Lay Summary

Manipulating the microbiome has recently entered popular culture, with various diets thought to aid the microbes that live within us. These microbes live within different locations of our body and accordingly help us digest food, modulate our immune system, and influence reproductive health. The role of the microbes living in and influencing the female reproductive tract remains understudied despite known roles in common conditions such as vulvovaginal candidiasis (affecting 75% of females in their lifetime), bacterial vaginosis (25% of females in their lifetime), cervical HPV infection (80% of females in their lifetime), endometriosis (6-10% of females of reproductive age), and polycystic ovary syndrome (10-12% of females of reproductive age).

Here, we review four different approaches used to manipulate the female reproductive tract and gastrointestinal system microbiomes: microbiota transplants, probiotics, prebiotics and dietary interventions, and the use of engineered microbial strains. In doing so, we aim to stimulate discussion on new ways to understand and treat female reproductive health conditions.
Harnessing the Power Within: Engineering the Microbiome for Enhanced Gynecologic Health

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Abstract

Although numerous studies have demonstrated the impact of microbiome manipulation on human health, research on the microbiome’s influence on female health remains relatively limited despite substantial disease burden. In light of this, we present a selected review of clinical trials and preclinical studies targeting both the vaginal and gut microbiome for the prevention or treatment of various gynecologic conditions. Specifically, we explore studies that leverage microbiota transplants, probiotics, prebiotics, diet modifications, and engineered microbial strains. A healthy vaginal microbiome for females of reproductive age consists of lactic acid-producing bacteria predominantly of the *Lactobacillus* genus, which serves as a protective barrier against pathogens and maintains a balanced ecosystem. The gut microbiota's production of short-chain fatty acids, metabolism of primary bile acids, and modulation of sex steroid levels have significant implications for the interplay between host and microbes throughout the body, ultimately impacting reproductive health. By harnessing interventions that modulate both the vaginal and gut microbiomes, it becomes possible to not only maintain homeostasis but also mitigate pathological conditions. While the field is still working towards making broad clinical recommendations, the current studies demonstrate that manipulating the microbiome holds great potential for addressing diverse gynecologic conditions.

Lay Summary

Manipulating the microbiome has recently entered popular culture, with various diets thought to aid the microbes that live within us. These microbes live within different locations of our body and accordingly help us digest food, modulate our immune system, and influence reproductive health. The role of the microbes living in and influencing the female reproductive tract remains understudied despite known roles in common conditions such as vulvovaginal candidiasis (affecting 75% of females in their lifetime), bacterial vaginosis (25% of females in their lifetime), cervical HPV infection (80% of females in their lifetime), endometriosis (6-10% of females of reproductive age), and polycystic ovary syndrome (10-12% of females of reproductive age). Here, we review four different approaches used to manipulate the...
female reproductive tract and gastrointestinal system microbiomes: microbiota transplants, probiotics, prebiotics and dietary interventions, and the use of engineered microbial strains. In doing so, we aim to stimulate discussion on new ways to understand and treat female reproductive health conditions.

Introduction

The human microbiome comprises trillions of bacteria, archaea, fungi, protists, and viruses that play crucial roles in the maintenance of health and progression of disease. There is considerable variation in the microbial composition associated with different body sites (The Human Microbiome Project Consortium, 2012; Costello et al., 2009) and many of these associations, particularly in the vagina, are linked to various gynecologic diseases. An individual's response to a particular type of therapy can be influenced by variation in the composition and functional potential of the microbiome both between people (McDonald et al., 2018) and across body sites (Walsh et al., 2018). This points to the possibility of developing optimized individual treatment plans through manipulation of the microbial community in a given body site.

Transformation of the microbiome from disease-promoting to health-promoting is a promising avenue to combat diverse human ailments. For example, the most well-documented clinically beneficial microbial manipulation approach is fecal microbiota transplantation (FMT) as a therapy for recurrent *Clostridioides difficile* infection (Rohlke and Stollman, 2012), in which healthy colonic flora is restored and can outcompete the pathogenic *C. difficile*. Taking it a step further, the live bacterial communities from human fecal matter of qualified healthy individuals were isolated and approved by the U.S. Food and Drug Administration (FDA) for oral use in April 2023, making this the second FDA approved microbiome-based therapeutic (FDA Approves First Orally Administered Fecal Microbiota Product for the Prevention of Recurrence of *Clostridioides difficile* Infection, 2023). In addition to FMT, other more accessible strategies to change the microbiome are currently under investigation, such as probiotic treatments (S.-K. Kim et al., 2019) and dietary interventions (Zeevi et al., 2015), which can alleviate
cardiometabolic, immune, and even neurological disorders (Gilbert et al., 2018). Another approach currently being developed is the use of engineered bacteria that produce therapeutic compounds within the body (Charbonneau et al., 2020).

Despite such remarkable progress, our understanding of microbiome dynamics in female dominant disorders or reproductive health remain critically understudied (Dothard, Allard and Gilbert, 2023a). This disparity likely stems from the disproportionate allocation of funding towards disorders more prevalent in males and neglect of conditions predominant in females despite their substantial disease burden (Mirin, 2021). Our review highlights the significant knowledge gap in the role of the vaginal and gut microbiome in the pathogenesis of gynecological conditions.

The vaginal and gut microbiota maintain discrete microbial ecologies based on abiotic and biotic factors such as pH, oxygen, nutrient availability, differences in epithelial cell structures, and immune surveillance, which, when disturbed, can result in organ-specific disease. The vaginal microbiota’s community composition has been classified into five unique community state types (CSTs), several of which are dominated by lactic acid-producing bacteria belonging to the Lactobacillus genus (Ravel et al., 2011; Kwon and Lee, 2022). These bacteria help create an acidic environment, maintaining the vaginal pH between 3.5 and 4.5, a key protective barrier against pathogenic microorganisms. This limits bacterial overgrowth linked with bacterial vaginosis (BV), and prevents pathogen colonization linked to cervical cancer (Lewis, Bernstein and Aral, 2017). However, CST-IV and subsequent CST subgroupings are dominated by anaerobic and microaerophilic bacteria, generally thought to comprise a non-optimal microbiome. Notably, many of the seminal studies delineating these groupings are not racially representative, and moving forward it is critical to be racially equitable when conducting such studies to avoid clinical disadvantages (Ravel et al., 2011).
While the vaginal microbiome is becoming increasingly characterized, the microbiota associated with the upper female reproductive tract, including the uterine cavity, fallopian tubes and ovaries, remains severely understudied. However, recent studies have indicated that the uterus is not sterile, and instead may be colonized by a low abundance of microorganisms (Moreno et al., 2016; Chen et al., 2017). This highlights the need for rigorous, validated techniques for transvaginal characterization of the upper reproductive tract microbiome to remove vaginal-microbiome contamination (Kennedy et al., 2023).

