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MRSA - one health worldwide

Genotypic and phenotypic characterization of *Staphylococcus aureus* isolates from human and animal origin in Portugal

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Background: Different methicillin-susceptible (MSSA) and methicillin-resistant (MRSA) *Staphylococcus aureus* clones have been encountered in isolates of human and animal origins. The objective of this study was to identify and characterize *S. aureus* from humans, and to compare their phenotypic and genotypic characteristics with animal isolates.

Material/methods: Fifty-eight *S. aureus* isolates recovered from different specimens of patients admitted at Portuguese hospitals, comprising community-acquired and nosocomial infections, were studied. Seventeen *S. aureus* strains isolated from animals were also studied. Antibiotic susceptibility testing was performed to all *S. aureus* isolates by disk diffusion and E-test, according to EUCAST guidelines. Different antibiotic resistant genes were searched by PCR. MLST, *spa* and *agr* typing methods were applied to evaluate diversity and genetic relatedness.

Results: The majority of the 58 clinical *S. aureus* was MRSA (70.7%), with reduced susceptibility to cefoxitin due to expression of the *mecA* gene; no *mecC* gene was detected. Additionally, 82.8% had decreased susceptibility to ciprofloxacin. Two (3.4%) linezolid-resistant *S. aureus* strains (CC5-ST105-t1094-*agr* 2 and CC8-ST239-t1223-*agr* 1) harboured mutations in the domain V of the 23S rRNA and/or in the *rlmN* gene, which explained the resistance phenotype. Decreased susceptibility to daptomycin (17.2%) was related with hospital environment clones, such as CC22-ST22-t032 and CC8-ST239-t037. Eleven (19%) *S. aureus* had a phenotype of multidrug resistance, with one (1.7%) characterized as hGISA (clone ST5/ST105-t002-*agr* 2). Among clinical strains, the most frequent *spa* types were t032 (ST22), followed closely by t002 (ST5/ST105); 2 new *spa* types (t14878 and t14933) were detected. Contrarily, all *S. aureus* isolated from animals were MSSA, showing susceptibility profiles to almost all antibiotics tested; four strains isolated from rabbits showed decreased susceptibility to ciprofloxacin. Furthermore, among *S. aureus* from animals we also identified CC398-ST398-t571 and CC130-t84 that have been described both in humans and animal infections, a new *spa* type (t15307), and three new ST (ST3254, ST3269 and ST3270). Globally, ST5 and ST34 were

found in both reservoirs, while ST22/ST105 and ST121 were the most frequently identified among human and animal isolates, respectively.

Conclusions: The identification of the same ST and *spa* types in *S. aureus* from humans and animals suggests a potential dissemination of strains between these two environments. In countries with high MRSA rates like Portugal, it is necessary to implement strategies in hospitals and also in veterinary areas in order to reduce the spread of this bacterium, which is a public health problem today.