

UDC [616.6-07:618.1](579.2:579.61)
DOI: 10.15587/2519-8025.2022.255743

UROGENITAL INFECTIONS OF WOMEN OF REPRODUCTIVE AGE CAUSED BY CONDITIONALLY PATHOGENIC MICROORGANISMS ON THE BACKGROUND OF TOBACCO SMOKING

Oksana Starishko, Tetiana Turytska, Anastasia Ovcharenko

The aim: to study changes in the microbiota of the urogenital tract of women of reproductive age in the Dnipro region, which is caused by conditionally pathogenic microorganisms on the background of smoking.

Material and methods: biomaterial of patients (scraping from the urogenital tract) who applied to the Center for Laboratory Medicine PE “VIS-MEDIC” in Dnipro region. We analyzed the components of the microbiota of the vagina of women of the surveyed groups (sign of age and smoking) in the period from 2018 to 2021. For the use in an analysis, microbiota data were obtained using the test system Femoflor Screen.

Results. Analysis of the results of the study revealed the dependence of the composition of the microbiota of the reproductive tract of women on the use of tobacco products. An increase in indicators for conditionally pathogenic microorganisms was shown. The rate of detection of elevated levels of *M. hominis* in samples of biological material varied between 6-8 % but was not recorded in all study groups of women. There was also an increase in the frequency of detection of elevated levels of *U. urealyticum*, *U. parvum* in samples of biological material, the values of which ranged from 9 to 50 %.

Conclusions. The obtained data allowed to assess the effect of tobacco on the composition of the microbiota of the urogenital tract of women and made it possible to use them in measures of social and preventive work, as an indisputable fact to quit smoking. Therefore, there is a need for further research to establish the role of microorganisms involved in restoring the composition of the microbiota after inflammatory processes in women who use and do not use tobacco products.

The results may be relevant for the diagnosis of inflammatory diseases, processes caused by opportunistic pathogens of the urogenital tract of women of reproductive age, potentially dangerous occurrence and development of infertility and the basis for social and preventive work among women on the background of smoking

Keywords: microbiota, urogenital tract, Femoflor Screen test, smoking, women, reproductive age, opportunistic pathogens, pathogenic microorganisms

How to cite:

Starishko, O., Turytska, T., Ovcharenko, A. (2022). Urogenital infections of women of reproductive age caused by conditionally pathogenic microorganisms on the background of tobacco smoking. ScienceRise: Biological Science, 1 (30), 16–25. doi: <http://doi.org/10.15587/2519-8025.2022.255743>

© The Author(s) 2022

This is an open access article under the Creative Commons CC BY license hydrate

1. Introduction

There is an increase in the number of cases of dysbiotic disorders of the urogenital tract of women. Therefore, it is of considerable interest to study the dynamics of changes in the composition of the microbiota of the urogenital tract of women of reproductive age in smoking.

Some infections may be asymptomatic or with minimal symptoms and may not be of concern to women. Asymptomatic course could lead to late medical treatment and the development of serious complications, cause reproductive dysfunction.

The functional significance of the indigenous microbiota is aimed at realizing the effect of colonization resistance. Thus, it provides a harmonious balance in the vaginal microbiocenosis and reduces the likelihood of colonization of opportunistic and pathogenic microorganisms of the urogenital tract [1, 2].

The microbiota consists of permanent “inhabitants” (indigenous or autochthonous microflora) and transient microorganisms (random or allochthonous microflora). The first group is dominant in the number of cells, but its species diversity is less pronounced. The second group includes a much wider range of species, but the number of their representatives is small, estimated at about 3–5 % of the total content of bacteria in the isolated material.

The composition of the microflora of the vagina depends on the condition of the epithelium lining the urogenital tract. This is due to the metabolism that occurs in epithelial cells. In general, the vaginal environment is used by microorganisms as an ecological niche, which includes the squamous epithelium of the inner surface of the vaginal wall, the cylindrical epithelium of the cervix and vaginal secretions. The vaginal environment itself determines the quantitative and species composition of the microflora of the urogenital tract [3, 4].

One of the most common disorders of the vaginal microbiota is bacterial vaginosis. It is an infectious non-inflammatory syndrome associated with vaginal dysbiosis, characterized by a high number of conditionally pathogenic microorganisms and a sharp decrease or absence of lactobacilli [5]. Excessive reproduction of opportunistic pathogens (both aerobic and anaerobic) could cause disease. The frequency of its detection in outpatient gynecological practice ranges from 15 to 19 %. In women with sexually transmitted infections – 24–40 %, in women with pelvic inflammatory disease – 35 %, in patients with complaints of vaginal discharge – 95 % [6].

Due to the inhibition of growth and activity of *Lactobacillus spp.* there is a shift in the acidity of vaginal secretions to the alkaline side with increasing concentrations of polyamines, various enzymes (mucinas, sialidases, collagenases, proteases, phospholipases A2 and C), organic acids, which, in turn, provokes biochemical changes. By rapidly destroying the protective layer of mucus, they promote the attachment of bacteria to epithelial cells and their subsequent penetration [7]. The immune system plays an important role: the reduction of non-specific resistance in these patients is one of the reasons for the recurrence of the process.

Widespread urogenital mycoplasmas and their frequent detection in healthy people makes it difficult to address the role of these microorganisms in the pathogenesis of urogenital tract diseases. Some researchers consider mycoplasmas to be conditionally pathogenic pathogens, justifying this by the possibility of isolating them from clinically healthy individuals, as well as asymptomatic clinical course of mycoplasmosis [8]. However, according to other authors [9, 10], mycoplasmas are pathogens, and their isolation from clinically healthy individuals should be considered a threatening carrier due to the prolonged action of persistent pathogens, as well as the possibility of increasing the virulence of mycoplasma strains. Difficulties in the diagnosis of mycoplasma infections, the prevalence of the disease, sexual transmission and irrational therapy determine the predominance of these infections over classical sexually transmitted diseases.