While the gut microbiome is a distinct microbiome site from the female reproductive tract, it displays sexual dimorphism (Sisk-Hackworth, Kelley and Thackray, 2023). When studied through this lens, it is referred to as the “microgenderome” (Flak, Neves and Blumberg, 2013) or, more accurately, the “microsexome” (Mulak, Larauche and Taché, 2022). The female gut microbiome is associated with sex differences in immunity and disease prevalence, and female reproductive physiology (Yoon and Kim, 2021). For example, glucuronide-conjugated estrogen and phytoestrogen can be deconjugated by bacterial β-glucuronidase, which may influence circulating levels of these sex hormones that disrupt steroid receptor-mediated physiological processes distal to the gut, with impacts on reproductive health and menopause (Baker, Al-Nakkash and Herbst-Kralovetz, 2017; Dothard, Allard and Gilbert, 2023b). Thus, sex differences in the microbiome are crucial to incorporate into studies of human health and disease.

This literature review focuses on pre-clinical studies and clinical trials targeting the vaginal and gut microbiome for the prevention or treatment of prevalent gynecologic conditions. Carefully selected for their potential impact, these studies demonstrate the potential of manipulating the microbiome for enhanced health, encouraging further exploration and research in this promising field. The studies we have chosen are illustrative rather than comprehensive and focus on 4 main methods of engineering the microbiome for gynecological health: transplant, probiotics, prebiotics and diet, and synthetically designed microbial strains. Finally, we strive to use gender-inclusive language and our use of the word
'female' refers to individuals assigned female sex at birth. We also explore the role of the vaginal microbiome in gender-diverse individuals, specifically transgender men and transgender women.

**MICROBIOME-LINKED GYNECOLOGICAL DISEASES DISCUSSED**

Before delving into methods of microbial manipulation, it is critical to understand the diseases for which they are currently under investigation. Here, we briefly review these diseases and their links to the microbiome.

**Bacterial Vaginosis (BV)**

One of the most common etiologies of vaginal symptoms is bacterial vaginosis (BV). BV impacts roughly a quarter of females globally, with some variation by region and ethnic background (Peebles *et al.*, 2019). It is a non-STI biofilm-based disease arising from vaginal dysbiosis classically associated with fewer Lactobacilli present in the vagina and an increase in anaerobes, such as *Gardnerella vaginalis*, *Fannyhessea* (previously *Atopobium* vaginae), and *Mycoplasma genitalium* (a few of the “BV-associated bacteria”). Lactic acid producing Lactobacilli (*Lactobacillus acidophilus*, *Lactobacillus crispatus*, *Lactobacillus jensenii*, and *Lactobacillus gasseri*) are dominant in the non-BV state and out-compete anaerobic bacterial adherence to the vaginal epithelium, thus preventing BV (Pramanick *et al.*, 2019; Yuanhui He *et al.*, 2020). Additionally, BV is linked with an increased risk of contracting other STIs, including HIV (Brotman, 2011; Abbai, Reddy and Ramjee, 2016; Armstrong *et al.*, 2022). Understanding BV-associated microbial disruption in humans is challenging due to the differences in the vaginal microbiome profile in individuals of different ethnic groups, with diet and lifestyle implicated in these differences (Ravel *et al.*, 2011). The current standard of care is antibiotics against anaerobic bacteria: either oral or intravaginal metronidazole, or intravaginal clindamycin is prescribed. There have been no new antibiotic treatments for BV in the past 50 years and with post-
treatment relapse rates reported up to 80%, it is imperative to consider novel therapeutic approaches (Abbe and Mitchell, 2023).

**Vulvovaginal Candidiasis (VVC)**

Vulvovaginal candidiasis (VVC, “yeast infection”) is commonly caused by overgrowth of the opportunistic yeast *Candida albicans*. Approximately 75% of females experience at least one yeast infection in their lifetime (Vaginal yeast infection (thrush): Overview, 2019), with 8% developing recurrent yeast infections after treatment. Growing resistance to treatment drugs is on the rise (Oerlemans et al., 2020; Jeanmonod and Jeanmonod, 2023). The current standard of care uses “-azole” drugs, which impairs yeast cell wall integrity. However, recurrence after administration of oral antibiotics for a different primary concern is common and may be related to an antibiotic-induced reduction of beneficial gut microbes, thus producing a non-optimal vaginal microbiome (Falagas, 2006). Lactobacilli are thought to modulate the entire vaginal microbial community, and the cell free supernatant of *L. crispatus*, *L. jensenii*, and *L. gasseri* significantly reduce *C. albicans* growth in vitro (Wang et al., 2017). One proposed mechanism is competition for adherence to the vaginal epithelium (Boris et al., 1998; Oerlemans et al., 2020). Given the intricate relationship between VVC and the host microbiome, manipulating the microbiome to prevent and treat VVC is a logical next step.

**Human Papillomavirus (HPV)**

Another common reproductive disease associated with the microbiome is infection with Human Papillomavirus (HPV), which is recognized as the causative form of cervical cancer. While certain forms of HPV are carcinogenic, HPV can be cleared spontaneously by 90% of females and the microbial dynamics leading to HPV clearance are a topic of active investigation (Veldhuijzen et al., 2010). Non-optimal vaginal microbiomes are associated with increased risk of HPV infection (Lehtoranta et al., 2022), positing that probiotic interventions could help prevent HPV infection and persistence. The BV-
associated bacteria *Gardnerella* and *Fannyhessea*, are commonly associated with HPV infection (Wei et al., 2021; Zhongzhou Yang et al., 2022). In fact, Lactobacillus-depleted microbiomes or those with predominantly BV-associated bacteria have higher rates of HPV persistence (Di Paola et al., 2017).

