Women's MICROBIOME *Mag*

| #1 | SEPTEMBER 2025

| OVERVIEW |

Women's vulvovaginal microbiota: how can it help in clinical practice?

BIOCODEX
Microbiota Institute

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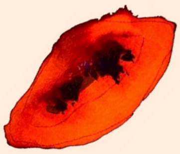

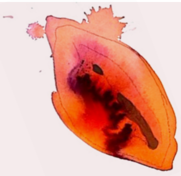

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Editorial

Placing microbiota at the centre of women's health

4 billion! Four billion women in the world – and just as much diversity! It's paradoxical when we know that, unlike the gut microbiota, the vaginal microbiota seems 'optimal' when it's not very diverse (about 200 species of bacteria) and is dominated by a small number of *Lactobacillus* species. Since so few patients know about this distinct quality (and one cannot blame them), **how many of them even know that they have a vaginal microbiota?** According to the latest survey by the International Microbiota Observatory and conducted with the help of Ipsos, **only 1 in 5 women claims to know precisely what it is.**

This knowledge deficit is not anecdotal. It reflects a triple blind spot – historical, cultural, and medical. It is not easy to emerge from centuries of obscurantism, prejudices, and taboos, especially since women have long been underrepresented in clinical research. In 2009, they accounted for only 38% of all participants included in study cohorts, despite representing nearly 50% of the general population[1].

> **Even today, discussion about the women's microbiota remains largely absent from medical consultations, despite its proven role in various pathologies such as endometriosis, recurrent urinary tract infections, or fertility disorders**

This first issue of the *Women's Microbiome Mag* is a modest contribution towards repositioning the **female microbiota (vulvar, intestinal, urinary, peri-anal, etc.)** to the heart of medical practice and to provide new frameworks, supported by committed experts, to better understand, diagnose, and support patients. At the same time, we seek to answer some crucial questions.

Why is the vaginal microbiota "optimal" when it is low in diversity? How does it behave throughout the menstrual cycle? What are the links between intestinal microbiota, endometriosis, and digestive disorders? And if we are to treat women better, do we also need to pay attention to the microbiota of their partners?

This magazine does not claim to cover everything (more will follow), but it does hope to increase focus on the importance of the women's microbiome.

To inform without simplifying, to educate without dogma, that is the ambition.

Most of all, **the *Women's Microbiome Mag* seeks to convince healthcare professionals and patients of the crucial role of the female microbiota in women's health.**

Happy reading.

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[1] Potterat MM, Monnin Y, Guessous I, *et al.*, Les femmes, oubliées de la recherche clinique. *Rev Med Suisse* 2015; 487: 1733-6. https://www.revmed.ch/view/531988/4308894/RMS_487_1733.pdf

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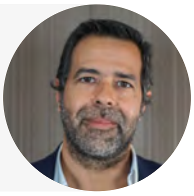


Women's vulvovaginal microbiota: how can it help in clinical practice?

The world of the human vaginal microbiome is a fascinating one, despite the limited knowledge about it. Evolution led to a unique scenario in which dominance by specific species of lactobacilli is the optimal state during reproductive years, despite huge interindividual variations – and even in the same woman over time. Understanding the vaginal microbiome and its potential is the key to improving women's health in areas such as sexually transmitted infections and recurrent vaginitis. Also, of utmost importance, it may be the answer to a problem to which there have been no satisfactory answers until now: preterm labour. In this article, we discuss the vaginal microbiome through an evolutionary lens, highlighting the apparent lack of a continuum between species. We discuss the current knowledge but also focus on future possibilities.

Historical perspective

The beginning of the long journey towards the understanding of the vaginal microbiome can be attributed to Albert Döderlein, at the end of the 19th century. In his book *Das Scheidensekret und seine Bedeutung für das Puerperalfieber* he pointed out that "normal", healthy women have the vagina dominated by Gram-positive bacilli, which he named *Lactobacillus acidophilus*.

KEY POINTS

- **The study of the vaginal microbiome is still evolving despite huge progress over the last decades.**
- **The optimal human vaginal microbiome in reproductive-aged women is dominated by lactobacilli.**
- **Non-dominance of the human vaginal microbiome by lactobacilli is associated with an increased risk of sexually transmitted infections, cervical cancer, and negative obstetrical outcomes.**
- **Future tests may allow a more accurate diagnosis of vaginitis and evaluation of the risk associated with specific dysbiotic profiles.**
- **While microbiome research is advancing rapidly, it is crucial to distinguish between investigational tests and their clinically relevant applications.**

This concept still shapes contemporary interpretations of the vaginal microbiome, but the reality is probably far more complex.

Understanding of vaginitis is still incomplete, and its management mostly empirical, despite being one of the most common causes for women to seek a medical appointment[1].

In 2011, Ravel *et al.* published one of the most important and mind-changing papers in terms of understanding of the human vaginal microbiome. In that paper they demonstrated that asymptomatic is not synonymous with "normal" (leading also to the question of what is a "normal" – or, probably more accurate, "optimal" – vaginal microbiome) and that there are striking differences according to ethnicity[2].

Diversity is the rule in nature, but the human vagina seems to be an exception: the accepted "optimal" vaginal microbiome is dominated by one or two species of lactobacilli (low alpha diversity). If we think about other organs or anatomical regions, dominance by one species is usually synonymous with disease (infection). If we perform the same exercise considering any ecological system, it represents the last step before collapse (e.g. monocultures of plants never occur in nature, and when performed artificially they must be limited in time). We can look for further explanations for this apparent "abnormality" (or "exception") in nature, but it does seem to lead to a dead end. Should we, instead, change the focus of our lens and investigate gene pools rather than species or genera to overcome this apparent biological abnormality?

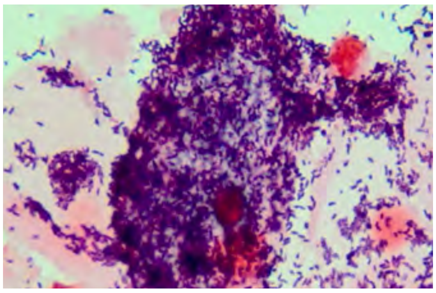
The ultimate goal of living beings seems to be passing genes to the next generations and evolution seems to be much driven by this primordial "instinct". Therefore, we can easily assume that the human vaginal microbiome should be a fulcral part of the end-product of evolution to optimise the reproductive process. If this premise is correct, we can expect:

1) evolutionary congruence (as has been shown, for instance, in the gut);

2) any differences should be more or less easily explained (mating process, diet, geographical location, etc.) and, naturally

3) higher similarity in closely related species.

Surprisingly, none of the three premises are satisfied. In nature, phylogeny cannot be related with the vaginal pH (a very indirect marker of the vaginal microbiome composition), and dominance by lactobacilli is unique to the human species. Even when comparing humans with other primates, the differences are huge and, currently, not easily explainable[3,4]. What made the human vagina so unique? Was it the fruit of random events or the evolutionary corollary of the continuous ovarian cycle, high risk of lacerations and infection at birth, or agriculture and the consequent high consumption of starch[3]?



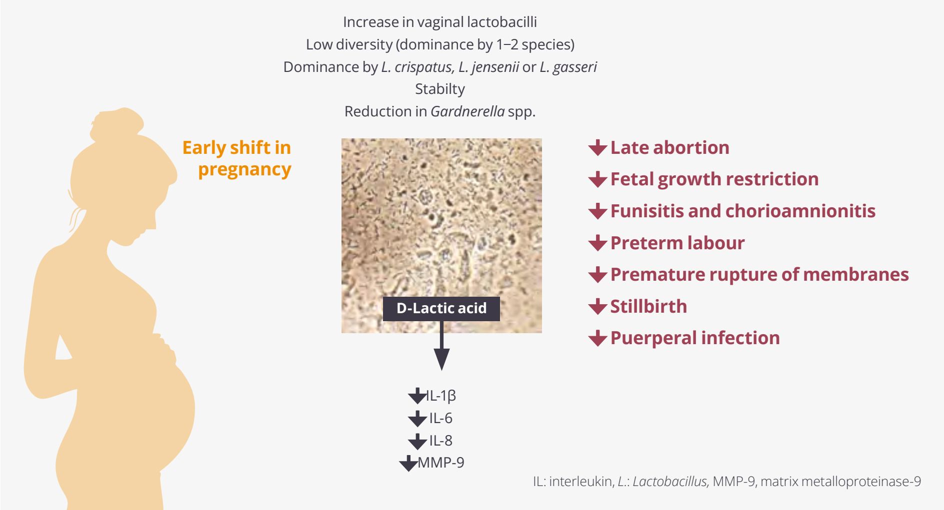
Bacterial vaginosis – clue cell in a Gram-stained smear (1000x). Courtesy of Prof. Piet Cools.

The microbiome and pregnancy

One issue seems to be beyond doubt: lactobacilli are fundamental for the success of pregnancy – but it is not so clear if the same applies to achieving a pregnancy[5].

