VAGINAL MICROBIOTA IN WOMEN WITH RECURRENT VULVOVAGINAL INFECTIONS: A REVIEW

Rabbimova Gulnora Toshtemirovna

Associate Professor of the Department of

Obstetrics and Gynecology No. 2, PhD

Samarkand State Medical University.

Annotation. Recurrent vulvovaginal infections (RVVI) represent a major health concern among women of reproductive age. The vaginal microbiota plays a crucial role in maintaining the mucosal immune barrier and preventing pathogenic colonization. This review summarizes current knowledge about the composition and dynamics of the vaginal microbiome in women with RVVI, focusing on bacterial vaginosis, vulvovaginal candidiasis, and aerobic vaginitis. Special attention is given to the role of Lactobacillus spp., emerging microbiota-based diagnostics, and therapeutic approaches such as probiotics and microbiota restoration. Understanding microbiota imbalance can lead to more effective prevention and treatment strategies.

Keywords: vaginal microbiota, recurrent infections, bacterial vaginosis, vulvovaginal candidiasis, Lactobacillus, probiotics, dysbiosis

Introduction. Recurrent vulvovaginal infections (RVVI), including bacterial vaginosis (BV), vulvovaginal candidiasis (VVC), and aerobic vaginitis (AV), affect millions of women globally, causing significant morbidity [1]. The vaginal ecosystem is normally dominated by Lactobacillus species that produce lactic

acid, hydrogen peroxide, and bacteriocins, ensuring protection against pathogenic organisms [2]. Disruption of this balance, or dysbiosis, is central to RVVI pathogenesis [3].

Normal vaginal microbiota. A healthy vaginal microbiome is typically characterized by low microbial diversity and dominance of Lactobacillus spp., particularly L. Crispatus, L. Jensenii, and L. Gasseri [4]. These species maintain acidic pH (~3.8–4.5), essential for inhibiting pathogens. Factors such as hormones, hygiene, sexual activity, and antibiotics can modulate the microbiota composition [5]. The vaginal microbiota in healthy women of reproductive age is typically characterized by **low species diversity** and **dominance of Lactobacillus spp.**, which form a key part of the host's innate defense system [4]. The most prevalent species include *Lactobacillus crispatus*, *L. gasseri*, *L. jensenii*, and *L. iners*. These bacteria produce **lactic acid**, which maintains a low vaginal pH (3.8–4.5), creating an environment unfavorable for most pathogenic organisms [2, 4].

In addition to acidification, certain *Lactobacillus* strains synthesize **hydrogen peroxide (H2O2)** and **bacteriocins**, which exhibit direct antimicrobial activity against pathogens such as *Gardnerella vaginalis*, *Escherichia coli*, and *Candida albicans* [2]. The adhesion of *Lactobacillus* to epithelial cells also provides a **physical barrier** to pathogen colonization [5].

The composition and stability of the vaginal microbiota are influenced by severalfactors:

– **Hormonal fluctuations**, especially estrogen levels, regulate glycogen deposition in epithelial cells, which in turn supports *Lactobacillus* growth [5];

– **Sexual activity**, semen exposure, and use of contraceptives can transiently alter microbial communities;

– **Antibiotic use** may reduce *Lactobacillus* populations and promote overgrowth of opportunistic organisms [4].

Studies using next-generation sequencing (NGS) revealed that even among healthy women, there is interindividual variability in dominant *Lactobacillus* species [4, 5]. Importantly, the presence of *L. crispatus* is generally associated with a more stable and protective microbiota, while dominance by *L. iners* is considered less protective and more variable, often preceding dysbiosis [4].

Dysbiosis and Pathogenesis of Recurrent Vulvovaginal Infections

Bacterial Vaginosis (BV). BV is the most common vaginal dysbiosis, characterized by the **replacement of Lactobacillus spp. with polymicrobial anaerobic flora**, including Gardnerella vaginalis, Atopobium vaginae, Prevotella spp., Mobiluncus spp., and others [6]. This transition is accompanied by elevated vaginal pH and the production of amines and biofilms that protect pathogens from host defenses and antimicrobial treatment [7].

The recurrence rate of BV after standard antibiotic therapy can exceed 50% within 6 months [7], highlighting the role of **persistent dysbiosis and biofilm resilience**. Molecular studies demonstrate that certain *G. vaginalis* strains with biofilm-forming capacity may persist despite treatment [6].