Conversely, certain microbes are associated with quicker HPV clearance; *L. gasseri*-dominated microbiomes seem to have faster clearance rates than microbiomes with low lactobacilli and high *Fannyhessea* (Brotman et al., 2014). It is notable that *Lactobacillus iners* is a common member of the vaginal microbiome in individuals regardless of HPV carrier status. However, *L. iners* dominated microbiomes (with decreased *L. crispatus* and *L. gasseri*) appear to have poorer outcomes and are associated with VVC (Verstraelen et al., 2009; Audirac-Chalifour et al., 2016; Jang et al., 2019; Sabbatini et al., 2021). Nonetheless, there appears to be a “chicken and egg” paradox between HPV and the vaginal microbiome residents, with one appearing to shape the other (Lebeau et al., 2022).

**Endometriosis**

Endometriosis is characterized by the translocation and growth of endometrial tissue outside of the uterus, causing a chronic inflammatory response. This debilitating condition affects approximately 6-10% of females of reproductive age (Saunders and Horne, 2021; Stephens et al., 2022). Endometriosis is a common cause of chronic pelvic pain, can cause infertility and dysmenorrhea, and is a risk factor for ovarian cancer (Kok et al., 2015). However, it is not easily diagnosed as surgical exploration is the gold standard. There is currently no known cure for endometriosis, and treatment aims to control symptoms. Current treatments include surgical removal of lesions and hormone suppressive therapy (Saunders and Horne, 2021; Stephens et al., 2022). There is a large unmet need for robust therapeutics and non-invasive biomarkers for diagnosis. Endometriosis pathogenesis is associated with compositional changes in the microbiota of both the reproductive tract and the gut (Khan et al., 2014, 2016; Chen et al., 2017; Yuan et al., 2018; Akiyama et al., 2019; Ata et al., 2019; Wessels et al., 2021).

For example, 64% of a cohort of 155 participants with endometriosis had *Fusobacterium* in the endometrium, while only 7% of participants without endometriosis were *Fusobacterium* positive.
Additionally, microbial metabolites such as short chain fatty acids are becoming increasingly implicated in the progression of endometriosis (Le et al., 2021; Chadchan et al., 2023). However, many of these studies are quite recent and do not explore the microbial changes after surgical or hormonal treatment. While these initial studies are quite promising, more work is needed in understanding the endometriosis-associated microbiome pre and post treatment.

**Polycystic Ovary Syndrome (PCOS)**

Polycystic ovary syndrome (PCOS) is a complex endocrine disease affecting roughly 6-10% of individuals with ovaries, primarily during reproductive years (Bozdag et al., 2016). It is diagnosed using the Rotterdam criteria, requiring 2 out of the following 3 features: clinical and/or biochemical hyperandrogenism, oligo- or anovulation, and polycystic ovarian morphology ('Revised 2003 consensus on diagnostic criteria and long-term health risks related to polycystic ovary syndrome', 2004). PCOS significantly affects physical and emotional well-being, resulting in infertility, menstrual irregularities, acne, excessive male-pattern hair growth, and an increased risk of anxiety and depression. Over 80% of individuals with PCOS also have metabolic dysfunction including insulin resistance (IR) with or without obesity, which can lead to an increased risk of type 2 diabetes, gestational diabetes, cardiovascular disease, and non-alcoholic fatty liver disease (Sanchez-Garrido and Tena-Sempere, 2020). While a connection exists between higher body mass index (BMI) and PCOS, it's not a direct cause-and-effect relationship. Elevated BMI, particularly in cases of obesity, can contribute to IR. This, in turn, disrupts hormone levels, potentially worsening PCOS symptoms. Notably, not all women with PCOS exhibit a high BMI, and conversely, not all women with a high BMI develop PCOS (Sam, 2007).

While the etiology of PCOS is unclear, substantial evidence demonstrating the importance of the gut microbiome in shaping glucose homeostasis and driving metabolic disorders has led to the hypothesis that alterations in the microbiome are also involved in the pathology of PCOS (Giampaolino et al., 2021; Rizk and Thackray, 2021). While there is inconsistency in the specific gut bacteria reported to be altered in PCOS, a recent meta-analysis of 17 studies showed that there is a consistent decrease in
alpha diversity (Sola-Leyva et al., 2023), indicating that reduced microbial biodiversity may be another hallmark of PCOS. Furthermore, recent studies are beginning to consider the effect of hyperandrogenism on the vaginal microbiome, where significant differences are observed in vaginal bacteria between individuals with and without PCOS (Hong et al., 2020). However, similar to HPV, PCOS also presents a “chicken and egg” paradox, with the interplay between host biology and disease shaping one another.

**Human Immunodeficiency Virus (HIV)**

HIV affects an estimated 39.0 million people globally, with females comprising 53% of those living with the virus (Global HIV & AIDS statistics — Fact sheet, 2023). HIV is primarily transmitted through unprotected sexual intercourse, sharing needles, and from birthing parent to child during childbirth or breastfeeding. Untreated HIV can progress to acquired immunodeficiency syndrome (AIDS), in which the immune system becomes severely compromised, leading to increased susceptibility to opportunistic infections and certain cancers. The virus can be present in vaginal and cervical fluids, as well as menstrual blood. A disrupted vaginal microbiome, such as the one found in BV, can increase inflammation and create an environment more conducive to viral transmission, highlighting the potential for vaginal microbiome optimization to reduce HIV transmission (Armstrong, Kaul and Cohen, 2023). Despite advances in effective antiretroviral therapy (ART) and pre-exposure prophylaxis (PrEP), HIV remains a major worldwide health concern due, in part, to the barriers that exist to testing and treatment access in many low- and middle-income countries.

