Name: Example, EBIOM
Date of birth: 10.04.1988
Sex: W
Sample ID: 3524451181

Date of sample collection: 04.11.2024
Date of receipt: 05.11.2024

3524430248

Microbiome analysis of the endometrium

The investigation of the endometrial mucosa for bacteria is based on the knowledge that (i) contrary to conventional opinion, bacteria are regularly detected there and (ii) the composition of these bacteria (called microbiota or simply microbiome) has an impact on the success of fertility treatment.

According to the literature [1-6], lactobacilli play a key role. An endometrial microbiome dominated by Lactobacillus microbiome is described as a healthy, normal state.

Test: EBIOM sequencing by NGS
Sample material: Endocervical - endometrial smear

Table 1: Relative abundance of bacterial species

Bacteria (genus)	**Result**	**Interpretation**
Lactobacillus	>99%	🟩

General notes: (1) The result corresponds to the percentage of reads (sequenced DNA fragments) per bacterial strain on genus level in relation to all reads that can be assigned to a bacterial genome. (2) The cut-off is 3%. (3) Analysis software: Illumina Basespace. (4) spp. = species. (5) When deciding on a possible therapy, please see "Interpretation of results" and "Further comments" on the back of the report.

Analysis of chronic endometritis

Pathogens of chronic endometritis	**PCR Results**
Chlamydia trachomatis	*Negative*
Mycoplasma genitalium	*Negative*
Neisseria gonorrhoeae	*Negative*
Ureaplasma urealyticum	*Negative*
Ureaplasma parvum	*Negative*

Shannon-Index: < 0.01

The Shannon Index is a measure of diversity and abundance. In simple terms, a high abundance of Lactobacillus and a low diversity of other bacteria causes a lower Shannon Index (< 1.0)

Interpretation of results:

- **Evaluation of the lactobacilli**
  Lactobacillus spp. dominate the endometrial microbiome (relative abundance >80%). The results do not indicate any therapeutic measures to influence the endometrial microbiome.
- **Potentially pathogenic bacteria**
  There was no DNA from pathogenic (red) bacteria detected in the sample.
- **Other bacteria**
  No other bacteria (blue) were detected in the sample.

Further comments:

No further comments

Literature:

[1] Moreno I, Franasiak JM. Endometrial microbiota-new player in town. Fertil Steril. 2017 Jul; 108(1):32-39.

[2] Moreno I, Codoñer FM, Vilella F, Valbuena D, Martinez-Blanch JF, Jimenez-Almazán J, Alonso R, Alamá P, Remohí J, Pellicer A, Ramon D, Simon C. Evidence that the endometrial microbiota has an effect on implantation success or failure. Am J Obstet Gynecol. 2016 Dec; 215(6):684-703.

[3] Jervis-Bardy J, Leong LE, Marri S, Smith RJ, Choo JM, Smith-Vaughan HC, Nosworthy E, Morris PS, O'Leary S, Rogers GB, Marsh RL. Deriving accurate microbiota profiles from human samples with low bacterial content through post-sequencing processing of Illumina MiSeq data. Microbiome. 2015 May 5; 3: 19.

[4] Moreno I, Garcia-Grau I, Perez-Villaroya D, Gonzalez-Monfort M, Bahçeci M, Barrionuevo MJ, Taguchi S, Puente E, Dimattina M, Lim MW, Meneghini G, Aubuchon M, Leondires M, Izquierdo A, Perez-Olgiati M, Chavez A, Seethram K, Bau D, Gomez C, Valbuena D, Vilella F, Simon C. Endometrial microbiota composition is associated with reproductive outcome in infertile patients. Microbiome. 2022 Jan 4;10(1):1. doi: 10.1186/s40168-021-01184-w. PMID: 34980280; PMCID: PMC8725275.

[5] Chen Q, Zhang X, Hu Q, Zhang W, Xie Y, Wei W. The alteration of intrauterine microbiota in chronic endometritis patients based on 16S rRNA sequencing analysis. Ann Clin Microbiol Antimicrob. 2023 Jan 12;22(1):4. doi: 10.1186/s12941-023-00556-4. PMID: 36635729; PMCID: PMC9838023.

[6] S2k-Leitlinie Bakterielle Vaginose AWMF-Registernummer 015-028, Version 5.0, Juni 2023