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Abstract (poster session)

Correlation between genotype (spa) and antibiotic susceptibility patterns and trends of vancomycin and daptomycin among methicillin-resistant Staphylococcus aureus isolates from sterile sites: TIST study (2006-2010)

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Background: Methicillin-resistant Staphylococcus aureus (MRSA) is a major pathogen that may cause breakthrough infections with significant morbidity and mortality. Certain MRSA clones with distinct antibiotic resistance have circulated worldwide. Objectives: The goals of this study were to delineate the distribution of spa types and their trend of antimicrobial resistance among MRSA isolates from sterile sites in Taiwan. Materials and Methods: MRSA isolates, confirmed by existence of mecA gene and resistance to cefoxitin disc, from sterile sites were collected during the 5-year period from 22 hospitals (Tigecycline In-vitro Surveillance in Taiwan – TIST 2006-2010) and tested of vancomycin (VA) minimal inhibitory concentration (MIC) with agar dilution and VA and daptomycin (DPC) MICs with E-test, respectively. The spa types were assigned by PCR and nucleotide sequencing. Correlation between spa types and MICs of VA and DAP and trends of antibiotic resistance were also analyzed. Results: A total of 687 MRSA were collected, among which most were isolated from blood (643, 93.6%). The mean VA MIC by agar dilution increased in 2007 (1.55 mg/L) with stepping down in the following years (1.32 and 1.11 mg/L in 2009 and 2010, respectively). Higher mean VA MIC was noted with E-test (1.86 mg/L, range: 0.75-4) than agar dilution (1.41 mg/L, range: 0.5-3) in 5-year period. DPC MIC varied during the study period with mean MIC of 0.28 mg/L (range: 0.09-4). Seventy-six spa types including 16 new types were identified, and there were 20 MRSA assigned as undetermined. Six major clones including HA-MRSA genotypes (spa t002, t037, and t1081; 377 isolates, 54.9%) and CA-MRSA genotypes (spa t473, t441, and t3525; 180 isolates, 26.2%) were identified. The mean MICs of VA and DPC in each year and in the 5-year period, determined even by agar dilution or E-test, were significantly lower in CA-MRSA than HA-MRSA ($p = 0.003$ to < 0.001). Interestingly, the decrease in mean VA MIC was significantly associated with decrease in proportion of HA-MRSA (62.9% in 2006 and 39.2% in 2010, respectively) ($p < 0.05$). Conclusions: Neither vancomycin-intermediate S. aureus (VISA) nor vancomycin creep was found in the 5-year survey. Limited HA-MRSA and CA-MRSA clones were identified in Taiwan with extremely distinct antibiotic resistance patterns of vancomycin and daptomycin.

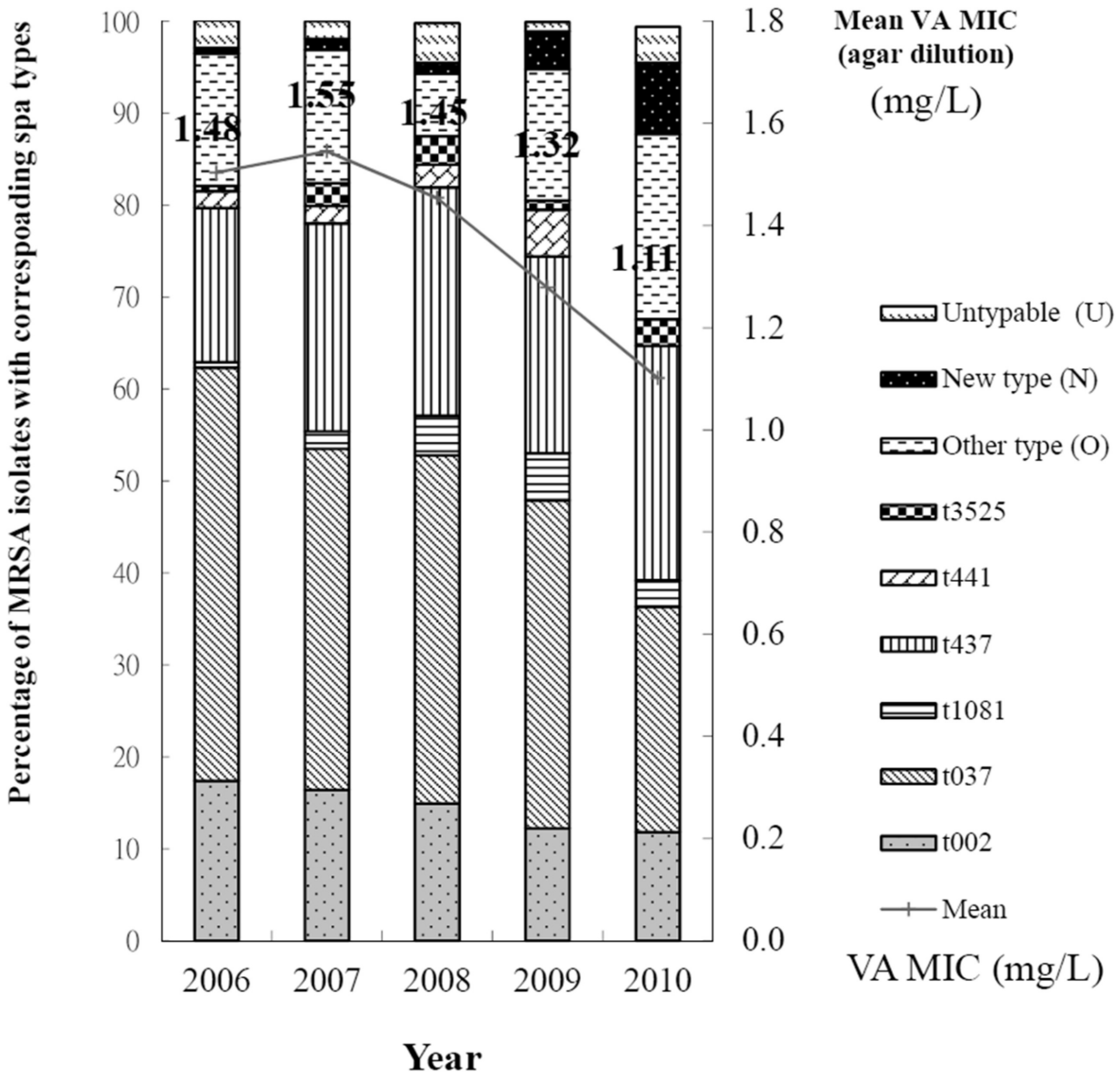

Figure 1. Distribution of *spa* types and their association with mean vancomycin MIC among 687 MRSA from sterile sites (TIST 2006-2010)