**MICROBIOTA TRANSPLANTS**

Microbiota transplants transfer microbes from a carefully screened healthy phenotype donor into a like-body site of a recipient with a diseased phenotype. Microbiota transplants can be used both as a beneficial therapeutic and an experimental tool for exploring pathology in animal models. Preclinical animal experiments and clinical trials using both FMTs and vaginal microbiota transplant trials (VMTs)
show promising results in female reproductive health. Regulation of microbiota transplants by the FDA is a major consideration due to the risk of infection as a side effect of transplantation, especially in immunocompromised patients. Microbiota screenings for opportunistic pathogens, infectious diseases, and multi-drug-resistant organisms can support microbiota transplant safety and efficacy (Carlson, 2020; Yockey et al., 2022) for both autologous and nonautologous donors. However, this introduces historical barriers to microbiota transplantation that may hinder access to patients, specifically due to the sourcing of screened donor material, logistic challenges of delivering the resulting fresh treatment preparations, and expenses associated with pathogen screening (Panchal et al., 2018; K. O. Kim et al., 2019).

Fecal Microbiota Transplant (FMT)

FMTs entail transfer of fecal microbes from a healthy donor to a recipient with a non-optimal microbiome. Multiple studies have demonstrated the therapeutic potential of FMTs in PCOS (Guo et al., 2016a; Zhandong Yang et al., 2022). For instance, letrozole-induced rat models of PCOS show improvement in estrous cyclicity after FMT from healthy rats or treatment with a probiotic containing Lactobacillus (Guo et al., 2016a; Zhandong Yang et al., 2022). Moreover, these results also implicate microbial disruption as a potential driver in PCOS pathogenesis. While the mechanism of action remains unclear, gut microbiome manipulation using FMT has led to decreased androgen levels and normalized ovarian morphology, further highlighting the influence of the gut microbiome on the female reproductive tract. Clinical studies will help determine whether FMT is a viable treatment option for patients with PCOS. Of note, previous studies demonstrate that a single administration of FMT in chronic metabolic conditions such as obesity and diabetes do not lead to long-term improvements in outcomes (Vrieze et al., 2012; Kootte et al., 2017). Hence, more frequent or persistent treatment may be necessary to see beneficial results in chronic metabolic conditions such as PCOS (Baunwall et al., 2020).
In addition to the therapeutic application of healthy FMT, investigators can use the transplantation of disease-associated FMT as a tool to provide deeper understanding of the underlying pathology of various gynecological diseases. For example, transplantation of disease-associated microbiota can trigger pathology including PCOS-like phenotypes in rodents (Qi et al., 2020; Han et al., 2021; Zhandong Yang et al., 2022), ovarian tumor development in mice (Wang et al., 2022), and endometriosis disease progression in mice (Chadchan et al., 2023). Such findings support the idea that the gut microbiome contributes to the progression or prevention of gynecological diseases.

Future studies can also focus on the potential for autologous FMT (aFMT), whereby a patient is both the donor and recipient (Suez et al., 2018). Autologous FMT consists of banking the host’s microbiome during a healthy state and later transplanting it to the same host when diseased, thus potentially improving long-term sustainability. If aFMT proves to be a successful intervention for gynecological diseases, it would require either better predictors of who will develop disease or more accessible stool banking opportunities. Given that FMT may work for a number of medical ailments, aFMT may have broad appeal.

**Vaginal Microbiota Transplant (VMT)**

The success of FMTs has laid the groundwork for transplantation of other microbiota sites, such as the vagina. Vaginal microbiota transplants (VMTs) have also shown considerable results in improving certain gynecological outcomes. VMT has been primarily investigated in BV, with the seminal study following five patients treated with VMT one week post intravaginal antibiotic treatment (Lev-Sagie et al., 2019). Four out of five showed marked symptom improvement and a shift to a remediated, *Lactobacillus*-dominated vaginal microbiome.

Additionally, preclinical experiments in animal models with VMT have revealed a more discrete and modular understanding of the causal factors of BV. However, it is important to note that the...
reproductive tract, physiology, timing of estrous, and microbiome of animals is considerably different to that of humans, and also varies between different animal models (Noguchi, Tsukumi and Urano, 2003; Guo et al., 2016a). Despite these caveats, we can still derive mechanistic understanding using these models. For example, one group made a rudimentary mouse model of BV using 8 successive days of vaginal inoculation with high levels of *G. vaginalis* (Yunxia Li et al., 2023). Both VMT and a synthetic bacterial consortia transplantation (comprised of isolates of *L. crispatus*, *Lactobacillus rhamnosus*, *Lactobacillus salivarius*, and *Lactobacillus plantarum* from vaginal discharge of healthy females) rescued the diseased phenotype (Yunxia Li et al., 2023), with the VMT more effective at suppressing inflammation. However, a major caveat of this study is that there are likely considerable differences between the human BV biofilm and this *G. vaginalis*-induced mouse model. Nonetheless, it is an encouraging first step in establishing a model for BV, which may ultimately help pave the way for the first FDA approved VMT.

VMT is also used in animal models to explore gynecological pathology, with one study transferring human vaginal lavage fluids from 10 females with endometriosis, 10 females with BV, and 10 healthy females into the vaginas of healthy rats (J. Wang et al., 2021). This led to significantly higher uterine inflammation in the endometriosis group as compared to the healthy and placebo controls. The endometriosis and BV lavage recipient rats showed epithelial lesions consistent with inflammation in the endometrial tissue. This study is a step towards untangling the complicated microbial dynamics that contribute to BV and endometriosis, as Koch’s postulates appear to be partially fulfilled. Thus, VMTs have potential use both in clinical treatment and in discovery-based research on disease etiology making them one a highly promising method of engineering the female reproductive microbiome.

**PROBIOTICS**

Probiotics, as defined by the International Scientific Association of Probiotics and Prebiotics are "live microorganisms that, when administered in adequate amounts, confer health benefits on the host"
Probiotics, unless claiming to help treat a disease, are not regulated by the FDA and their usage dates back many generations (McFarland, 2015). As we progress in our understanding of potentially beneficial microbes, it is critical to be cognizant of the contexts in which they are efficacious, rather than using the term “probiotics” as a panacea. Using probiotics for reproductive health have led to potentially promising results, which we will explore in depth using 3 conditions: BV, VVC, and HPV infection. We’ve included studies exploring both oral and vaginal probiotic administration. Although the precise route of oral probiotics to the vagina via the gastrointestinal tract is not fully understood, it’s crucial to note that probiotics don’t necessarily need direct access to the vagina to affect the reproductive tract microbiome (Borges, Silva and Teixeira, 2014). Furthermore, the indirect mechanisms through which orally administered probiotics influence the vaginal microbiome remain to be fully elucidated.

