Can MRSA-causing dermatological infections be transmitted between humans and dogs?

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Methicillin-resistant *Staphylococcus aureus* (MRSA) are associated with nosocomial infections and are frequently found in cutaneous and soft tissue infections [1]. Although *Staphylococcus pseudintermedius* are the main Staphylococcal species that cause infections in pets, several studies demonstrate that MRSA strains can infect pets and cause infections similar to those occurring in humans [2]. This study aimed to investigate the presence of MRSA in dogs and human infected diabetic foot ulcers, determine their genetic lineages and the ability to produce biofilms.

Nasal samples were collected from 54 dogs and 45 human infected foot ulcers from patients with type 2 diabetes. Samples were seeded on plates with ORSAB medium supplemented with 2 mg/L oxacillin to isolate MRSA strains and the *Staphylococcus* species were confirmed by Gram staining, DNase, catalase and molecular methods. Susceptibility to antibiotics was tested by the Kirby-Bauer disk diffusion method against 14 antimicrobial agents according to EUCAST (2018) guidelines. The presence of resistance and biofilm-related genes was studied by PCR using specific primers and conditions [3,4]. The genetic lineages of MRSA strains were characterized by *spa*-typing and MLST (multi-locus sequence typing).

It was possible to isolate 16/54 (29.6%) and 28/45 (62.2%) MRSA strains from the animal and human samples, respectively. *S. aureus* identification was confirmed by *nuc* and 16S genes, and MRSA isolates contained the *mec*A or *mec*C genes. All strains showed resistance to at least 3 antibiotics. Resistance to ciprofloxacin and erythromycin was detected in all strains isolated from dogs and in 19 and 18 MRSA strains of humans, respectively. The *erm*(C) gene was the most prevalent in erythromycin resistant isolates from both dogs and humans. All human isolates were classified as biofilm producers and presented several genes related to biofilm production and adhesion, being the *cna* gene the most prevalent one. Thirteen *spa*-type and 7 sequence type (ST) were identified in strains isolated from humans, and 4 *spa*-type and 1 ST were identified in MRSA from

dogs. The most frequently found *spa*-types were the t747 and t032 in humans and animals, respectively. ST22 was the most prevalent in both human and animal strains.

In this study, a high prevalence of MRSA was found in both humans and dogs. MRSA strains exhibited similar antibiotic resistance patterns among themselves. Most MRSA isolates belonged to ST22 which suggests that there was a transmission between humans and dogs, and most likely the transmission occurred from humans to dogs since ST22 that is related to nosocomial infections in humans. MRSA skin infections may be responsible for severe cases that may lead to necrosis. There is a concern related to the emergence of multidrug resistant MRSA strains and the limited number of antibiotics available for the treatment of these infections.

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