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GYNECOLOGICAL MICROBIOME ASSESSMENT

TEST ID: sample1
DATE: 2025-11-25

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THE VAGINAL BACTERIAL COMMUNITY STATE TYPE

Classification of the vaginal bacterial community into Community State Types (CST) is a specialized diagnostic tool used to evaluate microbial communities in the vaginal environment. This system categorizes vaginal microbiomes into five distinct groups (from CST I to CST V), aiding in the personalization of treatment strategies and enhancing understanding of vaginal health, particularly in managing conditions like bacterial vaginosis and other vaginal infections. A healthy vaginal microbiome is predominantly composed of Lactobacillus species, which make up about 90-95% of the total bacterial population. These beneficial bacteria help maintain vaginal health by producing lactic acid, which keeps the vaginal pH low, inhibiting the growth of harmful microorganisms. A decline in Lactobacilli enables anaerobic bacteria to multiply, disrupting the natural balance and potentially leading to bacterial vaginosis. **CST I** is the healthiest state, dominated by *Lactobacillus crispatus*, associated with a stable and protective vaginal environment. **CST II** is characterized by the presence of*Lactobacillus gasseri*, indicating a healthy but slightly less stable microbiome. **CST III** is dominated by *Lactobacillus iners*, which is associated with a more variable vaginal environment and a higher risk of dysbiosis. **CST IV** is marked by a diverse bacterial composition with a significant reduction in *Lactobacilli*, creating an environment where anaerobic bacteria can thrive. Common species include *Gardnerella vaginalis*, *Atopobium vaginae*, *Ureaplasma urealyticum*, *Mycoplasma hominis*, *Prevotella*, *Peptoniphilus*, *Megasphaera*, and *Mobiluncus*. This state is often linked to bacterial vaginosis. **CST V** is characterized by *Lactobacillus jensenii*, associated with a relatively stable and protective vaginal microbiome, though less common than CST I. The CST system plays a crucial role in diagnosing and managing vaginal health by identifying microbial imbalances and guiding appropriate treatment strategies, particularly for bacterial vaginosis and related infections. [1], [2]

Species name	Prevalence (%)
Lactobacillus crispatus	Negative (0.0%)
Lactobacillus gasseri	Negative (0.0%)
Lactobacillus iners	Positive (6.36%)
Lactobacillus jensenii	Negative (0.0%)
Other species	93.64%

Your CST type: **IV**.

SEXUALLY TRANSMITTED INFECTIONS

Sexually Transmitted Infections (STIs) are among the most common acute health conditions worldwide. While most STIs are not life-threatening, they can cause serious complications if left untreated. These infections are caused by bacteria, viruses, or other microorganisms transmitted through blood, semen, vaginal fluids, or other body secretions during oral, anal, or vaginal intercourse with an infected partner. Without prompt identification and treatment, STIs can lead to long-term health problems known as **Sexually Transmitted Diseases (STDs)**. Sexually transmitted diseases (STDs) can lead to various complications that affect both reproductive and systemic health. In terms of **reproductive health issues**, STDs may result in conditions such as pelvic inflammatory disease (PID), which can further increase the risk of ectopic pregnancy, infertility, and chronic pelvic pain. Beyond reproductive health, STDs can also pose **systemic health risks**, including neurological conditions and cardiovascular diseases. **Pregnancy-related complications** are another serious concern. STDs can lead to adverse outcomes such as fetal or newborn death, preterm birth, and neonatal health problems. These may include neonatal meningitis, eye infections, and pneumonia, all of which can have long-term consequences for the child's health. Additionally, STIs can increase the risk of **HIV infection**, making early detection, prevention, and treatment crucial for maintaining overall health. [3], [4]

Type of agent	Species name	Caused condition	Result and prevalence (%)
Bacteria	Chlamydia trachomatis	Lymphogranuloma venereum	Negative (0.0%)
	Neisseria gonorrhoeae	Gonorrhea	Negative (0.0%)
	Treponema pallidum	Syphilis (Lues)	Negative (0.0%)
	[Haemophilus] ducreyi	Ulcus molle	Negative (0.0%)
	Mycoplasmoides genitalium	Mycoplasmosis	Negative (0.0%)
Protozoan	Trichomonas vaginalis	Trichomoniasis	Negative (0.0%)

