Revisiting bovine pyometra-New insights into the disease using a culture-independent deep sequencing approach

The bacteria present in the uterus during pyometra have previously been studied using bacteriological culturing. These studies identified Fusobacterium necrophorum and Trueperella pyogenes as the major contributors to the pathogenesis of pyometra. However, an increasing number of culture-independent studies have demonstrated that the bacterial diversity in most environments is underestimated in culture-based studies. Consequently, fastidious pyometra-associated pathogens may have been overlooked. Therefore, the primary purpose of this study was to investigate the diversity of bacteria in the uterus of cows with pyometra by using culture-independent 16S rRNA PCR combined with next generation sequencing.

We investigated the microbial composition in the uterus of 21 cows with pyometra, which were obtained from a Danish slaughterhouse. Similar to the observations from the culture studies, Fusobacteriaceae, the family that F. necrophorum belongs to, was the operational taxonomic unit (OTU) observed in the largest quantities. By contrast, the Actinomycetaceae family, which includes T. pyogenes, constituted only 1% of the total number of reads. Thus we cannot confirm the previously reported role of species from this family in the pathogenesis of pyometra. Finally, we identified a large number of sequences representing three families of Gram-negative bacteria in the pyometra samples: Porphyromonadaceae, Mycoplasmataceae, and Pasteurellaceae. It is likely that these families comprise potential pathogenic species of a fastidious nature, which have been overlooked in previous studies. Our results increase the knowledge of the complexity of the pyometra microbiota and suggest that pathogens in addition to F. necrophorum may be involved in the pathogenesis of pyometra. (C) 2014 Elsevier B.V. All rights reserved.