Emergence of a Panton-Valentine leukocidin (PVL) positive MRSA strain in cystic fibrosis (CF) patients

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Objectives: Recent studies demonstrated the impact of methicillin-resistant Staphylococcus aureus (MRSA) on survival of CF patients. Community-acquired MRSA (CA-MRSA) have started to replace hospital-acquired MRSA (HA-MRSA) strains in hospital settings, and these definitions started to blur. An additional threat for CF patients is represented by PVL-positive MRSA strains, able to cause invasive lung infections including lung abscesses. The aim of this study was to assess the presence of PVL-positive MRSA strains, and to investigate their genetic background in order to obtain a more delineated epidemiological picture.

Methods: SCCmec typing was performed according to published protocols (Oliveira and de Lancastre, 2002), as well as Multi Locus Sequence Typing (MLST) analysis (Enright et al, 2000). PVL genes presence was tested using a previously published method (Lina et al., 1999).

Results: 38 MRSA strains, one/patient, median age 20.5 (range 2–48) were screened for the presence of PVL genes. Only 1 strain infecting a 9 years-old patient tested positive. 23 out of 38 strains (60%) belonged to HA-MRSA group, the remaining 15 (40%) to CA-MRSA. Several epidemic lineages, such as Southern Archaic clone were found, while the only PVL-positive strain belonged to ST152.

Conclusion: PVL-positive strains were described in CF population in US as well as in Brazil, but their diffusion remains still unclear. Further studies should be promoted to assess the epidemiology of PVL-positive MRSA strains infecting CF patients in order to avoid their spread.

Population structure and antimicrobial susceptibility of Pseudomonas aeruginosa from a national survey involving 24 cystic fibrosis units in Spain

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Objectives: To characterize a P. aeruginosa collection recovered from respiratory samples of Spanish CF-patients included in a national multicenter study (March-November, 2013).

Methods: 13 adult and 11 paediatric CF-Units from 17 Hospitals collected respiratory samples and clinical data of 15 non-selected consecutive patients during their routinely visit. Respiratory samples were microbiologically culture using stander CF-protocols and colonies were identified by both MALDI-TOF MS and MultiScan System. Antibiotic susceptibility was also tested by EUCAST disk diffusion. Genetic diversity was explored by Pulsed Field Gel Electrophoresis (PFGE) and Multi-Locus Sequence Typing (MLST).

Results: A total of 68 P. aeruginosa isolates were obtained from 340 respiratory samples (20%), being more frequently recovered from adult (27.7%) than paediatric (15.3%) patients. Antibiotic resistance rates were as follows: 67.6% levofloxacin, 52.9% gentamicin, 47.1% amikacin, 38.2% cefepime and aztreonam, 33.8% imipenem, 29.4% tobramycin, 27.9% meropenem, 25.0% ceftazidime and 13.2% piperacillin/tazobactam. Colistin was the most active compound (only 2 isolates exhibited resistance). A great genetic diversity was observed by PFGE and MLST techniques, even inside each CF-Unit. Non-previously described alleles were found, and new STs were assigned. The ST175 and ST111 clones, frequently implicated in nosocomial bacteremias in Spain, were scarcely represented.

Conclusion: In Spain, lung colonization/infection by P. aeruginosa was observed in 27.7% of the adults and 15.3% of children. These isolates correspond to unrelated genetic lineages and were multi-resistant to antibiotics.