Comparison of vaginal microbial community structure in healthy and endometritis d...

Article Review Summary of the article The objective of the current study was informed from previous studies that assessedthe protective properties of the normal flora in the reproductive tract. The article sought to characterise the vaginal microflora on the postpartum cows by comparing the healthy cows with those suffering from endometritis. The methods used the PCR, which was followed with denaturing gradient gel electrophoresis (PCR-DGGE), which was compared with real-time PCR. The study used sampling of five healthy and five cows with the condition of interest. Findings show thattwo species namely Weissella koreensis and Lactobacillus sakei subsp., were the dominant microflora in the vagina of the healthy postpartum cows, while those with endometritis did not exhibit a dominant bacteria specie. However, the sick cows exhibited increased diversity of microflora than the healthy cows. The study attributes disruption of the microflora with the onset of endometritis. This study proposes the use of microbial population in the development of probiotics that could treat endometriosis in bovines.

Critical analysis

The study by Wang et al., (2015), illustrates a good approach that aimed to characterise microflora, a gap that existed in previous studies that assessed the microflora in postpartum cows. It aimed to achieve the objective by comparing the abundance between cows suffering from endometritis against the healthy ones. The methods used such as PCR followed by denaturing gradient gel electrophoresis (PCR-DGGE), which was compared with real-time PCR, which signified a comprehensive method of attaining the objectives that Wang et al aimed to attain.

The researchers chose five cows among the healthy postpartum sample and

five in the post-partum endometritis group. This is the main challenge and weakness of the study. Correct sample size helps with generalisation of the finding. However, five cows per group cannot form adequate sample size for the attainment of these research tenets. In fact, when the sample size is too small like what happened in the current study, chances of generating error type two increases. Therefore, this study cannot be used for generalisation of its finding as stated by the researchers. Perhaps, if they have found a similar trend using a much larger sample size, the generalisation would be appropriate. Future studies should validate the findings of this study by using a large sample size.

The study failed in the aspect of representation of its method of data collection and the reflection of their finding for decision-making. For instance, the researchers collected their samples (two groups of cows) from the same firm (single firm). Therefore, sampling method was not randomised. The approach used by the researcher was not appropriate because when samples are acquired from a single place, the finding is likely to be skewed and therefore not representative. If they could have used more than five firms, their findings could have been sensible and randomised to offer a representative outlook.

Reference

Wang J., Sun, C., Liu, C., Yang, Y. Lu, W. (2015). Comparison of vaginal microbial community structure in healthy and endometritis dairy cows by PCR-DGGE and Real-time PCR, Anaerobe (2015), doi: 10. 1016/j. anaerobe. 2015. 11. 004