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ÁREA DO TRABALHO: MICROBIOLOGIA AMBIENTAL

TÍTULO DO TRABALHO: Bacterial Load And Methicillin-Resistant Staphylococcus Spp. In Household Dust, And Residents' And Dogs' Colonization Evaluation

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RESUMO:

The Staphylococcus genus comprises Gram-positive cocci found in the microbiota of humans and animals. It includes more than 80 species and subspecies, which can be coagulase-positive, coagulase-negative, or variable. As opportunistic pathogens, they can cause infections ranging from mild to severe, transmitted through direct or indirect contact. Preventing the transfer of resistance genes within and between species is a challenge, particularly regarding beta-lactams. The mecA and mecC genes encode an alternative penicillin-binding protein (PBP) with low affinity for beta-lactams and are carried by the mobile genetic elements known as SCCmec.We investigated the role of humans, dogs, and household dust in carrying MRS in three house groups: A-only with humans (n=20), B- humans with healthy dogs (n=20), and C- humans with antibiotic-treated dogs (n=14). We also analyzed the efficiency of an air purification system in decreasing the bacterial load and mecA gene in household dust. Nasal swabs, feces and household dust (from humans and dogs) were collected before and during air intervention. Gram-positive cocci isolated from rich and selective media with or without cefoxitin, were submitted to catalase and coagulase tests and Phoenix-M50 identification. Antimicrobial susceptibility was assessed using automated methods and broth microdilution to determine the minimal inhibitory concentrations (MICs) of vancomycin, daptomycin, linezolid, and tigecycline. Bacterial load and the mecA gene were quantified by qPCR in DNA extracted from household dust. We found 67 methicillin-resistant coagulase-negative Staphylococcus carrying mecA (group A=26, group B=22, and group C=19). Forty-two out of 67 (62,6%) isolates were in household dust from 11/20 houses in Group A, 13/20 in Group B, and 6/14 in Group C. Only one MRS was obtained from a dog (1,5%), and this isolate belonged to a dog under antibiotic treatment in Group C. Twenty-three isolates were collected from humans (7/20 humans of Group A, 3/20 of Group B, and 5/14 of Group C). The most common species identified were Staphylococcus haemolyticus (24 isolates, 35,8%) and Staphylococcus epidermidis (23 isolates, 34.3%). Resistance to macrolides was the most prevalent. One MRS isolate, recovered from household dust in Group A, was resistant to tigecycline, with a MIC of 1 mg/L. In conclusion we found a correlation between the presence of dogs and the increased amount of

household dust. Dust bacterial load was the same irrespective of the air purifier system or the dog's presence. The air intervention showed no statistical difference in the mecA/bacterium ratios. Dust from houses without dogs had the highest mecA/bacterium ratios than those with the animal.