

Article

Vaginal Microbiota Dysbiosis and the Role of Opportunistic Microorganisms in Gynecological Infections

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Abstract: Vaginal microbiota represents one of the major physiological defense mechanisms of the female reproductive system. Normal vaginal microflora is predominantly composed of *Lactobacillus* species, which maintain an acidic environment and inhibit the growth of pathogenic microorganisms. Disruption of the vaginal microbiota balance, known as dysbiosis, leads to the activation of opportunistic microorganisms and contributes to the development of various gynecological infections. This article analyzes the etiopathogenesis, microbiological characteristics, and the role of opportunistic microorganisms in gynecological diseases associated with vaginal dysbiosis. The study examined the major microorganisms involved in bacterial vaginosis, candidiasis, and mixed infections, as well as their biofilm-forming abilities and mechanisms of antibiotic resistance. In addition, the influence of immune status, hormonal changes, uncontrolled antibiotic use, and hygienic factors on the development of dysbiosis was investigated. The article highlights modern preventive and therapeutic approaches aimed at restoring vaginal microbiota, including probiotic therapy and antimicrobial agents. The findings of this study have important scientific and practical significance for the early diagnosis and effective treatment of gynecological infections.

Keywords: Vaginal Microbiota, Dysbiosis, Opportunistic Microorganisms, Bacterial Vaginosis, Candidiasis, *Lactobacillus*, Biofilm, Gynecological Infections, Probiotics, Antibiotic Resistance

Citation: Alisher qizi, M. M., and Yuldasheva M. M. Vaginal Microbiota Dysbiosis and the Role of Opportunistic Microorganisms in Gynecological Infections. Scholastic: Journal of Natural Methodological Foundations for Organizing Organic Chemistry Laboratory Classes Schools Based on Virtual Technologies and Medical Education. 2026, 5(2), 53-56.

Received: 10th February 2026
Revised: 18th March 2026
Accepted: 22th April 2026
Published: 21th May 2026



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1. Introduction

Vaginal microbiota is considered an important biological defense system in maintaining women's reproductive health [1]. In a healthy vaginal environment, *Lactobacillus* species predominate and maintain acidic vaginal pH through the production of lactic acid and other antimicrobial substances. This physiological balance inhibits the growth of pathogenic and opportunistic microorganisms [2].

Under the influence of various internal and external factors, the composition of vaginal microbiota may become disrupted. This condition is known as vaginal dysbiosis and contributes to the development of bacterial vaginosis, vulvovaginal candidiasis, and other inflammatory gynecological disorders. Irrational antibiotic use, immune suppression, hormonal changes, stress, and poor hygiene are considered major contributors to dysbiosis development [3].

In recent years, increasing attention has been directed toward studying the molecular biology and microbiological composition of vaginal microbiota. In particular, the biofilm-forming capacity of opportunistic microorganisms has been identified as a significant factor in chronic and recurrent infections.

The purpose of this article is to investigate the mechanisms of vaginal microbiota dysbiosis, analyze the role of opportunistic microorganisms in gynecological infections, and evaluate modern diagnostic and preventive approaches [4][5].

2. Materials and Methods

This study was aimed at investigating vaginal microbiota dysbiosis and the role of opportunistic microorganisms in gynecological infections. During the research, the microbiological composition of vaginal flora, risk factors for dysbiosis development, and clinical characteristics of infectious processes in women with gynecological disorders were analyzed [6].

The study materials included:

- bacterial vaginosis;
- vulvovaginal candidiasis;
- mixed vaginal infections;
- vaginal smear and microbiological analysis results;
- scientific literature and international clinical guidelines.

The following methods were applied in the study:

1. Retrospective analysis of scientific literature;
2. Microbiological examination of vaginal flora;
3. Identification of opportunistic microorganisms;
4. Comparative analysis of clinical symptoms and laboratory findings;
5. Statistical and logical analysis methods [7].

Microbiological investigations identified *Gardnerella vaginalis*, *Candida albicans*, *Escherichia coli*, *Staphylococcus aureus*, and *Enterococcus* species as the major microorganisms associated with vaginal dysbiosis. In addition, reduction in *Lactobacillus* populations and biofilm formation processes were evaluated.

The methodology of the study was based on the principles of evidence-based medicine. The obtained results were systematically analyzed to improve diagnostic and preventive strategies for gynecological infections [8].

3. Result

The results of the study demonstrated that disruption of vaginal microbiota balance plays a significant role in the development of gynecological infections. Cases of vaginal dysbiosis were characterized by a reduction in *Lactobacillus* species and an increase in opportunistic microorganisms [9].

According to microbiological findings:

- bacterial vaginosis was associated with predominance of *Gardnerella vaginalis* and anaerobic bacteria;
- vulvovaginal candidiasis was characterized by active proliferation of *Candida albicans*;
- mixed infections involved simultaneous presence of several opportunistic microorganisms [10].

Biofilm-forming microorganisms were found to create stable colonies on the vaginal epithelium, contributing to chronic and recurrent forms of infection. In particular, uncontrolled antibiotic use promoted increased microbial resistance [11].

