

P1953 Correlation Between *spa* Types and Susceptibility Patterns and Trends of Vancomycin and Daptomycin among Methicillin-resistant *Staphylococcus aureus* Isolates from Sterile Sites: TIST Study (2006-2010)



Wei-Yao Wang*, Tzong-Shi Chiueh, Po-Ren Hsueh, Jang-Jih Lu, and Shin-Ming Tsao
Fong-Yuan Hospital, Taichung and National Defense Medical Center, Taipei, Taiwan

Background and Purposes

Background: Since its discovery in 1960, methicillin-resistant *Staphylococcus aureus* (MRSA) has become a major pathogen that causes breakthrough infections including bacteremia and sepsis with significant morbidity and mortality. Certain MRSA clones with varied antibiotic resistance have been reported and disseminated worldwide. **Purpose:** The goals were to delineate the distribution of *spa* types and their association with vancomycin and daptomycin resistance among MRSA from sterile sites in Taiwan.

Materials & Methods

Bacterial isolation and identification: MRSA were collected from patients with invasive infections in a nationwide program during a 5-year study period [Tigecycline In Vitro Surveillance in Taiwan (TIST) Study (2006-2010)] and were identified according to CLSI and existence *mecA* by PCR. Vancomycin resistance of MRSA was determined by agar dilution and E-test. Daptomycin resistance was determined by E-test. Molecular typing of MRSA according to polymorphism in gene encoding surface protein A (*spa*) was done by PCR and nucleotide sequencing. M-W-U test was used for nonparametric comparison between two consecutive samples.

Results

A total of 687 MRSA isolates from sterile sites were collected during the 5-year study period. Most MRSA isolate were cultivated from blood (643, 93.6%), followed by pleural effusion (19, 2.8%), ascites (10, 1.4%), biopsied tissues (7, 1.0%), and synovial fluid (4, 0.6%) (Table 1)

Table 1. Sites and number of MRSA isolates from sterile sites (TIST 2006-2010)

Specimens (no./%) ^a /Year	2006	2007	2008	2009	2010	Total (%)
Blood	156 (93.4)	152 (95.6)	150 (93.2)	92 (93.9)	93 (91.2)	643 (93.6)
Pleural effusion	5 (3.0)	7 (4.4)	4 (2.5)	1 (1.0)	2 (2.0)	19 (2.8)
Ascites	5 (3.0)	0 (0)	3 (1.9)	1 (1.0)	1 (1.0)	10 (1.4)
Synovial fluid	1 (0.6)	0 (0)	0 (0)	1 (1.0)	2 (2.0)	4 (0.6)
Biopsied tissue	0 (0)	0 (0)	3 (1.9)	2 (2.0)	2 (2.0)	7 (1.0)
Others	0 (0)	0 (0)	1 (0.6) ^b	1 (1.0) ^b	2 (2.0) ^c	4 (0.6)
Total	167 (100)	159 (100)	161 (100)	98 (100)	102 (100)	687 (100)

^a: one isolate from lymph node.
^b: one isolate from bronchoalveolar lavage (BAL) fluid.
^c: one isolate from cerebrospinal fluid (CSF) and the other isolate from urine collected from the percutaneous nephrostomy (PCN) tube.

Table 2. Means and ranges of vancomycin and daptomycin MICs of MRSA isolates from sterile sites (TIST 2006-2010)

Year	No. of isolates	MIC (mg/L)					
		VAN (agar dilution)		VAN (E-test)		DPC (E-test)	
		Mean	Range	Mean	Range	Mean	Range
2006	167	1.48	1-3	2.09	1-3	0.29	0.094-1
2007	159	1.55	1-3	1.86	0.75-4	0.36	0.094-4
2008	161	1.45	1-3	1.79	1-3	0.23	0.094-0.75
2009	98	1.32	0.5-3	1.77	1-4	0.21	0.094-1
2010	102	1.11	1-1.5	1.68	0.75-3	0.29	0.094-0.75
Total	687	1.41	0.5-3	1.86 ¹	0.75-4	0.28 ²	0.094-4

VAN: vancomycin; DPC: daptomycin
¹: Comparison of vancomycin MIC with agar dilution and E-test: $p < 0.001$.
²: Correlation of vancomycin MIC by E-test with daptomycin MIC by E-test: $r = 0.39$.

