterium spp.* - $10^{3.5}$. As in the 1st group, *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas spp.* - 53.1%; in quantitative terms, their content exceeded 10^4 in 22.7% of women. Compared with the indicator in the 1st group, it increased by 137.3% ($p < 0.05$). Frequencies of *Atopobium vaginalis* and *Peptostreptococ spp.* did not change, despite the fact that their absolute content increased, especially the latter (by 134.9%; $p < 0.05$). Also increased the frequency of occurrence of *Megasphaera spp.* + *Veillonella spp.* + *Dialister spp.* and *Lachnobacterium spp.* + *Clostridium spp.* - respectively, up to 26.6% and 29.7% of cases, which was statistically significant compared with the 1st group (by 76.1% and 96.7%, respectively; $p < 0.05$ for both cases). In contrast to the 1st group, microorganisms of the species *Sneathia spp.* Appeared in the 2nd. + *Leptotrichia spp.* + *Fusobacterium spp.* They were detected in 12.5% of cases in an amount of less than 10^4 . *Ureaplasma urealyticum* + *parvum* was found in 39.8% of cases, while in 26.6% of patients their content exceeded 10^4 . In the 2nd group, the appearance in 8.0% of cases of *Mycoplasma hominis* + *genitalium* and the number up to 10^3 was noted. Yeast-like fungi were found with approximately the same frequency as in the 1st group (92.2%) of cases and in small quantities (only in 6% of women above 10^4). Differences of the 2nd group were a decrease in the volume of exchange rate, the number of lactobacilli with an increase in the incidence and the content of conditionally pathogenic microflora. Compared with normocenosis, representatives of *Sneathia spp.* *Leptotrichia spp.* + *Fusobacterium spp.* and *Mycoplasma hominis* + *genitalium*.

In the 3rd group, the changes characteristic for the 2nd group were even more pronounced. ICPM was more than -1 lg GE / sample, which allowed to diagnose II degree imbalance. There was a more pronounced decrease in MBP, which was less than in the 1st group by 12.5% and less than in the 2nd group - by 10.9% ($p < 0.05$ in both cases). The number of lactobacteria drastically decreased, the share of which ranged from 0 to 98.6%, while the amount of lactobacteria was below 20% in 6.0%, from 20% to 90% in 65.0% and in more than 90% in 29% patients of this group. The magnitude of the MBP varied from 4.5 to 8.0 lg GE / sample (median 7.5). The average number of lactobacilli decreased by 35.1% compared with the 1st group and by 29.4% compared with the 2nd ($p < 0.05$ in both cases) with an even greater increase in the number of opportunistic microorganisms. Accordingly, the RNB was 1.8 lg EG / sample (exceeded that in the 1st group by 15.5 times and in the 2nd group by 3.1 times; $p < 0.05$ in both cases). Among the optional anaerobic microorganisms, enterobacteria were found with a maximum frequency (99.1%), staphylo- and streptococci - in 35.0% and 39.3% of cases, respectively. In the majority of patients (95.7%) their absolute amount was greater than 10^4 (median for enterobacteria 5.1 lg GE / sample). In the 3rd group, the number of streptococci was significantly higher - it exceeded that in the 1st and 2nd groups, respectively, by 81.8% and 71.8% ($p < 0.05$ in both cases).

The frequency of distribution of obligate anaerobic microorganisms was 31.3%, which was significantly higher than in the 1st group (1.6 times). As in the other groups, *Mobiluncus spp.* + *Corynebacterium spp.* (84.6%) and *Eubacterium spp.* (82.9%). In quantitative terms, their content was higher than in the 1st group (respectively, by 58.1% and 125.5%; $p < 0.05$ in both cases). The number of *Eubacterium spp.* exceeded the indicator of not only the 1st group, but also the 2nd (by 26.7%; $p < 0.05$). Median for *Mobiluncus spp.* + *Corynebacterium spp.* amounted to $10^{3.2}$; for *Eubacterium spp.* - $10^{3.5}$.

As in the other groups, *Gardnerella vaginalis* + *Prevotella bivia* + *Porphyromonas spp.* - 69.2%; in quantitative terms, their content exceeded 10^4 in 59.8% of women, and compared to the indicator in the 1st group was higher by 4.3 times, and compared to the indicators of the 2nd group - by 1.8 times ($p < 0.05$ in both cases). In the 3rd group, the frequency of occurrence of *Atopobium vaginalis* and *Peptostreptococ spp.* compared with other groups was significantly higher. Thus, their frequency exceeded that in the 2nd group, respectively, 2.0 and 1.2 times ($p < 0.05$ in both cases). Their content was significantly higher (in comparison with the 1st group, respectively, by 4.8 times and by 3.6 times; $p < 0.05$ in both cases). The content of *Atopobium vaginalis* exceeded 10^4 in 33.3% of women, and *Peptostreptococ spp.* - at 22.2%. Content *Megasphaera spp.* + *Veillonella spp.* + *Dialister spp.* exceeded that 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 exceeded 10^4 . In the 3rd group, the frequency of detection of *Sneathia spp.* + *Leptotrichia spp.* + *Fusobacterium spp.* was statistically significantly

higher than in the 2nd group and reached 23.1%. In 18.8% of women their content exceeded 10^4 . *Ureaplasma urealiticum* + *parvum* was found in 45.3% of cases, in 34.2% of women their content exceeded 10^4 . In addition, their absolute content was statistically significantly higher than that in the 1st (1.9 times) and 2nd (1.3 times) groups. The appearance of *Mycoplasma hominis* + *genitalium* in the 3rd group was observed in 11.1% of cases, while above 10^4 their content was in 6.8% of women. Yeast-like fungi were found with the same frequency as in other groups (80.3% of cases). У 10.3% of women, their number exceeded 10^4 . Differences of the 3rd group were an even greater decrease in the volume of exchange rate, the number of lactobacilli with an increase in streptococci and obligate anaerobes.

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