The rates of infection of the population with urogenital mycoplasmosis in different countries are quite variable and range from 10 to 50 % of all infectious urogenital pathology of a human [11]. Quite common there is combination of mycoplasmas with other pathogens of urogenital infections. According to many authors, among the examined patients with a primary diagnosis of chlamydia, *Mycoplasma spp.* stood out in 64 %, among patients with trichomoniasis – in 20–71 %, and in gonorrhoea – in 15–66 % [6]. Unfortunately, there are currently no statistically significant data on the prevalence of urogenital mycoplasmosis in different population groups in Ukraine. Regarding ureaplasmas, most observations indicate that these microorganisms are more common in women of reproductive age, especially in persons with increased sexual activity, inflammatory diseases of the genitals, as well as in pregnant women [12, 13].

Smoking is one of the most common bad habits, which quickly turns into a disease characterized by both psychological and physical dependence on tobacco. For the female body, the effects of smoking are very unfavourable.

The influence of these factors on a woman's body contributes to an imbalance between normobiota, conditionally pathogenic and pathogenic microorganisms.

The aim of the research – to characterize the dynamics of changes in the microbiota of the urogenital tract of women of reproductive age in the Dnipro region during smoking according to the results of molecular genetic analysis.

2. Materials and methods of the research

The research was performed based on the educational and scientific laboratory of the Department of General Medicine with a course of physical therapy of Oles Honchar Dnipro National University and the Center for Laboratory Medicine “VIS-MEDIC” (Dnipro, Ukraine). A study of the composition of the microbiota of women of reproductive age was conducted and archival data of surveys of 600 women over 18 years of age for the period 2018–2021, who applied for the survey at their own request, were processed. Scrapings of epithelial cells of women from the vagina (posterior vaults), urethra, cervical canal were used as the studied material.

The study was conducted in accordance with the principles of bioethics of the Council of Europe Convention on Human Rights and Biomedicine (04.04.1997), the World Medical Association Helsinki Declaration: Ethical Principles of Human Medical Research (1964–2013), ICH GCP (1996, last revision – ICH VI, 2003), Order of the Ministry of Health of Ukraine No. 690 of 23.09.2009. All participants were informed about the goals, organization, research methods and signed an informed consent to participate in it, and all measures were taken to ensure anonymity of patients.

The results of scientific research were reviewed and approved by the Committee on Bioethics at the Faculty of Medical Technologies of Diagnosis and Rehabilitation of Oles Honchar Dnipro National University (Minutes No. 1 of January 5, 2022).

Collection, pre-processing and storage of biomaterial were carried out by doctors of the Center for Laboratory Medicine “VIS-Medic” (Dnipro). The procedures were performed following the instructions for the set of reagents for the isolation of nucleic acids “TEST-NK-PLUS” (NPO DNA-Technology, Russia).

Urogenital scrapings were taken with sterile disposable probes and brushes in 1.5 ml Eppendorf-type plastic tubes with transport medium (sterile 0.9 % sodium chloride solution 500 µl) for bioassays.

All patients were divided into 4 groups according to age and those who used tobacco products (Table 1). The predominant group of surveyed women with complaints was the age group of 26–35 years. Of these, 199 women do not smoke (43.4 % of the surveyed contingent).

Studies of the material were performed by polymerase chain reaction (PCR).

The study of the microbiota of the urogenital tract was performed using the test system “Femoflor Screen” (LLC “NGO DNA-Technology, Russia”) according to the manufacturer's instructions using iCycler iQ™ 5 (Bio-Rad, USA) in real time [14, 15]. The results are obtained in comparison with the manufacturer-regulated reference values specified in the instructions for the “Femoflor Screen test” system.

Table 1

Distribution of women by age and smoking

Age group, years	Indicator	Years							
		2018		2019		2020		2021	
		Number	%	Number	%	Number	%	Number	%
I, 18–25	Smoke	12	8	7	4.7	11	7.3	6	4
	Do not smoke	35	23.3	35	23.3	19	12.7	19	12.7
II, 26–35	Smoke	18	12	16	10.7	16	10.7	15	10
	Do not smoke	37	24.7	47	31.3	53	35.3	62	41.3
III, 36–45	Smoke	16	10.7	14	9.3	14	9.3	12	8
	Do not smoke	32	21.3	27	18	35	23.3	34	22.7
IV, >45	Smoke	–	–	2	1.3	1	0.7	–	–
	Do not smoke	–	–	2	1.3	1	0.7	2	1.3
Total		150	100	150	100	150	100	150	100

Isolation of DNA from biological material. A necessary condition for the correct quantitative analysis of urogenital tract biota is compliance with the technique of scraping epitheliocytes. An indicator of the adequacy of obtaining biological material was a sufficient amount of human genomic DNA in the sample, the source of which are epithelial cells that were sampled with the correct technique of taking biomaterial. Material collection control indicator (CCI) is estimated in absolute values, its minimum threshold is 10^4 . If the CCI is less than 10^4 , the real-time PCR result of the amount of biota was considered unreliable. In this case, re-collection of biological material was performed, because in the case of low CCI levels, the calculated ratios of different groups of microorganisms could be erroneous [14, 16].

Total bacterial mass (TBM) is an indicator that can be used to judge the total number of bacteria present in the test bioassay. The indicator is estimated in absolute values. For vaginal scrapings in healthy women, this value is 10^6 – 10^8 CU, for the urethra and cervical canal - an order of magnitude less – 10^5 – 10^7 CU [14].

Decrease of TBM below the specified limit values, accordingly, testified to the insufficient population of the studied biotope with bacteria, possibly due to antibiotic therapy, hypoestrogenism of various origins [14].

One strip, with a paraffin-sealed amplification mixture, was labelled for each test sample, negative control sample (K–) and positive control sample (K +). One strip is designed to study one sample (Table 2).

Table 2

Marking of test tubes for PCR [14]

Sample 1	Probes 1–8
Sample 2	Probes 1–8
«K–»	Probes 1–8
«K+»	Probes 1–8

1. Shake the tube with Taq polymerase MAX solution for 3–5 s and centrifuge for 1–3 s on a vortex microcentrifuge.

2. Added to each tube of strips, without damaging the paraffin layer, 10 μ l of a solution of Taq polymerase MAX.

3. Added to each tube of strips 1 drop of mineral oil (20 μ l). The lids of the strips were closed.

4. To prevent contamination before the introduction of DNA, open the lid of only the strip in which the sample was made, and close it before applying the next. DNA preparations were introduced with filter tips.