In a 2020 study, investigators assessed the efficacy of LACTIN-V, a strain of L. crispatus, in 152 premenopausal participants aged 18-45 years with recurrent BV (Cohen et al., 2020). After metronidazole treatment, LACTIN-V was administered intravaginally daily for 5 days and then twice weekly for 10 weeks. At 12 weeks post treatment, 30% of LACTIN-V users relapsed vs. 45% in the placebo group. However, at 24 weeks the groups had similar relapse rates (12% LACTIN-V vs. 17% placebo) and the amount of vaginal LACTIN-V decreased over time, most likely highlighting the transience of probiotics. Nevertheless, LACTIN-V usage was also associated with decreased inflammatory markers (Armstrong et al., 2022).

The efficacy of probiotics may be dictated by the strain and the dosing regimen. For example, one report showed that the intermittent use of a probiotic with various strains of Lactobacillus and Bifidobacterium for 2 months was useful in treating BV with similar efficacy to oral metronidazole and better than no treatment (Van De Wijgert et al., 2020). They reported no significant therapeutic effect of an intermittent 2-month use of a probiotic with L. rhamnosus. In contrast, Reid et al. (2003),
reported that daily use of oral *L. rhamnosus* GR-1 and *Lactobacillus fermentum* RC-14 for 60 days showed significant improvements in the microbial composition of patients with asymptomatic BV (Reid *et al.*, 2003). Thus, perhaps adherence to daily vs. intermittent regimen timing may be a driving factor in the usefulness of probiotics.

The importance of when probiotics are administered is further highlighted by a study reporting lower relapse rates when administering probiotics directly after menstruation. Larsson *et al.* (2008) administered daily clindamycin treatment for 7 days, followed directly by vaginal administration of *L. gasseri* and *L. rhamnosus* for 10 day blocks over the course of 4 months (Larsson *et al.*, 2008). At the end of the study (6 months), 35% of participants on probiotics relapsed compared to 54% of participants on a placebo pill. Furthermore, the probiotic treatment group relapsed significantly later than the placebo group. Menstruation is important to consider because there appears to be a higher concentration of non-*Lactobacillus* species during menstruation, when menstrual blood also raises the vaginal pH, which may contribute to compositional instability (Eschenbach *et al.*, 2000). Further research addressing timing of treatment in relation to the menstrual cycle is needed.

Similar to BV, the idea of recolonizing the vagina for protection against vulvovaginal candidiasis (VVC, “yeast infection”) has been discussed for generations (Wood *et al.*, 1985). Clinical VVC trials using Lactobacilli have had varying efficacy and there is more research needed before making strong clinical recommendations. Oerlemans *et al.* conducted a trial with a vaginal gel comprising *L. rhamnosus*, *L. plantarum*, and *Lactobacillus pentosus* used once daily for 10 days (Oerlemans *et al.*, 2020). There was little benefit compared to fluconazole usage, with 55% of participants not responding to the gel alone and requiring fluconazole therapy. However, participants who responded to the probiotic gel had similar fungal burden as those on antifungal fluconazole therapy at 4 weeks. Similarly, in a separate study, investigators observed yeast depletion at 4 weeks using an oral capsule of *L. rhamnosus* GR-1 and *L. fermentum* RC-14 (Reid *et al.*, 2003). However, the gel trial found that fluconazole reduced the number of Lactobacilli, which are thought to be beneficial in
protecting against VVC, suggesting that further studies of dual therapy with fluconazole and Lactobacilli may be warranted for a more effective treatment.

In fact, others have investigated such dual therapy. A randomized control trial with fluconazole usage +/- probiotic capsules containing *L. rhamnosus* GR-1 and *L. reuteri* RC-14 (Martinez *et al.*, 2009) demonstrated potential clinical efficacy. At 4 weeks, participants taking probiotics and fluconazole had significantly less discharge compared to the placebo pill and fluconazole group. Those on probiotics had significantly less culturable yeast. These findings suggest a beneficial role for Lactobacilli in dual therapy, while also showcasing the necessity to standardize endpoint measurement techniques (Zhou *et al.*, 2009; Macklaim *et al.*, 2015).

Finally, while most literature surrounding probiotics discusses bacteria, it is important to be cognizant of other potentially beneficial microbes such as fungi. One study in particular using a mouse model of VVC showed promising results using both live and inactivated *Saccharomyces cerevisiae*. By day 4 of probiotic administration, there were comparable results to fluconazole usage. In particular, the live yeast aided in accelerated pathogen clearance (Pericolini *et al.*, 2017).

The efficacy of probiotics has also been investigated in cervical infection with high risk HPV, the primary cause of cervical cancer (Ou *et al.*, 2019). Studies of probiotics for prevention or treatment of cervical HPV infection have had variable success. A 2013 study found that people with precancerous cervical lesions were twice as likely to clear any cytological abnormalities when drinking Yakult, which contains *Lactobacillus casei* Shirotta, for 60 days (Verhoeven *et al.*, 2013). In contrast, other investigators reported no difference in high risk HPV clearance in patients taking a daily oral pill with *L. rhamnosus* GR-1 and *L. reuteri* RC-14 (Ou *et al.*, 2019). In addition to the studies testing different strains, Yakult has roughly 20 billion CFUs whereas the pill with *L. rhamnosus* GR-1 and *L. reuteri*...
RC-14 5.4 billion CFUs (YAKULT Product Information, no date). Thus, the dosage and/or species may lead to varying results.

In a study following co-infection between cervical HPV and yeast or BV, investigators reported that taking a vaginal *L. rhamnosus* supplement for 6 months along with initial treatment for the yeast or BV was associated with a twice higher chance of clearing the HPV as compared to those taking the probiotic for 3 months. Unfortunately, this study did not have a control group without probiotics, which would have been helpful in examining the impact of medication-driven management of dysbiosis (Palma *et al.*, 2018). The tablets used in that study had 10,000 CFU/tablet rather than the billions found in the previous 2 studies, ultimately leading to a total dose which may be permissible due to direct vaginal administration.

