## Title: MOLECULAR TYPING OF *Mycobacterium bovis* ISOLATES FROM THE CENTRAL-WEST REGION OF BRAZIL

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Abstract: Bovine tuberculosis (BTB) is caused by Mycobacterium bovis, a bacteria belonging to the Mycobacterium tuberculosis complex. It is a pathogen that, besides causing economic impacts in the livestock sector, presents imminent risks to human health, since it is a zoonotic bacteria. In order to conduct a molecular epidemiology study in the central-west region of Brazil, the largest beef producer and exporter region in the country, molecular typing of M. bovis isolates obtained from the area were carried by the spoligotyping technique. Molecular typing can provide epidemiological data on M. bovis isolates, aiding in the control of BTB by indicating possible links between sick animals, as well as aiding in the the detection of outbreaks and cross-contamination between samples. The spoligotyping technique was used on 15 isolates from the state of Mato Grosso, 19 isolates from Mato Grosso do Sul and 15 isolates from Goiás, all obtained from 2010 to 2013, totaling 49 isolates from the central-west region of the country. It was possible to identify 19 different M. bovis spoligotypes, 14 described in the literature and 5 new spoligotypes. The identified spoligotypes were: SB0121 (17 isolates), SB0140 (6 isolates), SB1145, SB1966, SB0881 and SB0295 (3 isolated by spoligotyping) SB1144 (2 isolates), SB1136, SB1055, SB0134, SB1050, SB0873, SB0332 and SB0120 (1 isolated by spoligotyping). The spoligotype SB0121 has been described in Brazil and other countries, spoligotype SB0140 has been found in Brazil, Paraguay, Argentina and Uruguay and spoligotype SB1145 has been detected only in Brazil. Molecular typing by the spoligotyping technique allowed for the detection of polymorphisms among the M. bovis isolates from cattle from the central-west region of Brazil, demonstrating that these spoligotypes circulate all over the country, including other Latin-American and European countries. The use of the spoligotyping technique detected 19 distinct spoligotypes that circulate throughout the centralwest region of Brazil, among them, five new genotypic profiles, that should be better characterized in order to aid health authorities in the control and eradication of bovine tuberculosis from this region of the country.

Keywords: Molecular Epidemiology, Spoligotyping, bovine tuberculosis.

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