Current Research in Medical Sciences
p ISSN: 2538-6212

Student Research Committee
Babol University of Medical Sciences

Review Article

The Detrimental Impact of Dysbiosis in Gynecology and Obstetrics, Alongside the Positive Role of Probiotics in Prevention and Treatment: A Review Article

Zeinab Mohseni Afshar[1], Romina Fili[2], Fereshteh Behmanesh[3*]

1. Infectious Diseases and Tropical Medicine Research Center, Health Research Institute, Babol University of Medical Sciences, Babol, I.R. Iran
2. Student Research Committee, Babol University of Medical Sciences, Babol, Iran
3. Social Determinants of Health Research Center, Health Research Institute, Babol University of Medical Sciences, Babol, I.R. Iran

Article Info.

Received: 12 Jun 2025
Revised: 18 Aug 2025
Accepted: 12 Oct 2025
Published: 29 Nov 2025

*** Corresponding Author:**

Fereshteh Behmanesh, Ph.D
E-mail: f.behmanesh2015@gmail.com
Tel: +9811-32199594

Cite this article
Mohseni Afshar Z, Fili R, Behmanesh F. The Detrimental Impact of Dysbiosis in Gynecology and Obstetrics, Alongside the Positive Role of Probiotics in Prevention and Treatment: A Review Article, Curr Res Med Sci. 2025; 9: 98-109.

Abstract

Reproductive tract microbiome dysbiosis contributes to various gynecological and obstetric issues, including vaginal infections, adverse pregnancy outcomes, endometriosis, pelvic pain, sexually transmitted diseases, vulvodynia, and pelvic organ prolapse. Probiotics offer a promising approach to mitigating these problems through mechanisms such as microbiome regulation, immune system strengthening, antioxidant effects, and production of anti-mutagenic compounds. Common probiotics used to modulate reproductive dysbiosis include: *Limosilactobacillus reuteri* RC-14, *L. fermentum*, *L. gasseri*, *L. rhamnosus*, *L. acidophilus*, *L. crispatus*, *L. casei*, *L. salivarius*. Given the increasing prevalence of antibiotic resistance and associated limitations, probiotics represent a valuable therapeutic strategy; however, further research is required to optimize strain selection and dosage for specific conditions. Investigations should consider diverse populations, varying dosages, and different routes of administration (e.g., oral vs. vaginal suppositories) to determine the optimal approach for maximizing therapeutic benefits. The aim of the this study is to review the detrimental impact of reproductive tract microbiome dysbiosis on various gynecological and obstetric conditions, while also exploring the positive role that probiotics may play in the prevention and treatment of these conditions. The review seeks to evaluate how dysbiosis contributes to vaginal infections, adverse pregnancy outcomes, endometriosis, pelvic pain, sexually transmitted diseases, vulvodynia, and pelvic organ prolapse, as well as to assess the mechanisms through which probiotics may mitigate these problems, including microbiome regulation, immune system strengthening, antioxidant effects, and production of anti-mutagenic compounds.

Keywords: Dysbiosis, Microbiome, Probiotics, Obstetrics, Gynecology

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

Copyright © 2023 Babol University of Medical Sciences. Published by Babol University of Medical Sciences. This work is licensed under a Creative Commons Attribution-NonCommercial 4.0 International license (https://creativecommons.org/licenses/by-nc/4.0/). Noncommercial uses of the work are permitted, provided the original work is properly cited.

[DOI: 10.22088/crms.9.1.98] [Downloaded from crms.mubabol.ac.ir on 2026-10-17]

Introduction

The human body is a place with abundant concentration and diversity of microbes. These microorganisms populate any body organ and system, including the skin, gastrointestinal (GI), urogenital, oropharyngeal, and respiratory tracts. Microbes can be classified as beneficial, known as the microbiota, or harmful, known as pathogens..
They reside in or on the human body, maintaining a state of homeostasis with one another. Whenever the balance of the microbiota and pathogen is disrupted, a condition known as "dysbiosis", infection or disease occur. Today, it has been well understood that this imbalance is the main underlying cause of several inflammatory, infectious and malignant disorders. Accordingly, the discovery of probiotics, discussed in subsequent sections, has revolutionized both preventive and therapeutic medicine [1, 2].
The female reproductive system is one of the human body organs that is most tightly linked with microbiota balance. As soon as the microflora composition of the genital tract is changed, certain essential functions are impaired. In fact, successful human reproduction is influenced by the microbiota balance, and microbiome plays a role in reproductive cyclicity, pregnancy and delivery [3, 4]. On the other hand, disruption of the female genital microflora composition (dysbiosis) also leads to genital infections and the subsequent consequences like infertility. Thus, microbiota imbalance can be a trigger for several gynecological and obstetric events [5, 6].
Probiotics are live microorganisms that, in sufficient quantities, confer a health benefit on the host [7]. Probiotics offer a valuable approach to modulating microbiota dysbiosis and, with specific strains and dosages, can shift the microbiota towards a healthier state [8]. Their use is favored over antibiotics as long-term probiotic use avoids the serious side effects, particularly disruption of the natural microbiome, associated with antibiotics [9]. In addition, probiotics benefit female reproductive health by reducing gynecological diseases and strengthening vaginal immunity [10].Several review studies have examined the role of the female reproductive tract microbiome and gynecological disorders. Doroftei et al. (2023) reviewed the adverse impacts of microbial alterations in the vagina, cervix, and endometrium on pregnancy outcomes. Their narrative review analyzed studies from 2010-2023, finding that low levels of Lactobacillus species and core microbiota members can lead to eubiosis-to-dysbiosis transitions, impairing metabolic and endocrine network homeostasis [11]. Blancafort and Llácer (2023) reviewed the effect of probiotics on fertility outcomes and their capacity to improve the feminine genital tract microbiota, especially addressing the 50% of women with bacterial vaginosis who are asymptomatic [12]. Souza et al. (2023) systematically reviewed the influence of vaginal microbiome and Lactobacillus species on female fertility, analyzing 18 studies encompassing 2,011 women and concluding that fertile women exhibited dominance of Lactobacillus species while infertile women showed dysbiotic profiles [13]. Xholli et al. (2023) explored the relationship between gut microbiota and endometriosis, revealing altered gut microbiota in endometriosis patients, including reduced diversity, microbial composition imbalances, and increased pathogenic bacteria [14]. Kobayashi (2023) reviewed the role of gut and reproductive tract microbiota in endometriosis pathogenesis, highlighting how dysbiosis leads to estrobolomic and metabolomic changes that may contribute to disease development [15]. Wu et al. (2022) systematically reviewed disturbances in vaginal microbiome composition related to HPV infection and cervical carcinogenesis, finding higher alpha diversity in patients with HPV infection, cervical lesions, and/or cancer compared to controls [16].
Despite extensive research in this field, there remain significant gaps in the comprehensive understanding of dysbiosis impact across the full spectrum of gynecological and obstetric disorders, as well as the precise role of probiotics in prevention and treatment. Most existing studies have focused on specific aspects of the microbiome-disease relationship, with fewer studies comprehensively examining both the detrimental effects of dysbiosis and the positive role of probiotics in a single review. Furthermore, a complete understanding of the specific mechanisms of probiotic effectiveness, optimal

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

strain selection, and appropriate dosage for specific conditions still requires further investigation. The present study aims to fill these gaps.