The available data clearly show that a vagina not dominated by lactobacilli during pregnancy is associated with negative obstetrical and puerperal outcomes, including preterm labour, premature rupture of membranes, and puerperal infections (Figure 1). Of note, one million babies die every year from prematurity-related complications[6].

Figure 1. Vaginal lactobacilli dominance is associated with beneficial obstetrical and puerperal outcomes.



IL: interleukin, *L.*: *Lactobacillus*, MMP-9, matrix metalloproteinase-9

We are used to repeating that lactobacilli have a protective role and that their presence is desirable, but to assume that means we must ignore some obvious facts, such as that this dominance does not occur in children, during breastfeeding, nor in postmenopausal women. Therefore, we can theorise that our symbiotic relation with lactobacilli serves us a purpose during the reproductive years. We can consider that this purpose includes a reduction in the risk of sexually transmitted infection (STIs) (which pose a risk to the success of reproduction and to the offspring), of ascending genital infections (and consequent abortion, stillbirth, and preterm birth), as well as of puerperal complications. The role of the microbiome in achieving pregnancy seems to be more limited. For instance, populations with high rates of vaginal dysbiosis do not seem to be less fertile[7]. In the same way, the impact of the cervicovaginal microbiome on the outcome of fertility treatments is also unclear[5].

One of the biggest evolutionary differences between humans and other mammals has to do with delivery – the difficult balance between being born with a large cephalic perimeter and negotiating it with a pelvis that had to adapt to bipedalism. Humans have the most difficult deliveries – perhaps surpassed only by hyenas. Can this hold the key to understanding the uniqueness of the human vaginal microbiome? Whatever the evolutionary purpose was, for most women of reproductive age, even out of pregnancy, the dominance of lactobacilli in the vagina is the desirable state. But lacking lactobacilli, despite representing a dysbiotic state, is not synonymous with disease.

Our understanding of the role of the vaginal microbiota is still very limited. Even apparently simple questions, such as how lactobacilli colonise the vagina still does not have a clear answer.

The vulvovaginal microbiome in heath and disease

The most noticeable effect of an altered microbiome is vaginitis. Most women will suffer at least one episode of candidiasis and, in some populations, more than half of reproductive-aged women have bacterial vaginosis (BV), asymptomatic most of the time (figure 2A and 2B). We have a limited understanding of what drives these shifts ("normal" – colonisation/asymptomatic state – symptomatic)[8].

> **The vaginal microbiome may confer different profiles of risk or protection.**

However, the bacterial profile of the vagina, regardless of symptoms, may confer different profiles of risk or protection. In general, it is considered that *Lactobacillus* spp. tend to confer health benefits. However, not all species are equal and only a limited number of the existing species are usually found in dominating states in the vagina. *L. iners*, with a significantly smaller genome and different metabolic profile, is usually associated with dysbiotic or transition states[9].

Figure 2. Microphotographs of wet mount microscopy preparations (phase contrast 400x). (A) Normal lactobacilli, presence of *Candida* spp. blastospores (circle); (B) Bacterial vaginosis (absence of lactobacilli and overgrowth of anaerobic and facultative bacteria).

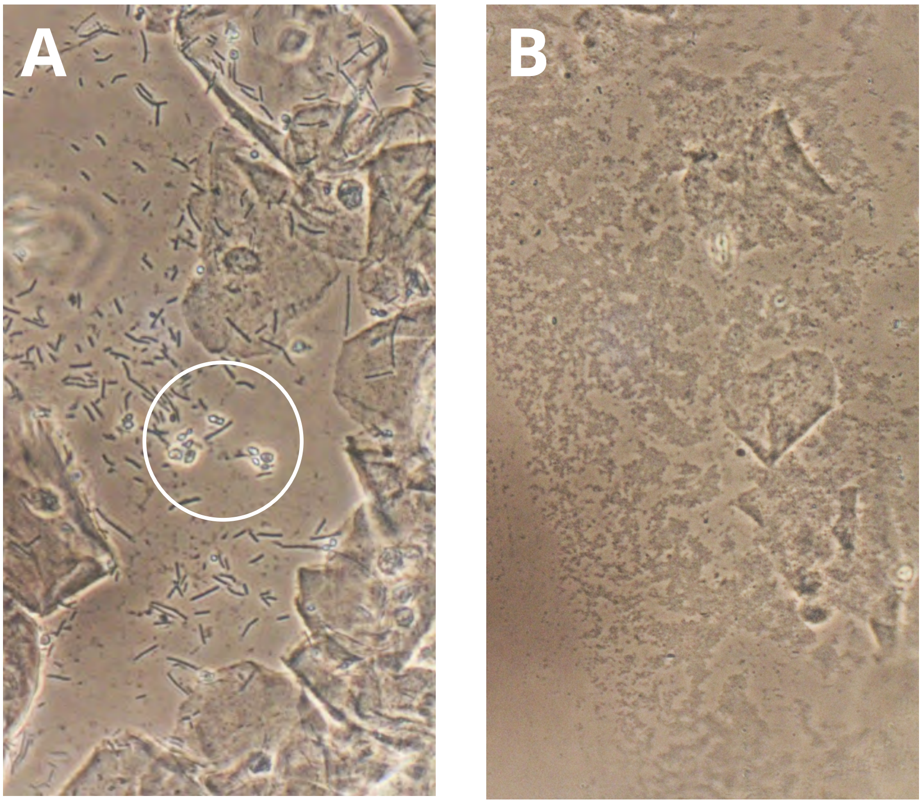


Table 1. Gynaecological and obstetrical conditions and their associations with the vulvovaginal microbiome.

Group	Condition	Association/characterisation of the vaginal bacterial microbiome
Vaginitis	Candidiasis	The relation between lactobacilli and *Candida* spp. is complex and controversial. *Candida* spp. can coexist with any vaginal microbiome pattern. Some studies have shown a slightly lower overall prevalence of *Lactobacillus* spp., and an increased proportion of *L. gasseri, L. iners, Gardnerella* spp., *Prevotella* spp., *Megasphera* spp., *Roseburia* spp., and *Fannyhessea (Atopobium) vaginae*. Other studies, however, have shown a higher risk in women with lactobacilli dominance.
	Bacterial vaginosis	Absence of lactobacilli and overgrowth of a variable mixture of predominantly anaerobic and facultative bacteria, which in low loads are part of the normal vaginal microbiota (i.e. *Gardnerella* spp., *Mycoplasma hominis, Fannyhessea (Atopobium) vaginae, Bacteroides, Clostridiale, Fusobacterium* spp., *Mobiluncus* spp., *Peptostreptococcus* spp., *Porphyromonas* spp., *Prevotella* spp.).
STIs	HIV	HIV infection is associated with BV and women with a lactobacilli-dominated vagina have less risk of acquiring HIV. A *L. crispatus*-dominated vaginal microbiome is less associated with inflammation, which may explain the advantage associated with it.
	HPV	The prevalence of HPV infection is higher in women without dominance by lactobacilli (CST III and IV, the prevalence of which also increase with the severity of disease). Women with lactobacilli dominance are less likely to become HPV-positive and, if positive, are more likely to become negative.
	HSV2	HSV2 is associated with BV, but the directionality of the relationship is unknown.
	Other STIs	The risk of incident trichomoniasis, gonococcal, and/or chlamydial infection is strongly associated with dysbiosis (Nugent intermediate and BV score). Of note, *Trichomonas vaginalis* itself often drives the vaginal microbiome towards a BV state.
Other infections	Urinary tract infections	The normal urinary microbiome seems to be dominated by lactic acid-producing species (*Lactobacillus* spp. and *Streptococcus* spp.). Women with recurrent cystitis have been found to have increased rates of colonisation by *Escherichia coli* and depletion of lactobacilli. Postmenopausal women using topical or oral oestrogens have fewer episodes of urinary tract infections, and the possible explanation has to do with the role of oestrogens in the dominance of lactobacilli in the vagina. *Gardnerella* spp. may be a promoter for the development of *E. coli* and women with BV seem to be more prone to urinary tract infections.
Cancers	Cervical cancer	Associated with lactobacilli depletion and high diversity. *Sneathia* spp. may be a marker of high-grade intraepithelial neoplasia and cervical cancer. *L. iners* is not only associated with HPV infection, but also with a higher chance of progression.
	Endometrial cancer	*Porphyromonas* spp. and *Fannyhessea (Atopobium) vaginae* are associated with endometrial cancer. The gut microbiome may actually be more relevant than the vaginal and endometrial one (estrobolome).
	Tubal and ovarian cancer	Possible role of intracellular bacteria (*Brucella* spp., *Mycoplasma* spp., and *Chlamydia* spp.).
Other	Vulvodynia	No systematic associations have been identified; a lower diversity seems to be more common in women with vulvodynia.
Reproduction	Fertility	The impact of the vaginal microbiome on fertility seems to be limited, but some studies have suggested that *L. crispatus* and *L. iners* are more common in fertile couples. No apparent correlation with BV and lower rates of fertility. A lower quantity of lactobacilli in the endometrium is possibly associated with infertility.
	Fertility treatment outcomes	No systematic correlation between lactobacilli dominance and outcomes, but some studies have associated a lower richness and diversity with better outcomes. High loads of *Gardnerella* spp. >20% are associated with poorer IVF outcomes.
Obstetrical outcomes	Miscarriages	Association with lactobacilli depletion, CST-IV and lower alpha diversity.
	Preterm birth	Lower risk in women with dominance by *L. crispatus*. In White women *L. iners, Gardnerella* spp. and *Ureaplasma* spp. are associated with an increased risk. In Black women BVAB1, *Sneathia amnii, Prevotella* spp., *Fannyhessea (Atopobium) vaginae* and *Gardnerella* spp. seem to be associated with a higher risk.

