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Microbial community state type stratification and quantitative culture-based assessment of vaginal microbiota in reproductive-age women

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Abstract. The vaginal microbiota plays a crucial role in maintaining female reproductive health; however, subclinical forms of dysbiosis remain insufficiently characterised, particularly regarding the integration of molecular, culture-based, and morphological assessment methods. The purpose of the study was to evaluate the structural, quantitative, and morphological characteristics of the vaginal microbiota in reproductive-age women and to determine the correspondence between molecular microbiome stratification and culture-based morphological findings. Thirty reproductive-age women were selected from 1,000 initially screened participants. Quantitative culture analysis with determination of CFU/mL was performed, along with Gram-stained smear microscopy using digital image documentation and molecular classification of the vaginal microbiota based on 16S ribosomal ribonucleic acid gene sequencing. Microbial concentrations ranged from 10^2 to 10^7 CFU/mL. The lactobacillary population showed the greatest variability, with a mean value of $(1.6 \pm 1.1) \times 10^6$ CFU/mL. Samples were classified into three microbial community types: type I accounted for 30%, type III for 13.3%, and type IV for 56.7%. Type I was characterised by dominance of *Lactobacillus crispatus* at $(3.8 \pm 1.7) \times 10^6$ CFU/mL and a mean acidity of 3.6 ± 0.3. Type III was associated with *Lactobacillus iners* at $(1.5 \pm 0.8) \times 10^6$ CFU/mL and a moderate increase in acidity to 4.5 ± 0.3. Type IV demonstrated reduced lactobacilli at $(4.9 \pm 3.2) \times 10^2$ CFU/mL, increased anaerobic bacteria to 10^3-10^4 CFU/mL, and elevated acidity to 5.6 ± 0.4. The morphological patterns of Gram-stained smears corresponded closely to the molecularly defined microbial types. The integration of quantitative culture analysis with standardised smear microscopy represents an informative tool for stratifying vaginal microbiota states in settings where molecular diagnostics are limited

Keywords: pathogenic flora; *Lactobacillus* dominance; anaerobic bacterial communities; microbiology of the reproductive system; culture-based microbiology; Gram-stained smear analysis

INTRODUCTION

The vaginal microbiota represents a specialised microbial ecosystem of the female reproductive tract and plays a central role in maintaining reproductive health. The stability of this microbial ecosystem contributes to the barrier function of the mucosal surface, maintenance of optimal acidity, and colonisation resistance against pathogenic and opportunistic microorganisms. Disturbances in the balance of vaginal microbial communities may result in dysbiotic states that alter the protective functions of the mucosal environment. Despite significant advances in microbiome research, the mechanisms underlying the development and dynamics of different ecological states of the vaginal microbiota remain insufficiently understood.

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Studies indicated that the vaginal microbiota is characterised by relatively low taxonomic diversity and predominance of bacteria belonging to the genus *Lactobacillus*, which maintain acidic vaginal pH and suppress the growth of opportunistic microorganisms. The study by R. Mirzaei *et al.* [1] demonstrated that the microbiota of different compartments of the female reproductive tract forms a continuous microbial ecosystem, and alterations in vaginal microbiota composition may be associated with inflammatory and neoplastic conditions. The researchers emphasised the importance of analysing the structural organisation of the microbiome for understanding mechanisms underlying pathological processes. M.J. Kim *et al*. [2] reported that recurrent vaginitis is associated with a significant decrease in the proportion of *Lactobacillus* spp. and an increase in bacterial diversity. In their study, more than half of the examined patients demonstrated a microbiota profile corresponding to the dysbiotic community state type (CST) IV, suggesting that structural changes within the microbial community play an important role in the development of chronic inflammatory processes.

