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Original article

CHANGES IN THE MICROBIOME AND IMMUNITY ASSOCIATED WITH THE INCREASING INCIDENCE OF INFLAMMATORY DISEASES

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Abstract: **Background:** In recent years, there has been a significant increase in the frequency of inflammatory diseases in women of reproductive age, likely due to changes in the microbiome, which prompted this study.

Aim: To study the dynamics of the taxonomic profile of the microbiota and the state of local immunity of the skin, nasopharynx, vagina, and feces in women living in Ukraine during 2010–2025.

Materials and Methods: A total of 136 women aged 20–39 years who underwent a preventive examination by a family doctor and were examined by a dermatologist, gynecologist, and otorhinolaryngologist were included in the study. In 2010–2011, 44 women were examined; in 2017–2018, 47; and in 2024–2025, 45. The microbial spectrum of the skin, oropharynx, vagina, and feces, including Gram-positive and Gram-negative bacteria, was analyzed using a VITEK 2 COMPACT bacteriological analyzer ("bioMérieux", France) with AES: Global CLSI-based + Phenotypic software. The humoral component of local immunity was assessed based on the level of secretory immunoglobulin A, which was determined using an enzyme-linked immunosorbent assay.

Results: It has been established that significant changes have occurred in the human microbiome over the past 15 years. Thus, the total number of bacteria on the skin has increased, with a statistically significant increase observed in 2024–2025 compared to 2010–2011. This was particularly evident in the increased numbers of *Staphylococcus aureus*, *Streptococcus pyogenes*, fungi of the genus *Candida*, and *Malassezia spp*., accompanied by a decrease in *Staphylococcus epidermidis* and *Staphylococcus hominis*. In the oropharyngeal microbiome, a significant increase in opportunistic streptococci, opportunistic staphylococci, fungi of the genus *Candida*, and an integral indicator of the number of opportunistic flora was detected during this period. In vaginal secretions, the replacement of normal microflora (*Lactobacillus spp.*) with opportunistic microorganisms, both aerobic and anaerobic, was observed, while in feces, a decrease in normal flora and an increase in the numbers of staphylococci, non-fermenting *Escherichia coli*, and fungi of the genus *Candida* were observed. Changes in the microbiome were accompanied by a decrease in the concentration of secretory immunoglobulin A in biological media, which, in turn, deepened the disruption of the microbiome and led to a decrease in normal flora and an increase in opportunistic pathogens.

Conclusion: In women of reproductive age, a deterioration in the state of microbiocenosis has been observed in recent years against a background of decreased local immunity, which is one of the important factors contributing to the increased frequency of inflammatory processes. Their microbial landscape is characterized by the replacement of normal microflora of the skin, nasopharynx, vagina, and intestine with conditionally pathogenic microorganisms. The results obtained, in our opinion, justify the need for timely implementation of individualized therapeutic and preventive measures in women, which may contribute to the restoration of the microbiome and reduce the frequency of relapses of inflammatory diseases.

Keywords: microbiome, local immunity, women of reproductive age, skin, oropharynx, vagina.

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INTRODUCTION

In recent decades, both worldwide and in Ukraine, the frequency and structure of skin, oropharyngeal, vaginal, and intestinal diseases have significantly increased and changed (1, 2).

The increase in the frequency of inflammatory diseases poses a threat to the health and lives of the population (3, 4). Migration processes caused by the war in Ukraine significantly increase the risk of epidemic complications due to overcrowding, deterioration of sanitary conditions, and limited access to medical services (2, 5).

Today, the dynamics of the incidence and structure of skin, oropharyngeal, vaginal, and intestinal diseases are indicative. Thus, studies by Korolenko VV (6) showed an increase in the incidence rates of trichophytosis and microsporia in the population of Ukraine during 2009–2019 by 32.9%, the prevalence of psoriasis by 16.6%, and the incidence of sexually transmitted diseases during 2000–2019 (syphilis by 15.5 times and gonorrhea by 6.8 times).

The frequency of atopic dermatitis (AD) is up to 20% among the pediatric population and up to 10% among adults in European countries. As of 2020, the prevalence of AD among the pediatric population in Ukraine ranged from 9.0 to 28.5% (4).

The most common diseases include oral pathology, rhinitis, pharyngitis, otitis media, and sinusitis (7). The frequency of tonsillitis worldwide ranges from 2% to 15% of the total population (8).