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A healthy vaginal microbiome includes various species of *Lactobacillus*. In a healthy vaginal flora, *Lactobacillus* species dominate, making up about 90-95% of all bacteria. These species produce hydrogen peroxide and lactic acid, which lower the vaginal pH and create an acidic environment. They also produce bacteriocins, which effectively inhibit the overgrowth of other bacteria in the vagina. If these normal *Lactobacillus* species are absent or significantly reduced, the vaginal ecosystem becomes imbalanced. This enables previously low-level organisms, such as fungi or strict and facultative anaerobic bacteria, to proliferate. Examples of bacterial vaginosis-related bacteria include *Gardnerella vaginalis*, *Atopobium vaginae*, *Ureaplasma urealyticum*, *Mycoplasma hominis, Prevotella*, *Peptoniphilus*, *Megasphaera*, *Mobiluncus*, and other bacteria that thrive in a higher pH environment due to the lack of *Lactobacillus* [5]. Anaerobic bacteria causing bacterial vaginosis act synergistically during infection and can form a multi-species biofilm on the vaginal wall. Bacterial vaginosis can increase the risk of several sexually transmitted infections, such as HIV, *Neisseria gonorrhea*, *Chlamydia trachomatis*, *Trichomonas vaginalis*, and *herpes simplex virus type 2* [6].

Bacterial vaginosis associated microorganisms:

Taxon name	Result and prevalence (%)
Dialister spp.	Positive (0.54%)
Escherichia coli	Negative (0.0%)
Fannyhessea vaginae	Positive (62.39%)
Gardnerella greenwoodii	Negative (0.0%)
Gardnerella swidsinskii	Negative (0.0%)
Gardnerella vaginalis	Positive (23.84%)
Klebsiella spp.	Negative (0.0%)
Leptotrichia spp.	Negative (0.0%)
Megasphaera spp.	Negative (0.0%)
Metamycoplasma hominis	Positive (2.33%)
Mobiluncus curtisii	Negative (0.0%)
Peptoniphilus spp.	Negative (0.0%)
Prevotella spp.	Positive (2.94%)
Proteus spp.	Negative (0.0%)
Sneathia spp.	Negative (0.0%)
Ureaplasma urealyticum	Positive (0.79%)

Aerobic vaginitis is clearly distinguishable from fungal infections and bacterial vaginosis. Incorrect or delayed diagnosis can often lead to treatment failures and severe complications such as pelvic inflammatory disease, infertility, preterm birth, fetal infections, and an increased risk of bacterial and viral sexually transmitted infections. The clinical features of aerobic vaginitis include a reduction in Lactobacillus populations, an increased presence of aerobic bacteria originating from the gastrointestinal tract, and vaginal inflammation. The most commonly detected aerobic bacteria include *Streptococcus agalactiae*, *Streptococcus pyogenes*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Escherichia coli*, and enterococci, primarily *Enterococcus faecalis* [7], [8]. Additionally, the presence of other bacteria such as *Klebsiella*, *Pseudomonas*, *Proteus*, *Haemophilus influenzae*, *Acinetobacter*, and *Citrobacter* has also been identified [9], [10].

Taxon name	Result and prevalence (%)
Acinetobacter spp.	Negative (0.0%)
Citrobacter spp.	Negative (0.0%)
Enterococcus faecalis	Negative (0.0%)
Escherichia coli	Negative (0.0%)
Haemophilus influenzae	Negative (0.0%)
Klebsiella spp.	Negative (0.0%)
Proteus spp.	Negative (0.0%)
Pseudomonas spp.	Negative (0.0%)
Staphylococcus aureus	Negative (0.0%)
Staphylococcus epidermidis	Negative (0.0%)
Streptococcus agalactiae	Negative (0.0%)
Streptococcus pyogenes	Negative (0.0%)

GROUP B STREPTOCOCCUS SCREENING

Group B *Streptococcus agalactiae* (GBS) is carried by 5-25% of women in their vaginal flora. Screening for GBS is particularly important in pregnant women, as this bacterium poses a significant risk to newborns. In recent decades, neonatal GBS infections have been associated with considerable morbidity and mortality during the perinatal period. GBS is also recognized as the leading cause of early-onset neonatal sepsis. The primary source of neonatal infection is maternal colonization of the vaginal tract. GBS is transmitted vertically during childbirth and can affect up to 80% of newborns born to colonized mothers. Screening for GBS is recommended between the 35th and 37th weeks of gestation. Maternal GBS colonization is also linked to an increased risk of urinary tract infections and certain pregnancy complications, such as endometritis, chorioamnionitis, preterm birth, and intrauterine fetal death [11], [12].