In another study, J. Novak *et al.* [3] investigated vaginal microbiota dominated by *Lactobacillus iners*. The researchers found that this microbiota profile is characterised by relative instability and an increased tendency to shift toward dysbiosis. This phenomenon is associated with the fact that *L. iners* produces lower amounts of lactic acid and exhibits reduced antagonistic activity against anaerobic bacteria. Further studies have highlighted the complex interactions between bacterial and fungal components of the vaginal microbiome. C. Zhao *et al*. [4] demonstrated that different forms of vulvovaginal candidiasis are associated with specific alterations in bacterial microbiota composition. Their findings suggested that fungal infections may modify the structure of bacterial communities by altering the balance of dominant microorganisms. An important area in microbiome research is the application of molecular methods for microbiota analysis. H.N. Brochu *et al*. [5] performed molecular profiling of the vaginal microbiome in patients with bacterial vaginosis and identified clear differences in the structure of bacterial communities. The researchers noted that sequencing of the 16S ribosomal ribonucleic acid (rRNA) gene provides a more accurate characterisation of microbiota taxonomic composition compared with conventional culture-based methods.

However, several studies also highlighted methodological limitations of molecular approaches. C.A. Broedlow *et al*. [6] demonstrated that the use of different sequencing protocols may result in discrepancies in the molecular diagnosis of bacterial vaginosis. Such variability may arise from both technical differences in analytical methods and significant strain-level diversity within certain bacterial species, particularly *Gardnerella vaginalis*. Other studies emphasised the importance of integrating different microbiological approaches for a comprehensive evaluation of vaginal microbiota. L. Mancabelli *et al*. [7] showed that the combination of molecular and culture-based techniques allows a more accurate assessment of the functional characteristics of the vaginal microbiome. Culture-based methods remain essential for determining the absolute abundance of microorganisms and evaluating their functional potential.

Thus, contemporary research confirmed that the vaginal microbiota represents a complex and dynamic ecosystem whose structure may vary under the influence of numerous biological and environmental factors. Despite significant progress in molecular microbiome profiling, there remains a clear need for integrated analytical approaches combining molecular, culture-based, and morphological methods. Such approaches enable not only identification of the taxonomic composition of microbial communities but also evaluation of their quantitative and functional characteristics. The purpose of this study was to investigate quantitative culture-based characteristics of vaginal microbiota across different CST and to assess the agreement between molecular microbiome classification and classical microbiological diagnostic methods.

MATERIALS AND METHODS

The study was conducted between 2023 and 2025 at medical institutions in Uzhhorod and Odesa, Ukraine. The study design was observational and cross-sectional. A total of 1,000 reproductive-age women underwent initial clinical examination. The participants sought gynaecological consultation for preventive purposes or routine medical evaluation. Women were included in the study if they met the following criteria: age 18-45 years; absence of clinical signs of acute infectious diseases; no antibacterial therapy during the previous 4 weeks; no antifungal therapy during the previous 2 weeks; provision of written informed consent. The exclusion criteria were: pregnancy or postpartum period; clinically confirmed sexually transmitted infections; systemic inflammatory or autoimmune diseases; hormonal therapy or use of hormonal intrauterine devices; incomplete clinical or laboratory data. The study was conducted in accordance with the ethical principles of the Declaration of Helsinki [8]. The study protocol was approved by the Local Ethics Committee of Uzhhorod National University (Protocol No. 11, December 30, 2022). All participants provided written informed consent prior to enrolment in the study.

Vaginal samples were collected using sterile swabs from the posterior vaginal fornix during gynaecological examination. All specimens were transported to the laboratory within 2 hours at a temperature of +4 to +8°C. Quantitative determination of microorganisms was performed using serial tenfold dilutions, followed by inoculation of 100 µL aliquots of the appropriate dilutions onto universal, selective, and anaerobic culture media. Incubation was carried out at 37°C under aerobic, microaerophilic, or anaerobic conditions depending on the microbial group. De Man-Rogosa-Sharpe agar was used for isolation of *Lactobacillus* spp.; blood agar for Gram-positive cocci; mannitol salt agar for staphylococci; selective anaerobic media for bacterial vaginosis-associated anaerobes; and *Sabouraud dextrose* agar and chromogenic media for yeast-like fungi. Identification of isolates was performed based on morphological characteristics and standard biochemical test systems (PLIVA-Lachema, Czech Republic) in accordance with the manufacturer's instructions. Colony-forming units per millilitre were calculated with consideration of the dilution factor, and the results were expressed in logarithmic format (log CFU/mL). Smears were prepared from vaginal secretion, stained using the standard Gram staining procedure, and examined under oil immersion at ×1,000 magnification. For each specimen, at least 10 randomly selected fields of view were analysed with digital