Probiotics, particularly *Lactobacillus* and *Bifidobacterium* strains, show promise in alleviating symptoms of PCOS in both women and several different mouse models (Guo *et al.*, 2016b; F. Zhang *et al.*, 2019; J. Zhang *et al.*, 2019; Yufeng He *et al.*, 2020). Another study suggested that co-supplementation of probiotics with vitamin D improves mental health, testosterone levels, and hirsutism in women with PCOS (Ostadmohammadi *et al.*, 2019). Probiotics alone and synbiotics (co-supplementation of probiotics with prebiotics including resistant dextrin and inulin), improved some clinical markers of PCOS such as free androgen index, and sex hormone-binding globulin, but had no effect on others, including testosterone and hirsutism (Shamasbi, Ghanbari-Homayi and Mirghafourvand, 2020). Meta-analyses also indicate positive effects on certain markers of insulin sensitivity and lipid profiles, however no significant changes on other metrics of glycemia and bodyweight (Liao *et al.*, 2018). Probiotics are a promising avenue of clinical symptom management for PCOS, however, further research is needed to fully optimize these interventions.
There are various other important health conditions that have shown to be responsive to probiotics, such as urinary tract infections (UTI), PCOS, ovarian cancer, and Group B Streptococcus (the leading cause of neonatal bacterial meningitis), which we urge the reader to further explore (Hanson et al., 2022; Yuling Li et al., 2023). Notably, direct manipulation of the vaginal microbiome using L. crispatus has been shown to improve UTI outcomes, pointing to potential microbial cross-talk within the urogenital track (Hanson et al., 2022). Thus, while still an active area of research, probiotics provide a potentially exciting and accessible avenue to engineer the vaginal microbiome. In particular, dose, strain, and timing of administration seem to be key effectors.

**DIET AND PREBIOTICS:**

Given the association between poor diet and a non-optimal microbiome (Martinez et al., 2021; Makarova and Zyriax, 2023), there may be significant therapeutic utility in using diet to alter microbial composition within and beyond the gut. High fiber foods, particularly those rich in soluble fiber, are broken down by enteric bacteria through a process called fermentation, producing short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate. SCFAs have several beneficial effects on the body, including providing a source of energy for the cells lining the colon, promoting a healthy gut environment, and potentially reducing inflammation (Caetano and Castelucci, 2022; Duan et al., 2023). The fermentation of fiber in the gut is governed by several factors including microbial composition, pH, fiber type, and time. A diverse array of gut bacteria enhances the range of fibers that can be fermented, enteric bacteria have optimal pH ranges for fermentation, and the longer the fiber remains in the gut, the more opportunity there is for bacteria to ferment it (Cronin et al., 2021). The metabolic byproducts or bioactive compounds produced by probiotic microorganisms during their fermentation process are known as postbiotics, and can be taken in supplement form. Furthermore, introduction of prebiotics to the diet, which can select for specific gut microbial species can help facilitate a health promoting gut microbial metabolism, for example, fiber supplements can promote the synthesis of SCFAs (Deehan et al., 2020). Prebiotics, such as fructooligosaccharides (FOS), galactooligosaccharides (GOS), inulin and...
lactulose, have shown improved metabolic markers and immunomodulation potentially by stimulating
the growth of beneficial bacteria like *Bifidobacterium* and *Lactobacillus* (Fernandes *et al.*, 2017; Enam
and Mansell, 2019; Deehan *et al.*, 2020).

In a mouse model of PCOS, a study showed that a 21-day treatment with 0.05 g inulin/100 g body
weight led to a reduction in the number of cystic follicles and corpora lutea, along with improvements in
inflammatory cytokine levels and insulin sensitivity (Xue *et al.*, 2019). These positive effects were
attributed to the increased abundance of *Bacteroides* and *Bifidobacterium* in the gut, with
*Bifidobacterium* showing strong anti-inflammatory properties. These findings highlight the potential role
of inulin in therapy, achieved via gut microbiota modulation. Furthermore, prebiotics can be combined
with probiotics to work synergistically to enhance the health promoting effects on the host. This
combination, known as synbiotics, aims to support the survival and activity of probiotics by providing
them with a favorable environment for growth and colonization. One clinical trial demonstrated that
dietary administration of a synbiotic supplementation of fructooligosaccharides, inulin, and various
*Bifidobacterium* and *Lactobacillus* species significantly reduced testosterone and BMI, both factors
linked to PCOS symptoms. By targeting these factors simultaneously, such interventions hold potential
in alleviating various facets of PCOS, including improving hormonal balance, and enhancing metabolic
function. This approach proved significantly more effective than relying solely on lifestyle and dietary
modification (Chudzicka-Strugala *et al.*, 2021). Nonetheless, further investigation is needed to
understand the specific mechanisms of gut bacteria in PCOS and related metabolic disorders.

Although clinical guidelines do not currently specify a particular diet for optimal PCOS management
(Moran *et al.*, 2020), dietary interventions have potential to mitigate hyperandrogenism, obesity, and
insulin resistance. In a review that pooled data from 20 RCTs involving 1,113 participants, Shang et al.
reported the maximized benefits of Mediterranean and low-carbohydrate diets for optimizing fertility.
outcomes, and calorie restriction for ameliorating hyperandrogenism (Shang et al., 2021). An additional study analyzed 14 individuals with PCOS that received a high-fiber diet composed of whole grains, traditional Chinese medicinal foods, and prebiotics (WTP diet) for twelve weeks (X. Wang et al., 2021). Adherence to the diet resulted in alleviation of PCOS clinical phenotypes such as inflammatory state, lower BMI, and decreased levels of leptin (a brain-gut hormone that dictates satiety) and fasting plasma insulin. However, those on the WTP diet also displayed higher testosterone levels and, after an initial dip at 4 weeks, and higher fasting blood glucose levels. Given these conflicting outcomes, small sample size, and relatively short timeline, further research into the WTP is warranted. Nonetheless, this experiment explored the interesting question of whether fiber intake can mitigate PCOS symptoms. This was also investigated in a case control study that demonstrated an inverse correlation between dietary fiber consumption, obesity, and insulin resistance among individuals with PCOS and BMI-matched controls (Cunha et al., 2019). Additionally, a 3-month intervention of starch resistant to digestion in the small intestine (wheat/corn dextrin; 20 g/day) compared to an insoluble fiber control in people with PCOS demonstrated a significant improvement in testosterone, fasting blood glucose, total cholesterol, LDL-C, HDL-C, triglyceride, and hsCRP (a marker of inflammation) (Gholizadeh Shamasbi et al., 2019). These studies indicate that increased dietary fiber or prebiotics supplements may modulate the gut microbiome and consequently improve symptoms of PCOS. Additional studies are needed to determine which dietary fibers and doses are optimal for treating PCOS either alone or in combination with other therapies.

