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Towards the veterinary diagnostics of the future

Main topic : Omics and big data, metagenomics: Open ended diagnosis

First results of exploration of the bacterial population in uterine samples from cows with metritis based on 16S metagenomics by high-throughput sequencing

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Introduction

Metritis is the inflammation of the uterus that develops in the immediate postpartum period following bacterial infection and is known to cause economic losses in cattle industry.
Thanks to high-throughput sequencing, the bacterial population in samples from cows showing signs of metritis was explored using a metagenomic analysis based on the 16S rRNA gene. Previous similar study, performed on lungs with pneumonia, led to discover new pathogens of interest (1).

Material and methods

A panel of 19 cows clinically ill were sampled by field veterinarians using uterine swab. For each case, a cow from the same herd and in the same post-partum stage but showing no sign of metritis was sampled in order to form a controle group. Routine tests were performed in parallel on these samples such as bacterial culture and targeted PCR (*Coxiella burnetii*, *Mycoplasma bovis*, *Histophilus somni*, *Chlamydophila* spp., *Ureaplasma diversum*, BoHV-4,)
16S metagenomics sequencing was performed targeting V4 and V7 of the 16S rRNA gene (primers from Thermo Fisher Scientific), and using Nextera XT Index kit and Miseq sequencer (Illumina). Data were processed with the software Geneious, with NCBI as the reference database.

Results

In all the tested swabs, more than 900 different taxa were detected by the sequencing method, confirming the high bacterial diversity in the samples, both in the cases group and in the controls group. Among these bacteria, many are commensal or of environmental origin. On the other hand, several bacteria are detected in cows with clinical metritis, whereas their prevalence in « healthy » cows is low. Some of them are well known for their pathogenicity ; these include *Trueperella pyogenes* and *Streptocossus* sp. Other bacteria, such as *Helcococcus ovis* or *Psychrobacter pulmonis* are reported in the literature as pathogenic for the ruminants but no data is available regarding their implication in genital disorders in cattle. Finally, bacteria such as *Oscillibacter* sp. appear to be more prevalent in cases samples, but there is no published information about their pathogenicity in cattle.

Conclusions

These first results are promising and open new avenues for the understanding and etiological diagnosis of metritis in cattle. However, further analysis on a larger panel of samples, e.g. with targeted PCR for specific agents, are needed to consolidate these results.