Taxon name	Result and prevalence (%)
Streptococcus agalactiae	Negative (0.0%)

The recognition of viral infections occurring in the vaginal environment is of great importance, as they may not only cause local symptoms but also have long-term health effects. These can affect fertility, the course of pregnancy, and the health of the newborn. Our screening detects the presence of the following clinically most relevant viruses:

HUMAN PAPILLOMAVIRUS (HPV)

Human papillomaviruses (HPVs) primarily infect epithelial cells of the skin and mucous membranes. It is estimated that approximately 80% of individuals acquire HPV infection during their lifetime, usually before the age of 50. From a clinical perspective, the most significant group is the genus Alphapapillomavirus, which infects epithelial cells of the anal and genital region. HPV types are classified into low- and high-risk categories based on their oncogenic potential. High-risk types, such as HPV16, 18, and 31, are associated with precancerous and cancerous lesions of the anal and genital region and are particularly prevalent among sexually active populations. HPV is detectable in more than 99% of cervical cancers, over 90% of anal cancers, and nearly 70% of penile, vulvar, and vaginal cancers. Preventive strategies include vaccination and the use of condoms, both of which significantly reduce the risk of transmission. [13], [14], [15]

Taxon name	Caused condition	Result
Human papillomavirus 16 (HPV16)	Cervix carcinoma (high risk), warts	Negative
Human papillomavirus 18 (HPV18)	Cervix carcinoma (high risk), warts	Negative
Human papillomavirus 31 (HPV31)	Cervix carcinoma (high risk), warts	Negative
Other HPV (low risk)	Warts	Negative
Other HPV (high risk)	Cervix carcinoma, warts	Negative

HERPES SIMPLEX VIRUS TYPE 1 AND 2 (HSV-1/2)

Herpes simplex viruses (HSV-1 and HSV-2) are among the most common etiological agents of herpesvirus infections. Although both types cause similar infections, they typically affect different anatomical sites and may present with distinct clinical manifestations. Infection often remains subclinical, producing mild or no symptoms, which contributes to the frequent unrecognized carriage of the virus. HSV-1 primarily causes oral herpes, characterized by vesicular and subsequently ulcerative lesions on and around the lips and oral cavity. HSV-2 is most commonly associated with genital herpes, presenting with painful vesicular or ulcerative lesions of the genitalia, anus, or surrounding skin. Transmission occurs mainly through sexual contact, but vertical transmission may also occur during childbirth, posing a serious risk to the neonate. Thus, early detection and adequate clinical management are of critical importance. A key feature of herpes simplex viruses is their ability to establish latency in the host after primary infection, with subsequent periodic reactivation triggered by factors such as stress, illness, or immunosuppression, leading to recurrent disease episodes. [16], [17], [18], [19]

Taxon name	Caused condition	Result
Herpes simplex virus type 1 (HSV-1)	blisters, ulcers	Negative
Herpes simplex virus type 2 (HSV-2)	genital herpes	Negative

EPSTEIN-BARR VIRUS (EBV)

The Epstein–Barr virus (EBV) is a member of the herpesvirus family and is implicated in a wide spectrum of diseases. It is most widely known as the causative agent of infectious mononucleosis (Pfeiffer's disease, or "kissing disease"), which is transmitted primarily through saliva. EBV has also been linked to the development of certain malignancies (e.g., Burkitt's lymphoma), autoimmune diseases (e.g., multiple sclerosis), and some neurodegenerative disorders. The virus predominantly infects epithelial cells of the mucosa and B lymphocytes, which play a central role in humoral immunity. Although less common, vaginal infection can manifest with painful ulcerative lesions. [20], [21]

Taxon name	Caused condition	Result
Epstein-Barr virus (EBV)	Mononucleosis infectiosa, ulcers	Negative

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HUMAN CYTOMEGALOVIRUS (HCMV)

Human cytomegalovirus (HCMV) belongs to the group of herpesviruses infecting humans. It primarily targets epithelial cells of the mucosa and poses substantial health risks in immunocompromised individuals. Infection is most frequently associated with mononucleosis-like syndromes and pneumonia. HCMV can be transmitted through multiple body fluids, including blood, urine, saliva, breast milk, tears, semen, and vaginal secretions. Vaginal infection may present with fever and hemorrhagic ulcerative lesions of the genital and perianal regions. [22], [23]