Methods

Microbiota dynamics of the female reproductive tract

Similar to any human body organ, the female reproductive system has its own micro-niche composition with regular interpersonal variations. In fact, the vaginal microbiome is a dynamic ecosystem, which depends upon the host factors and their interplay with the environment for example, ethnicity, seasonal cycles, or climate can influence every individual's vaginal microbiome. Moreover, age, menstrual cycle, pregnancy, menopause, and other hormonal changes of a female affect the spatio-temporal diversity of the reproductive tract microbiota [5, 17].

Defining a healthy female reproductive tract (FRT) microbiota is challenging. The female neonate acquires vaginal microflora shortly after birth. During the course of a female's life, the vagina is exposed to hormonal changes, sexual activity, constant secretions and medication use. Moreover, the composition of microbiota differs in various anatomical sites of the reproductive tract. For example, the quantity of endometrial bacteria is significantly lower than that of vaginal bacteria. It means that the cervix probably serves as a partial barrier for ascending microflora. However, microbial communities that inhabit the vagina of a healthy nonpregnant female predominantly consist of four *Lactobacillus* species (*L. crispatus*, *L. iners*, *L. jensenii* or *L. gasseri*). Lactobacillus species are significant in maintaining normal pH through the production of lactic acid and regulation of glycogen metabolism. Moreover, they can provide an acidic and antimicrobial environment through production of bacteriocins and hydrogen peroxide, which protect against the invading pathogens. However, other vaginal microbiome of a healthy female of reproductive age includes several aerobic and facultative or obligate anaerobic species, including *Gardnerella*, *Prevotella*, *Atopobium*, and *Mobiluncus*; the dominance of these pathogens in the vagina of a female is usually associated with increased mucosal inflammation through increasing pro-inflammatory cytokines and numbers of CD4+ T-cells, disruption of epithelial barrier, and production of immunomodulatory metabolites [18, 19]. On the other hand, the microbiota composition of the vulva consists of *Lactobacillus* along with several other genera including *Corynebacterium*, *Staphylococcus* and *Prevotella*, which resemble the vaginal, skin and fecal commensals [20].

In the menstruation period, the composition of vaginal microbiota depends upon estrogen levels, with overall increase in *Gardnerella vaginalis* abundance and decrease in *Lactobacillus* species (except for *L. iners*) [21]. During pregnancy, the microbial composition alters as a decrease in the abundance and composition of the vaginal microbiome occurs to enable sufficient fetal development, while maintaining maternal health. The richness and diversity of vaginal commensals of a pregnant female vary according to gestation progression. Nevertheless, a change towards a *Lactobacillus*, Actinomycetes and Bacteroidetes-dominated community occurs in order to preserve the vaginal immunity [22, 23]. On the other hand, a change occurs in the vaginal bacterial community after pregnancy, with a significant decrease in abundance and diversity of *Lactobacillus* species. In fact, postpartum vaginal commensals resemble the gut microfloral communities and this alteration usually persists up to one year after the end of pregnancy [24, 25]. And last, but not least, the vaginal microbiome alteration during menopause is on behalf of decreased abundance of *Lactobacilli* and increased amount of other bacterial species. This occurs as a result of estrogen loss which causes vaginal atrophy and decreased immunity [26-28].

In general, any change in the urogenital microfloral profile of an individual is associated with certain infections and diseases, mentioned as follows:

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

Role of microbiome in fertility and pregnancy outcome

The female microbiota affects almost all stages of reproduction, including gametogenesis, fertilization, embryo migration, implantation and parturition. Thus, any alteration in the commensals composition may lead to infertility and detrimental pregnancy outcome.

Vaginal microbiota and chorioamnionitis

Intra-amniotic infection (IAI), also known as chorioamnionitis (CAM), has also been determined to be associated with a deranged vaginal microbiome. It has been demonstrated that decrease of *L. crispatus* amount and increase of certain anaerobic groups are related to occurrence of chorioamnionitis. Moreover, prediction of the severity of CAM may also been feasible through vaginal flora analysis [29-31].

Vaginal microbiota and fertility

Today, the endometrial cavity is no longer assumed to be sterile, rather, it has been demonstrated to be populated with a variety of microorganisms. The presence of commensals within the FRT has been demonstrated to contribute in reproductive health and fertility. It has been shown that dysbiosis plays an important role in infertility and restoration of endometrial and vaginal microbiota could increase the success of reproductive techniques in infertile couples and improve the reproductive outcome [32, 33].

On the other hand, it has been demonstrated that vaginal dysbiosis is tightly associated with the occurrence of intrauterine adhesion (IUA), which is a significant underlying cause of amenorrhea, repeated miscarriages and infertility [34].

Vaginal microbiota and preterm birth

Vaginal dysbiosis has been suggested to serve as a cause for preterm birth (i.e. delivery before 37 weeks' gestation). In general, it has been demonstrated that the vaginal richness, diversity, and evenness of microbiota is decreased during pregnancy in those females with subsequent preterm labor; this alteration occurs between the first and second trimesters. An increase in the abundance of *Gardnerella* and a decrease in the abundance of *Lactobacillus* species have been demonstrated in the vaginal commensals of a female with preterm delivery [35, 36].

Vaginal microbiota and premature rupture of membranes

Premature rupture of membranes (PROM) is another adverse pregnancy outcome that may lead to preterm labor, low birth weight, fetal loss and even life-threatening maternal and neonatal septicemia. PROM is associated with endometrial and vaginal infections like bacterial vaginosis, which is the result of the shift from Lactobacilli dominance to a mixed microflora including *G.vaginalis* [37-40].