Recurrent aphthous stomatitis affects 5–25% of the population, and its prevalence ranges from 5% to 60%, depending on the population, environmental factors, or diagnostic criteria of the study (9).

Studies by Y. Abiko et al. (10) determined the influence of chronic stress on the development of this disease and concluded that psychological stress is more strongly associated with episodic manifestations of recurrent aphthous stomatitis than physical stress.

Every year, a progressive increase in the frequency of vulvovaginitis, cervicitis, and urethritis of mixed bacterial-fungal-trichomonal etiology has been noted in women (11). The frequency of bacterial vaginosis varies from 19% to 68%, while the proportion of aerobic vaginitis reaches 5–24% (12).

Every year, in countries around the world, particularly in Ukraine, the number of people suffering from diseases of the digestive system is increasing (13), including intestinal diseases (14).

Undoubtedly, the increase in the incidence in the population may be due to better diagnostics and the periodicity of the long-term epidemic process. However, many researchers attach importance to disturbances of the microflora, the presence of infectious agents, and the state of immunity in the development of numerous pathologies of the skin, oropharynx, vagina, and intestines due to environmental and social factors, the widespread prevalence of bad habits, and changes in nutrition (15, 16).

Against this background, a change in the ratio between pathogenic and non-pathogenic microorganisms in chronic nasopharyngeal infections is also observed. However, the pathogenicity of microorganisms attributed to a single pathogen may not only depend on its biological properties in monoculture but may also be an integrated result of the action of several symbionts (17, 18).

Characteristic changes in the intestinal microbiota are also observed in inflammatory bowel diseases, irritable bowel syndrome, and colorectal cancer (19, 20).

It is known that the interaction of microflora clearly manifests the phenomenon of microbial antagonism. On the one hand, this antagonism consists of the production of antagonistic substances (antibiotics, bacteriocins, lysozyme) by transit strains and strains of resident microflora; on the other hand, there is resistance to these same factors of microbial antagonism (21).

The mutual influence of microflora and local immunity is extremely important in biotopes, since local immunity is formed under the influence of microflora, and its deviations lead to certain changes in the balance of microflora in the biotope, which is likely to be one of the main factors contributing to the chronicity of diseases (22).

This is confirmed by the data from a study by Postolenko V.Yu. et al. (23), who established changes in the taxonomic profile of the microbiota in the presence of changes in local immunity in the endometrium of women. The authors note that the imbalance of the endometrial microflora was accompanied by significant disturbances in local immune defense.

The above prompted us to study the dynamics of the human microbiome over the past 15 years.

The aim: To study the dynamics of the taxonomic profile of the microbiota and the state of local immunity of the skin, nasopharynx, vagina, and feces in women living in Ukraine during 2010–2025.

MATERIALS AND METHODS

The study included 136 women of reproductive age (20–39 years) who underwent a preventive examination by a family doctor and were examined by a dermatologist, gynecologist, and ENT specialist. Forty-four women were examined in 2010–2011; 47 in 2017–2018; and 45 in 2024–2025.

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Samples were not collected from all study sites (skin, oropharynx, vagina, and stool) for every patient; this was due to factors such as the patient's condition at the time of the visit (e.g., menstruation) or a patient's reluctance to provide samples from specific sites, despite having signed the informed consent form prior to the study. Consequently, the tables present the actual number of examinations performed for each site across the various years of the study.

Exclusion criteria: the presence of chronic diseases, mental illnesses, acute inflammatory processes, or oncological diseases.

A study of the microbial spectrum of the skin, oropharynx, vagina, and feces was conducted. Clinical samples were delivered to the laboratory within 1 hour after material collection. Microbiological studies were performed in the bacteriological laboratory of the Municipal Non-Profit Institution "Healthy Family" of the Zaporizhzhia Regional Council. The determination of Gram-positive and Gram-negative bacterial species was performed using a VITEK 2 COMPACT bacteriological analyzer («BioMérieux», France) with AES: Global CLSI-based software.

The state of the humoral component of local immunity was assessed by the level of secretory immunoglobulin A (SIgA), which was determined using an enzyme-linked immunosorbent assay.