Prebiotics can also be therapeutically beneficial in endometriosis. Chadchan et al. investigated the role of gut bacteria and SCFAs in promoting or protecting against the growth of endometriosis lesions (Chadchan et al., 2021). SCFAs, as previously mentioned, are byproducts of bacterial fermentation and regulate host metabolism. The study found that feces from mice with endometriosis contained less n-butyrate, one of the most abundant SCFAs, in contrast to those without endometriosis. Treatment with n-butyrate reduced the growth of both mouse endometriotic lesions and human endometriotic lesions in
a preclinical mouse model, acting in part through G-protein-coupled receptors, GPR43 and GPR109A (Chadchan et al., 2021). GPR43 and GPR109A receptor inhibition in an endometrial cell line partially restored cell viability in n-butyrate-treated cells, highlighting potential therapeutic targets.

Certain prebiotics have also been implicated in potentially mitigating BV pathogenesis. One study showed that lactulose promotes the growth of vaginal Lactobacilli in monoculture and in communities cultured from healthy vaginal swabs. Importantly, this promotion did not extend to BV-associated bacteria or C. albicans (Collins et al., 2018).

Overall, diet and prebiotics have emerged as powerful strategies with potential for improving gynecologic health. By promoting a healthy gut microbiome, hormonal balance, and overall well-being, these interventions offer promising, non-invasive avenues for managing conditions such as PCOS, BV and endometriosis. Further research is needed to uncover the intricate connections between diet, gut microbiota, and reproductive health, paving the way for personalized interventions and improved outcomes.

ENGINEERED MICROBIAL STRAINS

Engineered probiotics use bacteria that are genetically designed to express a specific function as an alternative to traditional pharmaceutical treatments. Treatment with genetically modified organisms should be considered drug therapy and not, like traditional probiotics, a dietary supplement. The treatment vesicle is a chassis, a bacterial strain that serves as a platform for genetic modification. The choice of chassis is crucial based on manipulability, safety, and scalability, and most studies have selected chassis that are easy to engineer, food grade, or a predominant species. Recent studies show that there are also some chassis that can be scaled with the use of a prebiotic (Shepherd et al., 2018), or using bacteria derived from the system itself, i.e. native bacteria (Russell et al., 2022) which can implement a more persistent change. The engineered therapeutic functions themselves include, but are
not limited to, the production of small molecules, metabolic enzymes, nano-bodies, toxins, and immunomodulators. These engineered probiotics have been designed to treat a range of diseases, including GI disease, infection, dysmetabolism, rare genetic disorders, and cancer (Ma et al., 2022; Brevi and Zarrinpar, 2023). While studies evaluating individual strains or consortiums of bacteria have been somewhat successful in treating vaginal and reproductive conditions, gene edited probiotics which express deliberate functions are on the horizon for more targeted treatment of these conditions (Vieira-Baptista et al., 2022).

For example, several biotechnology companies and academic groups are developing genetically enhanced probiotics against HIV by inserting potent antiviral genes into bacteria that naturally colonize the vagina. Unlike conventional microbicide delivery systems such as gels and films, once administered, engineered probiotics can serve as a more sustained, self-replicating delivery method for treatment of HIV. The risk of this more sustained treatment method, however, is the persistence of any potentially harmful effects for the patient or the environment, and is as of now a risk of unknown impact.

Researchers engineered *L. jensenii* 1153 to produce the potent HIV entry inhibitor cyanovirin-N (CV-N) using chromosomal integration. Pre-clinical testing in macaques showed consistently high levels of colonization with CV-N expressing *L. jensenii* after vaginal administration, with no significant antibody response, and the strain was easily cleared with topical antibiotic administration. In a repeated low dose challenge model, HIV acquisition was reduced by 63% in macaques, and this engineered bacterium is being explored as a platform to co-express microbicide against HIV and other STIs (Liu et al., 2006; Lagenaur et al., 2011). More work is needed to examine safety and efficacy in humans.

Furthermore, increased activated genital CD4+ T cells (associated with *L. crispatus* deficiency) and elevated levels of high-risk bacteria indicate higher HIV risk, initially discovered in a cohort of South African females (Gosmann et al., 2017). Investigators are leveraging this discovery to develop targeted...
engineered bacteria to locally modulate CD4+ expression in the vaginal microenvironment (Gosmann et al., 2017). *L. acidophilus* ATCC 4356 engineered to display human CD4 on its surface can adsorb HIV-1 particles by binding to its envelope protein and successfully reduce infection in vitro and in a murine model (Wei et al., 2019). *Lactobacillus* has also been modulated to express broadly neutralizing nanobodies (VHH) against HIV, which may be a promising immunization method for females at high risk of HIV-1 transmission (Kalusche et al., 2020).

Engineered strains are also being actively explored as a method to combat *C. albicans*-driven VVC. Investigators engineered a commercial *Saccharomyces boulardii* strain to produce medium-chain fatty acids (MCFAs) with anti-biofilm and anti-hyphal effects *in vivo*. MCFAs also upregulated the expression of virulence-related genes in the strain of *C. albicans*, SC5314. The constitutive production and secretions of MCFAs serve as a proof-of-concept for the potential of probiotic yeast as a therapeutic strategy for *C. albicans* and other opportunistic pathogens in the reproductive tract (Ling et al., 2023).

