RESUMO SIMPLES - MICROBIOLOGIA E IMUNOLOGIA

SURVEY AND ANTIMICROBIAL RESISTANCE PROFILE OF STAPHYLOCOCCUS SPP. ISOLATED FROM DOGS IN THE ANIMAL SHELTER AND MONITORING SECTOR OF UFRRJ

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The genus Staphylococcus comprises bacteria that are commonly found on the skin of humans and animals. These commensal microorganisms are functionally categorised into Coagulase-Positive Staphylococci (CPS) and Coagulase-Negative Staphylococci (CNS), and can act as opportunistic pathogens. Staphylococcus pseudintermedius and other Methicillin-Resistant Staphylococcus species (MRSP, MRS) are frequently found in the microbiota of healthy dogs. The incidence of community-acquired and healthcare-associated infections caused by MRS, particularly Methicillin-Resistant Staphylococcus aureus (MRSA), is increasing annually. Adoption should be encouraged for families of all social backgrounds when acquiring a pet dog. Living with rescued animals can enrich family life and contribute to the well-being of the dogs themselves. However, household environments can facilitate the exchange of bacterial species and antimicrobial resistance genes between dogs and their owners. Through this exchange, bacteria of public health concern may acquire resistance genes. In Staphylococcus spp. the mecA gene, is responsable for

promoting resistance to all beta-lactam antimicrobials except fifth-generation cephalosporins, significantly limiting the available treatment options. This study aimed to identify and characterize the beta-lactam resistance profile in 83 Staphylococcus spp. isolates from various species, obtained from swabs collected from the body surfaces of healthy dogs available for adoption at the Animal Reception and Monitoring Sector (AMA) of UFRRJ. The goal was to enhance the understanding of mecA gene distribution among Staphylococcus spp. strains in the canine population at AMA and to investigate the role of CNS species as reservoirs of this gene in canine microbiota. The study was approved by CEUA-UFRRJ under the number 6239180418. Swabs were collected from 5 anatomical sites (left ear, right ear, interdigital, nasal and rectal ampoule) in 15 healthy dogs housed within the Projeto AMA animal shelter dependencies, at UFRRJ, resulting in 75 specimens. Samples were transported to the lab in Stuart's transport medium, then inoculated onto 5% Sheep's Blood Agar and incubated at 37ºC for 24/48h. Macromorphological characteristics were recorded and Gram's stain as well as the catalase test were performed as screening tools to select Gram-positive, catalase-positive cocci in arrangements such as the typical "bunch of grapes" for phenotypical identification, done through biochemical tests. The bacterial isolates exhibiting phenotypical traits consistent with the Staphylococcus spp. genus were identified at species level using the MALDI-TOF method at the Medical Microbiology Research Laboratory (LIMM) at UFRJ. Total DNA was extracted using the thermal lysis protocol for genotypical characterisation. The 16S rRNA gene was characterised by amplifying the material using polymerase chain reaction and specific primers for Staphylococcus spp genus. The mecA beta-lactam resistance gene was detected using a universal primer specifically designed for animal samples targeting different mecA variants. A total of 83 Staphylococcus spp. isolates were obtained from a sample of 75 specimens, with 50.6% identified as CPS and 49.4% as CNS. These represented 14 distinct species. The most prevalent species was S. pseudintermedius (37.3%), followed by S. sciuri (16.9%) and S. intermedius (12.0%). A total of 21.7% of the isolates harboured the mecA gene, of which 61.1% were CNS and 38.9% were CPS. Data analysis revealed the presence of methicillin-resistant isolates among both CNS and CPS in the shelter environment. These finds underscores the need for sanitary surveillance measures and highlights the importance of a One Health approach in the context of antimicrobial resistance.

Palavras-chave: staphylococcus; antimicrobial resistance; one health.