NEXT-GENERATION SEQUENCING - ANALYSIS OF THE VAGINAL MICROBIOME

SYNLAB MVZ Weiden • Zur Kesselschmiede 4 • 92637 Weiden

Medical report

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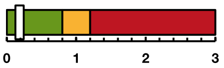
Patient information

Patient:	**MUSTERMANN, ERIKA**
Date of birth:	01.01.2000
Sample-ID:	1234567890
Request date:	02.01.2025
Report date:	08.01.2025
Pregnancy:	☐ yes ☑ no **WG:** -
Specimen type:	Vaginal swab
Diagnosis:	Routine check-up

Results overview

Species diversity

0,18



normal range

Community State Type

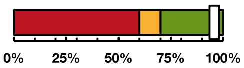
II

good

L. gasseri dominiert
positive properties

Lactobacilli proportion

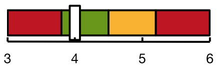
95,72%



normal range

pH Value

4,00



normal range

Vaginal mycosis

not detected

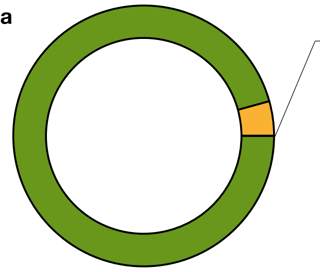
Trichomonas vaginalis

not detected

The vaginal microbiome composition

Composition of the vaginal microbiota

🟩	Protective	95,73%
🟨	Accompanying	4,27%
🟥	Pathogenic	0,00%



Composition of the pathogenic vaginal microbiota

Bacterial vaginosis - associated bacteria	0,00%
Sexually transmitted pathogens	0,00%
Aerobic vaginitis/acute vaginal infection	0,00%
Gastrointestinal/cutaneous/oral contamination	0,00%
Cervicitis - associated bacteria	0,00%
Potential risk of infection for the fetus	0,00%

Medical findings

Physiological vaginal flora with a normal proportion of lactobacilli. Lactobacillus gasseri predominates among the lactobacilli (Community State Type II). This species promotes vaginal health by lowering the pH through the production of D-lactate and L-lactate, thereby inhibiting the growth of undesirable microorganisms. The species diversity (Shannon index) is within the normal range. The proportion of pathogenic microbes is unremarkable. There is no evidence of a vaginal mycosis. No trichomonads were detected. The pH value is in the physiological range.

Overall healthy vaginal microbiome without abnormalities.

Therapy recommendations

Due to the unremarkable findings, no treatment recommendations are made.

The vaginal microbiome composition

Protective vaginal microbiota

Result

95,73%

Vaginal microbiome composition

Lactobacilli are the main bacteria species in the physiological vaginal microbiome. They represent a physiological protective microbiota against other bacteria in the microbiome and even against STDs. By metabolizing sugars to D/L-lactate, they lower the pH-value. In addition, many lactobacilli release hydrogen peroxide and other bactericides.

These and other factors, in particular the so-called surface active molecules (SAMs) create a microbial protective film, which prevents uprising infections caused by pathogens, that otherwise would result in a shift in equilibrium and the formation of a pathological biofilm.

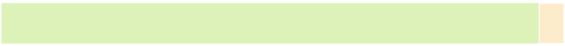
However, not all lactobacilli are equally protective. For example Lactobacillus iners (CST III) does not form D-lactate but predominantly L-lactate, which has no protective effect. Thus, the exact knowledge of the lactobacilli species - which is challenging to achieve with classic cultivation methods - is decisive for the evaluation of the vaginal microbiome.