Statistical processing of the research results was performed using standard computer programs. The arithmetic mean (M) and standard error of the arithmetic mean (m) were determined using the paired Student's t-test or the Wilcoxon signed-rank test, depending on the normality of the distribution of differences, which was determined using the Shapiro–Wilk test. A significance level of 0.01 was used. Correlation analysis with determination of pairwise correlation coefficients (r) was used to clarify structural relationships. A significance level of 0.05 was used; differences between the data were considered statistically significant at $p < 0.05$.

Mathematical analysis and statistical processing of the data were carried out using the EXCEL statistical package and the Statistica 13.0 licensed package, StatSoft Inc., serial number JPZ8041382130ARCN10-J.

The study was approved by the ethics committees of the medical institutions. The study was conducted in accordance with the main provisions of the "Rules of Ethical Principles for Conducting Scientific Medical Research with Human Participation", approved by the Declaration of Helsinki (1964–2013), ICH GCP (1996), EEC Directive No. 609 (dated 11/24/1986), and orders of the Ministry of Health of Ukraine No. 690 dated 09/23/2009, No. 944 dated 12/14/2009, and No. 616 dated 08/03/2012. All patients were informed about the goals, organization, and methods of the study and signed an informed consent form to participate in it, and all measures were taken to ensure the anonymity of the patients.

RESULTS

Descriptive Statistics

Dynamic changes in the skin microbiota over 15 years were analyzed, and an increase in the total number of bacteria on the skin was observed, with a statistically significant increase in 2024–2025 compared to 2010–2011 (Table 1).

Over the years, the numbers of *Staphylococcus aureus*, *Streptococcus pyogenes*, fungi of the genus *Candida*, and *Malassezia spp.* have increased on the skin, while those of *Staphylococcus epidermidis* and *Staphylococcus hominis* have decreased. The latter two belong to beneficial microorganisms that occupy the niche and prevent the proliferation of pathogen-

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Table 1. *Changes in the skin microbiome (LgCFU/cm2) (M ± m)*

Microorganisms	2010-2011 yy.	2017-2018 yy.	2024-2025 yy.
	n = 31	n = 34	n = 32
Total bacteria	3.1 ± 0.21	3.5 ± 0.23	4.1 ± 0.27*
Staphylococcus aureus	0.49 ± 0.06	0.84 ± 0.11*	1.07 ± 0.12*
Staphylococcus epidermidis	0.73 ± 0.08	0.46 ± 0.06*	0.29 ± 0.04*●
Staphylococcus haemolyticus	0.35 ± 0.05	0.41 ± 0.06	0.38 ± 0.05
Staphylococcus saprophiticus	0.37 ± 0.05	0.44 ± 0.05	0.48 ± 0.07
Staphylococcus hominis	0.63 ± 0.05	0.45 ± 0.05	0.28 ± 0.04*●
Streptococcus pyogenes	0.16 ± 0.04	0.23 ± 0,04	0.27 ± 0.04*
Candida fungi	1.42 ± 0.17	1.80 ± 0.20	2.13 ± 0.21*
Malassezia spp.	1.13 ± 0.12	1.26 ± 0.15	1.77 ± 0.16*●

Notes: * - $P < 0.05$ for differences from the 2010-2011 group; ● - $P < 0.05$ for differences from the 2017-2018 group.

Table 2. *Results of bacteriological examination of the oropharyngeal mucosa in different years (Lg CFU/ml) (M ± m)*

Microorganisms	2010-2011 yy.	2017-2018 yy.	2024-2025 yy.
	n = 33	n = 32	n = 30
Conditionally pathogenic streptococci	1.85 ± 0.23	2.18 ± 0.23	2.66 ± 0.28*
Conditionally pathogenic staphylococci	1.79 ± 0.22	2.03 ± 0.24	2.46 ± 0.27*
Haemophilus influenzae	1.23 ± 0.24	1.45 ± 0.31	1.58 ± 0.23
Candida fungi (albicans and nonalbicans)	0.45 ± 0.21	0.68 ± 0.29	1.23 ± 0.26*
Enterobacteria	0.24 ± 0.15	0.32 ± 0.17	0.34 ± 0.17
Enterococci	0.24 ± 0.15	0.32 ± 0.17	0.45 ± 0.20
NFGNB	0.24 ± 0.15	0.35 ± 0.21	0.40 ± 0.23
Integral indicator of the amount of conditionally pathogenic flora	6.04 ± 0.62	7.33 ± 0.69*	8.12 ± 0.76*

Notes: * - P < 0.05 for differences from the 2010-2011 group.

