

17th World Congress of the Academy of Human Reproduction

*15–18 March 2017
Rome, Italy*

TITLE

EVOLUTIONARY PERSPECTIVE FOR HUMAN REPRODUCTION OF VAGINAL MICROFLORA DYSBIOSIS

AUTHOR/S

Ventolini G (US) [1]

ABSTRACT

Evolutionary vaginal microbiome composition studies are crucial to understanding human reproduction. Microbioma has not been characterized in the vaginal pathology of non-human primates (NHPs).

Differences between humans and NHPs include: acidic vaginal pH (humans) and acidic-alkaline (baboons), utero-cervical junction anatomy sharp ante flexion (women) compared to ventro flexion (baboons), and increased microbioma diversity in baboons. This diversity is determined by vaginal size: 10–12 cm (humans) versus 7 cm (baboons).

Recently, we analyzed 64 baboons' pathology records and vaginally evaluated the presence of human subtypes of *Lactobacillus* spp. and Bacterial Vaginosis-related spp. in baboons (*Papio* spp.) using a real-time assay polymerase chain reaction (qPCR).

Lactobacillus iners, *Gardnerella vaginalis*, *Atopobium vaginae*, *Megasphaera* I, and *Megasphaera* II were not detected.

L. jensenii, *L. crispatus*, *L. gasseri* and BVAB2 were present.

These microbioma differences might be responsible for the development of specific vaginal protective mechanisms (baboons do not display increased numbers of infection-related still births and/or preterm births). Additionally, factors associated with specific pattern of placental development: shallow trophoblast invasion in baboons (cytotrophoblast's viral infection decreases their invasive capacity) versus human's deep trophoblast invasion promoted by decreased viral load through abundant *L. crispatus*

INSTITUTE

[1] Texas Tech University Health Sciences Center PB