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ePoster Session

Understanding staphylococcal pathogenesis and evolution

Variation of *Staphylococcus aureus* antimicrobial profiles and toxin determinants in São Tomé and Príncipe from 2010 to 2014

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Objectives

Staphylococcus aureus is a versatile human pathogen that has been acquiring multiple resistance and virulence traits over time, namely methicillin resistance (methicillin-resistant *S. aureus* - MRSA) and Panton-Valentine leukocidine (PVL). *S. aureus* surveys in Portuguese-speaking African countries are scarce. The aim of the present study was to assess the evolution of antimicrobial susceptibility profiles, toxin determinants and clonal types among *S. aureus* isolates recovered from patients and health care workers (HCW) in São Tomé and Príncipe during three consecutive surveillance studies performed in 2010, 2012 and 2014.

Methods

A total of 508 nasal swabs (n=135 in 2010, n=201 in 2012 and n=172 in 2014) were recovered from patients (n=352) and HCW (n=156). Antimicrobial susceptibility testing was performed for a panel of 17 antibiotics and methicillin resistance was confirmed by detection of the *mecA* gene. Presence of codifying genes for three leukocidins (PVL, *lukE-lukD*, *lukM*), three hemolysins (*hlb*, *hlg*, *hlgv*) and five super-antigenic toxins (*eta*, *etb*, *etd*, *sel*, *sep*) was tested on all isolates. Molecular characterization included PFGE, *spa* typing, MLST and SCC*mec* typing for MRSA.

Results

A total of 119 *S. aureus* were recovered from 508 swabs (24 in 2010, 30 in 2012 and 64 in 2014) out of which 24.4% (n=29) were resistant to methicillin (21%, 29% and 23%, respectively). Antimicrobial susceptibilities changed over time: while MSSA isolates acquired full resistance to penicillin but lost resistance to trimethoprim-sulfamethoxazole (from 42% to 27%) and ciprofloxacin (from 26% to 2%), MRSA isolates increased resistance to erythromycin (from 40% to 80%) and tetracycline (from 20% to 80%). Concerning virulence determinants, although all MRSA harboured γ-hemolysin variant and *lukE-lukD*, the prevalence of these determinants decreased substantially among MSSA (100% to 57% and 100% to 59%, respectively). Moreover, despite an abrupt decrease of SEL in the entire collection (from 63% in 2010 to 13% in 2014), there was a sudden emergence of ETA among MSSA in 2014 (14%). Except for a single MRSA, PVL was exclusively found among MSSA and remained extremely high over time (around 50%). During the three surveillance studies most MRSA isolates (83%) belonged to two clonal types: ST8-IVg/V (PFGE type C, *spa* t064/t451), and ST88-IVa (PFGE B, *spa* t186/t786/t1814), 45 and 38% respectively. Similarly, most MSSA isolates were distributed over three main lineages: ST15 (PFGE K, *spa* t084) (30%), ST152 (PFGE M, *spa* t355/t1299/t9564) (16%) and ST508/2446 (SLV/DLV of ST45) (PFGE L, *spa* t635/t861/t2771/t5602/t10763) (14%), corresponding to major MSSA clones in the African continent.

Conclusions

Despite the relatively stable clonal profile of *S. aureus* isolates circulating in São Tomé and Príncipe between 2010 and 2014, the increasing trend on antimicrobial resistance in MRSA and virulence content in MSSA, namely PVL, is of major concern warranting the implementation of additional infection control measures.