image documentation. Bacterial morphotypes, their relative abundance, spatial density, and the presence of mixed microbial consortia were assessed.

Classification of samples into community state types was performed based on previously obtained 16S rRNA gene sequencing results of the vaginal microbiota, as described in detail by S.Y. Borshosh & N.V. Boyko [9]. Sequencing of the vaginal microbiota was performed through amplification of variable regions of the 16S rRNA gene, followed by bioinformatic processing and taxonomic assignment of the obtained sequences. The resulting microbial profiles were classified according to the CST concept originally described by A. Gerede *et al.* [10]. Based on the taxonomic composition of the microbiota, the samples were assigned to three microbial community types: CST I – microbiota dominated by *Lactobacillus crispatus*; CST III – microbiota dominated by *Lactobacillus iners*; CST IV – polymicrobial anaerobic microbiota characterised by a reduced abundance of lactobacilli. The molecularly defined community state type profile was used as a reference standard for subsequent comparison with culture-based and microscopic characteristics.

Statistical analysis was performed using SPSS Statistics software. The normality of data distribution was evaluated using the Shapiro-Wilk test. For comparison of quantitative variables between the three CST groups, one-way analysis of variance (ANOVA) was applied for normally distributed data, whereas the Kruskal-Wallis test was used for non-parametric variables. Post hoc pairwise comparisons were performed using the Tukey test or Dunn's test where appropriate. Agreement between morphological assessment and molecular classification was evaluated using Cohen's kappa coefficient. Differences were considered statistically significant at $p < 0.05$. The main limitation of the study is the relatively small final sample size resulting from the application of strict selection criteria. In addition, the composition of the vaginal microbiota may change under the influence of individual hormonal, behavioural, and environmental factors that cannot always be fully standardised in a clinical research setting.

RESULTS AND DISCUSSION

The mean age of the examined women was 29.8 ± 6.4 years (range 19-44). Most participants were sexually active and had no clinical signs of acute vaginal infection at the time of examination. No statistically significant differences in age distribution were observed between CST groups ($p > 0.05$). The lactobacillary population demonstrated the greatest variability among the detected microbial groups. Its concentration ranged from $(5.1 \pm 3.4)\times10^2$ to $(3.4 \pm 2.1)\times10^6$ CFU/mL, reaching 10^7 CFU/mL in individual samples, with a mean value of $(1.6 \pm 1.1)\times10^6$ CFU/mL. In contrast, other representatives of the vaginal microbiota showed relatively stable concentrations (Table 1). These findings indicate that variation in *Lactobacillus* density represents the principal axis of microbiota shifts, whereas facultative bacteria reflect the degree of reduction in colonisation resistance.

According to 16S rRNA gene sequencing, samples were classified into three community state types: CST I – 9 cases (30%), CST III – 4 cases (13.3%), and CST IV – 17 cases (56.7%). Comparative analysis of microbiological indicators across CST groups revealed significant differences in the concentration of *Lactobacillus* spp., levels of anaerobic bacteria, and vaginal pH values (Table 2).