Vaginal microbiota and miscarriage

It has been recently demonstrated that the FRT dysbacteriosis can play a role in miscarriage and pregnancy loss. The underlying mechanism might be attributed to the disequilibrium in the Th1/Th2 immune response posed by the microbial imbalance. On the other hand, genital infections which are main causes of pregnancy loss are per se precipitated by the change in the bacterial microflora of the FRT [41-43].

Role of probiotics in fertility and pregnancy outcome

Probiotic effects on pregnancy are debated. One study found no impact on preterm birth or pregnancy length versus placebo [44]. However, evidence increasingly supports probiotic benefits; one recent systematic review suggests combined antibiotics/probiotics may improve outcomes in PPROM cases [45]. Probiotics may be linked to longer pregnancies, increased birth weight, reduced chorioamnionitis, and improved vaginal flora. Specifically, oral probiotics containing Clostridium may help prevent preterm birth before 32 weeks [46]. A daily 6-month *Ligilactobacillus salivarius* intervention in pregnant women with recurrent miscarriage or infertility, abnormal vaginal flora, and pH increased pregnancy success rates by 56% while

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

decreasing vaginal pH and increasing vaginal lactobacilli [7]. Common probiotics used to modulate reproductive dysbiosis include: *L. reuteri* RC-14, *L. fermentum*, *L. gasseri*, *L. rhamnosus*, *L. acidophilus*, *L. crispatus*, *L. casei, L. salivarius* [47]. Also, probiotics can influence fertility by:

1. Improving sperm parameters, testicular health, and testosterone levels through antioxidant effects;

2. Supporting a healthy vaginal microbiome and preventing bacterial vaginosis (BV) and inflammation [48].

Role of microbiome in female genitourinary infections

Female genital and sometimes gut dysbiosis is tightly linked with abundant adverse reproductive health outcomes like sexually transmitted diseases and other genitourinary infections.

Bacterial vaginosis

BV is a common vaginal infection in women [49]. in females of reproductive age. This condition is also associated with dysbiosis. In fact, decreased lactobacilli abundance can lead to reduced lactic acid production and increased vaginal pH, which can result in increased load of anaerobic and facultative-anaerobic bacteria like *G. vaginalis*, Bacteroidetes, *Mobiluncus*, and *Prevotella* species [50, 51].

Sexually transmitted infections

Not only BV, but also other sexually transmitted infections (STIs) are closely related to vaginal dysbacterosis. These STIs include *Neisseria gonorrhoeae*, *Chlamydia trachomatis*, *Trichomonas vaginalis*, human papillomavirus (HPV), herpes simplex virus (HSV) and human immunodeficiency virus (HIV). As a matter of fact, lactic acid has an inhibitory impact on STIs through modulation of cervicovaginal epithelial cell functions and exertion of immunomodulatory effects. Thus, decreased lactic acid production as a result of dysbiosis and decreased lactobacilli diversity and abundance can lead to decreased protection against STIs [52-54]. On the other hand, loss of lactobacilli dominance can be followed by an increased risk of HPV infection, persistence, and the associated cervical malignancies [55-58]. In addition, dysbiosis may decrease body defense against HIV infection and promote HIV disease progression, which per se facilitates other STIs occurrence and persistence [59-61].

Endometritis and pelvic inflammatory disease

There are sparse reports that are suggestive of the relative similarity of the upper FRT and the lower FRT microbiota. This would be the result of ascending microbial seeding of the uterine cavity with vaginal commensals. Thus, dysbiosis seems to play an important role in acute or chronic endometritis [62]. On the other hand, STIs that seem to be the result of dysbiosis are the main contributors to upper genital tract infections or pelvic inflammatory diseases (PID). In fact, Lactobacillus species can protect the host against STIs and the consequent PID [63-66].

Role of probiotics in female genitourinary infections

Probiotics in various forms of dietary supplements, capsules, and vaginal suppositories have beneficial effects on the vaginal environment through various means:

1. Reducing vaginal PH by producing lactic acid and hydrogen peroxide;

2. Producing antimicrobial compounds and stimulating the immune system;

3. Inhibiting the attachment of pathogenic bacteria by adhering probiotics to the vaginal epithelium;

4. Using the same nutrients as pathogens [49].

A meta-analysis study by Wang, Z., et al. (2019) showed that probiotics could have a potential effect in relieving BV [67]. Due to the dynamic environment of the genital tract and the risk of local infections, probiotics are recommended for both women susceptible to recurrent urogenital infections and healthy women to help prevent

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

genital mucosal superinfections [68].**Role of microbiome in gynecological cancers**

Alteration of the female gut and vagina microbiome may lead to the onset or progression of gynecologic cancers like endometrium, cervical and ovarian malignancies. For example, elevated level of Proteobacteria and Firmicutes phylum bacteria, namely *Atopobium* and *Porphyromonas*, is associated with endometrial cancer, increased level of *C. trachomatis*, *Lactobacillus* and *Mycobacterium* have been reported in ovarian cancer, and high loads of human papillomavirus, Fusobacterial and *Sneathia* species are accompanied by cervical cancers. Moreover, vaginal and vulvar cancers have also been linked to gut and vaginal dysbiosis [69, 70]. Furthermore, disruption of estrogens metabolism by the commensals imbalance may predispose to breast cancer [71].

Role of probiotics in gynecological cancers

Probiotic bacteria may reduce cancer risk through several mechanisms, including the production of anti-mutagenic compounds, degradation of carcinogens, induction of apoptosis, and modulation of both carcinogenic compound concentrations and the host immune response. In cervical cancer management, probiotics contribute by enhancing immunity, balancing the vaginal microbiome, and decreasing the risk of secondary infections [72]. Furthermore, long-term administration of *Lactiplantibacillus plantarum* LS/07 induces immunomodulation, potentially decreasing tumor necrosis factor (TNF)- α and increasing CD4(+) T-Cells levels [73].

Role of microbiome in other gynecological disorders

Endometriosis and chronic pelvic pain

Endometriosis is the presence of endometrium-like tissue outside the uterine cavity. This chronic inflammatory condition has been deemed to be the result of microbiome alteration. In fact, gut dysbiosis (with increased levels of Proteobacteria, *Streptococcus*, Enterobacteriaceae and *Escherichia coli*) leads to a change in estrogen metabolism and the resultant increase in levels of circulating estrogen, which is the underlying pathogenic mechanism for endometriosis. Moreover, decreased abundance of *Lactobacillus* species and increased abundance of anaerobes like *Prevotella*, *Atopobium*, *Mobiluncus*, and *Gardnerella* species are associated with vaginal dysbiosis, stimulation of the immune system and the consequent inflammation and endometriosis [26, 74, 75].