Table 3. *Changes in the vaginal microbiome (LgCFU/ml) (M ± m)*

Microflora	2010-2011 yy.	2017-2018 yy.	2024-2025 yy.
	n = 28	n = 31	n = 30
Lactobacillus spp.	6.8 ± 0.37	6.2 ± 0.38	5.7 ± 0.31*
Eshericia coli	2.6 ± 0.18	3.2 ± 0.27	4.3 ± 0.34*
Proteus	2.3 ± 0.22	2.6 ± 0.29	3.0 ± 0.33
Clustridium spp.	2.5 ± 0.21	2.8 ± 0.27	3.1 ± 0.25
Staphilococcus spp.	2.7 ± 0.24	3.2 ± 0.26	4.5 ± 0.33*●
Streptococcus spp.	2.0 ± 0.16	2.7 ± 0.20*	3.7 ± 0.29*●
Corinebacterium spp.	2.4 ± 0.21	2.6 ± 0.23	3.1 ± 0.29
Yeast-like fungi of the genus Candida	2.1 ± 0.18	2.7 ± 0.25	3.5 ± 0.29*
Gardnerella vaginali	1.2 ± 0.18	1.5 ± 0.21	1.9 ± 0.25
Mobiluncus spp.	1.5 ± 0.21	1.8 ± 0.23	2.4 ± 0.31

Notes: * - P < 0.05 for differences from the 2010-2011 group; ● - P < 0.05 for differences from the 2017-2018 group.

ic flora. Thus, there was not only an increase in the amount of microflora on the skin but also a shift toward more beneficial microflora.

The results of the bacteriological examination of the oropharyngeal mucosa in different years are presented in Table 2. During this period, the amount of microflora increased, although this increase did not reach critical levels for the development of disease.

A significant difference was found between the results for the presence of opportunistic streptococci, opportunistic staphylococci, *Candida* fungi, and the integral indicator of the number of opportunistic flora in 2010–2011 and 2024–2025. No significant difference was found between the corresponding indicators in 2017–2018 and 2024–2025, although a trend toward an increase in microflora was noted.

The microbiome of vaginal discharge was also analyzed, and the results of this analysis are presented in Table 3.

A decrease in *Lactobacillus* spp. in the vaginal microbiome was observed over the 15-year period, accompanied by an increase in *Escherichia coli*, *Staphylococcus* spp., *Streptococcus* spp., and yeast-like fungi of the genus *Candida*, as well as a tendency toward an increase in *Gardnerella vaginalis* and *Mobiluncus* spp. Thus, the normal microflora (*Lactobacillus* spp.) was replaced by conditionally pathogenic microorganisms, and the number of both aerobic and anaerobic flora increased.

The results of the bacteriological examination of feces are presented in Table 4. During the observation period, patients showed a decrease in lactic acid flora and an increase in the numbers of staphylococci, non-fermenting *Escherichia coli*, and fungi of the genus *Candida*.

Taking into account the changes detected in the biotopes in recent years, the level of local immunity was studied by measuring the concentration of SIgA

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Table 4. *Results of bacteriological examination of feces (Lg CFU/ml) (M ± m)*

Microflora	2010-2011 yy.	2017-2018 yy.	2024-2025 yy.
	n = 34	n = 37	n = 34
Bifidobacteria	8.86 ± 0.23	8.52 ± 0.21	8.14 ± 0.19*
Lactobacteria	7.12 ± 0.19	6.73 ± 0.17	6.45 ± 0.15*
Staphylococcus	1.84 ± 0.20	2.12 ± 0.21	2.53 ± 0.24*
Streptococcus	6.92 ± 0.19	7.15 ± 0.18	7.31 ± 0.16
Escherichia coli	7.32 ± 0.31	7.64 ± 0.37	7.81 ± 0.26
Non-fermenting Escherichia coli	0.42 ± 0.14	0.83 ± 0.27	1.2 ± 0.20*
Proteus	0.61 ± 0.12	0.78 ± 0.18	0.83 ± 0.19
Enterobacter	2.35 ± 0.20	2.51 ± 0.12	2.73 ± 0.16
Fungi of the genus Candida	0.94 ± 0.14	1.16 ± 0.17	1.48 ± 0.15*

Notes: * - P < 0.05 for differences from the 2010-2011 group; ● - P < 0.05 for differences from the 2017-2018 group.

