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**POPULATION LEVEL OF ASSOCIATIVE MICROBIOTA OF VAGINAL MUCOSA IN
WOMEN WITH TRICHOMONAL VULVOVAGINITIS AND ITS SEPARATE
MICROECOLOGICAL INDICES**

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Trichomonal vulvovaginitis (urogenital trichomoniasis in women) is a widespread disease of the urogenital tract, which occupies one of the first places by spreading among sexually transmitted infections. According to the WHO, about 180 million people in the world get trichomoniasis every year, including 120 million (66.67%) women.

The aim of the research work was to study the population level of the associative microbiota of *T. vaginalis* and quantitative microecological indicators of the ecosystem "macroorganism - microbiome" of vulvovaginal content in women of the reproductive age with trichomonal vulvovaginitis. The research work is based on the results of bacteriological, microscopic and protistological examination of 171 women of reproductive age, in whom trichomoniasis vulvovaginitis was verified. Identification of isolated taxons was performed by morphological, tinctorial, cultural and biochemical properties. If necessary, the factors of pathogenicity or antigenic structure were determined. During study of the population level of each taxon, taking into account that the number of microbiota in 1 ml of content reaches millions, the results were expressed in decimal logarithms of the number of viable (colony-forming) microbial units (lg CFU/ml).

In women with vulvovaginal trichomoniasis, the population level of all taxons that persist in the biotope, changes and these changes are of different order. The population level of the most important in the vulvovaginal composition with a multifunctional role in the biotope bacteria of the genus *Lactobacillus* decreases 46.76 % (almost 2 orders), *Bifidobacterium* 26.57 % (by one order), and bacteria of the genus *Propionibacterium* are not found in the biotope. Against this background, the population level of opportunistic pathogens is growing. Thus, the population level of yeast-like fungi of the genus *Candida* increases 75.54 % (2 orders), *E.coli* 78.72% (almost 3 orders), *B.fragilis* - by 53.70 %, bacteria of the genus *Peptococcus* - by 69.85 %, *E. faecalis* - by 26.26 % and *S.epidermidis* - 24.24 %. Pathogenic and opportunistic bacteria (*S. aureus*, *P. niger*, *S. agalactiae*, *N. gonorrhoeae*, *C. vaginalis*) in vulvovaginal content reach a critical population level, and opportunistic *M. curtisii* in the biotope is in a moderate population level. Changes in the population level of each taxon that persists on the vaginal mucosa in patients with trichomonal vulvovaginitis lead to changes in the quantitative dominance and significance of the microbe in the associated microbiocenosis. It is shown that the coefficient of quantitative dominance of physiologically useful bacteria of the genus *Lactobacillus* in patients is reduced by 6.33 times, bacteria of the genus *Bifidobacterium* - by 18.31 times, and the dominance in microbiocenosis of vulvovaginal content of coagulase-negative *S. epidermidis* by 2.4 times is reduced. The dominant role of opportunistic pathogens in the microbiocenosis of vulvovaginal contents in women of reproductive age with trichomoniasis significantly increases: yeasts of the genus *Candida* – by 33.60 times, *B. fragilis* – by 27.03 times, bacteria of the genus *Peptostreptococcus* – by 15,03 times, *E. faecalis* – by 9.75 times, *E. coli* – by 4.15 times. Other pathogenic and opportunistic bacteria that have colonized the vulvovaginal contents have a moderate value of the quantitative dominant coefficient and significance in the associative microbiocenosis of the vaginal mucosa.

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**MICROBIAL ASSOCIATIONS OF THE VAGINAL MUCOSA IN TRICHOMONAL
VULVOVAGINITIS**

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Trichomoniasis is a multifocal disease. The site of *Trichomonas vaginalis* infection in women is the vaginal mucosa, which is invaded by protozoa during sexual contact with a patient or a carrier.



