

Correlation of molecular types with antimicrobial susceptibility profiles among 670 *mecA*-positive MRSA isolates from sterile sites (TIST study, 2006-2010)W. Wang¹, T. Chieuh², S. Tsao³¹Feng-Yuan Hospital, Taichung, Taiwan²Tri-Service General Hospital and National Defense Medical Center-, Taipei, Taiwan³Chung Shan Medical University Hospital, Taichung, Taiwan

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is the most frequent organism that causes severe healthcare- and community-associated infections. Association of molecular types and antimicrobial susceptibility test (AST) profiles has been reported. The goal is to correlate various molecular types with AST profiles of MRSA isolates from Taiwan.

Materials and Methods: MRSA from sterile sites were collected during 5 years from 22 hospitals (Tigecycline *In-vitro* Surveillance in Taiwan – TIST 2006-2010) and AST including seventeen antibiotic regimens and inducible macrolide-lincosamide- streptogramin B (MLSb) phenotype were determined by Vitek-II automated system. Molecular types including SCC*mec*, *spa*, and *dru* were determined by PCR and nucleotide sequencing. Multidrug resistance (MDR) was defined an isolate with resistance to more than or equal to three non-β-lactam antibiotics. Correlation with molecular types with antibiotic resistance was determined by Fisher's exact test.

Results: Totally 670 *mecA*+ MRSA were collected, among which most were from blood (627, 93.6%). The susceptibility rates determined by Vitek-II were as followed: linezolid and teicoplanin (100%), vancomycin (99.9%), tigecycline (99.7%), daptomycin (95.1%), fusidic acid (85.5%), rifampicin (68.7%), trimethoprim (53.7%), moxifloxacin (36%), tetracycline (34.2%), and less than 10% for cefoxitin, cefazolin, penicillin, oxacillin, erythromycin, clindamycin, and ampicillin/sulbactam. MRSA with MDR (542, 80.9%) was associated with molecularly HA-MRSA (e.g., SCC*mec*II&III; *spa* t002&t037; *agr* group II; *dru*4, 12, and 14). (*p* from < 0.001 to < 0.01). MLSb (57, 8.5%) correlated with molecular types of SCC*mec*III&V, *spa* t3525, and *agr* group III (*p* < 0.01). The compound annual growth rate of susceptibility from 2006 to 2010 ranged from -2% of fusidic acid to 13% of clindamycin and 17% of erythromycin, respectively.

Conclusions: MRSA from Taiwan had varied AST profiles and some with increasing susceptibility within 5 years. Strains with particular molecular phenotypes had corresponding AST profiles that were distinct from those of endemic MRSA clones reported.

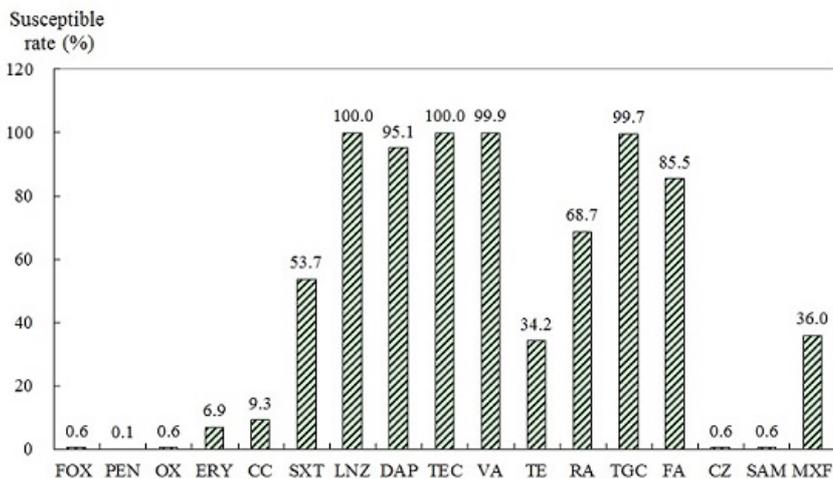


Fig. 1. Antibiotic susceptibility profiles of 670 *mecA*+ MRSA from sterile sites (TIST, 2006-2010). FOX: cefoxitin; PEN: penicillin; OX: oxacillin; ERY: erythromycin; CC: clindamycin; SXT: sulfamethoxazole; LNZ: linezolid; DAP: daptomycin; TEC: teicoplanin; VA: vancomycin; TE: tetracycline; RA: rifampicin; TGC: tigecycline; FA: fusidic acid; CZ: cefazolin; SAM: ampicillin-sulbactam; MXF: moxifloxacin.