Finally, the basic science surrounding the role of the gut microbiome in reproductive disease are leading to the development of live bacterial therapeutics. One study showed elevated *B. vulgatus* in females with PCOS and in murine models was linked to a bile acid - IL22 axis as a potential mediator of PCOS pathology. This suggests that genetically engineering a bile acid-modifying or IL22-expressing engineered bacteria could be effective for the treatment of PCOS (Qi et al., 2019).

The development of live therapeutics is a rapidly growing field, with an increasing number of scientists recognizing the need for the fusion of synthetic biology, clinical medicine, and basic science. As the field grows, it will hopefully closely integrate these three areas to provide optimal and personalized therapies.

**CONCLUSIONS AND FUTURE DIRECTIONS**
Manipulating the microbiome to enhance gynecologic health has vast, untapped potential. It opens up exciting possibilities for restoring microbial equilibrium, and preventing microbiome-associated conditions. Although more work is needed for clinical care recommendations, these studies highlight the potential impact of such strategies in preventing and treating major contributors to female infertility and gynecological maladies, such as endometriosis, PCOS, and BV. One exciting avenue includes leveraging the microbiome to improve pharmaceutical efficacy. Notably, the composition of the vaginal microbiome has been found to impact the effectiveness of tenofovir, an HIV treatment drug, in females (Klatt *et al.*, 2017). Furthermore, the advancements and strains of interest mentioned in the probiotics section demonstrate feasibility for further development of engineered probiotics for therapeutic purposes. While many live bacterial therapeutics are still under development and have been studied *in vivo* or in murine models, their effectiveness in preclinical or early clinical trials is yet to be established. An innovative technology known as the vagina-on-a-chip has recently been developed to replicate the vaginal epithelial microenvironment and its interactions with the microbiome, enabling preclinical validation. This microfluidic culture model of vaginal mucosa can be used to assess colonization, characterize interactions between engineered probiotics and host vaginal epithelium, measure host innate immune response, and test the safety and efficacy of live bacterial therapeutics under development (Mahajan *et al.*, 2022).

Despite these advances, progress in this area has been hindered by historical research gaps and gender disparities (Mirin, 2021). Until the NIH Revitalization Act of 1993, clinical trials primarily focused on male subjects and often excluded females. Furthermore, the prevailing gender disparities extend beyond clinical trials because venture capitalists, who are predominantly men, have limited understanding of the market for female technologies (Mann, 2022). The historical deficiency in funding and underrepresentation of females in clinical trials has significantly impacted our comprehension of female-dominant conditions. This, coupled with systemic gender biases in medical education and training, has led to many women feeling unheard in healthcare settings, with their pain...
often disregarded and treatment options primarily focused on symptom management rather than curative approaches (Ferrero, Evangelisti and Barra, 2018; Hoeger, Dokras and Piltonen, 2021).

Furthermore, few studies have interrogated the microbial community composition within the genital tracts of gender-diverse individuals, representing a key knowledge gap. A complete review of this literature is described by (Krakowsky et al., 2022)). In brief, transgender individuals experiencing gender dysphoria as a result of gender incongruence can elect to undergo gender-affirming care, which alleviates gender dysphoria through increasing congruence of external and internal gender identity. This can be achieved through elective surgeries such as phalloplasties, neovaginoplasties, and/or orchiectomies. Transgender women who have undergone neovaginoplasty have been observed to develop a neovaginal microbiome with an abundance of *Lactobacillus* species present (Petricevic et al., 2014). Gender-affirming care may also include hormone replacement therapy with testosterone or estradiol. As both of these sex hormones indirectly influence the vaginal microbiome through changes in epithelial integrity (Baldassarre, Giannone, et al., 2013; Baldassarre, Perrone, et al., 2013) and gut microbes influence the levels of circulating sex hormones through microbial estrogen-deconjugating genes (Baker, Al-Nakkash and Herbst-Kralovetz, 2017) and microbial-testosterone interactions (Li et al., 2022), understanding the impacts of gender affirming therapy on vaginal and neovaginal microbiomes of transgender individuals is critical to accurately providing healthcare. The vaginal microbiome of transgender men undergoing testosterone is understudied— a single 2019 study reports non-*Lactobacillus* dominance and high microbial diversity in the transman vaginal environment (Winston McPherson et al., 2019) More work must be done in this area using studies with larger sample sizes to provide equitable microbial healthcare in patients across the gender spectrum.

Another knowledge gap is the understanding of temporal dynamics within the female gut and vaginal microbiome. There are clear circadian dynamics within host-microbe relationships, however, much of
the research investigating these diurnal rhythms focus on only male gut microbiota (Frazier and Leone, 2022). There is some consensus that vaginal microbiome composition fluctuates with menstrual cycle phase, however, further evidence is needed regarding the links to gut microbiota with cycle phase, and the role of hormonally-based contraception (Song et al., 2020; Krog et al., 2022). Genetically engineered mice that express human genes related to menstrual cycle regulation and attempt to mimic hormonal patterning have been developed. However, this model lacks physiological menstruation, and therefore cannot be used to study the vaginal environmental shift that occurs during menstruation (Liu et al., 2020). As a result, there is a need for more human studies that analyze the influence of menstrual bleeding on the vaginal microbiome.

This review has highlighted the potential of microbiome manipulation to improve female reproductive health. However, this field is still in its infancy, and much more research and funding is needed to fully understand the role the microbiome plays in female gynecological conditions so that we can wield its power. In writing this, we seek to encourage further research in this promising field and emphasize the importance of exploring microbiome-based interventions in the realm of gynecologic health.

**FIGURE 1:**

Overview of four strategies designed to support the role of the microbiome in gynecological health.

These approaches, as evidenced by clinical trials and preclinical studies, aim to manipulate the microbiome of the gut or vagina to improve gynecologic health and thereby hold the potential for preventing, managing, and treating a range of gynecological issues.

1. **Microbiota Transplants:** Transfer of health-associated bacteria to remediate the vaginal and gut microbiome.

2. **Pre & Probiotics:** The consumption of beneficial bacteria or specific nutritional components to maintain and promote health.
3. **Diet**: Support of beneficial microbes through dietary components.

4. **Engineered Microbial Strains**: Designing genetically engineered bacteria to achieve health outcomes.

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