Adapted from Ventolini G, *et al.*[14], de Seta F, *et al.*[15], Brandão P, *et al.*[5], and Sacinti KG, *et al.*[16]. Some conditions such as lichen sclerosus, vulvar intraepithelial neoplasia and vulvar cancer were not included due to the scarcity of data.
BV, bacterial vaginosis; CST, community state type; HIV, human immunodeficiency virus; HPV, human papillomavirus; HSV, herpes simplex virus; IVF, *in vitro* fertilisation; STI, sexually transmitted infection.

Little is known about the relationship between *Candida* spp. and the vaginal microbiome.

While there are no current recommendations to treat asymptomatic dysbiosis (e.g. BV), it has been associated with obstetrical and non-obstetrical complications (including risk of acquiring STIs [HPV, HIV])[8] (Table 1). Once efficacious (preferably non-antibiotic) strategies are available, it may be advisable to screen and treat dysbiosis in women at increased risk of STIs or even in those infected with HPV. This, however, may prove more complex than it appears. The STI-like behaviour of BV has long been acknowledged, but recent data have confirmed it, as well as suggesting that reduction of recurrences may require treatment of partners, which may represent a great obstacle to prevention strategies[10].

BV is a common syndrome, in which there is depletion of lactobacilli and an overgrowth of several strictly and facultative anaerobic bacteria, associated with formation of a biofilm that seems to contribute to the frequent relapses after treatment. The composition of BV is variable from woman to woman – and probably even in the same woman over time[11]. Currently it is possible to diagnose BV using molecular tests, but it is expected that with the increasing knowledge of the vaginal microbiome, these tests will allow for the "profiling" of BV, the evaluation of the resistome, and a more rationale choice of treatments[8].

The relationship between *Candida* spp. and the vaginal microbiome is very complex and far from fully understood. While candidiasis can exist with any vaginal microbiome, it tends to be more common with lactobacilli dominance (and the consequent low pH)[12].

Several gynaecological conditions have been associated with specific microbiome characteristics and, almost systematically, a reduction in lactobacilli confers an increased risk for STIs and gynaecological cancers (even of the upper genital tract). However, a causal relationship between the microbiome deviations and the specific conditions is not always straightforward. We can, however, expect to one day assess or modulate the risk of cancer through the evaluation of the vaginal microbiome – especially for cervical cancer[13].

The interest and knowledge in the vulvar microbiome is more recent and the amount of data is scarce, but its role in entities such as vulvodynia, vulvar dermatoses, vulvar intraepithelial neoplasia and cancer is being studied[14-16].

Bacterial vaginosis – fluorescence *in situ* hybridization (FISH) (*Gardnerella* spp. in yellow and *Prevotella* spp. in red) (400x). Courtesy of Prof. Alexander Swidsninski.

What's next?

Giant strides are being made towards the understanding of the vulvovaginal microbiome. Until we fully understand the microbiome, we can start by respecting it and its functional role, recognising that each woman is unique (and that this uniqueness is mutable), avoiding unnecessary use of antibiotics and antiseptics, and properly diagnosing STIs and vaginitis, rather than relying on empiricism. Accurate diagnosis will minimise wrong treatments, with a potential long-term impact.

At this stage, it is essential to distinguish what is investigational and what is clinically relevant. We are in a process of learning and attempting to use investigational techniques and concepts in clinical practice that often leads to unnecessary testing, expenses, and treatments – for instance, metagenomics is a very useful research tool, but it currently has no place in the clinical evaluation of vaginitis.

In the last two decades we have amassed a huge quantity of information, which will soon translate into better health care for women, including specific dietary recommendations, and pre- and probiotics. We can expect that this knowledge will substantially reduce preterm labour, gynaecological cancers, as well as the recurrence of vaginitis and cystitis.

The next chapters will undoubtedly be the most exciting ones!

CONCLUSION

The human vaginal microbiome is still incompletely understood and some of our current assumptions may need to be updated or adapted as new data emerge. Its full understanding and the potential to manipulate it may be unravelled once the apparent lack of evolutionary logic is completely understood.

However, we can be certain that lactobacilli are of benefit for most reproductive-aged women and that they are fundamental for the success of pregnancy, regardless of geography or ethnicity.

The increasing knowledge in this field is leading to progress in the diagnosis and management of vaginitis and, in the near future, it will enable the reduction of the risk of serious issues, such as STIs and preterm labour.

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The Foundation for Endometriosis Research:

a catalyst for research on endometriosis in France

The Biocodex Microbiota Institute partners with a variety of professional organizations, including medical societies, patient associations, and research foundations involved in women's health. In this issue, we look at the work done by the Foundation for Endometriosis Research and talk to their experts who discuss the importance of the female microbiota in research and clinical practice.

Founded in France in 2021 by the ENDOmind Association under the aegis of the Foundation for Medical Research, the Foundation for Endometriosis Research aims to accelerate research on a disease that affects one in 10 women: endometriosis. Each year, the Foundation funds research projects aimed at understanding the pathology of endometriosis, improving diagnosis and developing more effective treatments.

In 2024, the Foundation for Endometriosis Research Executive Committee decided to more clearly define its research priorities for endometriosis and maximise its research impact. To this aim, the Foundation co-constructed and co-funded an innovative collaboration with the Curie Institute in Paris, seeking to compare the cellular microenvironments of endometriosis lesions and ovarian cancer. This ambitious project is starting in 2025 and illustrates the Foundation's desire to encourage cross-disciplinary and innovative research approaches.

Furthermore, the Foundation for Endometriosis Research has initiated a multidisciplinary scientific investigation with European experts on the links between microbiota and endometriosis. The Foundation will call for expressions of interest later in 2025, with the objective of launching new research work at the start of 2026, with financial support.

By focusing its efforts on strategic themes, the Foundation for Endometriosis Research confirms its role in accelerating research and ultimately contributing to improving the quality of life for the millions of women affected by this still little-known disease.

Key achievements of the Foundation for Endometriosis Research:

An International Scientific Committee, consisting of **12 scientific and clinical experts**, who are among the world's leading experts in endometriosis

1 Executive Committee, consisting of five gynaecologist professors, doctors, and midwives with expertise in endometriosis

2 educational modules launched, designed to raise researchers' awareness of ongoing innovative research into endometriosis

Key achievements of the Foundation for Endometriosis Research

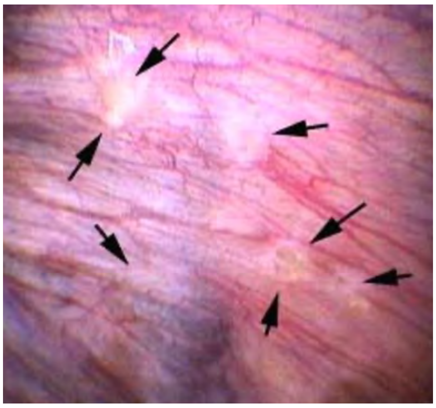
5 calls for projects launched, **14 projects funded**, **€500,000 of funding in 4 years**

1 research project set up in collaboration with the **Curie Institute** in Paris

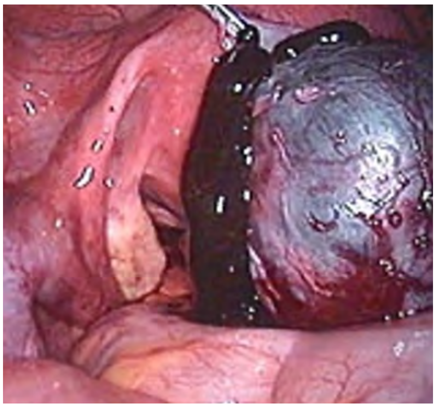
3 annual conferences held for the general public on advances in endometriosis research

More information:
https://www.fondation-endometriose.org/

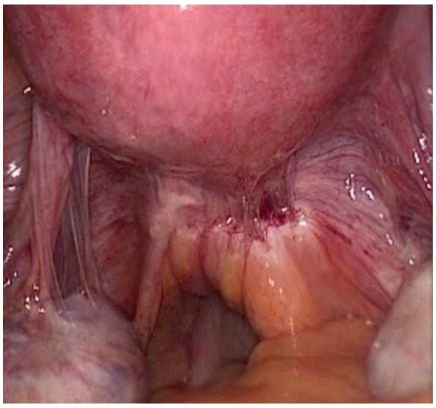
(i) Superficial peritoneal endometriosis



(ii) Ovarian endometriosis



(iii) Deep endometriosis



Images courtesy of Prof. Andrew Horne, University of Edinburgh, UK

Prof. Andrew Horne
Professor of Gynaecology and Director of the Centre for Reproductive Health at the University of Edinburgh in the UK, with specialisation in the management of endometriosis.