Genus	Species	Rel. Abundance
Bifidobacterium	spp.	0,00%
Lactobacillus	spp.	95,72%
Lactobacillus	acidophilus	0,00%
Lactobacillus	casei	0,00%
Lactobacillus	crispatus	0,00%
Lactobacillus	delbrueckii	0,00%
Lactobacillus	fermentum	0,00%
Lactobacillus	gasseri	69,25%
Lactobacillus	helveticus	0,00%
Lactobacillus	iners	0,00%
Lactobacillus	jensenii	0,00%
Lactobacillus	paracasei	0,00%
Lactobacillus	plantarum	0,00%
Lactobacillus	reuteri	0,24%
Lactobacillus	rhamnosus	0,00%
Lactobacillus	salivarius	0,00%

Bacterial vaginosis - associated bacteria (BVAB)

Result

0,00%



Vaginal microbiome composition

The prevalence of bacterial vaginosis (BV) in Europe is around 23%. The main causative pathogens are Gardnerella vaginalis followed by Atopobium vaginae. In addition, there are numerous other potentially pathogenic bacteria, which largely elude the classic cultural detection methods but can clearly be detected with the new NGS technology.

Since there are different pathogenic subtypes (A - D) of Gardnerella vaginalis, its detection does not automatically correlate with bacterial vaginosis. Therefore knowing the entire spectrum of pathogens in a occurring bacterial vaginosis, enables the application of targeted antibiotics and probiotics, if necessary.

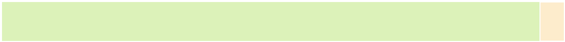
Genus	Species	Rel. Abundance
Actinomyces	spp.	0,00%
Anaerococcus	spp.	0,00%
Atopobium	spp.	0,00%
Bacteroides	fragilis	0,00%
Bacteroides	spp.	0,00%
Clostridium	spp.	0,00%
Dialister	spp.	0,00%
Eggerthella	spp.	0,00%
Gardnerella	vaginalis	0,00%
Lachnospira	spp.	0,00%
Leptotrichia	amnionii	0,00%
Mageeibacillus	indolicus	0,00%
Megasphaera	spp.	0,00%
Mobiluncus	spp.	0,00%
Parvimonas	micra	0,00%
Peptoniphilus	spp.	0,00%
Porphyromonas	spp.	0,00%
Prevotella	spp.	0,00%
Sneathia	sanguinegens	0,00%
Sneathia	spp.	0,00%

The vaginal microbiome composition

Sexually transmitted pathogens

Result

0,00%



Vaginal microbiome composition

Genus	Species	Rel. Abundance
Chlamydia	trachomatis	0,00%
Haemophilus	ducreyi	0,00%
Klebsiella	granulomatis	0,00%
Mycoplasma	genitalium	0,00%
Mycoplasma	hominis	0,00%
Neisseria	gonorrhoeae	0,00%
Neisseria	meningitidis	0,00%
Treponema	pallidum	0,00%
Trichomonas	vaginalis	negative
Ureaplasma	parvum	0,00%
Ureaplasma	urealyticum	0,00%

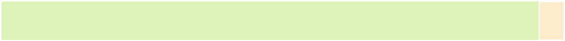
NGS is used to reliably detect sexually transmitted pathogens. Trichomonads are protozoa and cannot be detected by 16S-RNA sequencing. Therefore a singular PCR analysis for the detection of these often underdiagnosed pathogens is performed. If one of these pathogens is detected, a partner diagnostics should be carried out. Corresponding therapy recommendations can be found in our medical report.

The most common symptoms of STDs are: Urethral or vaginal discharge, painful or painless genital ulceration, inguinal swelling and lower abdominal pain. As STDs can occur without pain or symptoms, they are often undiagnosed and untreated.

