TITLE: METATAXONOMIC ANALYZES OF CAPRINE MILK BEFORE AND AFTER THE TREATMENT OF CLINICAL MASTITIS

AUTHORS: [1]POLVEIRO. R.C.; [1]LIMA, M. C.; [2]VIDIGAL, P. M. P.; [1]YAMATOGI R. S.; [1]MOREIRA, M. A. S.

[1] LABORATORY OF BACTERIAL DISEASES (LDBAC), PREVENTIVE VETERINARY MEDICINE AND PUBLIC HEALTH SECTOR, VETERINARY DEPARTMENT; [2]NUCLEUS OF ANALYSIS OF BIOMOLECULES (NUBIOMOL).

INSTITUTION: UNIVERSIDADE FEDERAL DE VIÇOSA; (P.H. ROLFS AVENUE, UNIVERSITY CAMPUS. 36570-900, VIÇOSA, MG, BRAZIL).

ABSTRACT:

Staphylococcus aureus, followed by coagulase-negative staphylococci, *Streptococcus* spp*,* Enterobacteria, *Arcanobacterium pyogenes*, *Corynebacteria*, *Pasteurellaceae*, *Pseudomonas spp*., *Mannheimia haemolytica*, *Trueperella pyogenes,* are the main agents of clinical caprine mastitis. In the last decades, some antimicrobials have been used without success in the therapy of clinical mastitis caprine (CM), which culminates in the return of the disease, called recidivant goat mastitis (RM), which determines the elimination of these animals from the herd. Sequencing of the 16S rRNA gene, by means of Next-Generation Sequencing, can provide a greater depth and amplitude of the microorganisms involved in the affection of the mammary gland. The objective of this study was to perform the classification of the bacterial agents involved in CM, before and after treatment, with the appearance of RM, and thus identify the bacterial microbiome alterations of the milk. Eleven CM animals were treated for seven days with enrofloxacin (20 mg / kg, 1X / day). Milk samples were collected before and 21 days after treatment (RM). Milk samples from three clinically healthy goats were used as controls. The DNA was extracted with the QIAmp DNA kit kit (QIAGEN). Sequencing was carried out with an IluminaMiseq sequencing platform, targeting the V4 region (515f-806r) of the 16S rRNA ribosomal subunit gene. The bioinformatics analyzes were performed in the QIIME pipeline and the USEARCH program. Sequences were grouped in Operational Taxonomic Units (OTUs), with 97% similarity. The taxonomic classification method used was the Ribosomal Database Project (RDP) classifier. The results showed that in the CM samples the most abundant genera in reads were *Trueperella* (TP), *Mannheimia* (MH), *Staphylococcus* (SC), *Bacteroides* (BC), *Alkalibacterium* (AK), *Corynebacterium* (CY), family Enterobacteriaceae (FE), with emphasis on *Escherichia coli* (ES). In the (RM) group, the genera SC, TP, MH, *Streptococcus*, ES species, and family Bacillaceae, increased the number of reads in most samples. Exclusively, MH and TP occupied over 80% of the number of reads in the (RM) goats samples. In the control group, SC, BC, AK, FE, *Shewanella* spp, CY and SC presented a number of abundant and similar reads among the samples. The metataxonomic analyzes of the milk samples (CM and RM) showed the genera and species of the main etiological agents within the same herd, which denotes a complexity in the treatment of mastitis.

Keywords: 16S rRNA, goat, mastitis, metataxonomic, milk.