Genetic diversity of *Staphylococcus pseudintermedius by* Multilocus Sequence Typing" (MLST) isolate from animals

SILVA, A. A¹.; CANDIDO, S.L¹.; PITCHENIN, L. C¹.; GODOY, I.¹; REIS, H.L.V¹.; LIMA, L.F.S¹.; NAKAZATO, L¹. ; DUTRA, V¹.

¹Laboratório de Microbiologia e Biologia Molecular Veterinária, Universidade Federal de Mato Grosso – UFMT

Av. Fernando Corrêa da Costa, nº 2367 - Bairro Boa Esperança. Cuiabá - MT - 78060-900

Staphylococcus pseudintermedius (S. pseudintermedius) is an opportunistic bacteria pathogen in dogs and has been associated with diseases in other animals, including humans. Genetic variability of this organism has been associated with methicillin resistance and hosts pathogenicity with some genotypes more prevalent in Europe. Due to the lack of data on the genetic diversity of S. pseudintermedius in Brazil, the objective of this study was to genotyping by molecular technique "Multilocus Sequence Typing" (MLST) isolated from S. pseudintermedius from animals from Veterinary Hospital (UFMT) during 2013 to 2016. Fifty-five isolates from lesions, including wild animal isolates, were analyzed. All isolates were submitted to DNA extraction, Polymerase Chain Reaction to amplify seven conserved genes (ack, cpn60, fdh, pta, purA, sar and tuf), amplicons purification and DNA sequencing. Eight isolates had all genes of MLST performed which seven were from dogs and one from bovine. All isolates were characterized as new sequence types (ST741, ST742, ST743, ST744, ST745, ST746, ST747, ST748). Allele profiles of genes were compared to public database of S. pseudintermedius (PubMLST). All isolates had a different profile and no Clonal complex was observed in Mato Grosso isolates. The analysis by the eBurst software showed that isolates did not show clonal proximity with others already described in Brazil and other countries based on PubMLST database, called "Singletons". Structural population of these eight isolates show high diversity and is not associated to clonal complex described in other countries of Europe which is associated to antibiotic resistance as Methicillin or host preference. Further studies in Brazil containing MLST sequence typing are required to elucidate the molecular epidemiology of S. pseudintermedius in South America.

Key Words: S. pseudintermedius, MLST, Dogs, Resistance