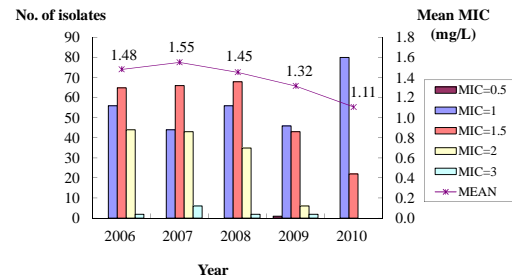


Figure 1. Distribution and mean of vancomycin MIC by agar dilution among 687 MRSA isolates from sterile sites (TIST 2006-2010)

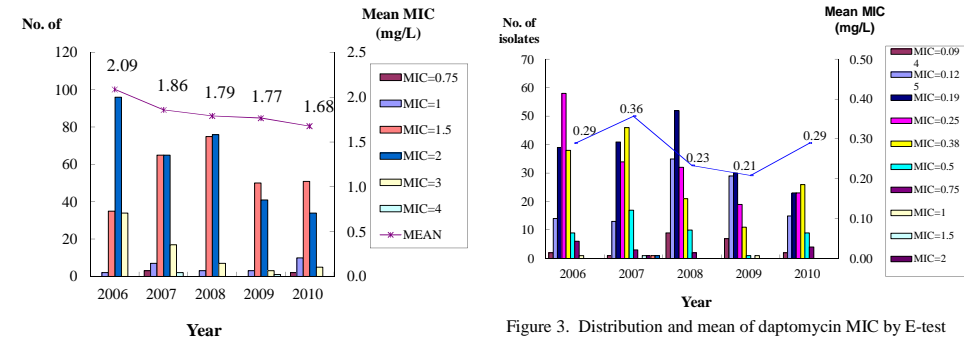


Figure 3. Distribution and mean of daptomycin MIC by E-test among 687 MRSA from sterile sites (TIST 2006-2010)

Table 3. Distribution of *spa* types among 687 MRSA isolates from sterile sites (TIST 2006-2010)

Genetic origin	<i>spa</i> type	No. of isolates (%)						
		Year						
		2006	2007	2008	2009	2010	Total	
HA-MRSA ¹	t002	29 (17.4)	26 (16.4)	24 (14.9)	12 (12.2)	12 (11.8)	103 (15.0)	
	t037	75 (44.9)	59 (37.1)	61 (37.9)	35 (35.7)	25 (24.5)	255 (37.1)	
	t1081	1 (0.6)	3 (1.9)	7 (4.3)	5 (5.1)	3 (2.9)	19 (2.8)	
	Total	105 (62.9)	88 (55.3)	88 (54.6)	52 (53.2)	40 (39.2)	377 (54.9)	
CA-MRSA ²	t437	28 (16.8)	36 (22.6)	40 (24.8)	21 (21.4)	26 (25.5)	151 (22.0)	
	t441	3 (1.8)	3 (1.9)	4 (2.5)	5 (5.1)	0 (0)	15 (2.2)	
	t3525	1 (0.6)	4 (2.5)	5 (3.1)	1 (1.0)	3 (2.9)	14 (2.0)	
	Total	32 (19.2)	43 (27.0)	49 (30.4)	27 (27.6)	29 (28.4)	180 (26.2)	
Unknown	Other type	24 (14.4)	23 (14.5)	11 (6.8)	14 (14.3)	21 (20.1)	93 (13.5)	
	New type	1 (0.6)	2 (1.2)	2 (1.2)	4 (4.1)	8 (7.8)	17 (2.5)	
	Untypable	5 (3.0)	3 (1.9)	7 (4.3)	1 (1.0)	4 (3.9)	20 (2.9)	
Total	All types	167 (100)	159 (100)	161 (100)	98 (100)	102 (100)	687 (100)	

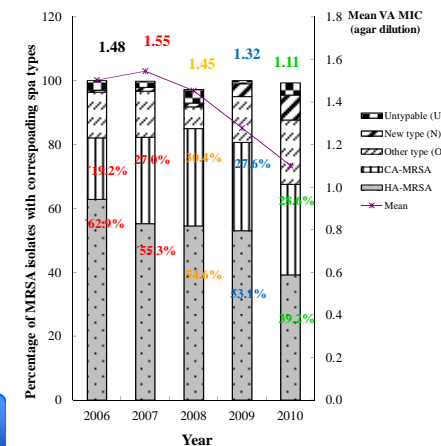


Figure 4. Distribution of HA-MRSA and CA-MRSA and correlation with vancomycin MIC by agar dilution among 687 MRSA from sterile sites (TIST 2006-2010)

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 found with significant difference in susceptibility patterns of vancomycin and daptomycin between them.