Título: OCCURRING of CYTOTOXINS, EXFOLIATIVE TOXINS AND PYROGENIC TOXINS GENES IN *Staphylococcus Pseudientermedius* OF DOMESTIC AND WILD SPECIES

Autores Pitchenin, L.C. ¹, Brandão, L.N.S. ¹, Rosa, J.M.A. ¹, Kagueyama, F.C. ¹, Rocha, I.S.M. ¹, Maruyama, F. H., Dutra, V. ¹, Nakazato L. ¹

Instituição ¹Departamento de Pós-graduação em Ciências Veterinária, Universidade Federal de Mato Grosso (UFMT), Av. Fernando Corrêa da Costa, nº 2367 - Bairro Boa Esperança. Cuiabá - MT - 78060-900 Fone/PABX: +55 (65) 3615-8000 / FAX: +55 (65) 3628-1219

Resumo:

Staphylococcus pseudintermedius is a coagulase-positive species of SIG (Staphylococcus intermedius Group). It is an opportunistic pathogen that can cause infections in several places and also has zoonotic potential. Although knowledge about the pathogenic process of S. pseudintermedius is limited, it is known the arrest of several virulence factors of this pathogen. Toxins are included in these factors, and epidemiological studies of their distribution in S. pseudintermedius are virtually nonexistent. They can be classified into three main groups: pyrogenic toxin with superantigens properties (SEs and TSST), exfoliative toxins and cytotoxins (leucocidins, hemolysin). In this study the occurrence of 8 toxin genes (sea, sec, tst, SIET, EXI, LuK FI, SI Luk and y hlg) was studied in 58 isolates of S. pseudintermedius by Polymerase Chain Reaction in 4 domestic animal species (dogs, cats, cattle and pig) and two wild species (1 cub (Cerdocyon thous) and 1 Hand raccoon (Procyon cancrivorus), from various sites of infection. All samples showed the gene of at least one type of toxin, alone or combined. The highest occurrences were related in Luk SI (94,83%), Luk FI (91.38%) and EXI (91.38%) and the smallest in hlg y (5.17). There wasn't any association between the toxin and the infected species or site of infection. Many genes showed large differences in occurrence when compared to previous studies (sea, sec, tst, EXI, hlg y), however most studies have only been performed in healthy dogs, in this studied, different species and all isolates were from animals which had infection. Also geographical location differences, clinical conditions, clonal profile and presence of regulatory systems may explain these differences. The extensive occurrence of these genes indicates an important role in the severity of infections caused by these commensal microorganisms to become pathogenic.

KEYWORDS: *Staphylococcus intermedius*, virulence factors, enterotoxin, toxic shock syndrome, hemolysin, leucocidinas, dogs, cat