Dr. William Fusco
Gastroenterologist and microbiome clinical researcher at the Agostino Gemelli Polyclinic, Rome, Italy.

Fondation Recherche Endométriose
sous l'égide de la FRM

Interdisciplinary Interview

Endometriosis, Digestive Symptoms, and the Microbiome: Perspectives of a Gynaecologist and a Gastroenterologist

What is the prevalence of endometriosis?

A.H.: Endometriosis is surprisingly common – as common as asthma and diabetes. It affects an estimated 1 in 10 women.

W.F.: In my practice of irritable bowel syndrome (IBS), it's even more common – certainly more than 25%.

What are the signs and questions to ask to avoid missing a diagnosis?

A.H.: Signs are varied and diagnosis can be difficult. The main symptom is chronic pelvic pain, which can often be debilitating, disrupting life and work. But, patients can also present with painful sex, chronic fatigue, diarrhoea and/or constipation and urinary symptoms. Any cyclical symptom can be a red flag for endometriosis.

W.F.: Increased peristalsis and softer stools during menstruation are normal, but significant and cyclical diarrhoea may not be so. Pain is expected, but not to the point of being bedridden.

A.H.: Another symptom that causes alarm is infertility. But I reassure patients with endometriosis: two-thirds of them won't have trouble getting pregnant, and those who do generally respond well to surgery or IVF.

W.F.: I would add that endometriosis is chronic, but that doesn't mean it's untreatable. It's important that any specialist involved with the care of these patients reinforces that message.

How common are digestive symptoms in women with endometriosis?

A.H.: The true prevalence isn't known, but nearly all my patients have digestive symptoms – bloating, bowel changes, heartburn. Lesions on the bowel wall explain some symptoms, but many have superficial peritoneal disease, making the link harder to define.

W.F.: I have observed similarly, and would state that inflammatory bowel disease (IBD) is four times more common in women with endometriosis compared with the general population (4% vs 1%). IBD and endometriosis are both autoimmune conditions; having one increases the risk of the other.

Is there a need for multidisciplinary management?

A.H.: Endometriosis is a systemic inflammatory disorder. As gynaecologists, we're not equipped to manage digestive symptoms. In Edinburgh, I've recently set up a joint gynaecology–gastroenterology clinic.

W.F.: When the abdominal pain strictly relates to menstruation, the gastroenterologist may find it difficult to add much. When the relationship is more loosely defined, we should investigate. Persistent digestive symptoms despite treatment may signal coexisting IBS.

Also, be mindful of medications, particularly nonsteroidal anti-inflammatory drugs (NSAIDs). Occasional use is fine in young patients, but chronic use may require a proton pump inhibitor (PPI), which can cause dysbiosis. There's no universal rule — we must tailor care to each patient.

Are gut and vaginal microbiota involved?

A.H.: There's growing interest in the role of the gut and vaginal microbiomes in endometriosis. Some studies suggest associations, but they're small and flawed. We need large cohort studies. I believe the microbiome plays a role, but it's still unclear as to which comes first — microbiome changes or endometriosis. If microbiota drive symptoms, this could open the path to new treatments.

W.F.: It's an exciting field. In patients with endometriosis, we observe gut dysbiosis with reduced short-chain fatty acids like acetate, propionate and butyrate that protect gut permeability. The same pattern can be seen in other gastroenterological conditions, like IBS or IBD, but we don't yet understand the relationship. Maybe one day, we'll personalise care by restoring exact missing strains. For now, we don't know what causes what, so mechanistic studies are needed.

Should we recommend specific diets to patients with endometriosis?

W.F.: There's no universal diet for endometriosis and we shouldn't offer false hope. Allergies, lactose intolerance, and coeliac disease might be involved. The best step is to refer patients to a nutritionist.

A.H.: No specific "endometriosis diet" exists, but many patients report symptom relief after dietary changes. In my clinic, patients work with a dietitian to carefully adjust their diets. In our international survey of 2,500 patients with endometriosis, some found relief by stopping consumption of alcohol and caffeine, or foods containing gluten. However, without guidance, dietary restriction can be harmful.

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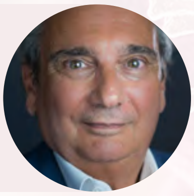
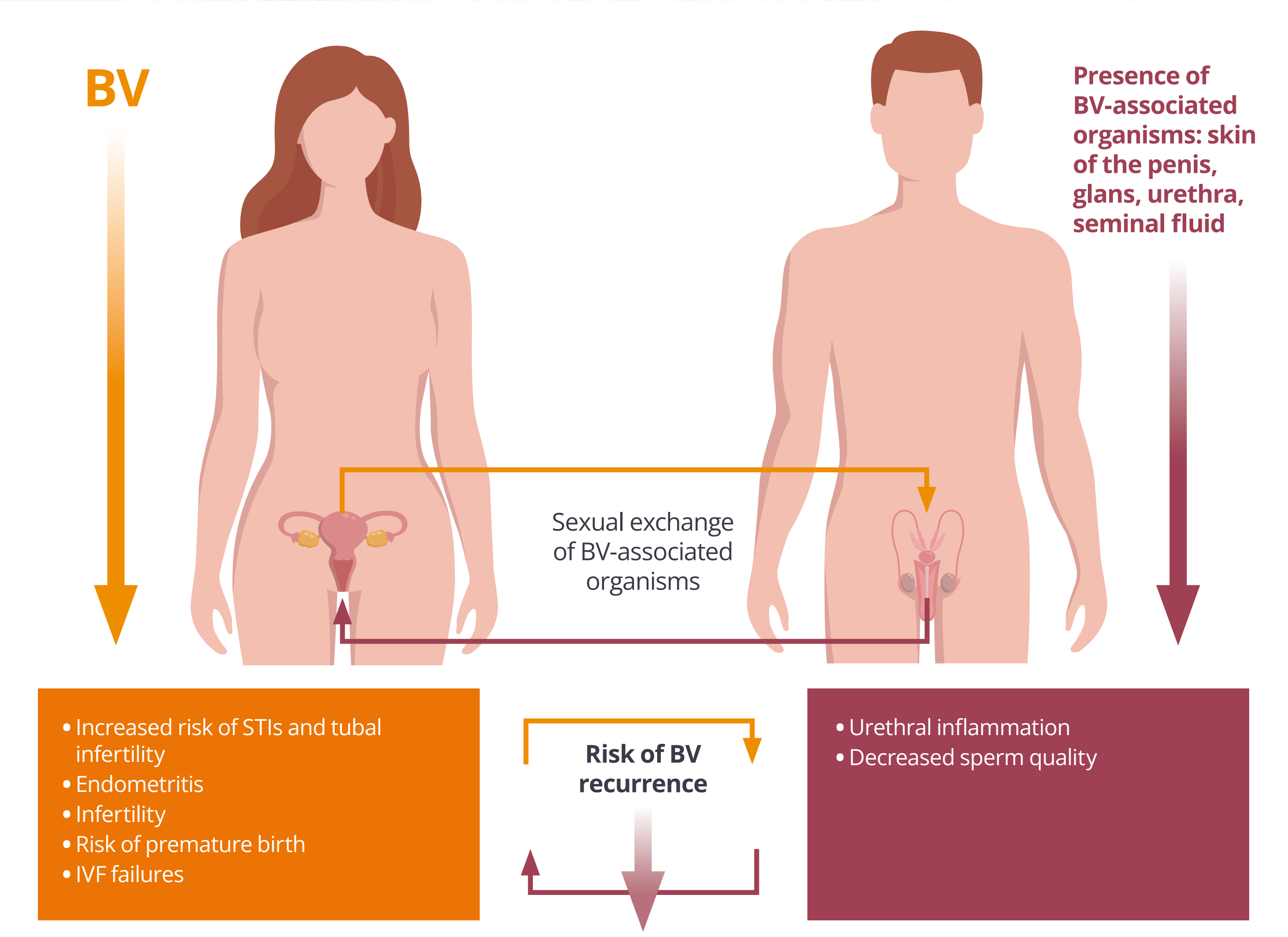


The male genital microbiota impact on women's health

Talk about vaginal infections, fertility, or pregnancy complications often focuses solely on women. But there is another important player: the male urogenital tact (MUGT). The wide variety of microbes in the MUGT can significantly affect female reproductive and vaginal health (Figure 1). Understanding these influences may improve outcomes for women, especially those with persistent vaginal infections, fertility challenges, and pregnancy complications.