5. Introduced to each test strip for the test samples (one strip for each sample), without damaging the paraffin layer, 5.0 μ l of DNA isolated from the sample.

6. 5.0 μ l of a negative control sample that had passed the DNA isolation step was added to each tube of a K– labelled strip without damaging the paraffin layer. 5.0 μ l of a positive control sample was added to each tube of K+ -labelled strip without damaging the paraffin layer.

7. The strips were centrifuged on a vortex microcentrifuge for 1–3 s.

8. Installed all the strips in the detection amplifier unit.

9. Run the software RealTime_PCR in the mode “Work with the device”. During the first PCR, the Femoflor.ini file was downloaded.

10. In the following performances, the Femoflor Screen test was added to the protocol, the number and identifiers of samples, including negative and positive control samples, were indicated, the location of the strips on the thermoblock matrix was noted according to their installation and PCR was performed. When selecting the Femoflor Screen test, the program was displayed in the Amplification Program Startup window (Table 3).

The DNA probes used to detect the amplification products of the genome fragments of the identified microorganisms include fluorescent labels Fam, Rox and Cy5. The DNA probes used to detect the amplification products of the internal control sample and control the sampling include the Hex fluorescent dye. The use of several fluorescent dyes could reduce the number of tubes, as it is possible to simultaneously record the results of amplification reactions that take place in one tube.

An oligonucleotide with a Rox fluorescent label, Marker, was added to tube No. 5. It is used by the device as a marker to determine the position of striped tubes (strips) in the bar (Table 4).

The relative level of a conditionally pathogenic microorganism was calculated using amplifier software by calculating decimal logarithms or orders between the absolute values of a particular microorganism and total bacterial mass (Table 5).

Table 3

Amplification program [14]

No. of block	Temperature, °C	minutes	seconds	Cycles number	Optical measurement mode	Block type
1	80.0	0	30	1		Cycle
	94.0	1	30			
2	94.0	0	30	5		Cycle
	64.0	0	15		√ ^{3s}	
3	94.0	0	10	45		Cycle
	64.0	0	15		√ ^{3s}	
4	94.0	0	5	1		Cycle
5	10.0	Saving		Saving

Note: detection of optical measurements of research results

Table 4

Composition of “FEMOFLO SCREENS” strips, color marking and detection channels of amplification products [14]

No. of tube	Detection channels				Color buffer marking
	Fam	Hex	Rox	Cy5	
1	Total bacterial mass	IC	–	–	Blue
2	Normoflora – <i>Lactobacillus spp.</i>	IC	–	–	Colorless
3	<i>Gardnerella vaginalis/ Prevotella bivia/ Porphyromonas spp.</i>	IC	–	–	
4	<i>Ureaplasma (urealyticum + parvum)</i>	IC	–	–	
5	<i>Candida spp.</i>	UCR	Marker	–	
6	<i>Mycoplasma hominis</i>	IC	<i>Mycoplasma genitalium</i>	–	

Table 5

Criteria for quantitative assessment of biota for the set of reagents “Femoflor” [14]

Indicator	Absolute gEq / sample	Relative indicator	Evaluation of the indicator
Control of material collection	>10 ⁴	none	enough for analysis
	<10 ⁴		not enough for analysis, re-taking the material is required
Total bacterial mass (TBM)	10 ⁶ –10 ⁸	none	within the norm
	<10 ⁶		reduced level
<i>Mycoplasma hominis</i>	>10 ⁴	none	within the norm
	<10 ⁴		the level is raised
<i>Ureaplasma (urealyticum+parvum)</i>	>10 ⁴	none	within the norm
	<10 ⁴		the level is raised
<i>Candida spp.</i>	>10 ³	none	the level is raised
	<10 ³		within the norm
<i>Lactobacillus spp.</i>	>10 ⁶⁻⁸	from 0 to –0.3 (100 %–50 %)	within the norm
		from –0.3 to –1 (50 %–10 %)	moderately low level
	<10 ⁵⁻⁶	< –1 (10 %)	significantly reduced level
<i>Gardnerella vaginalis</i>	>10 ⁴⁻⁵	Less than –3 (0.1 %)	within the norm

Statistical processing of the results was performed using Microsoft Excel 2016 software products to build graphical images. In the text of the article nominal variables are shown in the form of absolute and percentage values. (n, %). The choice of statistical procedures considered the methodological requirements of the International Congress on the Harmonization of Clinical Trials ICH / GGP.

3. Research results

When the hormonal background changes and the immune defense decreases in the microecosystem of the

vagina, the conditions for quantitative and qualitative microbial abnormalities are created and, the more significant hormonal and immune disorders, the more pronounced dysbiotic. In this regard, vaginal dysbacteriosis and bacterial vaginosis (BV) should be considered not as an independent process of a purely bacterial nature, but as a symptom complex accompanying systemic disorders, and take into account this feature in the diagnosis and treatment of gynecological diseases.

To solve the tasks, the components of the vaginal microbiota of women of the surveyed groups (a sign of

age and smoking) were analyzed in the period from 2018 to 2021.

Representatives of the genus *Mycoplasma spp.* as part of the microbiota of the urogenital tract of women of reproductive age who smoke and do not smoke.

According to the recommended criteria of the norm according to the instruction to the Femoflor Screen test system, the content of *Mycoplasma hominis*, *Mycoplasma genitalium*, *Ureaplasma urealyticum*, *Ureaplasma*

ma urealyticum, *Ureaplasma parvum* is considered to be 10^4 gEq / sample, and the content of *Mycoplasma hominis*, *Mycoplasma genitalium*, *Ureaplasma urealyticum*, *Ureaplasma parvum* more than 10^4 gEq / sample is considered a sign of a pathological process.

The frequency of detection of the corresponding norm and elevated level of gEq *M. hominis* in samples of biological material among women of different age groups who do not smoke, for the period 2018–2021 is presented in Fig. 1, 2.

