

TITLE: DETECTION OF *MYCOBACTERIUM BOVIS* CIRCULATING IN THE STATE OF MATO GROSSO - BRAZIL, USING THE NESTED REAL TIME PCR TECHNIQUE

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ABSTRACT:

Mycobacterium bovis is a bacterium belonging to the *Mycobacterium tuberculosis* complex (CMT) and causes bovine tuberculosis (bTB), a disease that affects cattle, other domestic and wild animals, as well as man, and is therefore a zoonosis that causes losses to cattle industry and public health. Epidemiological surveillance of the disease is carried out mainly by inspection of carcasses in slaughterhouses where samples of suspected bTB lesions are collected and submitted for laboratory analysis to confirm the diagnosis, requiring rapid, sensitive and specific tests for disease control and eradication in cattle. This work aimed to identify the strains of *M. bovis* circulating in the State of Mato Grosso during the year 2018. In order to investigate the presence of bTB, DNA extracted directly from lesions suggestive of bTB from slaughterhouses under the Federal Inspection Service (SIF), was submitted to Nested Real Time PCR (Nested qPCR) technique, using specific primers for both CMT detection and *M. bovis* species. A total of 136 were individually processed using 3 g of lesion suggestive of bTB, and used for DNA extraction with commercial Dneasy Blood and Tissue kit (Qiagen®), following the manufacturer's recommendations. Then the DNAs of the samples were submitted to Nested qPCR technique for the identification of CMT and *M. bovis*, using primers and probes for the Rv2807 gene, present only between the CMT species and primers and probes for the TbD1 gene, present only in *M. bovis*. As a result, 28% (38/136) of samples were classified as positive for CMT and 19% (26/136) for *M. bovis*, where 6.61% (9/136) were animals destined to sanitary slaughter. Among *M. bovis* positive animals, 57.7% (15/136) were females, 44% (60/136) were aged 24-36 months and 39% (53/136) over 36 months. With the identification of *M. bovis* circulating in the State of Mato Grosso by molecular method, it was possible to assist the surveillance service in the tracking and sanitation of remaining foci of bTB in the State, providing a faster diagnosis, aiding in the eradication stage of bTB in the State.

Keywords: Bovine tuberculosis, *Mycobacterium tuberculosis* complex, Nested qPCR

Development Agency: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Fundação de Amparo à Pesquisa do Estado de Mato Grosso (FAPEMAT)