Figure 1. Consequences of exchanges of bacteria associated with vaginosis during sexual contact between males and females.



Abbreviations
BV, bacterial vaginosis; IVF, *in vitro* fertilisation; STIs, sexually transmitted infections.

What do we know about the male genital microbiota?

The MUGT includes several distinct microbial environments: the skin of the penis, the urethra, semen, and the urinary tract. Each has a unique bacterial community, influenced by factors like circumcision, sexual practices, hygiene, and lifestyle.

Penile skin and foreskin

The skin of the penis harbours bacteria similar to those found on other cutaneous (skin) surfaces — mainly *Corynebacterium* and *Staphylococcus genera*[1, 2]. In uncircumcised men, the area under the foreskin (the balanopreputial sulcus) is dominated by anaerobic bacteria such as *Anaerococcus, Peptoniphilus, Finegoldia,* and *Prevotella,* some of which are also found in women with bacterial vaginosis (BV)[1, 2]. Circumcision significantly reduces these anaerobes, which may explain why women with circumcised partners have a lower risk of BV[2].

Urethra

Sampling the urethra directly is painful, so most studies use the first-void urine as a proxy to study urethral microbiota. This fluid contains a mix of bacteria like *Lactobacillus, Streptococcus, Sneathia, Veillonella, Corynebacteria,* and *Prevotella*[3]. Interestingly, some of these are linked to BV (e.g. *Gardnerella vaginalis*) and aerobic vaginitis (*S. agalactiae*)[4].

Semen

Semen is not just sperm — it also includes fluids from the prostate and seminal glands. Studies show that a *Lactobacillus*-dominated seminal microbiota is linked to better sperm quality, while other bacteria (e.g. *Ureaplasma, Mycoplasma, Prevotella,* and *Klebsiella pneumoniae*) are associated with lower fertility[5].

Urine

The male urinary microbiota is less studied, but lower levels of *Streptococcus, Lactobacillus, Pseudomonas,* and *Enterococcus* genera have been found in men with abnormal sperm concentration compared with men with normal sperm concentration[6]. Men with abnormal sperm motility may have high levels of *Dialister micraerophilus* bacteria, which contribute to a proinflammatory sperm microenvironment[6].

MUGT microbiota vary with circumcision status, sexual practices, and the composition of the female partner's vaginal microbiota[7]. Interestingly, the urethral microbiota of homosexual men does not seem to be modified by the type of sexual intercourse (oral or anal)[8]. Bacterial exchanges between partners during sexual contact are the rule; why these exchanges lead to vaginal dysbiosis in some cases and not others is unclear.

Seminal microbiota are also influenced by several physiological functions (age, hormonal changes) and lifestyle or epigenetic factors (tobacco, alcohol, obesity, high-fat diet, exposure to toxins)[5]. These modifiable factors are potential targets for intervention.

How does the MUGT impact female health?

The transmission of microorganisms responsible for bacterial and viral sexually transmitted infections (STIs) including HIV and herpes simplex virus infection during sexual contact is the most obvious consequence of how the MUGT impacts female health. The female complications of bacterial STIs (gonorrhoea, infections by *Chlamydia trachomatis* or *M. genitalium*) are well known (inflammation and infection of the upper genital tract, risk of tubal infertility).

Many studies have shown that the epidemiological profile of women with BV is comparable to that of women with STIs, suggesting possible sexual transmission of the bacteria involved in BV. The presence of BV-associated bacteria in the foreskin and urethra of partners of women with BV and a concordance of vaginal and male urethral bacterial strains support the sharing of these strains or sexual transmission of BV.

Treating the male partner with oral antibiotics (metronidazole) has had very limited impact on recurrence rates in women with recurrent BV, although combining metronidazole with a topical antibiotic applied to penile skin in partners of women with BV may reduce the risk of recurrence[9].

The impact of the MUGT on uterovaginal health is not limited to passive bacterial transfer. Seminal fluid contains proinflammatory substances (such as prostaglandins) that can interfere with immune responses and inflammation within the female genital tract[10].

KEY POINTS

- **The male genital microbiota plays an influential but under-recognised role in female reproductive health, particularly in recurrent genital infections and fertility challenges.**
- **Routine STI screening may miss important bacteria that are not traditionally classified as pathogens but disrupt the female genital microbiota.**
- **Male-partner treatment for recurrent BV may need to go beyond oral antibiotics, incorporating topical therapies and addressing shared risk factors.**

CONCLUSION

The male urogenital microbiota matters — not just for men's health, but for women's too. While research is still evolving, it is clear that male partner dynamics, lifestyle, and microbial exchange influence female urogenital health. The evidence increasingly supports a more holistic, couple-based approach to managing reproductive concerns, by incorporating male partner care into routine sexual and reproductive health strategies to improve outcomes for both partners, especially in cases of persistent or recurrent vaginal infections. Encouraging healthier habits in men — including quitting smoking or improving the diet — might improve semen microbial health and reduce the risk of negative outcomes for their female partners.

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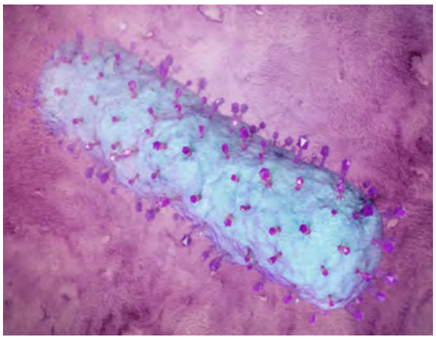
Defining Vaginal Community Dynamics: daily microbiome transitions, the role of menstruation, bacteriophages and bacterial genes

Comments on the article by Hugerth et al. (Microbiome 2024)[1]

This high-resolution metagenomic study investigates daily transitions in the vaginal microbiome across a menstrual cycle in 49 healthy young women. By analysing taxonomic, viral, and functional gene data from daily samples, the authors introduce a dynamic classification system called Vaginal Community Dynamics (VCDs), which categorises women into four groups: *constant eubiotic, constant dysbiotic, menses-related dysbiosis,* and *unstable dysbiotic.* These patterns reflect how individual microbiomes respond to menstruation, sexual activity, and other exposures, and demonstrate that vaginal health cannot be adequately assessed from static samples alone. Notably, bacteriophage abundance and bacterial gene content — such as bacteriocins — may contribute to the stability or instability of microbial communities. This work highlights the complexity and individuality of vaginal microbiome behaviour and has implications for improving diagnostics and personalised care in gynaecology.



Bacteriophages attacking E coli cell, Science Photo Library

What do we already know about this subject?

The vaginal microbiota plays a key role in defending against pathogens, maintaining mucosal immunity, and supporting reproductive health. Dominance by *Lactobacillus* species, especially *L. crispatus,* maintains a low pH and inhibits pathogenic colonisation[2]. Dysbiosis — defined by a loss of lactobacilli and overgrowth of anaerobic species such as *Gardnerella* or *Prevotella* — is associated with increased risks of bacterial vaginosis (BV), preterm birth[3], infertility[4], sexually transmitted infections, human papillomavirus (HPV) infections and gynaecological cancers[5]. Previous studies have shown that hormonal changes, menstruation, and sexual intercourse can influence the composition of the vaginal microbiome[6]. Many of these studies relied on infrequent sampling and lacked resolution to assess short-term fluctuations or determine the drivers of transitions between eubiosis and dysbiosis. The contributions of viral dynamics and functional bacterial genes have remained largely unexplored.

What are the main insights from the study?

This study introduces the concept of VCDs, offering a new framework for classifying microbiome behaviour across the menstrual cycle. Unlike community state types (CSTs), which describe static microbiome compositions, VCDs capture temporal patterns that may better reflect microbiome resilience and vulnerability. The four VCDs — constant eubiotic, constant dysbiotic, menses-related dysbiosis, and unstable dysbiotic — represent distinct profiles of microbial stability. Women in the constant eubiotic group maintained *Lactobacillus* dominance throughout the cycle, while those with constant dysbiosis had persistent BV-associated communities. Menses-related dysbiosis was characterised by temporary shifts during menstruation, often reverting mid-cycle, whereas the unstable group experienced abrupt fluctuations after exposures like sexual intercourse, suggesting greater ecological fragility.

One of the key findings was that instability in the vaginal microbiome is associated with increased bacteriophage activity and a higher prevalence of *L. iners.* This species is frequently linked to transitional or less stable states, and phage abundance may reflect active lytic cycles that destabilise dominant bacteria via "kill-the-winner" dynamics. Additionally, women with transient dysbiosis showed increased abundance of potential pathogens such as *Sneathia* spp. during and after menstruation, pointing to specific periods of vulnerability.

Strain-level analysis revealed differences in bacterial gene content, including bacteriocins produced by *Gardnerella leopoldii* that may inhibit lactobacilli. These genes were more prevalent in unstable and dysbiotic VCDs, supporting a possible mechanistic role in shaping community structure. Although these genetic findings require further validation, they highlight the importance of moving beyond species-level classification to understand microbial function and its impact on host health.

