

O0987 Clonal dynamics among methicillin-resistant *Staphylococcus aureus* isolates causing bacteraemia over an 18-year period in a Spanish teaching hospital

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Background: MRSA is an important cause of morbidity and mortality worldwide. Different MRSA clones causing invasive infections have been identified. The aim of this work is to provide an analysis of the MRSA genetic lineages causing bacteremia in a university-affiliated hospital (Hospital Universitari de Bellvitge, HUB) over an 18-year period.

Materials/Methods: Since 1990 all MRSA isolates obtained from clinical samples of patients attended at HUB are prospectively stored. In this study, we analyzed MRSA isolates obtained from blood cultures from 2000 to 2017. Isolates were identified by standard microbiological methods. Antimicrobial susceptibility was studied by microdilution following EUCAST criteria. Bacteraemia episodes were classified according to the Friedman's criteria as community-, nosocomial- or health-care-acquired. Molecular characterization of isolates was carried out by PFGE, MLST and SCCmec typing. Results were analyzed in three periods: 2000-2005, 2006-2011 and 2012-2017.

Results: The percentage of MRSA among *S.aureus* infections increased from 19% in 2000 to 24% in 2017. The study includes 510 bacteraemia episodes. The proportion of nosocomial-acquired infections throughout the three periods decreased (68.8%-51.7%-22.2%; $p < 0.001$); whereas the health-care-acquired infections increased (31.3-47.7-74.3%; $p < 0.001$). Major Clonal Complexes (CC) 5, 8 and 22 grouped (43.9%) isolates. Isolates of CC5 (ST5/ST125/ST146-SCCmecIV) were dominant in 2000-2005 (65%) and 2006-2011 (44%); during 2012-2017 represented 39% of all MRSA isolates. Isolates of CC8 (SCCmecIV) increased steadily from 4% in 2000-2005 to 39% in 2012-2017. And ST22-SCCmecIV emerged in 2006-2011(8%) and represented 15% of all MRSA isolates during 2012-2017. Antibiotic resistance profiles were variable within a single clone. A significant decrease ($p < 0.05$) of resistance rates was observed for most of the studied antimicrobials through the three periods: ciprofloxacin (95.3-66.1-75.7%), tobramycin (87.0-71.3-59.7%), erythromycin (68.8-64.9-56.3%), clindamycin (45.5-41.4-21.5%), gentamicin (29.7-28.7-8.3%), rifampicin (24.5-64.9-1.4%), tetracycline (12.5-1.1-2.8%) and chloramphenicol (12.0-3.4-2.1%).

Conclusions: In spite of the increased health-care-acquired infections in our setting, the number of MRSA clones remained limited. Three major clones grouped most of the isolates: CC5 (*Paediatric* clone) dominant in our clinical setting since 2000, CC8 currently (2012-2017) as frequent as CC5, and the emerging ST22. This epidemiological shift has been associated with a decrease in the number of nosocomial-acquired infections and on the antimicrobial resistance rates.