On the other hand, chronic pelvic pain (CPP) is another inflammatory condition with endometriosis being one of the causes. This annoying syndrome, which considerably affects the quality of life, has also been observed to be associated with alterations of the vaginal and rectal microbiome profiles [76, 77].

Polycystic ovary syndrome

Polycystic ovary syndrome (PCOS) is the most prevalent endocrinopathy in females of reproductive age, which mainly results from insulin resistance (IR). Females with PCOS exhibit ovarian cysts, anovulation/menstrual irregularity, and hyperandrogenism, and occasionally overweight, insulin resistance, anxiety and depression. Furthermore, it is sometimes associated with follicular dysplasia, abortion or infertility [78].

It has been suggested that alteration of the phylogenetic profile of the gut commensals may have a role in the evolution of PCOS. However, the association between vaginal microbiota and PCOS has not yet been established. Studies have demonstrated a lower diversity of stool microbiota, with decreased abundance of *Lactobacillus* species, namely *L. crispatus* and the increased abundance of *Mycoplasma* and *Prevotella* in females with PCOS. Moreover, the abundance of GABA-producing bacteria like *Parabacteroides distasonis*, *Bacteroides fragilis* and *E. coli*, is also increased which is associated with increased serum luteinizing hormone (LH) to follicle stimulating hormone (FSH) ratios. This type of dysbiosis reveals a potential gut–brain axis in PCOS. This disturbance in gut microbiota increases the gut mucosal permeability and

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

consequently increased passage of lipopolysaccaride (LPS) from Gram-negative colonic bacteria into the systemic circulation. This leads to the immune system activation and the resultant interference with insulin receptor function, androgen production by the ovaries and impaired follicle development [79-81].

Vulvodynia

Dysbiosis has also been suggested to contribute to the onset of vulvodynia, also known as idiopathic vulvar pain. This is perhaps the result of altered immune inflammatory response caused by the changed microbiota composition and abundance. In fact, females with low-diversity microbiota are more likely to develop vulvodynia, compared with those women with high-diversity microbiomes [82, 83].

Pelvic organ prolapses

Pelvic organ prolapse (POP) is a prevalent female syndrome presenting with various manifestations like uterine prolapse, rectal bladder prolapses, and anterior and posterior vaginal wall bulge. It has been demonstrated that vaginal dysbiosis has an impact on the occurrence of female POP; it means that the inflammation and fluctuations of estrogen levels caused by vaginal microecology disruption may be a trigger for POP [84, 85].

Role of probiotics in other gynecological disorders

PCOS-related insulin resistance may be mitigated by specific probiotics. For example, a 12-week supplementation with "*Lactobacillus acidophilus*", "*Lacticaseibacillus casei*", and "*Bifidobacterium bifidum*" significantly lowered Sex Hormone Binding Globulin (SHBG) and serum insulin levels in one study [86]. While a systematic review found that probiotics did not significantly reduce insulin and fasting blood glucose (FBG), even small reductions in these markers offer health advantages [87]. Furthermore, prior studies indicate that probiotic use exceeding 12 weeks leads to weight and fat loss in obese women [88]. Furthermore, daily intake of 100 mg of "Lactobacillus gasseri" reduced Visual Analog Scale (VAS) pain more effectively than a placebo in women with endometriosis [89]. Probiotics, by reducing immune responses and proinflammatory cytokines, alleviate inflammation and discomfort. They may also promote endometriotic lesion regression through Natural killer cell activation [90].

Association of sex behaviors and vaginal microbiome

an association has recently been demonstrated between vaginal commensals and sexual behaviors. As previously mentioned the vaginal microbiota contribute to in the development and persistence of STIs; this per se has a significant impact on sexual relationship [91]. On the other hand, it has been demonstrated that sexual practices affect the vaginal microbiota profile in women with various sexual orientation and behaviors. For example, inconsistent condom use, new or multiple numbers of sexual partners and homosexual affair have been shown to lead to decreased lactobacilli abundance and increased diversity and abundance of anaerobic bacteria including *G. vaginalis*; this is followed by increased risk of BV. Moreover, high-risk sexual behavior like female sex work is associated with increased diversity of the vaginal microbiome and decreased abundance of Lactobacillus species, which is the cornerstone of several gynecological infections and disorders [92-94].

Association of contraceptives and the female reproductive tract microbiome

It has been demonstrated that different contraceptives have various effects on the composition of FRT microbiota and vaginal health. For example, women who are on intramuscular injectable depot-medroxyprogesterone acetate (DMPA-IM) or oral contraceptives (OCPs) for contraception are at decreased risk of BV incidence and recurrence, mainly due to the increase in Lactobacillus levels [95, 96]. This is in contrast with copper or levonorgestrel intrauterine device (IUD) users who are at increased risk of BV as a result of alteration in the

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

vaginal bacterial composition [97-99].**Supporting and Conflicting Studies**

Multiple studies have confirmed the important role of *Lactobacillus* species in maintaining vaginal health. Zierden et al. demonstrated that *Lactobacillus* crispatus-dominated microbiota was associated with stronger cervicovaginal mucus barrier function, while polymicrobial communities increased permeability. This suggests that microbial composition plays a crucial role in preventing bacterial ascension, with potential implications for preterm birth risk [100]. Similarly, Takano et al. (2023) evaluated how various *Lactobacillus* species inhibit *Candida albicans* growth, biofilm formation, and epithelial adhesion, identifying lactate as a key factor in suppressing *C. albicans* biofilms and hyphal transition [101]. Rahman et al. (2023) showed that estrogen significantly influences Lactobacillus and *G. vaginalis* colonization, with mice treated with 17β-estradiol exhibiting increased glycogen levels supporting Lactobacillus colonization, whereas progesterone alone failed to restore microbial balance [102].

However, some studies have reported conflicting findings. Mao et al. (2023) investigated the association between vaginal and cervical microbiome dysbiosis and uterine fibroids, finding no significant difference in overall microbial diversity between women with fibroids and healthy controls, although alpha diversity was negatively correlated with the number of fibroids Mao [103]. Zhang et al. (2024) reviewed the relationship between vaginal microbiota, human papillomavirus (HPV) infection, and cervical cancer, highlighting that while vaginal dysbiosis (characterized by reduced *Lactobacillus* abundance and increased microbial diversity) contributes to HPV persistence and cervical lesion progression, the specific mechanisms and causal relationships remain complex [42]. Additionally, Wu et al. (2022) reported that *L. iners* may exert either protective or pathogenic effects on different HPV-related diseases, suggesting variability in the role of specific *Lactobacillus* species [16].

