

BLOOD BACTERIAL PROFILE OF FREE GRAZING BOVINE (*Bos taurus*) IN THE COMARCA LAGUNERA, DURANGO, MEXICO

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Introduction

Contrary to what was previously believed, blood is not a sterile medium and harbors a diverse community of bacteria. The Comarca Lagunera de Durango is a region in northern Mexico where many families subsist from livestock keeping small herds in non-technified free-range stables. In recent years, the number of diseases transmitted by ticks to cattle has been increasing, causing significant economic losses in the beef and dairy industry.

Materials and methods

In 2021, bovine blood was collected in stables in Ceballos, Bermejillo, and Nazas Durango, Mexico. In order to expand the microbiological panorama of this ruminant and provide reference bacteriological information that may be useful to support veterinary diagnoses under extensive management in the present study the objective was to analyze the composition and abundance of the bacterial taxa present in the blood of this ruminant in the Comarca Lagunera de Durango.

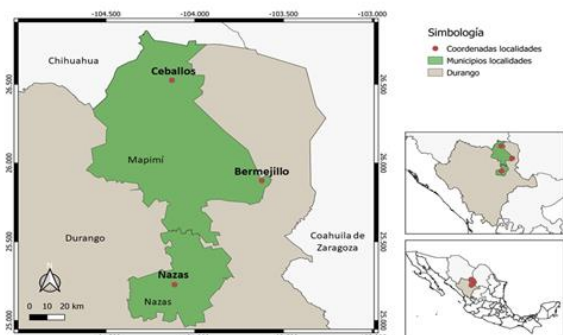
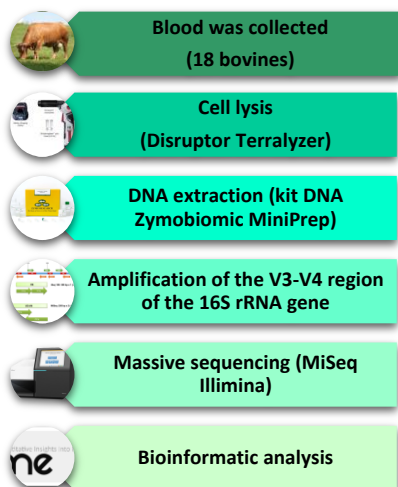


Fig. 1. Study areas.

Results

An average of 18,149 operational taxonomic units (OTUs) was obtained. A total of 31 bacterial phyla were recorded (Firmicutes 43.8%), 83 classes (Clostridia 26.5%), 176 orders (Clostridiales 26.5%), 436 families (Ruminococcaceae 16.8%), 1,806 genera (PAC000748_g 5.8%), and 4,000 bacterial species (836 known, 1,573 non-cultivable and 1,591 unknown). The dominant family blood was observed Ruminococcaceae, Bacillaceae and Corynebacteriaceae; These bacteria are related to taxa that inhabit the rumen of these animals, as well as in the food they consume.

The genders *Sporobacter*, *Bacillus* and *Corynebacterium* were the most abundant and highlighted the presence of potentially pathogenic species for bovines such as *Mycoplasma haemobos*, *M. wenyonii*, *Campylobacter fetus*, *Staphylococcus aureus*, *Coxiella burnetii*, *Bartonella bovis*, *Ehrlichia minasensis*, *Pasteurella multocida*, *Clostridium perfringens* y *C. chauvoei*. Going forward, it will be important to investigate the dynamics of these bacterial communities, their function, and how they self-regulate in the host's blood.

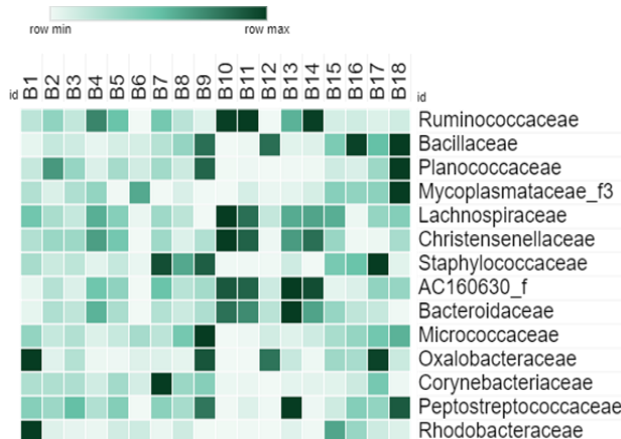


Fig. 2. Heatmap representing the relative abundance (%) of the dominant bacterial family for the bovines (*Bos taurus*) pools in the Comarca Lagunera de Durango.

Discussion

Jeon et al. (2017) analyzed blood from 12 adult Holstein cattle at a dairy farm in Florida, USA. In this study, it is reported that an average of 85,651 bacterial readings was obtained, where the phylum Tenericutes was dominant with 90.3% relative abundance, followed by Proteobacteria (6.9%) and Firmicutes (1.3%). In the present study with bovines from non-technified stables, an average of 46,214.1 bacterial readings was reported where the dominant phyla in bovine blood were Firmicutes (43.8%), Proteobacteria (17.7%), Actinobacteria (15.2%), Bacteroidetes (12.5%) and Tenericutes (4.0%). It is evident that at this taxonomic level the samples from the Comarca showed a more heterogeneous microbiota and low numbers of Tenericutes compared to the study by Jeon et al. (2017).

Literature cited

- Jeon, S. J., Cunha, F., Vieira-Neto, A., Bicalho, R. C., Lima, S., Bicalho, M. L., y Galvão, K. N. 2017. Blood as a route of transmission of uterine pathogens from the gut to the uterus in cows. *Microbiome*. 5(1), 1-13. DOI 10.1186/s40168-017-0328-9.