TITLE: Infertility and parity order in cows influences the diversity and composition of the cervicovaginal fungi microbiota

AUTHORS: D. CARLI, S.[1]; LOPES, C.E.[1]; DIAS, M.E.[1]; SAGGIN, B.F.[1]; VARELA, A.P.M.[2]; MAYER, F.Q.[2]; SIQUEIRA, F.M.[1]

INSTITUTION: [1]UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL, PORTO ALEGRE, RS, BRAZIL. [2]INSTITUTO DE PESQUISAS VETERINÁRIAS DESIDÉRIO FINAMOR, ELDORADO DO SUL, RS, BRAZIL.

ABSTRACT:
The microbiota is composed of fungi, bacteria, viruses, and protozoa that may determine the health or disease of the host. In this context, researchers have explored the uterine and vaginal bacteriome to understand the reproductive tract microbiota in cows. However, despite fungi having already been described as etiologic agents of endometritis and infertility in cows, few studies approached the composition of cows cervicovaginal fungal communities. Therefore, our study aimed to characterize the fungal community present in the cervix of cows with signs of infertility. Cervicovaginal mucus was collected from 21 Angus breed cows with a history of infertility in the year before the collection, showing an early return to estrus. According to the parity order, 11 of these cows were considered multiparous (4–12 years old) and ten nulliparous (3 years old). Additionally, five non-sexually active heifers (1.5 years old) were employed as a control group. The internal transcribed spacer 1 (ITS1) was amplified and sequenced to explored the cervicovaginal fungi community using QIIME2 software. Diversity metrics of the cervicovaginal fungal community revealed no statistical differences in the fungal community composition between infertile cows and non-sexually active heifers. Noteworthy, the cervicovaginal fungal microbiota had significative increased richness and evenness in nulliparous cows and non-sexually active heifers, while in multiparous cows, a decreased richness and evenness of the fungal microbiota were identified. Ascomycota and Basidiomycota made up the largest part of the fungal community, with a greater inclination for Ascomycota in all sample groups. *Candida* genus was more frequently in infertile cows. In contrast, *Eichleriella* and *Trichosporon* were highlighted in multiparous cows. Non-sexually active heifers and nulliparous cows had a similar pattern of fungi community sharing some exclusive genera. These results indicated that the source of the fungal community changes significantly after parturition and hence in older cows.

Keywords: Infertile cows; microbiota; high-throughput sequencing; fungi community, parity order.