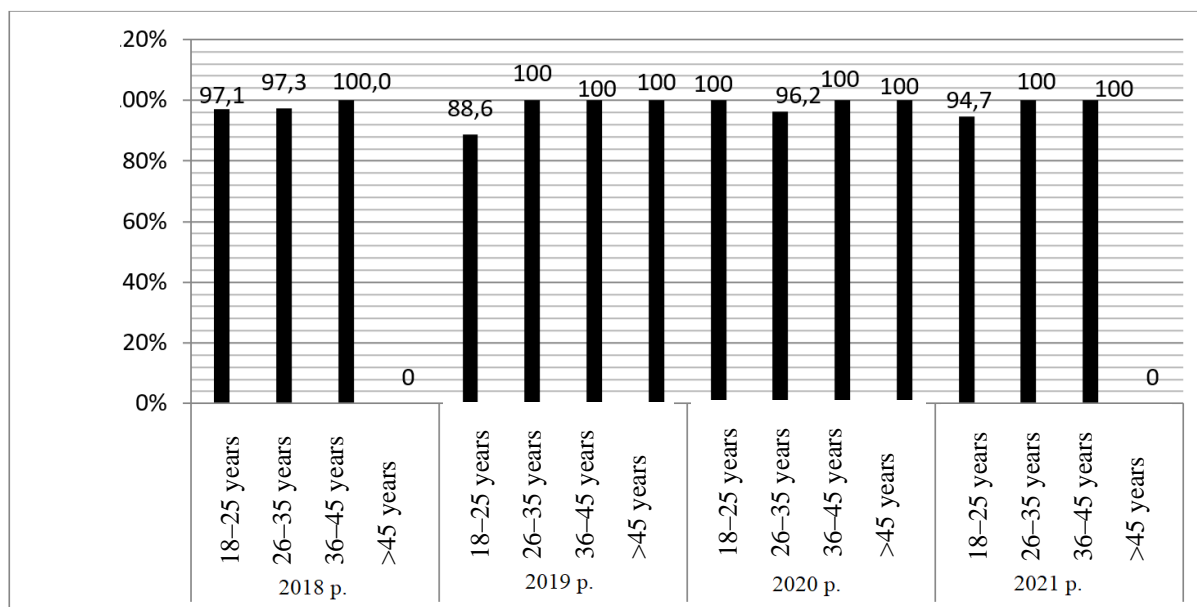


Fig. 1. Frequency of the corresponding level of *M. hominis* among women of different age groups who do not smoke (2018–2021)

Thus, it was found that the frequency of detection of normal gEq *M. hominis* in samples of biological material among women of age group I (n=108) who did not use tobacco products, had the following trend: in 2018 this indicator was detected in 34 people (97.1 %), in 2019 – for 31 people (88.6 %). In 2020, the frequency of detection of the corresponding level of *M. hominis* among non-smokers is the highest – in 100 % of patients, in 2021 – in 18 women (94.7 %).

During the period 2018–2021, a high percentage of the frequency of detection of the corresponding level of *M. hominis* in the biological material of patients was determined among women of the second age group (n=199) who do not smoke. In 2018, the level of gEq of this microorganism was detected in the samples of biological material of 36 people (97.3 %), but in 2019 and 2021 this indicator was found in 100 % of patients. In 2020, the norm of *M. hominis* in samples of biological material was detected in 51 people (96.2 %).

During the period 2018–2021, among women of the third age group (n=128) who do not smoke, the frequency of detection of the optimal level of gEq *M. hominis* in samples of biological material was 100 %. No patient in this age group showed an elevated level in mycoplasma gEq samples.

During the period 2018–2021, among women of the IV age group (n=5) who do not smoke, the level of *M. hominis* in the samples of biological material was 100 % corresponding to the norm.

The frequency of detection of elevated levels (Fig. 2) of gEq *M. hominis* in samples of biological material in women of the first age group who do not smoke, had a slight tendency to increase in the period 2018–2021.

The frequency of detection of elevated levels of gEq *M. hominis* in samples of biological material of women of the II age group who do not smoke is almost absent in only 3 people out of 199 found elevated gEq titers of this microorganism.

In the III and IV age groups among women with elevated levels of *M. hominis* who do not smoke, this microorganism was not detected at all.

For women who had a habit of smoking, we registered the following (Figs. 3, 4). During the study period, the frequency of detection of the corresponding norm of *M. hominis* in the biological material of women of all ages ranged from 92–100 %. Regarding the detection of elevated levels of *M. hominis* in samples of biological material, this indicator varied in the range of 6–8 %, but was not registered in all studied groups of women (Fig. 4).

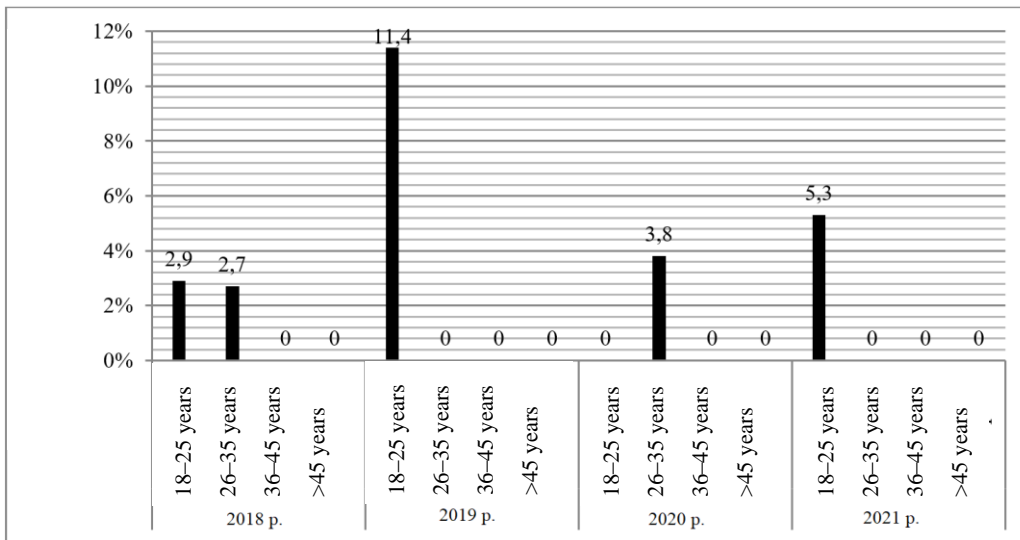


Fig. 2. Frequency of elevated levels of *M. hominis* among women of different ages who do not smoke (2018–2021)

