Comunicazione Orale

METHICILLIN-RESISTANT STAPHYLOCOCCI IN COLLECTIVE CATERING FACILITIES FOR VULNERABLE POPULATIONS: OCCURRENCE AND GENOMIC CHARACTERIZATION

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Aim. The spread of methicillin-resistant staphylococci represents an increasing global public health challenge. Although historically associated with healthcare settings, these organisms are now widely detected in community environments, including food-handling settings. In collective catering facilities, food handlers may serve as reservoirs and vectors of transmission through direct contact with food and food-contact surfaces.
This study aimed to investigate the dissemination of methicillin-resistant staphylococci in collective catering facilities serving vulnerable populations and to characterize their antimicrobial resistance profiles.

Methods. A total of 268 staphylococcal isolates, including coagulase-positive and coagulase-negative species, recovered from food handlers' hands and food-contact surfaces in collective catering kitchens, were analysed. Cefoxitin and oxacillin resistance, determined by the Kirby–Bauer disk diffusion method, was used as a phenotypic screening approach to identify presumptive methicillin-resistant isolates for molecular characterization. Species identification of resistant isolates was performed by MALDI-TOF MS, followed by whole-genome sequencing (WGS) and analysis focused on antibiotic and biocide resistance genes. Bioinformatic analyses were performed using a Galaxy instance. Raw sequencing reads were quality-trimmed with Trimmomatic, followed by de novo assembly using Unicycler. Genome assemblies were then analyzed with ResFinder online tool to identify antimicrobial resistance (AMR) genes.

Results. Twenty-one isolates (7.8%, 21/268) exhibited a phenotype consistent with methicillin resistance. Species identification revealed a predominance of Staphylococcus epidermidis (12/21), followed by Staphylococcus haemolyticus (6/21), Staphylococcus hominis (2/21), and Staphylococcus aureus (1/21).
The mecA gene was detected in all isolates, confirming the genetic basis of methicillin resistance. The blaZ gene, encoding a staphylococcal β-lactamase, was identified in 90.5% (19/21) of isolates, frequently co-occurring with mecA, indicating the coexistence of complementary β-lactam resistance mechanisms. Genes conferring resistance to macrolides, lincosamides, and streptogramins (MLS) were detected in 71.4% (15/21) of isolates, while determinants associated with aminoglycoside and fusidic acid resistance were each identified in 52.4% (11/21). Furthermore, the mupA gene, which confers high-level mupirocin resistance, was detected in one isolate, highlighting the presence of a clinically relevant resistance determinant in coagulase-negative staphylococci. Overall, a high number of antimicrobial resistance genes was observed, with isolates harbouring between two and eight resistance determinants.
Notably, qacA, qacB, and qacC genes, associated with reduced susceptibility to quaternary ammonium compounds, were detected in 33.3% of isolates (7/21), suggesting potential adaptation to selective pressures exerted by disinfectants commonly used in sanitation procedures.

Conclusions. The findings demonstrate the circulation of methicillin-resistant staphylococci, predominantly coagulase-negative species, in collective catering facilities serving vulnerable populations. The co-occurrence of antimicrobial resistance and disinfectant tolerance determinants highlights the potential of these environments to act as reservoirs of resistant bacteria, where horizontal gene transfer may occur, contributing to the persistence and dissemination of antimicrobial resistance.