Aerobic vaginitis/acute vaginal infection

Result

0,00%



Vaginal microbiome composition

Genus	Species	Rel. Abundance
Enterococcus	spp.	0,00%
Escherichia	spp.	0,00%
Staphylococcus	aureus	0,00%
Staphylococcus	epidermidis	0,00%
Staphylococcus	lugdunensis	0,00%
Streptococcus	agalactiae	0,00%
Streptococcus	anginosus	0,00%
Streptococcus	dysgalactiae	0,00%
Streptococcus	pyogenes	0,00%

Aerobic vaginitis (according to Donders/Belgium) is a condition, where women complain about an unpleasant fluorine and in which pH values of five to six are reported. The numerous leucocytes, which can be seen in the native compound with coccoid microbiota, are difficult to treat. A clear inflammatory reaction is the main difference to bacterial vaginosis. The cause is often a mixed microbiota of haemolytic streptococci, mostly Streptococcus agalactiae (B. streptococci) but also of groups A, C or G, or of the Streptococcus anginosus group, Staphylococcus aureus, enterobacteriaceae, enterococci and lastly Trichomonas vaginalis.

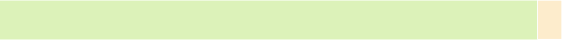
This acute inflammation is difficult to treat. Attempts at therapy with vaginal clindamycin cream for one to two weeks are possible, but often not sufficient. Additionally, hydrocortisone in a vaginal cream seems to improve the results. Substitution with lactobacilli or acidification for weeks to months is always advisable. This is especially recommended during pregnancy, as prematurity is also significantly increased by aerobic vaginitis-associated bacteria. Furthermore, acute infections can occur very rarely, some of which massively affect the patient. These are caused by Staphylococcus aureus and streptococci of groups A, C or G, some of which used to be called "childbed fever", up to their most threatening form, the Fournier's gangrene.

The vaginal microbiome composition

Gastrointestinal/cutaneous/oral contamination

Result

0,00%



Vaginal microbiome composition

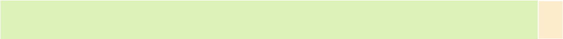
If the vaginal microbiome is not sufficiently colonised with lactobacilli, E. coli and other faecal bacteria can be translocated from the intestine into the vagina and urinary tract and cause infections. Therefore, particular attention should be paid to proper toilet hygiene.

Genus	Species	Rel. Abundance
Acinetobacter	johnsonii	0,00%
Acinetobacter	lwoffii	0,00%
Acinetobacter	ursingii	0,00%
Clostridium	spp.	0,00%
Enterococcus	avium	0,00%
Enterococcus	faecalis	0,00%
Enterococcus	faecium	0,00%
Escherichia	spp.	0,00%
Haemophilus	spp.	0,00%
Klebsiella	spp.	0,00%
Kluyvera	spp.	0,00%
Pseudomonas	spp.	0,00%
Ruminococcus	spp.	0,00%
Staphylococcus	capitis	0,00%
Staphylococcus	caprae	0,00%
Staphylococcus	epidermidis	0,00%
Staphylococcus	hominis	0,00%
Streptococcus	pneumoniae	0,00%
Veillonella	parvula	0,00%

Cervicitis - associated bacteria

Result

0,00%



Vaginal microbiome composition

In this group we have summarised typical pathogens associated with the clinical condition of cervicitis. Please refer to our medical report for corresponding therapy recommendations.

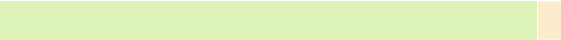
Genus	Species	Rel. Abundance
Actinomyces	spp.	0,00%
Chlamydia	trachomatis	0,00%
Neisseria	gonorrhoeae	0,00%
Streptococcus	pyogenes	0,00%
Trichomonas	vaginalis	negative

The vaginal microbiome composition

Potential risk of infection for the fetus

Result

0,00%



Vaginal microbiome composition

Genus	Species	Rel. Abundance
Chlamydia	trachomatis	0,00%
Haemophilus	influenzae	0,00%
Listeria	monocytogenes	0,00%
Mycoplasma	spp.	0,00%
Neisseria	gonorrhoeae	0,00%
Treponema	pallidum	0,00%
Ureaplasma	spp.	0,00%

Vaginal mycosis

Vaginal mycosis are widely spread among women. Statistically, three out of four women have a vaginal fungal infection at least once in their lifetime. In about 3-4 % of these women, the disease recurs.