Table 5. *Concentration of SIgA in biological media*

Indicator, unit of measurement	2010-2011 yy.	2017-2018 yy.	2024-2025 yy.
Saliva, μg/ml,	104.4 ± 2.65 n = 31	102.0 ± 3.15 n = 30	92.1 ± 3.66* n = 30
Vaginal discharge, mg/l	51.6 ± 1.21 n = 27	49.7 ± 1.48 n = 30	46.0 ± 2.03* n = 28
Faeces, μg/g (feces)	1266.3 ± 35.23 n = 31	1192.7 ± 39.90 n = 32	1108.7 ± 44.93* n = 32

Notes: * - P < 0.05 for differences from the 2010-2011 group.

in biological media: saliva, vaginal discharge, and feces (Table 5). As can be seen from Table 5, over the 15-year period, the concentration of SIgA in these media decreased significantly. This may have contributed to changes in the microbiota in these media. A negative correlation was established between the concentration of SIgA in saliva and the numbers of opportunistic streptococci (r = −0.37) and opportunistic staphylococci (r = −0.41) in the oropharyngeal mucosa.

When analyzing the concentration of SIgA in vaginal secretions, a moderate positive correlation was established with the concentration of *Lactobacillus* spp. (r = +0.53) and a negative correlation with the concentration of *Escherichia coli* (r = −0.57). A similar relationship was observed when determining the correlation between the concentration of SIgA in feces and the number of bifidobacteria (positive, r = +0.41), lactobacteria (positive, r = +0.44), and non-fermenting *Escherichia coli* (negative, r = −0.47) in feces. Thus, the observed decrease in the concentration of SIgA in biological media was associated with a decrease in lactic acid flora and an increase in opportunistic pathogens.

DISCUSSION

Studies of the microbiota of the skin, saliva, vaginal discharge, and feces, as well as secretory immunoglobulin levels in these environments, conducted in 2010–2011, 2017–2018, and 2024–2025 revealed changes in the microflora over this period. On the skin, significantly less beneficial microflora was found in 2024–2025, accompanied by its replacement with conditionally pathogenic microorganisms and an increase in fungi. It is likely that this process contributes, to some extent, to the development of inflammatory skin processes, the increased frequency of which has been indicated by the literature (24). Changes in the microbiota of the oropharynx were also detected, including an increase in conditionally pathogenic flora, which reduces the body's resistance to pathogenic flora and the influence of negative environmental factors. All this may contribute to an increase in the frequency of inflammatory processes of the nasopharynx, as has often been noted by other researchers (25).

The study showed the presence of similar dynamic changes in the microbiota of vaginal discharge. Over 15 years, a lower number of *Lactobacillus* spp. was recorded in vaginal discharge, while the number of conditionally pathogenic flora increased. Such a replacement, together with the additional negative impact of external factors, may increase the risk of developing inflammatory processes in the vagina. The increase in the frequency of inflammatory processes in the vagina

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in recent years, as reported by researchers (26), can probably be explained by changes in the vaginal biotope. In Ukraine, inflammatory diseases of the female genital organs are quite common among women of reproductive age (11), which negatively affects other gynecological pathologies and reproductive function disorders. The results also showed changes in the intestinal microbiota, including a decrease in lactic acid flora and an increase in staphylococci, non-fermenting *Escherichia coli*, and fungi. This finding may, to some extent, support the proposed mechanism underlying the increase in intestinal inflammatory processes observed in recent years in Ukraine (27).

The studies showed a deterioration in local immunity, as evidenced by a decrease in the concentration of secretory immunoglobulin in saliva, nasopharyngeal secretions, and vaginal secretions. A correlation between the concentration of secretory immunoglobulin and the amount of diverse microflora was noted. A decrease in the concentration of immunoglobulins was correlated with a decrease in beneficial microflora and was inversely related to the concentration of conditionally pathogenic flora. This could ultimately contribute to an increase in the frequency of inflammatory processes in humans, as has been reported in recent years (28).

CONCLUSION

During the study, a deterioration in the state of microbiocenosis in women of reproductive age was observed in recent years against a background of decreased local immunity, which is one of the important factors contributing to the increased frequency of inflammatory processes. Their microbial landscape was characterized by the replacement of normal microflora of the skin, nasopharynx, vagina, and intestine with conditionally pathogenic microorganisms.