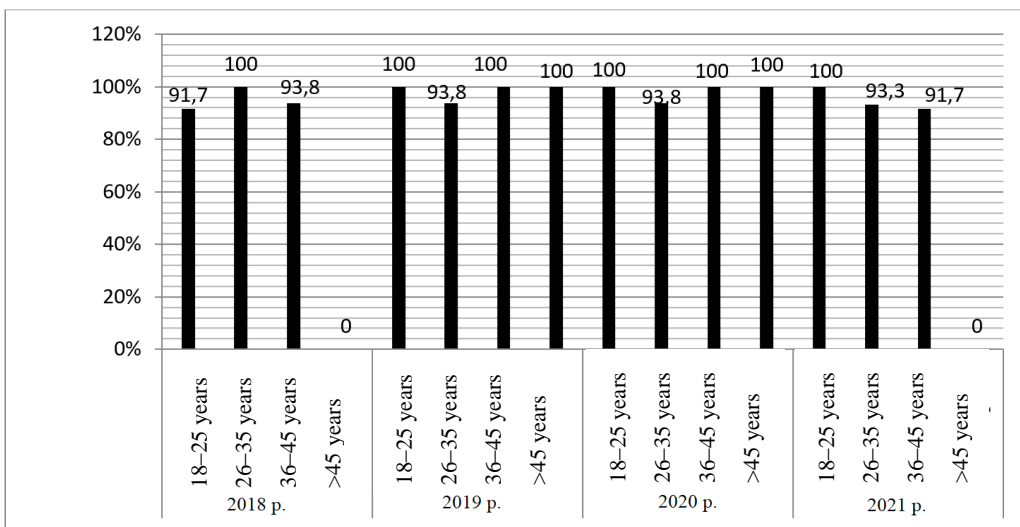


Fig. 3. Frequency of detection of normal levels of *M. hominis* among women of different ages who smoke (2018–2021)

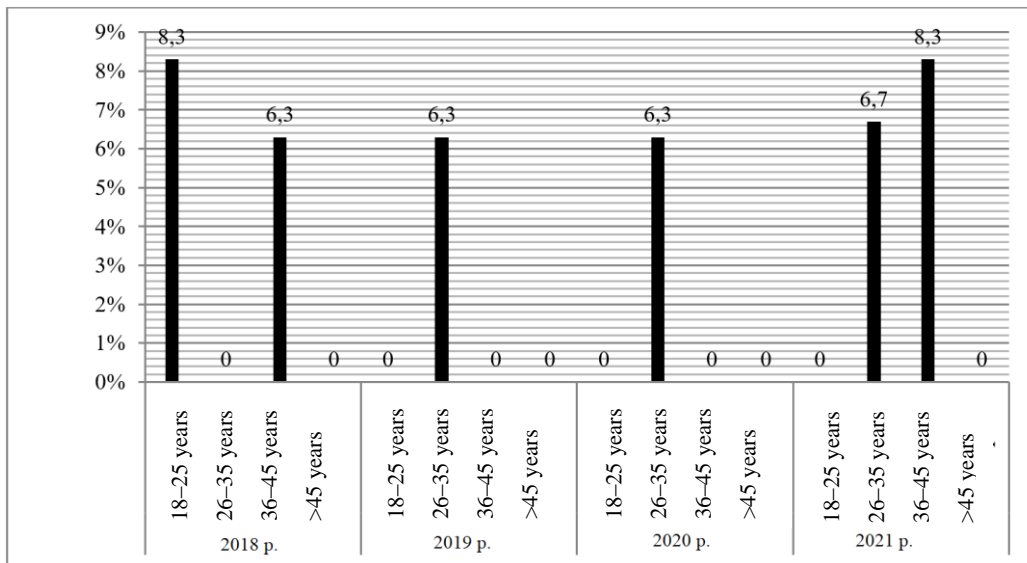


Fig. 4. Frequency of detection of elevated levels of *M. hominis* among women of different ages who smoke (2018–2021)

The analysis revealed that the most affected group at risk of dysbiosis in women who do not smoke was I (18–25 years) age group; in women who smoke – II (26–35 years) age group.

The frequency of detection of the corresponding norm and elevated levels of *M. genitalium* gEq in sam-

ples of biological material among women of different age groups who do not smoke, from 2018–2021 is presented in Fig. 5. It was found that the corresponding level of *M. genitalium* ranged from 96.2 % to 100 %, and the frequency of detection of elevated levels – from 2.9 % to 3.8 %.

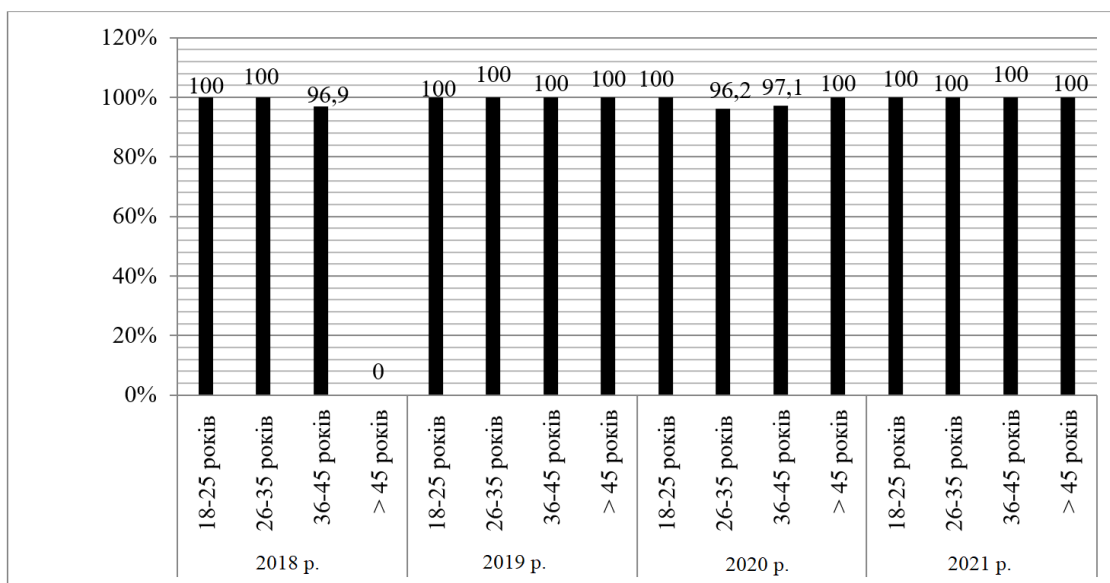


Fig. 5. The frequency of detection of normal levels of *M. genitalium* among women of different ages who do not smoke (2018–2021)