Table 1. Mean concentration of representatives of the vaginal microbiota

Microorganism	Mean concentration ± SD (CFU/mL)
Lactobacillus spp.	$(1.6 \pm 1.1)\times10^6$
Corynebacterium spp.	$(3.9 \pm 1.6)\times10^5$
Enterococcus faecalis	$(1.3 \pm 0.5)\times10^5$
Escherichia coli	$(6.8 \pm 2.9)\times10^2$
Streptococcus spp.	$(9.8 \pm 3.6)\times10^2$

Source: compiled by the authors based on research

Table 2. Comparative characteristics of quantitative indicators of vaginal microbiota according to CST

Parameter	CST I (n = 9)	CST III (n = 4)	CST IV (n = 17)	p-value	Statistical test
Lactobacillus spp., CFU/mL	$(3.8 \pm 1.7)\times10^6$	$(1.5 \pm 0.8)\times10^6$	$(4.9 \pm 3.2)\times10^2$	<0.001	Kruskal-Wallis
BV-associated anaerobes, CFU/mL	≤1.0 ×10²	≤1.0×10⁵	1.0 ×10⁵ - 1.0 ×10⁴	<0.001	Kruskal-Wallis
Escherichia coli / *Klebsiella* spp., CFU/mL	$(3.8 \pm 1.6)\times10^2$	$(7.8 \pm 3.2)\times10^2$	$(9.1 \pm 3.7)\times10^2$	0.04	Kruskal-Wallis
Enterococcus faecalis, CFU/mL	$(7.4 \pm 2.6)\times10^2$	$(1.2 \pm 0.5)\times10^5$	$(2.4 \pm 0.9)\times10^5$	0.02	Kruskal-Wallis
Candida spp., CFU/mL	≤1.0×10²	$(3.6 \pm 1.4)\times10^2$	≤1.0×10⁵	0.05	Kruskal-Wallis
Vaginal pH	3.6 ± 0.3	4.5 ± 0.3	5.6 ± 0.4	<0.001	One-way ANOVA

Source: compiled by the authors based on research

The predominance of CST IV is noteworthy. In population-based studies of apparently healthy women, including those by A. Gerede *et al.* [10], lactobacillus-dominated profiles usually prevail, whereas CST IV is observed less frequently. In contrast, in the present study CST IV constituted more than half of all samples, suggesting the presence of subclinical dysbiotic states in a predominantly asymptomatic cohort. In the CST I group, the microbiota was dominated by *Lactobacillus crispatus*. This type was characterised by high concentrations of lactobacilli, low levels of facultative microorganisms, and a mean vaginal pH of 3.6 ± 0.3. Morphologically, Gram-stained smears demonstrated a homogeneous pattern with predominance of long Gram-positive rods. Bacterial vaginosis-associated anaerobes were either absent or detected only in trace amounts, which corresponds to a classical eubiotic microbiota profile.

CST III represented a transitional microbiota state dominated by *Lactobacillus iners*. This group demonstrated moderate concentrations of lactobacilli, accompanied by a gradual increase in facultative microorganisms such as *Escherichia coli* and *Enterococcus* spp. The mean vaginal pH reached 4.5 ± 0.3. Morphologically, Gram-stained smears showed thinner and more variable rods, reflecting the ecological instability of this microbiota type. The CST IV group showed the most substantial shifts in microbial composition. This type was characterised by a marked reduction in *Lactobacillus* spp., increased concentrations of facultative Gram-negative bacteria, and a high prevalence of anaerobic microorganisms associated with bacterial vaginosis, including *Gardnerella vaginalis, Prevotella* spp., and *Atopobium vaginae*. Vaginal pH increased to 5.6 ± 0.4, reflecting the loss of colonisation resistance and the development of a dysbiotic microbial community.

Microscopic analysis of digitised Gram-stained smears confirmed the correspondence between morphological patterns and molecularly defined community state types. CST I demonstrated predominance of long Gram-positive rods with minimal diversity, CST III showed greater morphological variability, whereas CST IV was characterised by a dense polymicrobial pattern dominated by small Gram-negative rods and cocci. The agreement between morphological assessment and molecular CST classification was high (κ = 0.87), confirming the diagnostic value of integrated microbiological analysis (Table 3).

