An investigation of the microbiota in uterine flush samples and endometrial biopsies from dairy cows during the first 7 weeks postpartum

Metritis and endometritis commonly occur in dairy cows after calving. Although numerous studies have been performed to identify the causative pathogens, a complete overview has not been done. Metagenomic studies have analyzed the bacterial populations of uterine flush samples from postpartum (pp) dairy cows, but the microbiota in the uterine luminal fluid may differ from the microbiota of the endometrium itself, and important putative pathogens may have been overlooked. In the present study, we compared the microbiota of the uterine lumen and the endometrium of healthy, metritic, and endometritic cows. Samples were collected from 68 Holstein dairy cows at 1, 4, and 7 weeks pp, and the data were analyzed by deep sequencing of the V1 and V2 hypervariable regions of the 16S ribosomal RNA gene. The results showed that Porphyromonadaceae, Fusobacteriaceae, Leptotrichiaceae, and Mycoplasmataceae may be associated with uterine disease. The microbiota of the uterine flush samples and the endometrial biopsies were correlated, but the microbiota of the biopsies was more diverse. Fusobacteriaceae and Leptotrichiaceae were not observed in the biopsies at week 7, whereas they accounted for 20% and 13%, respectively, of the bacterial populations in the flush samples. The Mycoplasmataceae family was observed in much higher quantity in the flush samples than in the biopsies of the endometritis groups at weeks 4 and 7. Our findings support the observations of previous metagenomic studies and illustrate the importance of including endometrial biopsies to obtain more detailed knowledge of the pp uterine microbiota.

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