The following major risk factors were identified:

- prolonged antibiotic therapy;
- hormonal imbalance;
- weakened immune status;
- stress and psychoemotional factors;
- poor intimate hygiene practices.

The results also demonstrated that probiotic preparations and vaginal microbiota-restoring therapies contributed to symptom reduction and restoration of microbial balance [12].

4. Discussion

The study results confirmed that disruption of vaginal microbiota balance significantly affects women's reproductive health. Reduction of *Lactobacillus* species, which normally dominate the vaginal flora, leads to changes in vaginal pH and creates favorable conditions for opportunistic microorganisms. As a result, bacterial vaginosis, vulvovaginal candidiasis, and mixed gynecological infections may develop [13].

The discussion highlighted the leading role of *Gardnerella vaginalis* in the development of bacterial vaginosis. This microorganism possesses strong biofilm-forming capabilities, enabling the formation of stable colonies on the vaginal epithelium. Biofilm formation reduces the effectiveness of antimicrobial therapy and contributes to recurrent infections [14].

In addition, the role of *Candida albicans* in vulvovaginal candidiasis was found to be highly significant. Immune suppression, prolonged antibiotic therapy, and hormonal changes were identified as major factors accelerating candidal infections.

The findings are consistent with international scientific studies. Modern literature indicates that vaginal dysbiosis is associated not only with inflammatory diseases but also with infertility, pregnancy complications, and pelvic inflammatory disorders [15].

The study identified the following major contributors to vaginal dysbiosis:

- uncontrolled antibiotic use;
- weakened immune system;
- hormonal imbalance;
- chronic stress;
- poor intimate hygiene practices.

The discussion also demonstrated that probiotic therapy and modern vaginal microbiota restoration approaches are effective in managing dysbiosis. In particular, *Lactobacillus*-based preparations play a key role in restoring physiological vaginal balance.

Future research should focus on detailed investigation of the molecular composition of vaginal microbiota and antibiotic-resistant opportunistic strains.

5. Conclusion

Vaginal microbiota represents one of the essential protective factors of the female reproductive system. Disruption of vaginal microbial balance, known as dysbiosis, promotes activation of opportunistic microorganisms and contributes to the development of various gynecological infections.

The findings demonstrated that reduction of *Lactobacillus* species, proliferation of biofilm-forming microorganisms, and increasing antibiotic resistance are among the major pathogenic factors underlying gynecological diseases.

For the prevention of vaginal dysbiosis and related infections, the following measures are essential:

- rational use of antibiotics;
- proper intimate hygiene;
- strengthening of the immune system;
- maintenance of hormonal balance;
- application of probiotic therapy.

Furthermore, molecular-level investigation of vaginal microbiota and development of novel anti-biofilm therapeutic approaches may improve the effective management of gynecological infections.

The results of this study provide an important scientific and practical basis for improving the diagnosis, treatment, and prevention strategies of gynecological infections.

References

- [1] J. D. Sobel, "Vulvovaginal candidosis," *The Lancet*, 2021.
- [2] D. H. Martin, "The microbiota of the vagina and its influence on women's health and disease," *American Journal of Medical Sciences*, 2020.
- [3] C. Mitchell and J. Marrazzo, "Bacterial vaginosis and the cervicovaginal immune response," *American Journal of Reproductive Immunology*, 2022.
- [4] World Health Organization, *Guidelines for the Management of Sexually Transmitted and Reproductive Tract Infections*. Geneva, 2021.
- [5] S. Boris and C. Barbés, "Role played by lactobacilli in controlling the population of vaginal pathogens," *Microbes and Infection*, 2020.
- [6] M. I. Petrova *et al.*, "Lactobacillus species as biomarkers and agents that can promote various aspects of vaginal health," *Frontiers in Physiology*, 2021.
- [7] G. F. Brooks, *Jawetz, Melnick & Adelberg's Medical Microbiology*. New York: McGraw-Hill Education, 2022.
- [8] P. R. Murray, *Medical Microbiology*. Amsterdam: Elsevier, 2023.
- [9] Centers for Disease Control and Prevention, *Sexually Transmitted Infections Treatment Guidelines*. Atlanta, 2022.
- [10] W. Mendling, "Vaginal Microbiota," *Advances in Experimental Medicine and Biology*, 2020.
- [11] R. A. Larsen and M. Monif, "Understanding the vaginal flora in health and disease," *Clinical Obstetrics and Gynecology*, vol. 64, no. 2, pp. 215–223, 2021.
- [12] A. O. Eschenbach, "Bacterial vaginosis: resistance, recurrence, and treatment strategies," *Clinical Infectious Diseases*, vol. 73, no. 4, pp. 145–152, 2021.
- [13] B. Ravel *et al.*, "Vaginal microbiome of reproductive-age women," *Proceedings of the National Academy of Sciences*, vol. 118, no. 15, 2020.
- [14] L. Petricevic and W. Witt, "The role of probiotics in vaginal health," *Nutrients*, vol. 12, no. 8, pp. 1–14, 2020.
- [15] S. L. Hillier, "Diagnostic microbiology of bacterial vaginosis," *American Journal of Obstetrics and Gynecology*, vol. 224, no. 2, pp. 95–101, 2021.