Table 3. Agreement between morphological assessment and molecular classification of vaginal microbiota

Assessment method	CST I	CST III	CST IV
Molecular classification (16S rRNA sequencing)	9	4	17
Morphological assessment (Gram-stained microscopy)	8	4	16

Note: Cohen's kappa coefficient: 0.87, p-value: <0.001
Source: compiled by the authors based on research

Overall, the obtained results demonstrated a clearly structured spectrum of vaginal microbiota states ranging from stable lactobacillus-dominated eubiosis to polymicrobial anaerobic dysbiosis. The key quantitative marker of this transition is a reduction in *Lactobacillus* spp., particularly *Lactobacillus crispatus*, accompanied by increased vaginal pH and progressive expansion of anaerobic microbial consortia. The results of the present study demonstrated a clear stratification of vaginal microbiota states corresponding to different CST. In the examined cohort, CST IV represented the most prevalent microbiota profile. This finding differs from the observations reported by M.J. Kim *et al*. [2], who showed that the stability of the vaginal microbiome is associated with a high abundance of lactobacilli and relatively low microbial diversity. In addition, the conceptual model of bacterial vaginosis proposed by Y. Zhang *et al*. [11] indicated that lactobacillus-dominated microbiota usually represents the physiological state of the vaginal ecosystem. The predominance of CST IV in the present study therefore suggests that subclinical dysbiotic states may occur more frequently in apparently asymptomatic populations than previously assumed.

In the present study, CST I was characterised by the dominance of *Lactobacillus crispatus*, high concentrations of lactobacilli, and low vaginal pH values. Similar microbiota profiles have been described in several microbiome studies. For example, W. Dong *et al*. [12] reported that lactobacillus-dominated microbiota represents the most stable and protective microbial state of the vaginal ecosystem. Likewise, H. Xu *et al*. [13] emphasised that high concentrations of lactobacilli play a crucial role in maintaining vaginal microbial homeostasis and colonisation resistance against opportunistic microorganisms. These observations are also supported by the findings of A. Borrego-Ruiz & J.J. Borrego [14], who highlighted the important role of lactobacilli in maintaining vaginal acidity and suppressing the growth of anaerobic bacteria. Therefore, the CST I microbiota profile identified in the present study corresponds to a classical eubiotic vaginal microbiota state.

The CST III microbiota type observed in this study was dominated by *Lactobacillus iners*. Previous studies have shown that *L. iners* – dominated microbial communities often represent a transitional ecological state between eubiosis and dysbiosis. Similar observations were reported in clinical microbiological studies of vaginal microbiota in women with intermediate Nugent scores, where *L. iners* frequently predominated in microbiota profiles demonstrating ecological instability [9]. In particular, J. Novak *et al*. [3] demonstrated that *Lactobacillus iners* produces smaller amounts of lactic acid and exhibits reduced antagonistic activity against anaerobic microorganisms compared with other lactobacillus species. Similar conclusions were reported by C. Zhao *et al*. [4], who found that microbiota dominated by *L. iners* frequently displays increased ecological variability and may transition toward dysbiotic microbial states under certain conditions. The moderate concentrations of lactobacilli and increased variability of microbial composition observed in the CST III group of the present study therefore correspond well with previously described characteristics of this microbiota type.

The most pronounced microbiological alterations in the present study were observed in CST IV, which accounted for more than half of the analysed samples. This microbiota type was characterised by a substantial reduction in *Lactobacillus* spp. and an increased prevalence of facultative and obligate anaerobic microorganisms associated with bacterial vaginosis. Similar microbial patterns have been reported by C.A. Broedlow *et al*. [6] who demonstrated that dysbiotic vaginal microbiota is frequently associated with anaerobic taxa such as *Gardnerella vaginalis, Prevotella* spp., and *Atopobium vaginae*. Comparable findings were also described by L. Mancabelli *et al*. [7], who identified polymicrobial anaerobic communities as a characteristic feature of CST IV microbiota and reported that these communities are associated with increased microbial diversity and reduced abundance of lactobacilli. Furthermore, the influence of behavioural and environmental factors on

the structure of vaginal microbial communities has been described S. Ottinger *et al*. [15], who demonstrated that sexual behaviour and other host-related factors may significantly affect microbiota composition and contribute to dysbiotic microbial states.

