

O179

Oral Session

New transmission routes and genotypic diversity: are we looking at a new MRSA?

EMERGENCE OF EMRSA-15 AS A SIGNIFICANT CAUSE OF S. AUREUS BACTEREMIA IN ISRAEL

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Objectives

Study of the molecular epidemiology of *S. aureus* infections, particularly methicillin-resistant *S. aureus* (MRSA), is important for optimisation of infection control. *S. aureus* typing data in Israel are mainly limited to MRSA strains from single institutions and thus we undertook a nationwide analysis of methicillin-susceptible *S. aureus* (MSSA) and MRSA bacteremia isolates.

Methods

The study was performed at the national reference laboratory for *S. aureus* to which all blood isolates are submitted. Isolates recovered from 1,405 *S. aureus* bacteremia (SAB) cases in 18 hospitals during 2011-2013 in Israel were analysed. The presence of the *mecA* (encoding methicillin resistance) and *lukS/F-PV* (encoding PVL toxin) genes was determined by PCR for all isolates. Spa typing was performed for 1,065 strains (542 MRSA, 523 MSSA). EMRSA-15 was identified based on PFGE analysis, SCC*mec* typing, and urease test of all t032 MRSA strains and related spa types. Representative EMRSA-15 strains were analysed by MLST. Antibiotic susceptibility was determined by the CLSI disk diffusion method or VITEK2 for representative EMRSA-15 strains.

Results

Overall, 1,405 SAB isolates from 18 health care centers were analysed. The mean age of patients with MRSA and MSSA bacteremia was 71±17 and 61±26 years, respectively (P<0.001). The *mecA* gene was detected in 599 (42.6%) isolates. The *lukS/F-PV* gene (PVL) was found in 45 (3.2%) isolates (4% of MSSA and 2.2% of MRSA). Among 542 MRSA isolates, 71 spa types were identified, of which the four major types were t002 (30%), t001 (16%), t032 (13%) and t008 (6%). The 523 MSSA isolates included 180 types, the most common of which were t084 (7%), t002 (6%) and t701 (4%). MRSA t032 and 7 related spa types (t379, t022, t4204, t025, t3846, t020, t513) comprised 18% of MRSA isolates and were confirmed as EMRSA-15, only anecdotally reported in Israel to date. EMRSA-15 strains were resistant to erythromycin and ciprofloxacin. The 98 EMRSA-15 strains were urease negative and harboured SCC*mec* IVh. PFGE analysis showed local EMRSA-15 strains consisted of several pulsotypes identical or similar to European strains. Representative strains were confirmed as ST22. EMRSA-15 strains were isolated in 12 of 18 studied hospitals where they comprised 11%-30% of MRSA bacteremia. The overall EMRSA15 rate was 15%, 20% and 18% in 2011, 2012 and 2013.

Conclusions

A high rate (42.6%) of MRSA with limited diversity was observed among SAB isolates while PVL-positive MRSA strains were rare. Several clones of EMRSA-15 ST22-IVh have recently emerged in Israel as a significant cause of SAB. Since EMRSA-15 tends to spread internationally, displace local clones and add to disease burden, these clones should be the focus of control efforts. The genetic diversity and microevolution of EMRSA-15 in Israel warrants further study.