The results obtained justify the feasibility of timely implementation of individualized therapeutic and preventive measures in women, which will contribute to the restoration of the microbiome and reduce the frequency of relapses of inflammatory diseases.

Abbreviations

SIgA – secretory immunoglobulin A
LgКУО – logarithm of colony-forming units
n – sample size

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Note: The authors state that artificial intelligence was not used as a tool in this study.

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Sažetak

PROMENE MIKROBIOMA I IMUNITETA POVEZANE SA POVEĆANOM UČESTALOŠĆU INFLAMATORNIH BOLESTI

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Uvod: Poslednjih godina beleži se značajan porast učestalosti inflamatornih bolesti kod žena reproduktivnog doba, verovatno usled promena u mikrobiomu, što je bio povod za ovo istraživanje.

Cilj: Ispitati dinamiku taksonomskog profila mikrobiote i stanje lokalnog imuniteta kože, nazofarinksa, vagine i fecesa kod žena koje žive u Ukrajini u periodu od 2010. do 2025. godine.

Materijal i metode: U istraživanje je uključeno ukupno 136 žena uzrasta od 20 do 39 godina koje su obavile preventivni pregled kod izabranog lekara i pregledane od strane dermatologa, ginekologa i ORL specijaliste. U periodu 2010–2011. godine pregledane su 44 žene, u periodu 2017–2018. godine 47, a u periodu 2024–2025. godine 45 žena. Mikrobiološki spektar kože, orofarinksa, vagine i fecesa, uključujući Gram-pozitivne i Gram-negativne bakterije, analiziran je pomoću bakteriološkog analizatora VITEK 2 COMPACT („bioMérieux“, Francuska), uz korišćenje softvera AES: Global CLSI-based + Phenotypic. Humoralna komponenta lokalnog imuniteta procenjena je na osnovu nivoa sekretornog imunoglobulina A, koji je određen metodom enzimski imunosorbentnog testa.

Rezultati: Utvrđeno je da su se tokom poslednjih 15 godina dogodile značajne promene u humanom mikrobiomu. Ukupan broj bakterija na koži se povećao, pri čemu je statistički značajno povećanje zabeleženo u periodu 2024–2025. u poređenju sa periodom 2010–2011. godine. To je naročito bilo izraženo kroz povećanje broja *Staphylococcus aureus*, *Streptococcus pyogenes*, gljivica roda *Candida* i *Malassezia* spp., uz istovremeno smanjenje broja *Staphylococcus epidermidis* i *Staphylococcus hominis*. U orofaringealnom mikrobiomu tokom ovog perioda utvrđeno je značajno povećanje broja oportunističkih streptokoka, oportunističkih stafilokoka, gljivica roda *Candida*, kao i integralnog pokazatelja broja oportunističke flore. U vaginalnom sekretu uočena je zamena normalne mikroflore (*Lactobacillus* spp.) oportunističkim mikroorganizmima, kako aerobnim tako i anaerobnim, dok je u fecesu uočeno smanjenje normalne flore i povećanje broja stafilokoka, nefermentišućih *Escherichia coli* i gljivica roda *Candida*. Promene u mikrobiomu bile su praćene smanjenjem koncentracije sekretornog imunoglobulina A u biološkim sredinama, što je, sa svoje strane, produbilo poremećaj mikrobioma i dovelo do smanjenja normalne flore i povećanja broja oportunističkih patogena.

Zaključak: Kod žena reproduktivnog doba poslednjih godina uočeno je pogoršanje stanja mikrobiocenoze u uslovima smanjenog lokalnog imuniteta, što predstavlja jedan od važnih faktora koji doprinose povećanoj učestalosti inflamatornih procesa. Njihov mikrobni pejzaž karakteriše zamena normalne mikroflore kože, nazofarinksa, vagine i creva uslovno patogenim mikroorganizmima. Dobijeni rezultati, prema našem mišljenju, ukazuju na potrebu za pravovremenim sprovođenjem individualizovanih terapijskih i preventivnih mera kod žena, što može doprineti obnovi mikrobioma i smanjenju učestalosti recidiva inflamatornih bolesti.

Ključne reči: mikrobiom, lokalni imunitet, žene reproduktivnog doba, koža, orofarinks, vagina.

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