An important observation of this study was the relatively high prevalence of CST IV among women who did not present with pronounced clinical symptoms. This finding supports the concept of subclinical vaginal dysbiosis. For example, C. Adapen *et al*. [16] reported that dysbiotic microbial communities may persist in the vaginal environment without clear clinical manifestations for extended periods. In addition, epidemiological studies conducted by M. Gholiof *et al.* [17] demonstrated that alterations in vaginal microbiota composition may increase susceptibility to sexually transmitted infections and inflammatory conditions of the reproductive tract. These observations suggest that subclinical microbiota instability may represent an important factor in reproductive health.

Another important finding of the present study is the high level of concordance observed between molecular sequencing results, quantitative culture-based microbiological analysis, and morphological smear assessment. Similar conclusions were reported by M.J. Kim *et al*. [2], who emphasised that the integration of molecular microbiome profiling with classical microbiological methods allows a more comprehensive characterisation of vaginal microbial communities. Moreover, experimental studies conducted by J.B. Holm *et al*. [18] demonstrated that lactobacillus species may serve not only as key biomarkers of vaginal health but also as functional agents that regulate microbial interactions within the vaginal ecosystem. These findings support the diagnostic value of combining molecular and classical microbiological approaches.

The classification of microbial communities into CST profiles in the present study was based on previously established microbiome concepts. The CST classification system originally described by A. Gerede *et al*. [10] has become one of the most widely used frameworks for describing vaginal microbial community structure. Further refinement of CST classification methods was proposed by B. Oliva-Arancibia *et al*. [19], who confirmed the reproducibility of these microbial community profiles across different populations. More recently, M.T. France *et al*. [20] developed the VALENCIA classification approach for improved identification of vaginal microbial community types using molecular sequencing data. In addition, experimental studies by P.B. Heczko *et al*. [21] highlighted the important functional role of lactobacillus species in maintaining microbial stability within the vaginal ecosystem.

Overall, the findings of the present study confirmed that the reduction of *Lactobacillus* spp., particularly *Lactobacillus crispatus*, represents a key microbiological marker of the transition from stable eubiosis to dysbiosis. Increased vaginal pH, expansion of anaerobic microbial communities, and morphological polymorphism observed in Gram-stained smears reflect progressive disruption of vaginal microbial homeostasis. The integration of molecular microbiome profiling with quantitative culture-based and morphotypic microbiological approaches may therefore improve the diagnostic stratification of vaginal microbiota states and contribute to more accurate detection of dysbiotic conditions in reproductive health research and clinical practice.

CONCLUSIONS

The analysis of vaginal microbiota in reproductive-age women demonstrated the presence of clearly differentiated microbial community states corresponding to distinct community state types. Molecular classification based on 16S rRNA gene sequencing identified three microbiota profiles within the examined cohort: CST I, CST III, and CST IV. It was found that CST I accounted for 30% of samples, CST III for 13.3%, and CST IV for 56.7% of cases, indicating a predominance of dysbiotic microbiota patterns among the studied participants. The results indicated that the transition from eubiotic to dysbiotic microbiota states is primarily associated with a pronounced reduction in the concentration of *Lactobacillus* spp., particularly *Lactobacillus crispatus*. In the CST I group, the mean concentration of lactobacilli reached $(3.8 \pm 1.7) \times 10^6$ CFU/mL and was accompanied by a low vaginal pH of 3.6 ± 0.3, reflecting a stable lactobacillus-dominated microbial environment. In contrast, CST IV was characterised by a marked decrease in Lactobacillus spp. to $(4.9 \pm 3.2) \times 10^2$ CFU/mL, combined with an increase in anaerobic microorganisms associated with bacterial vaginosis and an elevation of vaginal pH to 5.6 ± 0.4. These findings demonstrated that a quantitative decline of lactobacilli represents a key microbiological marker of vaginal dysbiosis.