The aim of the research was to study the taxonomic composition, its associations and microecological indicators of the ecosystem "macroorganism-microbiome" of vulvovaginal content in women of the reproductive age with trichomonal vulvovaginitis. Bacteriological, microscopic and protistological examination was performed in 171 women of reproductive age in whom, on the basis of clinical manifestations (nonspecific vulvovaginitis), test results, specific gynecological examination and general laboratory examination (detection in vulvovaginal contents of neutrophils, monocytes/macrophages, mucus, epithelial and phagocytic cells, degenerative and reactively altered cells, as well as *T. vaginalis* cells stained with methylene blue by the Giemsa method), Trichomonas vulvovaginitis was diagnosed. At the same time, the vulvovaginal contents were removed from the posterior fornix and inoculated into sterile centrifuge test tubes. To the taken material, tenfold volume of standard buffer solution for better preservation of anaerobic bacteria and the possibility of seeding the diluted material on separate sectors of a Petri dish with the optimal agar medium for each taxon with following identification, was added.

It has been found that the microbiota of vulvovaginal content of women of the reproductive age with trichomonas vulvovaginitis represents itself associations, a mandatory component of which is *T. vaginalis*, and in majority (70.15 %) of cases there formed associations with pathogenic and opportunistic microorganisms of 3-5 different taxons. In 51 (29.82 %) patients, in addition to *T. vaginalis* and opportunistic pathogens there are found physiologically normal autochthonous obligate and the most important in the vulvovaginal contents with a multifunctional role in the biotope bacteria of the genus *Lactobacillus* or *Bifidobacterium*. *T. vaginalis* monoculture was not detected in any patient. According to the constancy index, frequency of occurrence, Margalef's species richness index, Whittaker's species diversity, Simpson's and Berger-Parker's species dominance indices *T. vaginalis* has a dominant role in all patients. The most important associates of this eukaryotic pathogen are opportunistic yeast-like fungi of the genus *Candida* (67.95 %), *Staphylococcus aureus* (y 57.31 %), as well as pathogenic for the biotope *G. vaginalis* (5.85 %), *N.gonorrhoeae* (5.26 %), and opportunistic anaerobic bacteria of the genus *Peptostreptococcus* (46.73%), *B. fragilis* (30.99 %) and *E. faecalis* (9.36 %), *E. coli* (8.19 %), *K pneumoniae* (5.85 %), *S. epidermidis* 6.43 %, *S. agalactiae* (4.09 %), *P. niger* (4.09 %) and others.

Thus, in the vulvovaginal content of women of the reproductive age with trichomonal vulvovaginitis there persist associations consisting of three (26.32 %), four (65.50 %) and five (8.19%) components. All three-component associations contain *T. vaginalis*, bacteria of the genus *Lactobacillus* and other opportunistic taxons. Four-component associations include *T. vaginalis*, 3 taxons of opportunistic bacteria and fungi of the genus *Candida*. Only 6 (3.5 %) patients have *T. vaginalis*, bacteria of the genus *Lactobacillus* (2.92 %) or *Bifidobacterium* (0.58 %). Five-component associations are formed with *T. vaginalis* and 4 opportunistic taxons, which suggests that vulvovaginal trichomoniasis is an infectious-inflammatory process of mixed etiology, a key role in it, except *T. vaginalis*, play pathogenic and opportunistic for the biotope bacteria and yeast-like fungi of the genus *Candida*.

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**ВИЗНАЧЕННЯ СКЛАДУ МІКРОБІОТИ ТОВСТОГО КИШКІВНИКА У ДІТЕЙ, ЯКІ
ВХОДИЛИ У ГРУПУ РИЗИКУ ПО РОЗВІТКУ ДИСБІОЗА КИШЕЧНИКА ТА
МЕТОДИ КОРЕКЦІЇ ЙОГО**

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Зміна кількісних або якісних характеристик нормальної мікрофлори створюють умови для розвитку умовно патогенних бактерій (УПБ) - представників родів клебсієл, ентеробактерів, протей, стафілококів, ацинетобактерів, псевдомонад і грибів роду *Candida*. Порушення нормальної мікрофлори характеризується зникненням або зменшенням кількості облігатних її представників та збільшенням популяційного рівня УПБ, які відсутні або зустрічаються в невеликих кількостях в нормі. В результаті такі дисбіотичні мікробні