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Discrimination of Staphylococcus intermedius group isolates

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Abstract

S. pseudintermedius species are frequent members of the normal flora of cats and dogs, in which they play a major role as opportunistic pathogens. These species are also known to develop multidrug resistance. Their transmission between humans and animals has already been documented and their zoonotic potential as well as the role of pets as reservoir of these antimicrobial-resistant bacteria is currently under investigation.

Phenotypic differentiation among staphylococcal species belonging to the Staphylococcus intermedius Group (SIG), i.e. S. intermedius, S. delphini and S. pseudintermedius, is not possible using conventional microbiological tests (e.g. biochemical reactions) and no commercial kits are available to separate these species taxonomically. Because of their close taxonomical relationship, misidentification of staphylococcal species in the SIG might thus occur. During this study, several SIG strains isolated from animals and humans have been recovered and analyzed. We have used genetic and proteomic methods such as partial rpoB and partial hsp60 gene sequences and Matrix Assisted Laser Desorption Ionization – Time Of Flight mass spectrometry (MALDI-TOF) respectively, to conclusively differentiate and identify each SIG strain analyzed in this study. rpoB gene is well established for gene sequencing to differentiate SIG strains and hsp60 is a common gene used for identification of staphylococcal strains. Results showed that genetic differentiation of SIG was possible by sequencing of rpoB gene and MALDI-TOF MS analysis allowed differentiation of staphylococcal strains at specie level. Moreover, MALDI-TOF MS gave some supplementary information about the heterogeneity of the strain analyzed. This work confirmed that MALDI-TOF MS is a powerful tool for the identification of SIG isolates being reliable, time-saving and cost effective in long term.