Beyond MRSA CC398: molecular characterisation and antibiotic resistance mechanisms of other MRSA-TetR genetic lineages circulating in Spanish hospitals

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Background: Methicillin-resistant Staphylococcus aureus (MRSA) is a public health threat. Livestock-associated (LA) clonal lineages have emerged as a clinical problem. Tetracycline is used in food animal production, and tetracycline resistance (TetR) is commonly used as a marker for CC398. The CC1 can be both, community and LA-MRSA, and its differentiation can be difficult. LA-MRSA CC1 isolates can carry the Immune Evasion Cluster (IEC) genes.

Materials/methods: Clinical and epidemiological samples were collected from 17 Spanish hospitals. TetR was used in a previous study to obtain a collection of MRSA CC398 strains. Here we analyzed the remaining MRSA-TetR non-CC398 strains. Molecular characterization by spa-typing and multilocus-sequence-typing were performed using PCR/sequencing. The presence of the scn gene (marker of the human IEC) was analyzed by PCR. Characterization of antibiotic resistance mechanisms was performed at phenotypic and genotypic levels. The virulence profile was determined through the detection of the lukF/S-PV genes, codifying the Panton-Valentine Leucocidin (PVL).

Results: A collection of 95 MRSA-TetR strains not belonging to CC398 was obtained. The 80% of isolates were obtained from clinical samples (65% from skin and soft tissue infections) and the remaining 20% from epidemiological surveillance. Thirty-two different spa-types were identified, with t127/CC1 being the most frequent (40%) and present in 14 of 17 hospitals. Three new spa-types were detected (t17234, t17235, t17236). The most prevalent clonal complexes were: CC1 (45%), CC45 (12%), CC5 (11%) and CC8 (8%). The scn gene was present in 73% of isolates (60% t127-scn+). The tetK gene was present in 95% of MRSA-TetR non-CC398 strains. The 71% of strains were resistant to macrolides/lincosamides (genes: 62% ermC, 53% msrA), with 58% of them showing an inducible resistance to clindamycin. Resistance phenotypes to other antibiotics were described: 32% tobramycin, 35% ciprofloxacin, 11% fusidic acid and 6% mupirocin. The PVL toxin was present in 16% of strains (only one t127).

Conclusions: TetR not only is a good marker for MRSA CC398, but also for other MRSA genetic lineages associated with livestock, as CC1. This genetic lineage can easily colonize humans, and should be subjected to a more strict surveillance.