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271-1 CASE STUDY OF METHICILLIN-RESISTANT Staphylococcus aureus (MRSA) CAUSING A FURUNCULOSIS OUTBREAK IN A HOUSEHOLD ENVIRONMENT

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Resumo:

Staphylococcus aureus is a common causative of skin infections, such as impetigo (superficial infection) and more invasive infections such as cellulitis, ulcers, folliculitis, and wounds. Methicillin-resistant *Staphylococcus aureus* (MRSA) have emerged in community acquired infections and is a major health concern in immunocompromised inpatients. A patient sought medical attention with recurrent furunculosis previously treated on an outpatient basis with cephalexin and ceftriaxone. He reported other similar and recent cases at his parents' home, where he often stays. Therefore, the aim of the study was to investigate a furunculosis outbreak in this family house that occurred in June 2023, in São Carlos, SP, Brazil. Pus of one intact pustule was cultured and he was initially treated with chlorhexidine baths and sulfamethoxazole-trimethoprim, with some improvement. The patient isolated agent was MRSA, also resistant to sulfamethoxazole-trimethoprim. Nasal swabs of the residents (person 1 and person 2), the person 3 (that often stays in the house), and two dogs, plus the house environments (living room, shower area, and bathroom sink) and the house dust were investigated for the presence of methicillin-resistant *Staphylococci* (MRS). Isolates were recovered from 5% sheep blood agar and mannitol agar with cefoxitin (4 mg/L). The colonies were submitted to Gram staining, catalase, and coagulase tests. The resistant isolates were identified with PMIC/ID-89 panels using Phoenix M50 (BD). All isolates of the same species, if involving a household or dogs, were compared by Pulsed Field Gel Electrophoresis (PFGE) to investigate clonality. The *mecA* gene was detected by PCR. Finally, the isolates' ability to form biofilm was compared to that of *S. aureus* ATCC 8095 (weak biofilm former) and ATCC 25923 (strong biofilm former). In addition to the patient, MRSA was isolated from the person 2 and shower area. However, other MRS were isolated from the person 3 (*S. epidermidis*), dogs 1 and 2 (*S. hominis* in both), the environment (*S. cohnii ssp cohnii, S. haemolyticus*, and *S. hominis* at the living room; *S. haemolyticus* at the shower area), and the house dust (*S. carnosus* and *S. pasteuri*). All the isolates were *mecA* positive. PFGE analysis showed that *S. aureus* from the patient was indistinguishable to the ones isolated in the living room and in the nasal swab of person 2. Eight strains exhibited the ability to form biofilm better than *S. aureus* ATCC 8095, of which the MRSA from the patient and from the shower area surpassed the biofilm formed by *S. aureus* ATCC 25923. Furthermore, the MRSA isolates presented resistance to erythromycin and sulfamethoxazole-trimethoprim. Therefore, treatment of the patient was changed to clindamycin. In conclusion, the same clone of MRSA involved in the patient infection was detected colonizing person 2 and in the shower area indicating environment dissemination. We also concluded that the house environment, house dust, and dogs had MRS of various species harboring the *mecA* gene, which may be a source of the methicillin resistance determinant to more virulent bacterial species.

Palavras-chave:

antimicrobial resistance, skin infection, MRSA

Agência de fomento:

International Centre for Antimicrobial Resistance Solutions; Joint Programming Initiative on Antimicrobial Resistance