Conclusion

This review article highlights the essential impact of dysbiosis on various obstetric and gynecological disorders. Thus, it seems that restoration of female normal microflora through probiotics can be used as a preventive and therapeutic target for several reproductive diseases. This can be true for all challenges including reproductive failures and gynecological cancers. Given the unclear mechanisms of action and inconsistent findings on effective strains and doses, further research is needed to determine the impact of probiotics on women's health, particularly in conditions like gynecological cancers.

Acknowledgment

Acknowledgment: The authors will thank of Vice President of Research and Technology of Babol University of Medical Sciences.

Conflicts of interest:

There are no conflicts of interest.

Funding:

No funding was received

Availability of data and material: Not applicable.

Author's contribution:

All the authors contributed to the conception and design of the study. MA Z, B F, and F R drafted the first version of the manuscript. All authors approved the final version.

List of abbreviations

GI: Gastrointestinal , FRT: Female Reproductive Tract, CAM: Chorioamnionitis, IUA: Intrauterine Adhesion, PROM: Premature Rupture Of Membranes, BV: Bacterial Vaginosis, STIs: Sexually Transmitted Infections, HPV: Human Papillomavirus, HSV: Herpes Simplex Virus, HIV: Human Immunodeficiency Virus , PID: Pelvic Inflammatory diseases, PCOS: Polycystic ovary syndrome, LPS: lipopolysaccaride, POP: Pelvic Organ Prolapse, SHBG: Sex Hormone Binding Globulin, FBG: Fasting Blood Glucose, VAS: Visual Analog Scale, DMPA-IM: Depot-

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

Medroxyprogesterone Acetate, OCPs: Oral Contraceptives, IUD: intrauterine device.

Consent for publication: Not applicable.

References

1. Sekirov I, Russell SL, Antunes LCM, Finlay BB. Gut microbiota in health and disease. Physiol Rev. 2010.
2. Hou K, Wu Z-X, Chen X-Y, Wang J-Q, Zhang D, Xiao C, et al. Microbiota in health and diseases. Signal Transduct. 2022; 7(1):1-28.
3. Knight R, Callewaert C, Marotz C, Hyde ER, Debelius JW, McDonald D, et al. The microbiome and human biology. Annu Rev Genomics. 2017; 18(1):65-86.
4. Martin BD, Schwab E. Current usage of symbiosis and associated terminology. Int J Biol Sci. 2012; 5(1):32-45.
5. Green KA, Zarek SM, Catherino WH. Gynecologic health and disease in relation to the microbiome of the female reproductive tract. Fertil Steril. 2015; 104(6):1351-57.
6. Punzón-Jiménez P, Labarta E. The impact of the female genital tract microbiome in women health and reproduction: a review. J Assist Reprod Genet. 2021; 38(10):2519-41.
7. Fernández L, Castro I, Arroyo R, Alba C, Beltrán D, Rodríguez JM. Application of Ligilactobacillus salivarius CECT5713 to achieve term pregnancies in women with repetitive abortion or infertility of unknown origin by microbiological and immunological modulation of the vaginal ecosystem. Nutrients. 2021; 13(1):162.
8. López-Moreno A, Aguilera M. Vaginal probiotics for reproductive health and related dysbiosis: systematic review and meta-analysis. J Clin Med. 2021; 10(7):1461.
9. Jarde A, Lewis-Mikhael A-M, Moayyedi P, Stearns JC, Collins SM, Beyene J, et al. Pregnancy outcomes in women taking probiotics or prebiotics: a systematic review and meta-analysis. BMC Pregnancy Childbirth. 2018; 18:1-14.
10. Mei Z, Li D. The role of probiotics in vaginal health. Front Cell Infect Microbiol. 2022; 12:963868.
11. Doroftei B, Ilie O-D, Armeanu T, Stoian I-L, Anton N, Babici R-G, et al. A narrative review discussing the obstetric repercussions due to alterations of personalized bacterial sites developed within the vagina, cervix, and endometrium. J Clin Med. 2023; 12(15):5069.
12. Blancafort C, Llácer J. Can probiotics enhance fertility outcome? Capacity of probiotics as a single intervention to improve the feminine genital tract microbiota in non-symptomatic reproductive-aged women. Front Endocrinol. 2023; 13:1081830.
13. Vieira de Souza S, Monteiro P, de Moura G, Oliveira Santos N, Fontanezi C, de Almeida Gomes I, et al. Vaginal microbioma and the presence of Lactobacillus spp. As interferences in female fertility: A review system JBRA Assist Reprod. 2023; 27:496-506.
14. Xholli A, Cremonini F, Perugi I, Londero AP, Cagnacci A. Gut microbiota and endometriosis: exploring the relationship and therapeutic implications. pharmaceut. 2023; 16(12):1696.
15. Kobayashi H. Gut and reproductive tract microbiota: insights into the pathogenesis of endometriosis. Biomed Rep. 2023; 19(1):43.
16. Wu M, Li H, Yu H, Yan Y, Wang C, Teng F, et al. Disturbances of vaginal microbiome composition in human papillomavirus infection and cervical carcinogenesis: A qualitative systematic review. Front Oncol. 2022; 12:941741.
17. Gao H, Liu Q, Wang X, Li T, Li H, Li G, et al. Deciphering the role of female reproductive tract microbiome in reproductive health: a review. Front Cell Infect Microbiol. 2024; 14:1351540.
18. Vitale SG, Ferrari F, Ciebiera M, Zgliczyńska M, Rapisarda AMC, Vecchio GM, et al. The role of genital tract microbiome in fertility: a systematic review. Int J Mol Sci. 2021; 23(1):180.
19. France M, Alizadeh M, Brown S, Ma B, Ravel J. Towards a deeper understanding of the vaginal microbiota. Nat Microbiol. 2022; 7(3):367-78.
20. Pagan L, Ederveen RA, Huisman BW, Schoones JW, Zwittink RD, Schuren FH, et al. The human vulvar microbiome: a systematic review. Microorganisms. 2021; 9(12):2568.
21. Song SD, Acharya KD, Zhu JE, Deveney CM, Walther-Antonio MR, Tetel MJ, et al. Daily vaginal microbiota fluctuations associated with natural hormonal cycle, contraceptives, diet, and exercise. MSphere. 2020; 5(4):10.1128/msphere. 00593-20.
22. Sparvoli LG, Cortez RV, Daher S, Padilha M, Sun SY, Nakamura MU, et al. Women's multisite microbial modulation during pregnancy. Microb Pathog. 2020; 147:104230.
23. Aagaard KM. Mode of delivery and pondering potential sources of the neonatal microbiome. EBioMedicine. 2020; 51.
24. Gevers D, Knight R, Petrosino JF, Huang K, McGuire AL, Birren BW, et al. The Human Microbiome Project: a community resource for the