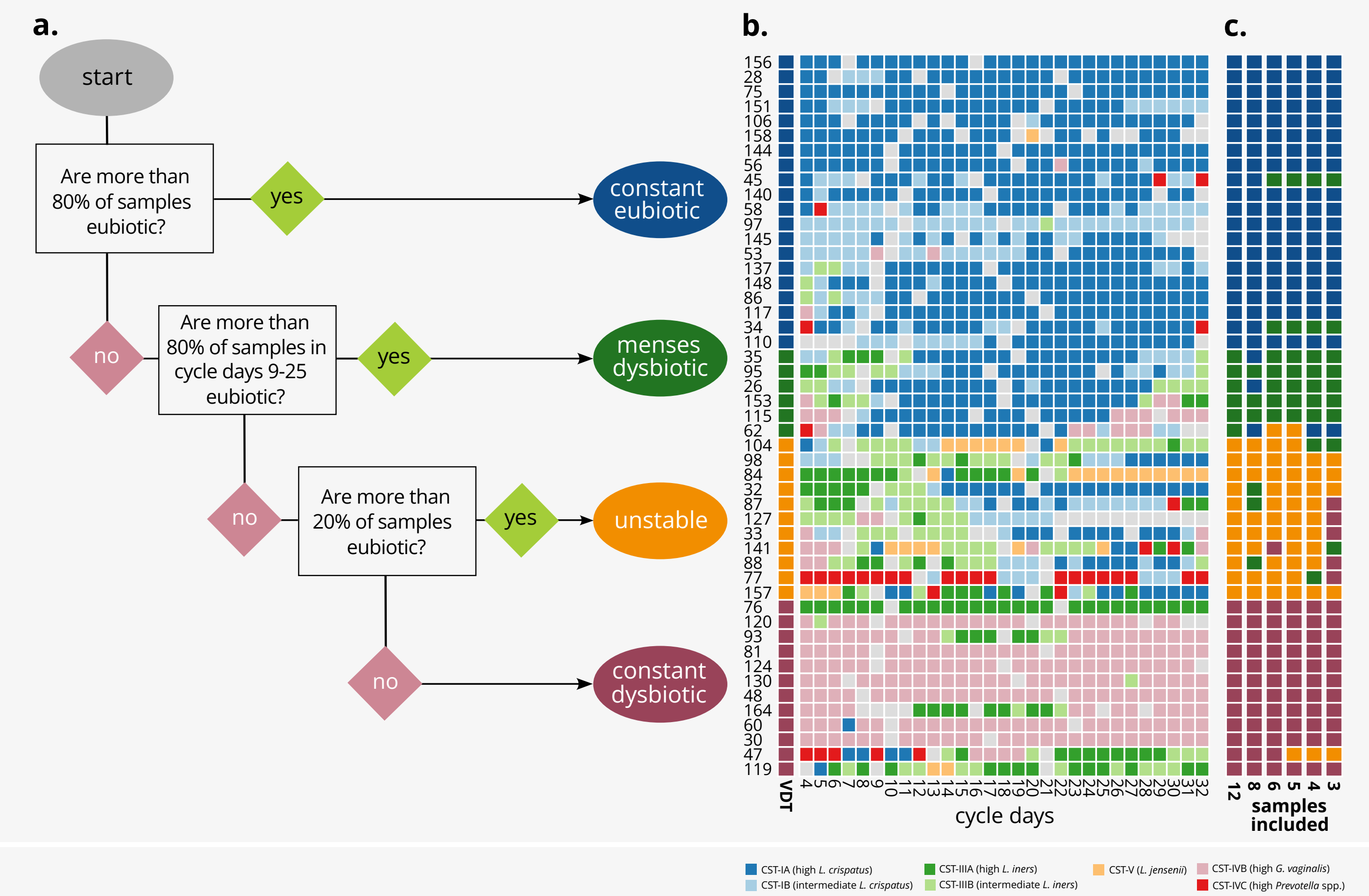
What are the consequences for clinical practice?

This study underscores the need to rethink how vaginal health is assessed and monitored in clinical practice. The recognition that vaginal microbiota are dynamic — and that stability patterns differ markedly between women — has implications for diagnostics, risk assessment, and therapeutic strategies. Sampling at a single time point, especially during menstruation, may fail to capture meaningful fluctuations or misrepresent a woman's baseline microbial state. Clinicians should consider collecting samples at multiple points in the cycle to better assess microbiome behavior, particularly in patients with recurrent symptoms or reproductive concerns.

The limitations of CST-based classification are evident in this study. Two women with the same CST may exhibit entirely different VCDs, one with stable eubiosis and the other with frequent dysbiosis. Incorporating VCD assessment could enable more personalised interventions, such as recommending prophylactic microbiome support for women with unstable patterns or targeting high-risk windows (e.g. post-menses) for infection screening.

The identification of phage-driven instability and strain-level bacterial traits opens avenues for precision medicine. Future therapies may need to address microbial function — such as biofilm formation or bacteriocin production — rather than composition alone. Understanding the dynamics of vaginal bacteriophages could also inform novel microbiome stabilisation strategies.

Figure 1. **Vaginal time series can be classified into four categories (Vaginal Community Dynamics) according to their proportions of eubiotic samples.**



a. A decision tree can separate a time series of samples into dynamic groups, based on the community state types (CSTs). Input from the user determines which CSTs are considered eubiotic (here: I, II, and V) and which days are to be considered free from the influence of menses (here: cycle day 9 to cycle day 25). Time series with ≥80% eubiotic samples are considered constant eubiotic; conversely, those with >80% dysbiotic samples are considered constant dysbiotic. For those in the 20–80% range, a second assessment is done on the days free of menses: if they are >80% eubiotic, the time series is considered menses-related dysbiotic, and otherwise unstable (changing from eubiosis to dysbiosis without a clear temporal pattern). **b.** A colour map with one individual per row and one day per column. The colour of each intersection depicts CST. Coloured bars on the left side show the vaginal community dynamics of each woman. **c.** Additional colour bars show the inferred vaginal community dynamics of each participant when using fewer samples for classification. Reproduced from Hugerth LW, *et al. Microbiome* **2024,** *12,* 153[1] (doi:10.1186/s40168-024-01870-5) under a CC-BY 4.0 license (creativecommons.org/licenses/by/4.0). No changes have been made to the figure.

KEY POINTS

- **The vaginal microbiome shows individual and dynamic patterns during the menstrual cycle that may affect reproductive outcomes.**
- **Transient or unstable dysbiosis is associated with higher phage counts, *Lactobacillus iners* dominance, and phases of increased risk.**
- **Strain-level functional traits, such as bacteriocin production, may help explain transitions to and persistence of dysbiosis.**

CONCLUSION

This study presents a significant advance in our understanding of vaginal microbiome behaviour by shifting the focus from static CSTs to dynamic community patterns. By classifying women into four categories of VCDs, the study offers a new lens for evaluating microbiome health and its clinical consequences. These insights call for more personalised, time-sensitive approaches to sampling, diagnosis, and intervention. Incorporating virome data and functional bacterial traits may further refine risk prediction and treatment strategies. Ultimately, a deeper ecological understanding of the vaginal microbiome could help reduce complications like bacterial vaginosis, preterm birth, and infertility — and support a more individualised standard of care for women's reproductive health.

The classification tool VALODY, designed to assign VCD categories based on VALENCIA CST assignments, is available on GitHub at https://github.com/ctmrbio/valody.

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Gut Microbiota

Gut microbiota composition in women with polycystic ovary syndrome

The gut microbiota is increasingly viewed as an invisible organ-like system that not only plays an important role in a woman's well-being but also affects the pathophysiology of some disorders such as polycystic ovarian syndrome (PCOS). Knowing about microbial metabolite pathways may elucidate effective treatments.

A recent meta-analysis that included 948 women with PCOS from 14 studies explored the relationships between gut microbiota among women from different regions and with different testosterone levels. Key findings revealed distinct gut microbiota compositions in PCOS patients compared with their healthy counterparts, and significantly different gut microbiota between PCOS patients with higher testosterone levels and those with lower testosterone levels. Also, gut bacterial genera differed among PCOS patients from different regions; European patients had high *Alistipes* levels, whereas Chinese patients had high *Blautia* and *Roseburia* levels.

These findings support current evidence showing that PCOS patients have fewer different types of bacteria and a less balanced microbial community compared with healthy women. The data also confirm the abundance in PCOS patients of specific bacterial genera such as *Escherichia/Shigella* and *Alistipes,* which are associated with insulin resistance and inflammation. This study implies that the gut microbiome is linked to various metabolic and hormonal disturbances associated with PCOS, which is compatible with previous research. Importantly, it demonstrates differences in bacterial taxa between Chinese and European women with PCOS, which may assist with personalised treatment strategies. Further research to determine PCOS-associated bacteria strains may enhance anti-PCOS microbial therapies and studies in different geographical regions would promote the global treatment of PCOS.

