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Correlation of molecular types with antimicrobial susceptibility profiles among 670 *mecA*+ MRSA isolates from sterile sites (TIST, 2006-2010)

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Introduction

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 patients with invasive infections in Taiwan.

Materials and Methods

MRSA from sterile sites were collected from 22 hospitals (Tigecycline *In-vitro* Surveillance in Taiwan – TIST 2006-2010) and AST including seventeen antibiotic regimens and inducible macrolide-lincosamide-streptogramin B (MLSBi) phenotype were determined by Vitek-II automated system. Molecular types including SCC*mec* [1], *spa* [2], and *dru* [3] were determined by PCR and nucleotide sequencing. Multidrug resistance (MDR) was defined as isolate with resistance to ≥ 3 kinds of 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, and most were isolated from blood (627, 93.6%). The susceptibility rates determined by Vitek-II were high in linezolid and teicoplanin (100%), vancomycin (99.9%), tigecycline (99.7%), daptomycin (95.1%), fusidic acid (85.5%) and low in β–lactams, erythromycin,

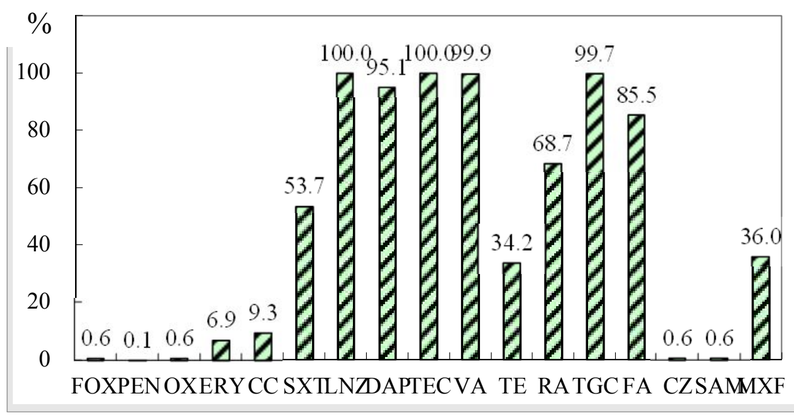

Figure 1. Drug susceptibility by Vitek-II of 670 *mecA*+ MRSA from sterile sites (TIST, 2006-2010). FOX: cefoxitin; PEN: penicillin; OX: oxacillin; ERY: erythromycin; CC: clindamycin; SXT: sulfamethoxazole; LNZ: linezolid; DAP: daptomycin; TEC: teicoplanin; VA: vancomycin; TE: tetracycline; RA: rifampicin;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

Results

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, Table 2). MLSBi (57, 8.5%) correlated with 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.

Table 1. Varied antimicrobial resistance profiles and their association with molecular types among 670 *mecA*+ MRSA (TIST, 2006-2010).

Antimicrobials	Resistance rate (%)	Significantly associated molecular types[2]
Moxifloxacin	64.2%	SCC*mec*II and III; *spa* t002, t037; *agr* group II; *dru*4, 12, 13, and 14
MLSBi	8.5%	SCC*mec*III and V; *spa* t3525; *agr* group III
Erythromycin	93.1%	SCC*mec*II and III; *spa* t002 and t037; *agr* group I; *dru*4 and 14
Clindamycin	90.7%	SCC*mec*II and III; *spa* t002 and t037; *agr* group I; *dru*4 and 14
Daptomycin	4.9%	SCC*mec*II; *spa* t002; *agr* group II; *dru*4
Tetracycline	65.8%	SCC*mec*III; *spa* t037 and t3525; *agr* group I; *dru*12, 13, and 14
Tigecycline	0.3%	SCC*mec*V
Fusidic acid	14.5%	*spa* t037; *dru*14
Rifampicin	31.3%	SCC*mec*II; *spa* t002; *agr* group II; *dru*4
SXT/TMP	46.3%	SCC*mec*III; *spa* t037; *agr* group I; *dru*12, 13, and 14
Multidrug resistance[1]	80.9%	SCC*mec*II and III; *spa* t002 and t037; *agr* group II; *dru*4, 12, and 14

[1]: with resistance ≧3 kinds of non-β-lactam antibiotic; [2]: p ranging from < 0.01 to < 0.001.

Table 2. Varied antimicrobial susceptibility profiles and their association with molecular types among 670 *mecA*+ MRSA (TIST, 2006-2010).

Antimicrobials	Susceptibility rate (%)	Significantly associated molecular types[2]
Moxifloxacin	35.8%	SCC*mec*IV and V_T; *spa* t437, t441, and t3525; *agr* group I and III; *dru*6, 8, 9, and 11
No MLSBi	91.5%	SCC*mec*II; *spa* t002 and t437; *dru*4
Erythromycin	6.9%	SCC*mec*IV and V; *spa* t1081 and t3525; *agr* group II, III, and IV; *dru*9 and 10
Clindamycin	9.3%	SCC*mec*IV and V; *spa* t1081 and t3525; *agr* group III and IV; *dru*6, 9, and 10
Daptomycin	95.1%	SCC*mec*IV; *spa* t437; *agr* group I; *dru*9 and 14
Tetracycline	34.2%	SCC*mec*II and IV; *spa* t002 and t437; *agr* group II and IIII; *dru*4
Tigecycline	99.7%	None
Fusidic acid	85.5%	SCC*mec*IV and V_T; *spa* t437; *dru*9 and 11
Rifampicin	68.7%	SCC*mec*IV and V_T; *spa* t437 and t441; *agr* group I; *dru*9, 11, and 14
SXT/TMP	53.7%	SCC*mec*II, IV, and V_T; *spa* t002, t437, t441, t1081, and t3525; *agr* group II, III, and IV; *dru*4, 6, 9, and 11
No multidrug resistance[1]	19.1%	SCC*mec*IV and V_T; *spa* t437, t1081, and t3525; *agr* group III and IV; *dru*6, 9, and 11

[1]: with resistance < 3 kinds of non-β-lactam antibiotic; [2]: p ranging from 0.01 to < 0.001.

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.

References

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