The vaginal microbiome is stable in prepubertal and sexually mature Ellegaard Göttingen Minipigs throughout an estrous cycle

Although the pig has been introduced as an advanced animal model of genital tract infections in women, almost no knowledge exists on the porcine vaginal microbiota, especially in barrier-raised Göttingen Minipigs. In women, the vaginal microbiota plays a crucial role for a healthy vaginal environment and the fate of sexually transmitted infections such as *Chlamydia trachomatis* infections. Therefore, knowledge on the vaginal microbiota is urgently needed for the minipig model. The aim of this study was to characterize the microbiota of the anterior vagina by 16S rDNA gene sequencing in prepubertal and sexually mature Göttingen Minipigs during an estrous cycle. The dominating phyla in the vaginal microbiota consisted of *Firmicutes*, *Proteobacteria*, *Actinobacteria*, *Bacteroidetes* and *Tenericutes*. The most abundant bacterial families were *Enterobacteriaceae*, unclassified families from *Gammaproteobacteria*, *Clostridiales Family XI Incertae Sedis*, *Paenibacillaceae*, *Lactobacillaceae*, *Ruminococcaceae* and *Syntrophaceae*. We found a higher abundance of *Lactobacillaceae* in the prepubertal Göttingen Minipigs compared to sexually mature non-pregnant Göttingen Minipigs. However, correlation tests and diversity parameters revealed a very stable vaginal microbiota in the Göttingen Minipigs, both before and after sexual maturity and on different days throughout an estrous cycle. The vaginal microbiota in Göttingen Minipigs was not dominated by lactobacilli, as it is in women and according to our results the minipig vaginal microbiota is very stable, in opposite to women. These differences should be considered when using the minipig as a model of the genital tract in women.

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