To conclude, characterising gut microbiota in PCOS patients from different countries may enable gut microbiota to act as a biomarker to distinguish different subtypes of PCOS, and thereby improve the clinical diagnosis and treatment of PCOS.

Yang Y, Cheng J, Liu C, *et al.* Gut microbiota in women with polycystic ovary syndrome: an individual based analysis of publicly available data. *EClinicalMedicine* 2024; 77: 102884.

Menopausal Microbiota

How the menopausal microbiome impacts women's overall health

Menopause-induced changes lower gut microbiome diversity and cause a shift toward greater similarity to the male gut microbiome. This review details the health-related consequences of these changes. During perimenopause, a gradual decline in hormone levels disrupts the gut microbiome balance and contributes to adverse health outcomes, including cardiometabolic disease and changes in oestrogen metabolism. Hormonal fluctuations during menopause change the oral microbiome, heightening the risk for dental caries, periodontitis, and oral infections such as candidiasis. Menopause-induced vaginal microbiota alterations increase susceptibility to bacterial vaginosis, vulvovaginal atrophy, and recurrent urinary tract infections. Menopause also alters the diversity and abundance of gut microbiota that have been linked to inflammation. Chronic dysbiosis-induced inflammation predisposes menopausal women to metabolic disorders and autoimmune diseases.

This article bridges the gap between endocrinology and microbiology, and emphasises the systemic impact of menopause beyond reproductive health. A key strength of the review is its holistic examination of menopausal-related hormonal fluctuations with corresponding shifts in gut and vaginal microbial composition and diversity. This opens the door to exploring microbiome-based biomarkers for managing menopausal symptoms such as genitourinary syndrome, metabolic changes, or inflammation. This article's interpretation of age-related changes in women's health enriches the growing interest in the human microbiome's role in disease. While hormone replacement therapy has shown promise in mitigating some of the adverse effects of oestrogen deficiency, its broader application is limited by its systemic risks. The targeted use of specific probiotics to restore gut microbial balance, coupled with dietary and lifestyle modifications, may offer safer, more individualised alternatives that mitigate adverse health effects of menopause.

Menopausal microbiome research is overrepresented with data from Western populations and a lack of detailed mechanistic insights. Since diet, lifestyle, and environmental factors significantly influence the microbiome, we need ethnically and geographically diverse research incorporating advanced "omics" approaches to fully elucidate these influences. More effective, personalised treatment strategies will then emerge that can improve the quality of life for menopausal women.

In conclusion, menopause is a whole-body transition involving significant changes in the microbial ecosystem. Understanding and addressing these changes can enhance patient outcomes and promote healthier ageing in women.

Nieto MR, Rus MJ, Areal-Quecuty V, *et al.* Menopausal shift on women's health and microbial niches. *npj Women's Health* 2025; 3: 3.

Vaginal Microbiota

The role of the vaginal microbiota in women's health

The human body hosts trillions of microorganisms, collectively known as the microbiome, residing in various locations and coexisting in a complex symbiotic partnership. Importantly, the vaginal microbiota influences women's reproductive and overall health. Understanding this ecosystem could revolutionise the prevention and treatment of these conditions.

This review highlights the links between dysbiosis of the vaginal microbiota and gynaecological disorders, as well as pregnancy-related complications. Specifically, reductions in lactobacilli and an increased vaginal microbiota diversity are associated with human papillomavirus (HPV) infection, the formation of cervical lesions, and cervical cancer. A loss of vaginal *Lactobacillus* dominance can create a proinflammatory environment that compromises successful embryonic implantation, leading to infertility. An imbalance in the vaginal microbiome can trigger inflammation leading to pregnancy complications. Having fewer *Lactobacillus* species in the vaginal microbiome increases the risks of premature rupture of membranes, preterm birth, miscarriage, and ectopic pregnancy. Vaginal dysbiosis may contribute to insulin resistance, a hallmark of gestational diabetes mellitus, and greater diversity in bacterial composition has been found in severe preeclampsia. Testing for *Prevotella bivia* colonisation during pregnancy may help to predict and mitigate against hypertensive disorders during pregnancy.

This review underscores the key relevance of the vaginal microbiome in women's reproductive and overall health. The composition of this microbiome can impact everything from fertility and pregnancy outcomes to infection susceptibility. The article covers various aspects of vaginal microbiota, including its relationship with immune system function, inflammation, and pathogen defence, and thereby offers a broad, holistic understanding of its role with generalisable insights into women's health at large. Enhanced knowledge around how the vaginal microbiome influences health presents an important advance for early disease detection and prevention, instead of treating infections or conditions after they appear. However, long-term study data are needed to clarify the long-term effects of vaginal microbiome imbalances. Moreover, while probiotics and other microbiome-based interventions show promise for maintaining a healthy vaginal microbiome, probiotic strains, dosages, and delivery mechanisms have yet to be standardised for clinical application. Much work remains to be done.

In sum, having fewer vaginal *Lactobacillus* species and increased vaginal microbial diversity is associated with obstetric and gynaecological complications. This review highlights the possibility of using microbiome-based diagnostics to detect imbalances in vaginal flora, potentially before symptoms manifest. Early intervention may prevent adverse consequences.

Paduch-Jakubczyk W, Dubińska M. The role of vaginal microbiota in women's health. *Actual Gyn* 2024; 16: 75-9.

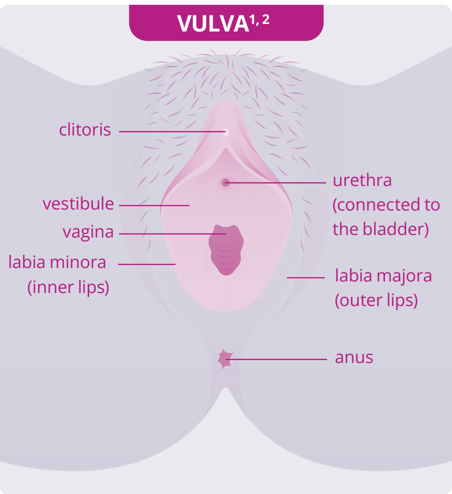
Women's microbiota:
The missing piece in intimate health

download

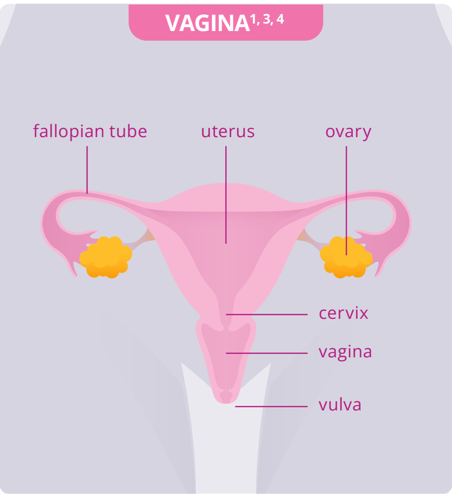
What are they and how to protect them?

LET'S TALK ABOUT ANATOMY

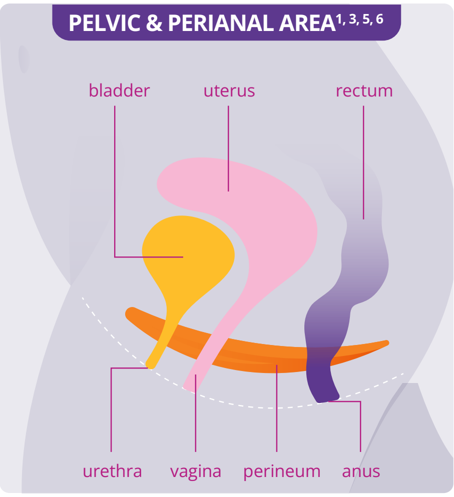
VULVA[1, 2]



VAGINA[1, 3, 4]



PELVIC & PERIANAL AREA[1, 3, 5, 6]



5 THINGS TO KNOW[1, 2, 3]

- **Vulva** is NOT vagina
- the **vulva, vagina, bladder** and **perianal** areas all harbour a **specific microbiota** (flora)
- the **vulvar** microbiota is a **microbial crossroad**, containing microorganisms of **skin, vaginal** and **gut** origin
- **women's microbiota** play a crucial **role in reproductive and overall health**
- **lactobacilli** are beneficial colonisers of the **female genital tract** that protect **against pathogenic microbes**

AN IMBALANCED MICROBIOTA IN THE FEMALE GENITAL TRACT MAY BE ASSOCIATED WITH CERTAIN DISEASES. . .

vulvar diseases[1, 2, 7, 8]
candidiasis, vulvodynia, vulvar lichen sclerosus. . .

urinary tract diseases[1, 6, 9]
urinary tract infections, incontinence. . .

vaginal diseases[1, 3, 4]
candidiasis, bacterial vaginosis, HPV, sexually transmitted infections. . .

perianal diseases[1, 10, 11]
perianal infection, dermatosis. . .