The frequency of detection of the corresponding level of *M. genitalium* among women of different age groups who smoke (2018–2021) ranged from 50.0 % to

100 % (Fig. 6), elevated levels – from 7.1 % to 50, 0 %. The most affected group at risk of dysbiosis in women who do not smoke and smoke was the III age group.

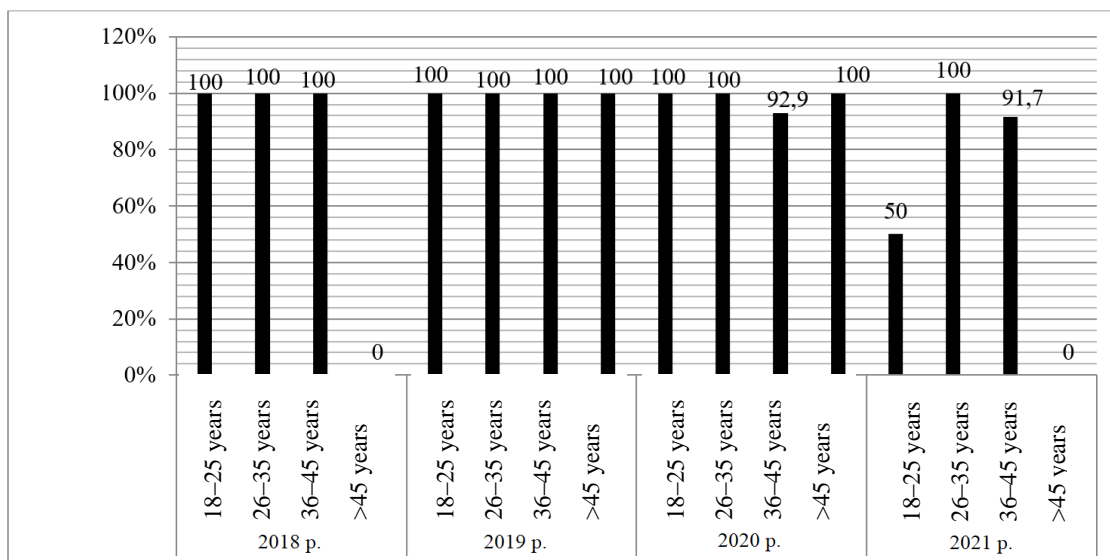


Fig. 6. Frequency of detection of normal levels of *M. genitalium* among women of different ages who smoke (2018–2021)

The frequency of detection of the corresponding norm and elevated levels of *U. urealyticum*, *U. parvum* in samples of biological material among women of different

age groups who do not smoke, from 2018–2021 is presented in Fig. 7. The study found that these figures ranged from 68.6 % to 100 % and from 4.8 % to 31.4 %, respectively.

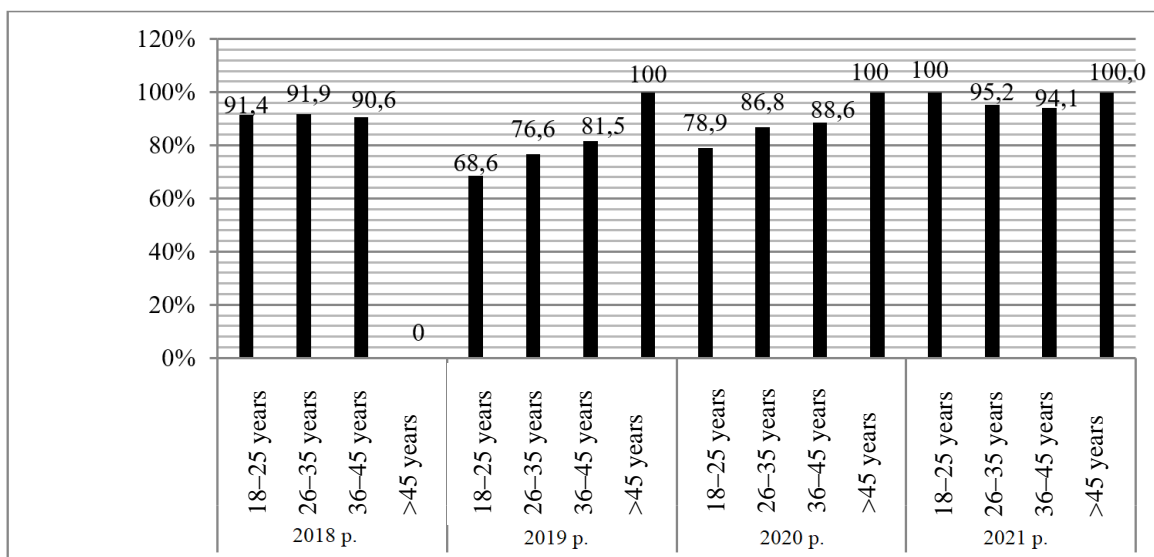


Fig. 7. The frequency of detection of normal levels of *U. urealyticum*, *U. parvum* among women of different ages who do not smoke (2018–2021)

Somewhat different results were recorded in women of all study groups on the background of smoking (Fig. 8). The percentage fluctuation of the normal level of *U. urealyticum*, *U. parvum* among women of dif-

ferent ages of smokers ranged from 50.0 to 100. It was also determined the increase in the frequency of detection of elevated levels of *U. urealyticum*, *U. parvum* in samples of biological material, which ranged from 9 to 50 %.

