THE RELATIONSHIP BETWEEN VAGINAL MICROBIOME AND BACTERIAL VAGINOSIS IN WOMEN OF REPRODUCTIVE AGE IN UZBEKISTAN

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Abstract: This article analyzes the relationship between the composition of the vaginal microbiome and the pathological condition associated with its disruption—bacterial vaginosis (BV)—in women of reproductive age in Uzbekistan. The theory of the microbiome is explained, and available Uzbek-language studies are reviewed. Changes in the microbiota of women of reproductive age, reduced dominance of lactobacilli, increased anaerobic bacteria, and their relationship with the development of BV are examined. Regional data on microbiocenosis and BV in Uzbekistan are also presented. Methodologically, a review of existing literature and clinical research outcomes is conducted, forming the basis for practical recommendations. The conclusion provides suggestions for monitoring the vaginal microbiome and preventing BV among reproductive-age women.

Keywords: vaginal microbiome, bacterial vaginosis, reproductive age, lactobacilli, microbiocenosis, women’s health in Uzbekistan, anaerobic bacteria.

INTRODUCTION: Women’s health is an essential component of public well-being, and the prevention and treatment of gynecological diseases in women of reproductive age are of particular importance. The vaginal microbiome (or vaginal microflora) is a community of microorganisms residing on the vaginal walls and within the vaginal cavity, where lactobacilli dominate under healthy conditions. Lactobacilli play a crucial protective role through various mechanisms such as producing lactate, lowering pH, and secreting hydrogen peroxide and bacteriocins. When this balance is disrupted, dysbiosis (microbiocenosis imbalance) develops, potentially leading to numerous gynecological and reproductive complications. Bacterial vaginosis is a common vaginal infection among women of reproductive age, characterized by a reduction in healthy lactobacilli and an increase in anaerobic bacteria (e.g., Gardnerella vaginalis, Atopobium vaginae, Mobiluncus spp.). BV often presents asymptomatically, yet it is associated with preterm birth, prenatal complications, increased risk of sexually transmitted infections, tubal infertility, and recurrent colpitis. Although several studies on women’s reproductive health have been conducted in Uzbekistan, research directly analyzing the relationship between the vaginal microbiome and bacterial vaginosis remains limited. For example, at

Samarkand State Medical University, the use of probiotics for BV was studied in 62 women aged 18–35. Additionally, an article titled "Vaginal Microbiocenosis, Bacterial Vaginosis and Its Treatment Methods" has been published. Therefore, this article analyzes the relationship between the vaginal microbiome and bacterial vaginosis in reproductive-age women in Uzbekistan, based on available literature, and provides practical recommendations.

RESEARCH METHODOLOGY: This article employs a literature review approach. Specifically, Uzbek- and English-language scientific articles, clinical studies, reviews, and classical gynecological microbiology sources of regional significance were collected and analyzed. Search stages:1. Articles were searched using Google Scholar and Uzbek scientific journal portals with keywords such as: "vaginal microbiome," "vaginal microflora," "bacterial vaginosis," "microbiocenosis," "women's gynecology in Uzbekistan."

2. Studies were selected based on the following criteria:

Included women of reproductive age (15–49 years);

Contained data on the vaginal microbiome or microbiocenosis;

Related to bacterial vaginosis;

Included examples from Uzbekistan or Central Asia.

3. Selected sources were analyzed in terms of authors, methodology, sample size, results, and conclusions.

4. Generalizations were made regarding the link between vaginal microbiome disturbances and BV development.

5. Clinical experiences in Uzbekistan, particularly the use of probiotics, were evaluated separately.

Limitations: Genetic sequencing and large-scale epidemiological studies on the vaginal microbiome are not yet widely performed in Uzbekistan. Therefore, this article includes both international and regional data.

MAIN BODY: The concept of the vaginal microbiome has gained increasing importance in gynecological practice in recent years. The vaginal microbiome is primarily dominated by Lactobacillus crispatus, L. jensenii, and L. gasseri. These bacteria maintain the vaginal pH between 3.8 and 4.5 by producing hydrogen peroxide, bacteriocins, and lactate. Under normal conditions, the microbiota remains stable; however, factors such as multiple sexual partners, unprotected intercourse, childbirth, antibiotics, vaginal douching, and hormonal contraception can disrupt this balance. When lactobacilli decrease and anaerobic bacteria proliferate, bacterial vaginosis develops. BV is among the most common vaginal pathologies in women of reproductive age. Globally, its prevalence reaches 20–30%. Although precise statistics are limited in Uzbekistan, existing studies indicate that BV cases are relatively widespread. For example, Karimova (2023), studying the effectiveness of probiotics in 62 women aged 18–35 with BV, found that a combination of clindamycin and probiotics (Ecofemin or

Laktozhinal) improved lactobacilli restoration and reduced BV symptoms. Qodirova and Kattakhodjayeva (2023) examined the effects of ultrasonic cavitation on vaginal microbiocenosis in women with recurrent vaginitis and BV, noting improved microflora after treatment. Factors contributing to BV include changes in sexual activity, antibiotic use, decreased immunity, pregnancy, postpartum period, vaginal douching, and hormonal contraception. Although evidence from Uzbekistan supports the link between the vaginal microbiome and BV, large-scale genetic studies remain insufficient.

RECOMMENDATIONS: 1. BV diagnosis in clinical practice should consider the ratio of lactobacilli to anaerobic bacteria.

2. Women should be educated about sexual hygiene, risks of unprotected intercourse, and the negative effects of vaginal douching.

3. Protocols should be developed for probiotic use after antibiotic therapy to restore the microbiome.

4. Regional studies on the vaginal microbiome using genetic sequencing should be conducted.

5. Collaboration between gynecologists and microbiologists should be strengthened.

ANALYSIS AND RESULTS: The analysis shows that disturbances in microbiocenosis are observed in BV cases in Uzbekistan, the sequence of lactobacilli reduction anaerobic bacteria increase BV development is evident, Probiotic treatment reduces BV symptoms, however, metagenomic studies are required to genetically confirm causality.

CONCLUSION: Scientific evidence indicates a clear relationship between the vaginal microbiome and bacterial vaginosis in reproductive-age women in Uzbekistan. Stability of the vaginal microbiome—primarily maintained by lactobacilli—is essential for healthy reproductive function. When this balance is disrupted, BV develops, increasing risks of complications related to childbirth and infertility. Therefore, regular monitoring of the vaginal microbiome, the use of probiotics after antibiotic therapy, and improving women's hygiene awareness are necessary.

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