KEY FACTORS INFLUENCING MICROBIOTA[1, 2, 4, 5, 12-17]

intimate microbiota

environmental factors	individual factors	bad hygiene practices
lifestyle	hormones	vaginal douches
diet	diseases	scented products, strong soaps
mental state	age	washing >2 times daily
drugs	genetic factors	full hair removal
	ethnicity	tight/ synthetic clothes

GOOD HABITS TO MAINTAIN A BALANCED MICROBIOTA[1, 13, 17-20]

The vagina is self-cleaning

- cotton underwear is best
- a gentle, soap-free cleanser
- external wash only 1-2 times daily
- sleep without underwear at night
- wipe front to back
- prebiotics
- probiotics

Sources

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2026 International Grant:
Microbiota & Women's Health

Since 2017, the Biocodex Microbiota Foundation has supported innovative research projects around the world to deepen our understanding of human microbiota's role in health and disease. To date, the role of women's microbiota remains largely underexplored. In 2024, only 493 publications on the vaginal microbiota were indexed on PubMed, compared with over 17,000 publications on the gut microbiota. In order to address this lack of knowledge, the Biocodex Microbiota Foundation is launching an international grant dedicated to women's health. This new grant is intended to help support international research proposals involving the microbiota and its implication in women's health and disease. The grant confirms the Foundation's commitment to accelerating research on microbiota and supporting the emergence of innovative solutions for women's health.

The topic of this 2026 international grant is "Women's Microbiota and Reproduction: Functional Exploration at the Host-Microbiota Interface". This topic was defined by the Microbiota & Women's Health International Scientific Committee composed of Dr. Pedro Vieira Baptista (Portugal), Prof. Pierre-Emmanuel Bouet (France), Assoc. Prof. Ina Schuppe Koistinen (Sweden), Prof. Maria Kyrgiou (United Kingdom), Prof. Jacques Ravel (USA), and Prof. Henriette Svarre Nielsen (Denmark). This grant is open to all researchers affiliated with a university, hospital or research institute, in the following (or related) fields — gynaecology, obstetrics; microbiology, infectious diseases; internal medicine; and oncology — with no geographical restrictions: applications from around the world are welcome. Previous recipients of other Biocodex Foundation grants (National Grant, Henri Boulard Award, Gut International Grant) are also eligible to apply.


MICROBIOTA & WOMEN'S HEALTH INTERNATIONAL GRANT

Your research could make a difference!

Topic of this new grant for 2026:

Women's Microbiota and Reproduction: Functional Exploration at the Host-Microbiota Interface.

Grant amount: €200,000

Application deadline: 30th September 2025

Winner announcement: January 2026

Contact: contact@biocodexmicrobiotafoundation.com

Details and application form

More information: Microbiota & Women's Health International Call for Projects | Biocodex Foundation

Continued Medical Education (CME)
Course for gynaecologists, GPs, midwives, and pharmacists

The Biocodex Microbiota Institute and Xpeer Medical Education invite you to take part in a free, accredited CME course on the significance of microbiota, particularly vaginal microbiota, for intimate health. The course is led by Prof. Alessandra Graziottin (Italy), a renowned gynaecologist, oncologist, sexologist, psychotherapist, and director of the Center for Gynecology and Medical Sexology at the San Raffaele Resnati Hospital in Milan. The course provides in-depth insights into the evolution of gut and vaginal microbiota from infancy to menopause, and describes how these microbiota impact hormonal balance, fertility, and intimate health throughout different life stages. Insights into the vaginal microbiota throughout different life stages include the potential for a sterile placenta, neonatal microbiota, and changes during infancy, puberty, fertile years, and menopause. You will be given practical recommendations and key takeaways for applying the necessary knowledge and skills in your clinical practice.

The course is available in five languages and is delivered in 5-minute micro-learning videos. This educational activity is supported by an unrestricted grant from the Biocodex Microbiota Institute.


by Prof. Alessandra Graziottin

Woman's microbiota

Free training on "Microbiota in intimate woman health through the lifespan"

With the support of an unrestricted grant from Biocodex Microbiota Institute

More information: https://www.biocodexmicrobiotainstitute.com/en/pro/xpeer-course-microbiota-intimate-woman-health-through-lifespan

International Microbiota Observatory
3rd EDITION - 2025

Microbiota Momentum: Bridging Awareness and Action

The vaginal microbiota is essential to women's health. But how well-known is it among women? What behaviours do they adopt to protect it? What information do they receive from their healthcare professionals? How have knowledge and attitudes about the vaginal microbiota changed since 2024?

What women know (and don't know) about their vaginal microbiota

- For the third year running, the Biocodex Microbiota Institute in France commissioned Ipsos in 2025 to conduct a major international survey on microbiota: the International Microbiota Observatory. This large survey was conducted by Ipsos among 7,500 people including nearly 4,000 women in 11 countries (the USA, Mexico, Brazil, Portugal, France, Germany, Italy, Poland, Finland, China and Vietnam).
- Within each country, a representative sample of the population aged 18 years and over was interviewed. Representativeness was ensured by the quota method applied to the respondent's gender, sex, age, occupation, and geographical region. A total of 3,862 women participated in the online survey, which was conducted from January 21 to February 28, 2025.
- The third wave of this study once again highlights women's lack of awareness about the vaginal microbiota, which remains largely unknown. However, the study also indicates that knowledge and behaviours have improved over the last two years, thanks to more widespread education from healthcare professionals.
- Age is a determining factor when it comes to the vaginal microbiota: women aged 60 years and over are less aware than those aged 25–34 years and mothers of children under 3 years. Education about the vaginal microbiota, including its roles and functions, must be highlighted and extended to all women, especially those aged 60 years and over.

The vaginal microbiota: an increasingly understood organ

Awareness and knowledge is on the rise among women

1 out of 4
know exactly what the vaginal microbiota is
(24%, +5 points vs 2023)

2 out of 3
are aware that each woman's vaginal microbiota is unique
(66%, +9 points vs 2023)

72%
are aware that antibiotics can alter the vaginal microbiota
(+1 point vs 2024)

60%
are aware that the vaginal microbiota changes throughout a woman's life
(+9 points vs 2023)

But, knowledge gaps persist regarding its functioning

55%
know that smoking affects the vaginal microbiota
(-1 point vs 2024)

45%
know that the gut microbiota influences the vaginal microbiota
(-1 point vs 2024)

Bridging the gap between awareness and action

Some positive habits are widely adopted by women . . .

84% wear **cotton underwear**
(+1 point vs 2023)

66% **avoid self-medication**
(+5 points vs 2023)

. . . as well as practices that are harmful to vaginal microbiota

54%
wash their body several times a day

38%
take vaginal douches
(-4 points vs 2023)

Women seek guidance from healthcare professionals

Only a minority of women are informed by their healthcare professionals about the role of the vaginal microbiota

37% have received information about the vaginal microbiota, its roles and functions
(+1 point vs 2023)

42% have received explanations on how to best preserve their vaginal microbiota
(+2 points vs 2023)

Vaginal microbiota and health: a large majority of women are asking for more information

85%
would like to receive more information from their healthcare professionals about the importance of the vaginal microbiota and its impact on health
(+3 points vs 2023)

Mothers and women aged 25–34 years are more aware than older-aged women

38%
of mothers with children under 3 years

32%
of 25–34 year-olds

19%
of over 60s

» Know exactly what the vaginal microbiota is

VS

24%
women of all ages

57%
of mothers with children under 3 years

44%
of 25–34 year-olds

28%
of over 60s

» Have been informed by a healthcare professional about the roles and functions of the vaginal microbiota

VS

37%
women of all ages

Methodology:

7,500 individuals were surveyed online from January 21 to February 28, 2025 in 11 countries: the USA, Mexico, Brazil, Portugal, France, Germany, Italy, Poland, Finland, China and Vietnam.

Within this sample, 3,862 women were interviewed.

Representative samples by country are ensured by the quota method applied to the respondent's gender, sex, age, occupation, and geographical region.

All point changes in percentages relate to data collected from the 2024 or 2025 International Microbiota Observatory surveys compared with the 2023 survey data. Newly introduced questions in the 2025 survey could not be analysed against previous surveys.

11
Countries

7,500
Respondents

3,862
Women

BMI-25.22

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Organisation Highlight

Foundation for Endometriosis Research and Expert Interview

Prof. Andrew Horne
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Dr. William Fusco
Gastroenterologist and microbiome clinical researcher at the Agostino Gemelli Polyclinic, Rome, Italy

What about Men?

Prof. Jean-Marc Bohbot
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Bacterial vaginosis: clue cell in a Gram-stained smear, page 4. Courtesy of Prof. Piet Cools.

Bacterial vaginosis: fluorescence *in situ* hybridization (FISH), page 7. Courtesy of Prof. Alexander Swidsninski.

Male and female reproductive organs, page 10. Shutterstock.

Woman patient with a senior gynecologist during the consultation, page 15. Shutterstock.

Mature female friends socializing, page 18. Shutterstock.

Female doctor explaining uterus model to woman, page 18. Shutterstock.

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