Vaginal microbiota and infectious infertility

This model identified infectious infertility with an accuracy of 89.8%



Image adapted from Whiteside, S. A. *et al. Nat. Rev. Urol.* **12**, 81–90 (2015), Macmillan Publishers Limited. Differences in the vaginal microbiota of women with or without infectious infertility have been reported in a new study. Identification of these differences could aid in the diagnosis of women with infectious infertility.

In total, 210 women were enrolled in the study. Of those in an infertile couple, 26 women had noninfectious infertility and 21 had infectious infertility. For comparison, 89 fertile women with no evidence of a sexually transmitted infection and 54 female sex workers were included.

Women with infectious infertility had previously experienced significantly more *Chlamydia trachomatis* infections than women with noninfectious infertility or fertile women. Women with infectious infertility had more IgG antibodies against chlamydial antigens than fertile women. Specifically, those with infectious infertility had more serum IgG antibodies against CPAF and HSP60 antigens than women with noninfectious infertility, and also had more IgG antibodies against HSP60 than female sex workers. For IgA antibodies, women with infectious infertility had increased antibodies against OMP2 and HSP60 antigens compared with fertile women.

In fertile women, bacteria belonging to the Lactobacillus genus dominated the vaginal microbiota; however, the prevalence of these bacteria was reduced in women in the other study groups. By contrast, the prevalence of bacteria from the Gardnerella, Prevotella, and Sneathia genera were reduced in fertile women compared with those in the other groups. Microbiota diversity was lowest in fertile women, and, of all the groups, the composition of vaginal microbiota of women with noninfectious infertility was only less diverse than that of female sex workers.

Using these data, the researchers developed a statistical model for predicting the underlying cause of female infertility. The model includes detection of potential pathogens by PCR and cultivation, serological status of *C. trachomatis* IgG and IgA antibodies, and the first ten taxa identified using microbiota sequencing. This model identified infectious infertility with an accuracy of 89.8%, prediction of infectious infertility was correct in 17 of 18 women, and all women with infectious infertility were separated from those with noninfectious infertility.

These results show that the composition of the vaginal microbiota differs between women with infectious infertility and those with noninfectious infertility. Including analysis of vaginal microbiota in a model for predicting the cause of infertility can help identify women with infectious infertility. Louise Stone

ORIGINAL ARTICLE Graspeuntner, S. et al. Microbiota-based analysis reveals specific bacterial traits and a novel strategy for the diagnosis of infectious infertility. PLoS one 13, e0191047 (2017)