P4.66 - ST8475: A NEW SEQUENCE TYPE IDENTIFIED IN METHICILLIN-RESISTANT STAPHYLOCOCCI (MRS) IN PORTUGAL

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ABSTRACT

Methicillin-resistant staphylococci (MRS) pose a challenge to public health, particularly in healthcare-associated infections, where they seriously threaten the effectiveness of antimicrobial therapy. MRS strains have also been implicated in community-associated infections, such as in companion animals, wild animals, fresh foods, and ready-to-eat foods, and livestock-associated infections, such as in poultry and cattle.

In this study, the antimicrobial susceptibility profile of one hundred *Staphylococcus* isolates from canine and feline infections and sixty-two *Staphylococcus* isolates from raw bovine milk was determined. Isolates with an MRS phenotype were tested for the presence of the methicillin-resistance genes, *mecA* and *mecC*. MRSA isolates were further characterized by *spa* typing and whole genome sequenced (WGS) for more in-depth characterization, including the determination of sequence types (ST)/clonal complexes (CC).

Six MRS isolates were identified from companion animals, including four *S. pseudintermedius*, one *S. hominis*, and one *S. haemolyticus*, while five *S. aureus* isolates from raw bovine milk presented an MRS phenotype. The *mecA* gene was detected as being responsible for the phenotype observed in all of them. The *spa* types identified were t011 and t2383, which are types normally associated with MRSA isolates in Europe. In turn, all MRSA isolates revealed a new ST, now designated as ST8475.

This study reveals the spread of MRS isolates not only in farm animals but also in companion animals, which could pose a risk to public health. Furthermore, not only *S. aureus* but also *S. pseudintermedius*, the species most commonly detected in companion animal, appears to be associated with the MRS phenomenon. More importantly, a new ST associated with MRSA isolates has been identified and submitted to the MLST database (ST8475). This could imply the emergence of a new genetic lineage in Portugal, and cattle as a possible reservoir of resistance.

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