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

healthy human microbiome. PLoS biology. 2012;10: e1001377.
25. Lloyd-Price J, Abu-Ali G, Huttenhower C. The healthy human microbiome. Genome Med. 2016; 8:1-11.
26. Muhleisen AL, Herbst-Kralovetz MM. Menopause and the vaginal microbiome. Maturitas. 2016; 91:42-50.
27. Park MG, Cho S, Oh MM. Menopausal changes in the Microbiome—a review focused on the genitourinary Microbiome. Diagnostics. 2023; 13(6):1193.
28. Kim S, Seo H, Rahim MA, Lee S, Kim Y-S, Song H-Y. Changes in the microbiome of vaginal fluid after menopause in Korean women. J Microbiol Biotechnol. 2021; 31(11):1490.
29. Urushiyama D, Ohnishi E, Suda W, Kurakazu M, Kiyoshima C, Hirakawa T, et al. Vaginal microbiome as a tool for prediction of chorioamnionitis in preterm labor: a pilot study. Sci Rep. 2021; 11(1):18971.
30. Guo X, Hong X, Qian H, Qiao D, Wang B, Yu H. Relationship between vaginal microbiota and chorioamnionitis: A prospective cohort study. Microb Pathog. 2024; 186:106458.
31. Prince AL, Ma J, Kannan PS, Alvarez M, Gisslen T, Harris RA, et al. The placental membrane microbiome is altered among subjects with spontaneous preterm birth with and without chorioamnionitis. Am J Obstet Gynecol. 2016; 214(5):627. e1-27. e16.
32. Hong X, Ma J, Yin J, Fang S, Geng J, Zhao H, et al. The association between vaginal microbiota and female infertility: a systematic review and meta-analysis. Arch Gynecol Obstet. 2020; 302:569-78.
33. Singer M, Borg M, Ouburg S, Morré SA. The relation of the vaginal microbiota to early pregnancy development during in vitro fertilization treatment—A meta-analysis. J Gynecol Obstet Hum Reprod. 2019; 48(4):223-29.
34. Dun S, Liu C, Li N. Changes of Vaginal Microecology of Women with Intrauterine Adhesions. Int J Womens Health. 2023;15: 857-67.
35. Peelen MJ, Luef BM, Lamont RF, de Milliano I, Jensen JS, Limpens J, et al. The influence of the vaginal microbiota on preterm birth: A systematic review and recommendations for a minimum dataset for future research. Placenta. 2019; 79:30-39.
36. Fettweis JM, Serrano MG, Brooks JP, Edwards DJ, Girerd PH, Parikh HI, et al. The vaginal microbiome and preterm birth. Nat Med. 2019; 25(6):1012-21.
37. Zhang D, Dong R, Jiang T, Ren S, Yue X, Zhai M, et al. The relationships of metals exposure and disturbance of the vaginal microbiota with the risk of PROM: Results from a birth cohort study. Ecotoxicol Environ Saf. 2025; 289:117420.
38. Khodzhaeva ZS, Guseinova GE, Muravyeva VV, Donnikov AE, Mishina ND, Priputnevich TV. Characteristics of the vaginal microbiota in pregnant women with preterm premature rupture of the membranes. Obstet Gynecol. 2019; 12:64-72.
39. Genovese C, Corsello S, Nicolosi D, Aidala V, Falcidia E, Tempera G. Alterations of the vaginal microbiota in the third trimester of pregnancy and pPROM. Eur Rev Med Pharmacol Sci. 2016; 20(16).
40. Yan C, Hong F, Xin G, Duan S, Deng X, Xu Y. Alterations in the vaginal microbiota of patients with preterm premature rupture of membranes. Front Cell Infect Microbiol. 2022; 12:858732.
41. Lebedeva OP, Popov VN, Syromyatnikov MY, Starkova NN, Maslov AY, Kozarenko ON, et al. Female reproductive tract microbiome and early miscarriages. APMIS. 2023; 131(2):61-76.
42. Zhang F, Zhang T, Ma Y, Huang Z, He Y, Pan H, et al. Alteration of vaginal microbiota in patients with unexplained recurrent miscarriage. Exp Ther Med. 2019; 17(5):3307-16.
43. Liu X, Cao Y, Xie X, Qin X, He X, Shi C, et al. Association between vaginal microbiota and risk of early pregnancy miscarriage. Comp Immunol Microbiol Infect Dis. 2021; 77:101669.
44. Solgi E, Tavakoli-Far B, Badehnoosh B, Khavandegar A, Bakhtiyari M. Vaginal and oral probiotics effect in the prevention of preterm delivery in patients visiting Kamali Hospital, Karaj, Iran in 2020. Eur J Obstet Gynecol Reprod Biol:X. 2022; 16:100169.
45. Baradwan S, AlSghan R, Sabban H, Khadawardi K, Ali ZAM, Felemban LHA, et al. Vaginal probiotics as an adjunct to antibiotic prophylaxis in the management of preterm premature rupture of membranes: A systematic review and meta-analysis of randomized controlled trials. Eur J Obstet Gynecol Reprod Biol. 2023; 291:112-19.
46. Kirihara N, Kamitomo M, Tabira T, Hashimoto T, Taniguchi H, Maeda T. Effect of probiotics on perinatal outcome in patients at high risk of preterm birth. J Obstet Gynaecol Res. 2018; 44(2):241-47.
47. López-Moreno A, Aguilera M. Probiotics dietary supplementation for modulating endocrine and fertility microbiota dysbiosis. Nutrients. 2020; 12(3):757.

