

The Effect of Seminal Microbiota on Semen Quality and IVF Results

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Introduction: Infections of the genitourinary tract (GUT) are responsible for about 15% of male factor infertility cases. Pathogens and the reactional seminal leukocytes can negatively affect spermatogenesis and obstruct the GUT.

Aim: To define the seminal microbiome and the correlation between bacteria and sperm quality and ability to fertilize.

Materials & Methods: In this prospective, non-interventional study, sperm samples were collected on day of ovum pick-up. Vaginal samples were collected the same day to evaluate the correlation between semen and the vaginal microbiome. The microbiome was identified by sequencing 16S ribosomal RNA based on next-generation sequencing and bioinformatics.

Results: A total of 17 pairs of samples were collected. The vaginal microbiome contained 76.6% lactobacillus, 11.6% streptococcus and 7.8% prevotella. The top 8 bacteria genera in the semen were corynebacterium (14.4%), prevotella (14.2%), streptococcus (12.4%), staphylococcus (11.1%), proionibacterium (10.7%), ureaplasma (9.5%), lactobacillus (9.4%), and veillonella (7.6%). No correlation was found between couples of male and female microbiomes. No clustering by male weight or age was found. We found no significant differences between the microbiomes of fertile vs. infertile males.

Conclusions: Based on these preliminary data, no effect of microbiome on infertility was found.

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