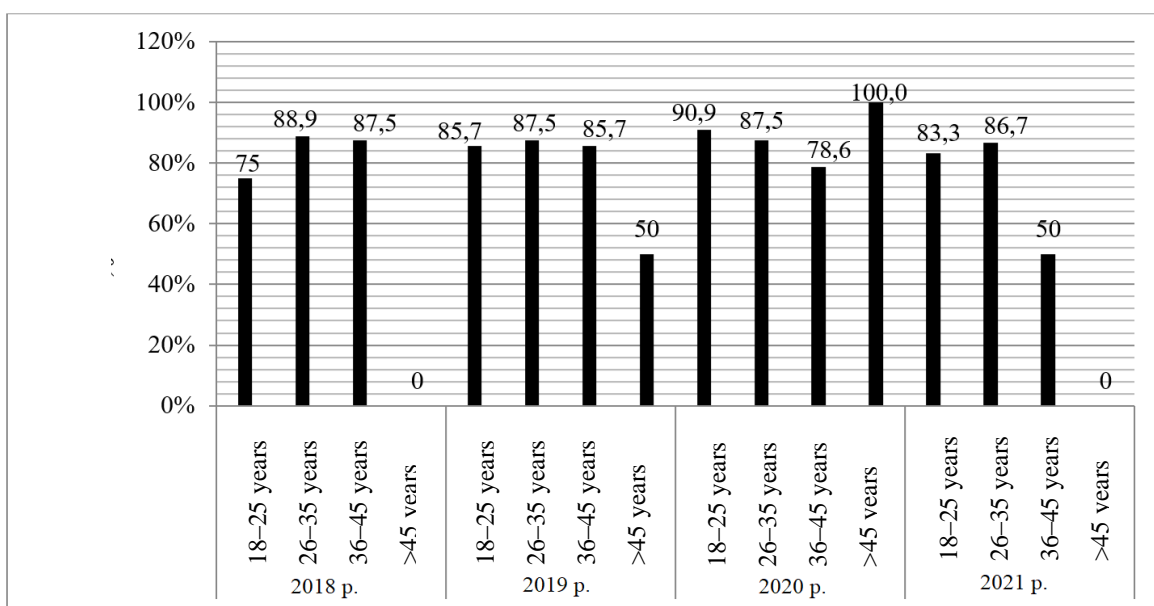


Fig. 8. Frequency of detection of normal levels of *U. urealyticum*, *U. parvum* among women of different ages who smoke (2018–2021)

Thus, summarizing the results we can highlight the following. The most affected group of women, with the frequency of detection of elevated levels of *U. urealyticum*, *U. parvum*, among non-smokers, were I and II age groups; in women who smoke with elevated levels of *U. urealyticum*, *U. parvum* – age group III.

The IV age group of women by the number of *U. urealyticum*, *U. parvum* is the least numerous of the surveyed contingent and is not indicative for comparison with other age groups.

4. Discussion of research results

The advantages of the obtained results are the establishment of the dependence of the effect of smoking on the composition of the microbiota of the urogenital tract of women of reproductive age. This makes it possible to diagnose inflammatory diseases caused by opportunistic pathogens.

The disadvantage is the study of incomplete microbiota of the urogenital tract of women of reproductive

age to obtain a complete picture of the effects of smoking on women's reproductive health.

According to the research (Nelson T. M. et al.) [17], smoking has been found to be a risk factor for dose-dependent bacterial vaginosis and is significantly associated with the risk of a number of sexually transmitted infections in women. Colonization of the mucous membrane by pathogenic and opportunistic microorganisms is associated with damage to the cervical epithelium due to cell DNA modification and suppression of local and systemic immune responses, which lead to a decrease in the number of indigenous microflora. It is shown that the main metabolite of nicotine – cotinine – is concentrated in cervical mucus, which indicates the possibility of direct impact on the vaginal microbiocenosis. Bacterial vaginosis is usually found in smokers twice as often as in non-smokers and is mostly found in young women.

The results of our research also found that smoking is associated with the development of bacterial vaginosis, which is caused by opportunistic pathogens.

Study limitations. The study was screening to establish the structure of the microbiota of women of reproductive age on the background of smoking. Therefore, it is advisable to study the full range of microbiota in women: lactobacilli, conditionally pathogenic and pathogenic microorganisms.

Prospects for further research. Imbalance in the microflora of the vagina leads to a decrease in the number of lactobacilli and an increase in the number of conditionally pathogenic flora, which is the cause of the inflammatory process. Analysis of the results shows that smoking is associated with an increase in opportunistic flora in the vaginal microflora of women. Therefore, there is a need for further research to determine exactly how smoking affects changes in the biocenosis of the urogenital tract of women of childbearing age.

5. Conclusions

The microflora of the urogenital tract is a microorganism that colonizes the mucous membrane in the

norm, able to perform a protective function against colonization by opportunistic and pathogenic microorganisms. It is the imbalance in the microflora of the vagina that leads to an increase in the number of conditionally pathogenic flora, which is the cause of the inflammatory process.

Analysis of the results of the study shows that the composition of the microbiota of the reproductive tract of women depends on the use of tobacco products.

An increase in indicators for conditionally pathogenic microorganisms was also shown. Therefore, there is a need for further research to establish the role of microorganisms involved in restoring the composition of the microbiota after inflammatory processes in women who use and do not use tobacco products.

By processing scientific data, doctors could more confidently assign a woman to one or another risk category during pregnancy, the role in fetal pathology, in some cases leading to miscarriage, dysbiotic phenomena in the gastrointestinal tract and make further predictions about treatment. The obtained data allowed to assess the effect of tobacco on the composition of the microbiota of the urogenital tract of women and made it possible to use them in measures of social and preventive work, as an indisputable fact to quit smoking.

Conflict of interests

The authors declare there is no conflict of interests.

Financing

The study was performed with no financial support.

Acknowledgments. The research was conducted within the scientific and technical work of the Department of General Medicine with a course of physical therapy on “Modern strategies for determining the health of the population for the most common diseases, their treatment, prevention and rehabilitation measures”, state registration number 0122U001470 Oles Honchar Dnipro National University, Dnipro.