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

48. Younis N, Mahasneh A. Probiotics and the envisaged role in treating human infertility. Middle East Fertil Soc J. 2020; 25:1-9.
49. Lehtoranta L, Ala-Jaakkola R, Laitila A, Maukonen J. Healthy vaginal microbiota and influence of probiotics across the female life span. Front Microbiol. 2022; 13:819958.
50. Ling Z, Kong J, Liu F, Zhu H, Chen X, Wang Y, et al. Molecular analysis of the diversity of vaginal microbiota associated with bacterial vaginosis. BMC genomics. 2010; 11:1-16.
51. Srinivasan S, Fredricks DN. The human vaginal bacterial biota and bacterial vaginosis. Interdiscip Perspect Infect Dis. 2008; 2008(1):750479.
52. O'Hanlon DE, Moench TR, Cone RA. In vaginal fluid, bacteria associated with bacterial vaginosis can be suppressed with lactic acid but not hydrogen peroxide. BMC Infect Dis. 2011; 11:1-8.
53. Aldunate M, Tyssen D, Johnson A, Zakir T, Sonza S, Moench T, et al. Vaginal concentrations of lactic acid potently inactivate HIV. J Antimicrob Chemother. 2013; 68(9):2015-25.
54. Gong Z, Luna Y, Yu P, Fan H. Lactobacilli inactivate Chlamydia trachomatis through lactic acid but not H2O2. PLoS One. 2014; 9(9):e107758.
55. Aryanian Z, Mohammadi M, Babazadeh A, Hatami P, Mohseni Afshar Z, Goodarzi A, et al. Knowledge and attitude of Iranian university students toward genital warts. Interdiscip Perspect Infect Dis. 2022; 2022(1):6730476.
56. Afshar ZM, Aryanian Z, Rajabalian MB, Narouie B, Dayani M, Aliasgharpour M, et al. Clinical and Public Health Considerations for HPV Infection in Men: A Narrative Review. Transl Res Urol. 2024; 6(1):10-17.
57. Qingqing B, Jie Z, Songben Q, Juan C, Lei Z, Mu X. Cervicovaginal microbiota dysbiosis correlates with HPV persistent infection. Microb Pathog. 2021; 152:104617.
58. Brusselaers N, Shrestha S, Van De Wijgert J, Verstraelen H. Vaginal dysbiosis and the risk of human papillomavirus and cervical cancer: systematic review and meta-analysis. Am J Obstet Gynecol. 2019; 221(1):9-18. e8.
59. Mohseni Afshar Z, Goodarzi A, Emadi SN, Miladi R, Shakoei S, Janbakhsh A, et al. A comprehensive review on HIV-associated dermatologic manifestations: from epidemiology to clinical management. Int J Microbiol Res. 2023; 2023(1):6203193.
60. Vujkovic-Cvijin I, Dunham RM, Iwai S, Maher MC, Albright RG, Broadhurst MJ, et al. Dysbiosis of the gut microbiota is associated with HIV disease progression and tryptophan catabolism. Sci Transl Med. 2013; 5(193):193ra91-93ra91.
61. Brenchley JM, Serrano-Villar S. From dysbiosis to defense: harnessing the gut microbiome in HIV/SIV therapy. Microbiome. 2024; 12(1):113.
62. Chen C, Song X, Wei W, Zhong H, Dai J, Lan Z, et al. The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. Nat Commun. 2017; 8(1):875.
63. Wang Y, Zhang Y, Zhang Q, Chen H, Feng Y. Characterization of pelvic and cervical microbiotas from patients with pelvic inflammatory disease. J Med Microbiol. 2018; 67(10):1519-26.
64. Kim S, Seo H, Rahim MA, Tajdozian H, Kim Y-S, Song H-Y. Characteristics of vaginal microbiome in women with pelvic inflammatory disease in Korea. Pol J Microbiol. 2021; 70(3):345-57.
65. Taylor BD, Darville T, Haggerty CL. Does bacterial vaginosis cause pelvic inflammatory disease? Sex Transm Dis. 2013; 40(2):117-22.
f66. Nurgalieva E, Dukhin A, Gushin A. The microbiota of the female genital organs of women with pelvic inflammatory diseases. RUDN Journal of Medicine. 2016; (2):197-201.
67. Wang Z, He Y, Zheng Y. Probiotics for the treatment of bacterial vaginosis: a meta-analysis. Int J Environ Res Public Health. 2019; 16(20):3859.
68. Ballini A, Santacroce L, Cantore S, Bottalico L, Dipalma G, De Vito D, et al. Probiotics improve urogenital health in women. Open Access Maced J Med Sci. 2018; 6(10):1845.
69. Rizzo AE, Gordon JC, Berard AR, Burgener AD, Avril S. The female reproductive tract microbiome—implications for gynecologic cancers and personalized medicine. J Pers Med. 2021; 11(6):546.
70. Borella F, Carosso AR, Cosma S, Preti M, Collemi G, Cassoni P, et al. Gut microbiota and gynecological cancers: a summary of pathogenetic mechanisms and future directions. ACS Infect Dis. 2021; 7(5):987-1009.
71. Jaye K, Chang D, Li CG, Bhuyan DJ. Gut metabolites and breast cancer: the continuum of dysbiosis, breast cancer risk, and potential breast cancer therapy. Int J Mol Sci. 2022; 23(16):9490.
72. Supriya Y, Sivamalar S, Nallusamy D, Sureka V, Arunagirinathan N, Saravanan S, et al. Application of probiotics in cervical cancer infections to enhance the immune response. Microb Pathog. 2024:106764.
73. Kassayova M, Bobrov N, Strojný L, Kiskova T, Mikeš J, Demečková V, et al. Preventive effects of probiotic bacteria Lactobacillus plantarum and