A high level of concordance between molecular microbiota classification, quantitative culture-based microbiological analysis, and morphological evaluation of Gram-stained smears was observed. The calculated Cohen's kappa coefficient ($\kappa = 0.87$, $p < 0.001$) confirmed strong agreement between these diagnostic approaches, indicating that standardised culture-based and microscopic methods can reliably reflect structural changes in vaginal microbial communities. The predominance of CST IV detected in a largely asymptomatic cohort suggests that dysbiotic microbiota states may persist in a subclinical form and remain undetected during routine clinical examination. From a clinical perspective, early identification of such microbial shifts may be important for the prevention of infectious and inflammatory disorders of the female reproductive tract. Further studies involving larger cohorts are required to clarify the influence of hormonal, behavioural, and environmental factors on the distribution of vaginal microbial community state types. Integrating molecular microbiome profiling with quantitative microbiological and morphotypic approaches may improve diagnostic strategies for assessing vaginal microbiota stability and contribute to more effective prevention and management of dysbiotic conditions in reproductive health.

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Стратифікація станів мікробної спільноти та кількісна культуральна оцінка вагінальної мікробіоти у жінок репродуктивного віку

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Анотація. Вагінальна мікробіота є ключовим фактором підтримання репродуктивного здоров'я жінки, однак субклінічні форми дисбіозу залишаються недостатньо вивченими, особливо в аспекті поєднання молекулярних, культуральних і морфологічних методів оцінки. Метою було оцінити структурні, кількісні та морфологічні характеристики вагінальної мікробіоти жінок репродуктивного віку та встановити відповідність між молекулярною стратифікацією мікробіому і культурально-морфологічними показниками. Обстежено 30 жінок репродуктивного віку, відібраних із 1 000 первинно оглянутих пацієнток. Проведено кількісний культуральний аналіз із визначенням КУО/мл, мікроскопію мазків, забарвлених за Грамом із цифровою фіксацією зображень, а також молекулярну класифікацію вагінальної мікробіоти на підставі секвенування гена 16S рибосомної рибонуклеїнової кислоти. Концентрації мікроорганізмів варіювали від 10^2 до 10^7 КУО/мл. Найбільш варіабельною була лактобацилярна популяція із середнім значенням $(1,6 \pm 1,1)\times10^6$ КУО/мл. Зразки було розподілено на три типи мікробної організації: перший тип становив 30 %, третій – 13,3 %, четвертий – 56,7 %. Перший тип характеризувався домінуванням *Lactobacillus crispatus* у концентрації $(3,8 \pm 1,7)\times10^6$ КУО/мл та кислотністю $3,6 \pm 0,3$. Третій тип асоціювався з *Lactobacillus iners* у концентрації $(1,5 \pm 0,8)\times10^6$ КУО/мл і помірним підвищенням кислотності до $4,5 \pm 0,3$. Четвертий тип характеризувався зниженням лактобацил до $(4,9 \pm 3,2)\times10^2$ КУО/мл, зростанням анаеробних бактерій до 10^3 - 10^4 КУО/мл і підвищенням кислотності до $5,6 \pm 0,4$. Морфологічна картина мазків повністю відповідала молекулярно визначеним типам мікробіоти. Поєднання кількісного культурального аналізу та стандартизованої мікроскопії може слугувати інформативним інструментом стратифікації стану вагінальної мікробіоти у випадках обмеженого доступу до молекулярних методів

Ключові слова: патогенна флора; домінування *Lactobacillus*; анаеробні бактеріальні спільноти; мікробіологія статевої системи; культуральна мікробіологія; аналіз забарвлених за Грамом мазків