The most common pathogens of vaginal mycosis are yeasts of the Candida type. Candida species in small numbers belong to the saprophytic inhabitants of the vaginal flora and are usually harmless.

Hormonal influences, general or local immune deficiencies, changes in the pH-value and/or disturbances of the normal microbial colonisation of the vagina favour the increase of yeasts and can subsequently lead to disease emergence. The most common type of fungal pathogen is Candida albicans, with an incidence of over 80%.

Genus	Species	Result
Candida	albicans	negative
Candida	dubliniensis	negative
Candida	glabrata	negative
Candida	krusei	negative
Candida	lusitaniae	negative
Candida	parapsilosis	negative
Candida	tropicalis	negative

Medical report validated by:
Dr. med. Dr. rer. nat. Hans-Wolfgang Schultis, Dr. med. Christian Aepinus, Anagnostina Orfanou

General information about the NGS microbiome analytics

► Analysis of the vaginal microbiome by NGS

Under the influence of oestrogens, the vaginal mucosa is physiologically dominated by lactobacilli (> 70%), which metabolise glucose to lactate, thus reducing the pH value. In addition to the lactobacilli, numerous other species (up to approx. ~ 180 in total) can be found, many of them in low bacterial counts, which belong to the normal vaginal microbiota.

Equilibrium shifts within the normal vaginal microbiota are central to the microbial pathogenicity of the vagina. Various clinical conditions (bacterial vaginosis (BV) / aerobic vaginitis, potentially pathogenic bacteria / sexually transmitted diseases (STD) / cervicitis / vaginal mycosis or gastrointestinal / cutaneous contamination) can be associated with increased numbers of pathogenic bacteria.

In contrast to the classic microbiological cultivation of bacteria supplemented by singular amplification methods (PCR), the molecular genetic method NGS (Next-Generation Sequencing) records all apathogenic and potentially pathogenic bacteria within the vaginal microbiome. This analytics is supplemented by a specific molecular-biological detection of trichomonads, which are often underdiagnosed with conventional methods. On the other hand viruses, e.g. herpes simplex virus 1/2 (HSV 1/2) and human papilloma viruses (HPV) are not recorded by this NGS technology.

The molecular-biologically measurable variety of the vaginal microbiota increases with pathologies being present as part of the shift in equilibrium (species diversity). This shift is measured using the Shannon-Index.

► Shannon - Index

The Shannon-Index is a mathematical dimension for recording the biodiversity (species diversity) in a community. The healthy, physiological vaginal microbiome is characterized by low biodiversity due to the dominance of lactobacilli (index treshold: < 0.8). An increased index is always a sign of increased biodiversity or a shift in balance and therefore a disturbed vaginal bacterial community.

► Community State Type (CST)

To simplify the interpretation of the vaginal microbiome, a classification based on typical constellations was introduced by Ravel et al. Along with the dominant bacteria, all other bacteria are also taken into account in terms of type and prevalence.

CST (community state type) I, II and V define favorable constellations with dominance of Lactobacillus crispatus, Lactobacillus gasseri and Lactobacillus jensenii, respectively. Lactobacillus iners is dominant in CST III and has less favorable properties. CST IV describes constellations of a bacterial vaginosis with a reduction of lactobacilli and increased abundance of vaginosis-associated bacteria. Meanwhile further CSTs have been introduced in order to record other pathologies as well.

► Next-Generation-Sequencing (NGS)

NGS technology enables the analysis of microbial compositions of complex samples using various sequencing strategies approved by the government.

SYNLAB NGS technology performs amplification and subsequent sequencing of the conserved ribosomal 16S rRNA gene. The sequencing data is processed using an bioinformatic analysis algorithm and phylogenetically profiled through database comparison.

► Result interpretation

The results of the NGS data analysis are quantified using relative abundance. DNA fragments corresponding to certain bacteria genus/species are compared to the entirety of all detected DNA fragments and depicted in percentage. The detection limit of our NGS test has been set to 0.1% relative abundance.