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

dietary fiber in chemically-induced mammary carcinogenesis. Anticancer Res. 2014; 34(9):4969-75.
74. Leonardi M, Hicks C, El-Assaad F, El-Omar E, Condous G. Endometriosis and the microbiome: a systematic review. BJOG: An International Journal of Obstetrics & Gynaecology. 2020; 127(2):239-49.
75. D'Alterio MN, Giuliani C, Scicchitano F, Laganà AS, Oltolina NM, Sorrentino F, et al. Possible role of microbiome in the pathogenesis of endometriosis. Minerva Ginecol. 2021; 73(2):193-214.
76. Jimenez N, Norton T, Diadala G, Bell E, Valenti M, Farland LV, et al. Vaginal and rectal microbiome contribute to genital inflammation in chronic pelvic pain. BMC Med. 2024; 22(1):283.
77. Hashemi N, Tondro Anamag F, Javan Balegh Marand A, Rahnama'i MS, Herizchi Ghadim H, Salehi-Pourmehr H, et al. A systematic and comprehensive review of the role of microbiota in urinary chronic pelvic pain syndrome. Neurourol Urodyn. 2024; 43(8):1859-82.
78. He F-f, Li Y-m. Role of gut microbiota in the development of insulin resistance and the mechanism underlying polycystic ovary syndrome: a review. J Ovarian Res. 2020; 13(1):73.
79. Lindheim L, Bashir M, Münzker J, Trummer C, Zachhuber V, Leber B, et al. Alterations in gut microbiome composition and barrier function are associated with reproductive and metabolic defects in women with polycystic ovary syndrome (PCOS): a pilot study. PLoS One. 2017; 12(1):e0168390.
80. Tremellen K, Pearce K. Dysbiosis of Gut Microbiota (DOGMA)–a novel theory for the development of Polycystic Ovarian Syndrome. Med Hypotheses. 2012; 79(1):104-12.
81. Liang Z, Di N, Li L, Yang D. Gut microbiota alterations reveal potential gut–brain axis changes in polycystic ovary syndrome. J Endocrinol Invest. 2021:1-11.
82. Park SY, Lee ES, Lee SR, Kim SH, Chae HD. Vaginal microbiome is associated with vulvodynia, vulvar pain syndrome: a case-control study. Sex Med. 2021; 9(2):100314-14.
83. Bedford L, Parker SE, Davis E, Salzman E, Hillier SL, Foxman B, et al. Characteristics of the vaginal microbiome in women with and without clinically confirmed vulvodynia. Am J Obstet Gynecol. 2020; 223(3):406. e1-06. e16.
84. Chen S, Zheng Q, Zhang L, Chen L, Wang J. Effect of Vaginal Microecological Alterations on Female Pelvic Organ Prolapse. Int Urogynecol J. 2024; 35(4):881-91.
85. Kim M, Lee S, Kim HS, Kwon MY, Yoo J, Kim MJ. Microbiome alterations in women with pelvic organ prolapse and after anatomical restorative interventions. Sci Rep. 2023; 13(1):17547.
86. Nasri K, Jamilian M, Rahmani E, Bahmani F, Tajabadi-Ebrahimi M, Asemi Z. The effects of synbiotic supplementation on hormonal status, biomarkers of inflammation and oxidative stress in subjects with polycystic ovary syndrome: a randomized, double-blind, placebo-controlled trial. BMC Endocr Disord. 2018; 18:1-8.
87. Cozzolino M, Vitagliano A, Pellegrini L, Chiurazzi M, Andriasani A, Ambrosini G, et al. Therapy with probiotics and synbiotics for polycystic ovarian syndrome: a systematic review and meta-analysis. Eur J Nutr. 2020; 59:2841-56.
88. Sanchez M, Darimont C, Drapeau V, Emady-Azar S, Lepage M, Rezzonico E, et al. Effect of Lactobacillus rhamnosus CGMCC1. 3724 supplementation on weight loss and maintenance in obese men and women. Br J Nutr. 2014; 111(8):1507-19.
89. Itoh H, Sashihara T, Hosono A, Kaminogawa S, Uchida M. Lactobacillus gasseri OLL2809 inhibits development of ectopic endometrial cell in peritoneal cavity via activation of NK cells in a murine endometriosis model. Cytotechnology. 2011; 63:205-10.
90. Norfuad FA, Mokhtar MH, Nur Azurah AG. Beneficial effects of probiotics on benign gynaecological disorders: a review. Nutrients. 2023; 15(12):2733.
91. Lewis FM, Bernstein KT, Aral SO. Vaginal microbiome and its relationship to behavior, sexual health, and sexually transmitted diseases. Obstet Gynecol. 2017; 129(4):643-54.
92. Plummer EL, Vodstrcil LA, Fairley CK, Tabrizi SN, Garland SM, Law MG, et al. Sexual practices have a significant impact on the vaginal microbiota of women who have sex with women. Sci Rep. 2019; 9(1):19749.
93. Mitchell CM, Fredricks DN, Winer RL, Koutsky L. Effect of sexual debut on vaginal microbiota in a cohort of young women. Obstet Gynecol. 2012; 120(6):1306-13.
94. Wessels JM, Lajoie J, Vitali D, Omollo K, Kimani J, Oyugi J, et al. Association of high-risk sexual behaviour with diversity of the vaginal microbiota and abundance of Lactobacillus. PLoS One. 2017; 12(11):e0187612.
95. Nijris ON, Hassen FG, Abbas Al-douri WK. Contraceptives impact on the bacterial vaginal flora and its relationship to frequent vaginal infection. Eurasia J Biosci. 2020; 14(1).
96. Balle C, Happel AU, Heffron R, Jaspan HB. Contraceptive effects on the cervicovaginal

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]

microbiome: Recent evidence including randomized trials. Am J Reprod Immunol. 2023; 90(5):e13785.
97. Achilles SL, Austin MN, Meyn LA, Mhlanga F, Chirenje ZM, Hillier SL. Impact of contraceptive initiation on vaginal microbiota. Am J Obstet Gynecol. 2018; 218(6):622. e1-22. e10.
98. Abdul-Aziz M, Mahdy MA, Abdul-Ghani R, Alhilali NA, Al-Mujahed LK, Alabsi SA, et al. Bacterial vaginosis, vulvovaginal candidiasis and trichomonal vaginitis among reproductive-aged women seeking primary healthcare in Sana'a city, Yemen. BMC Infect Dis. 2019; 19:1-10.
99. Joesoef M, Karundeng A, Runtupalit C, Moran J, Lewis J, Ryan C. High rate of bacterial vaginosis among women with intrauterine devices in Manado, Indonesia. Contraception. 2001; 64(3):169-72.
100. Zierden HC, DeLong K, Zulfiqar F, Ortiz JO, Laney V, Bensouda S, et al. Cervicovaginal mucus barrier properties during pregnancy are impacted by the vaginal microbiome. Front Cell Infect Microbiol. 2023; 13:1015625.
101. Takano T, Kudo H, Eguchi S, Matsumoto A, Oka K, Yamasaki Y, et al. Inhibitory effects of vaginal Lactobacilli on C andida albicans growth, hyphal formation, biofilm development, and epithelial cell adhesion. Front Cell Infect Microbiol. 2023; 13:1113401.
102. Rahman N, Mian MF, Nazli A, Kaushic C. Human vaginal microbiota colonization is regulated by female sex hormones in a mouse model. Front Cell Infect Microbiol. 2023; 13:1307451.
103. Mao X, Chen H, Peng X, Zhao X, Yu Z, Xu D. Dysbiosis of vaginal and cervical microbiome is associated with uterine fibroids. Front Cell Infect Microbiol. 2023; 13:1196823.

[Downloaded from crms.mubabol.ac.ir on 2026-10-17]

[DOI: 10.22088/crms.9.1.98]