***Vulvovaginal Candidiasis (VVC*).** VVC is caused primarily by *Candida albicans*, although non-albicans species such as C. glabrata *and* C. *tropicalis* are increasingly reported [8]. Unlike BV, the presence of *Lactobacillus* is often **not significantly reduced**, but **alterations in host immunity, local pH, and estrogen levels** promote fungal overgrowth [1, 8].

Recurrent VVC (RVVC), defined as four or more episodes per year, may result from **mucosal immune dysfunction**, including impaired neutrophil response and reduced antimicrobial peptide expression [1]. Use of antibiotics, hormonal contraceptives, and high estrogen states (e.g., pregnancy) are contributing factors [8].

Aerobic Vaginitis (AV). *AV is a less common but clinically significant dysbiosis, marked by* ***inflammation, epithelial disruption, and dominance of aerobic organisms*** *such as Escherichia coli, Staphylococcus aureus,* and *Streptococcus agalactiae* [9]. *Unlike BV, AV presents with* ***elevated leukocyte counts*** *and* ***epithelial atrophy*** *on microscopy. AV has been associated with adverse pregnancy outcomes and often coexists with other genital tract infections. The etiology includes* ***hormonal imbalance, mechanical trauma, and immunosuppression*** *[9]. Diagnosis is based on wet-mount microscopy showing toxic leukocytes and absence of* Lactobacillus.

In all forms of RVVI, **dysbiosis represents both a cause and a consequence of recurrent infection**, creating a vicious cycle that complicates treatment and demands a microbiota-oriented approach [3, 6].

t

a

- Next-generation sequencing (NGS) allows for precise microbiome profiling, aiding in distinguishing RVVI subtypes and tailoring treatments [10].

- While antibiotics like metronidazole and antifungals such as fluconazole are standard, recurrence rates remain high due to incomplete microbiota recovery [1].
- Probiotics and Microbiota Restoration. Probiotics, especially Lactobacillus rhamnosus GR-1 and Lactobacillus reuteri RC-14, show promise in restoring healthy flora [2]. Vaginal microbiota transplantation (VMT) is under investigation as a novel approach [6]. **Conclusion.** RVVI is closely linked to disturbances in vaginal microbiota. Emerging diagnostics and microbiota-targeted therapies

offer promising strategies for management. A deeper understanding of microbial interactions and host factors is critical for preventing recurrence and improving women's reproductive health.

1. Sobel J.D. Vulvovaginal candidosis // Lancet. – 2007. – Vol. 369(9577). – P. 1961–1971.
2. Reid G. Et al. Probiotic Lactobacillus dose required to restore and maintain a normal vaginal flora // FEMS Immunol Med Microbiol. – 2001. – Vol. 32(1). – P. 37–41.
3. Ma B. Et al. Vaginal microbiome: rethinking health and disease // Annu Rev Microbiol. – 2012. – Vol. 66. – P. 371–389.
4. Ravel J. Et al. Vaginal microbiome of reproductive-age women // Proc Natl Acad Sci USA. – 2011. – Vol. 108 Suppl 1. – P. 4680–4687.
5. Gajer P. Et al. Temporal dynamics of the human vaginal microbiota // Sci Transl Med. – 2012. – Vol. 4(132). – P. 132ra52.
6. Lev-Sagie A. Et al. Vaginal microbiome transplantation in women with intractable bacterial vaginosis // Nat Med. – 2019. – Vol. 25(10). – P. 1500–1504.
7. Bradshaw C.S. et al. High recurrence rates of bacterial vaginosis // J Infect Dis. – 2006. – Vol. 193(11). – P. 1478–1486.
8. Achkar J.M., Fries B.C. Candida infections of the genitourinary tract // Clin Microbiol Rev. – 2010. – Vol. 23(2). – P. 253–273.
9. Donders G.G. et al. Aerobic vaginitis: no longer a stranger // Res Microbiol. – 2017. – Vol. 168(9–10). – P. 845–858.
10. Srinivasan S., Fredricks D.N. The human vaginal bacterial biota and bacterial vaginosis // Interdiscip Perspect Infect Dis. – 2008. – Vol. 2008. – P. 750479