Taxon name	Caused condition	Result
Human cytomegalovirus (CMV)	Mononucleosis	Negative

MOLLUSCUM CONTAGIOSUM VIRUS (MCV-1/2)

Molluscum contagiosum, also referred to as water warts, is a common viral skin infection caused by the Molluscum contagiosum virus, a member of the Poxviridae family. Transmission typically occurs via direct contact or exposure to contaminated water environments, such as swimming pools, making acquisition possible even during casual bathing. The characteristic clinical presentation consists of small, dome-shaped, often pruritic papules, which may develop on various body sites, including the arms, legs, and genital area. Secondary scratching of the lesions may result in inflammation and subsequent scarring during healingv. [24], [25]

Taxon name	Caused condition	Result
Molluscum contagiosum virus subtype 1	Molluscum contagiosum (warts)	Negative
Molluscum contagiosum virus subtype 2	Molluscum contagiosum (warts)	Negative

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In addition to bacteria, fungi can also be present in the vagina, forming part of the vaginal mycobiome. Although their prevalence and abundance are not yet fully mapped, they occur much less frequently and with a lower microbial load compared to bacteria. Nevertheless, they play a significant role in vaginal health, both negatively (by causing infections) and positively (by supporting health). The most commonly detected fungal species includes the primary pathogen *Candida albicans*, which is the most studied and frequently detected fungal species. It is recognized as the leading cause of vulvovaginal candidiasis. However, other species have also been detected in the vagina, including *Candida parapsilosis*, *Candida tropicalis*, *Candida sake*, *Candida dubliniensis*, *Candida spencermartinsiae*, *Clavispora lusitaniae*, *Meyerozyma guilliermondii*, *Kluyveromyces marxianus*, *Pichia kudriavzevii*, and *Nakaseomyces glabratus*. While *C. albicans* is commonly present even in a healthy vaginal mycobiome, its overgrowth can cause vulvovaginal candidiasis, making it the most significant fungal pathogen in this context [26].

VULVOVAGINAL CANDIDIASIS

Vulvovaginal candidiasis is one of the most common infections of the female genital tract. Based on current knowledge, this condition is not classified as a sexually transmitted disease. However, it most frequently occurs at the onset of sexual activity and during the most sexually active years. Despite this, the occurrence of the infection is often unrelated to the number of sexual partners or the frequency of sexual activity. Vulvovaginal candidiasis, caused by opportunistic fungi, typically develops when the immune system is compromised, such as during dysbiosis or pregnancy. Microbial dysbiosis has long been associated with vulvovaginal candidiasis, as it has been observed that antibiotic-induced dysbiosis dramatically increases the risk of developing the infection. The majority of the cases (80–85%) are caused by *Candida albicans*, while non-*albicans* species account for only 5–20% of cases. Among infections involving non-*albicans Candida* species, most are linked to *Nakaseomyces glabratus* (5–10% of cases) or *Candida tropicalis* (about 5%). *Pichia kudriavzevii*, however, is a rare cause of fungal vaginitis [27].

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USUALLY PRESENT FUNGI SPECIES

Taxon name	Result and prevalence (%)
Candida albicans	Negative (0.0%)
Candida dubliniensis	Negative (0.0%)
Candida parapsilosis	Negative (0.0%)
Candida tropicalis	Negative (0.0%)
Clavispora lusitaniae	Negative (0.0%)
Kluyveromyces marxianus	Negative (0.0%)
Meyerozyma guilliermondii	Negative (0.0%)
Nakaseomyces glabratus	Negative (0.0%)
Pichia kudriavzevii	Negative (0.0%)
Saccharomyces cerevisiae	Negative (0.0%)
[Candida] sake	Negative (0.0%)
[Candida] spencermartinsiae	Negative (0.0%)

DETECTED TAXA IN THE SAMPLE

Every detected microbial taxon and their relative abundance in a descending manner:

Species name	Prevalence (%)
Fannyhessea vaginae	62.39%
Gardnerella vaginalis	23.84%
Lactobacillus iners	6.36%
Prevotella bivia	2.94%
Metamycoplasma hominis	2.33%
Ureaplasma urealyticum	0.79%
Dialister micraerophilus	0.54%
Gardnerella piotii	0.46%
Veillonella montpellierensis	0.35%

DETECTED VIRUSES

No viruses were found during the test.

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