References

1. Kalia, N., Singh, J., Kaur, M. (2020). Microbiota in vaginal health and pathogenesis of recurrent vulvovaginal infections: a critical review. *Annals of Clinical Microbiology and Antimicrobials*, 19 (1). doi: <http://doi.org/10.1186/s12941-020-0347-4>
2. Chee, W. J. Y., Chew, S. Y., Than, L. T. L. (2020). Vaginal microbiota and the potential of Lactobacillus derivatives in maintaining vaginal health. *Microbial Cell Factories*, 19 (1). doi: <http://doi.org/10.1186/s12934-020-01464-4>
3. Al-Nasiry, S., Ambrosino, E., Schlaepfer, M., Morré, S. A., Wieten, L., Voncken, J. W. (2020). The Interplay Between Reproductive Tract Microbiota and Immunological System in Human Reproduction. *Frontiers in Immunology*, 11. doi: <http://doi.org/10.3389/fimmu.2020.00378>
4. Kennedy, M. S., Chang, E. B. (2020). The microbiome: Composition and locations. *Progress in Molecular Biology and Translational Science*, 1–42. doi: [10.1016/bs.pmbts.2020.08.013](https://doi.org/10.1016/bs.pmbts.2020.08.013)
5. Bubalo, K. V., Holodok, L. P., Khlopova, O. V., Vinnikov, A. I. (2016). Doslidzhennia mikrobykh asotsiatsii mikoplazm z inshymy mikroorhanizmy urohenitalnoho traktu zhynok. *Visnyk problem biolohii i medytsyny*, 1, 244–248.
6. Boldyreva, M. N., Donnikov, A. E., Tumbinskaia, L. V. (2009). Issledovanie biotcenoza urogenitalnogo trakta u zhenshchin metodom PTcR s detekciei rezultatov v rezhime realnogo vremeni. *Moscow*, 42.
7. Nemova, I. S., Potaturkina-Nesterova, N. I., Orlina, M. A., Miasnikova, A. V. (2011). Monitoring mikrobiotcenoza urogenitalnogo trakta zhenshchin pri mikoplazmennykh infektsiakh. *Vestnik novykh meditsinskikh tekhnologii*, 1, 34–36.
8. Bilimova, S. I., Chistiakova, G. N., Remizova, I. I. (2010). Kompleksnaia otsenka vaginalnoi mikrobyoty metodom PTcR v rezhime realnogo vremeni. *Uralskii meditsinskii zhurnal*, 5, 135–138.
9. Kaptilyni, V. A. (2016). Metodika vziatia biologicheskogo materiala dlia molekuliarno-biologicheskogo metoda issledovaniia (PTcR-dagnostika). *Arkhiv akusherstva i ginekologii im. V. F. Snegireva*, 3, 156–160.
10. Kungurov, N. V. (2010). Pokazaniia i taktika terapii patcientov s urogenitalnoi mikoplazmennoi infektsiei v zavisimosti ot geneticheskoi variabelnosti genitalnykh mikoplazm. *Ekaterinburg*, 32.
11. Abdrakhmanov, A. R., Petrova, A. S., Sadykova, Z. R., Abdrakhmanov, R. M. (2017). Analiz sostoianii zhenskoi reproduktsivnoi sistemy, infitsirovanoi mikoplazmennoi infektsiei. *Zdorove i obrazovanie v XXI veke*, 10, 17–20.

12. Paira, D. A., Molina, G., Tissera, A. D., Olivera, C., Molina, R. I., Motrich, R. D. (2021). Results from a large cross-sectional study assessing Chlamydia trachomatis, Ureaplasma spp. and Mycoplasma hominis urogenital infections in patients with primary infertility. Scientific Reports, 11 (1). doi: <http://doi.org/10.1038/s41598-021-93318-1>
13. Moridi, K., Hemmaty, M., Azimian, A., Fallah, M. H., Khaneghahi Abyaneh, H., Ghazvini, K. (2020). Epidemiology of genital infections caused by Mycoplasma hominis, M. genitalium and Ureaplasma urealyticum in Iran; a systematic review and meta-analysis study (2000–2019). BMC Public Health, 20 (1). doi: <http://doi.org/10.1186/s12889-020-08962-5>
14. Instrukciia po primeneniiu nabora reagentov dlia issledovaniia biotcenoza urogenitalnogo trakta u zhenshchin metodom PTcR v rezhime realnogo vremeni Femoflor (2017). OOO "DNK-Tekhnologiiia".
15. Kaptilnyi, V. A. (2016). Metodika vziatii biologicheskogo materiala dlia molekuliarno-biologicheskogo metoda issledovaniia (PTcR-diaagnostika). Arkhiv akusherstva i ginekologii im. V. F. Snegireva, 3, 156–160.
16. Baranova, E. E., Bateneva, E. I., Galkina, I. S., Donnikov, A. E., Zorina, V. V., Tumbinskaia, L. V. et. al. (2013). PTcR v realnom vremeni: novye vozmozhnosti tekhnologii v reshenii reproduktivnykh problem. OOO "DNK-Tekhnologiiia", 63.
17. Nelson, T. M., Borgogna, J. C., Michalek, R. D., Roberts, D. W., Rath, J. M., Glover, E. D. et. al. (2018). Cigarette smoking is associated with an altered vaginal tract metabolomic profile. Scientific Reports, 8 (1). doi: <http://doi.org/10.1038/s41598-017-14943-3>

Received date 06.01.2022

Accepted date 17.02.2022

Published date 31.03.2022

Oksana Starishko, Senior Lecturer, Department of General Medicine with a Course of Physical Therapy, Oles Honchar Dnipro National University, Gagarina ave., 72, Dnipro, Ukraine, 49010

Tetiana Turytska, PhD, Associate Professor, Department of General Medicine with a Course of Physical Therapy, Oles Honchar Dnipro National University, Gagarina ave., 72, Dnipro, Ukraine, 49010

Anastasia Ovcharenko, Department of General Medicine with a Course of Physical Therapy, Oles Honchar Dnipro National University, Gagarina ave., 72, Dnipro, Ukraine, 49010

**Corresponding author: Oksana Starishko, e-mail: oksanason@i.ua*