

P0210 Molecular Epidemiology of Methicillin-Resistant *Staphylococcus aureus* Bloodstream Isolates in Changhua, Taiwan, 2007-2013

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Introduction and Purpose

Methicillin-resistant *Staphylococcus aureus* (MRSA) has continuously been an important medical pathogen. In Taiwan, MRSA prevailed in the most hospitals and accounted for 53-83% of all clinical *S. aureus* isolates. The molecular epidemiology of MRSA offers essential information for infection control and management of diseases caused by this pathogen.

The purpose of this study was to investigate the molecular characters of clinical bloodstream isolates and the epidemiological change from 2007 to 2013 of two regional hospitals in central Taiwan by a variety of molecular typing techniques.

Materials and Methods

A total of 409 consecutive non-duplicate MRSA bloodstream isolates (203 isolates of hospital A and 206 of hospital B) were collected over a 7-year period from two regional hospitals in Changhua, Taiwan.

Hospital setting:

Hospital A: 786-bed teaching hospital in the urban Changhua

Hospital B: 861-bed teaching hospital in the rural Changhua



Genotyping: SCCmec type, Spa type and MLST

All MRSA isolates were characterized by molecular typing targeting the staphylococcal chromosomal cassette (SCCmec) and protein A (spa) genes and antibiogram analysis. Detection of the mecA gene, Panton-Valentine leukocidin and sasX gene were performed. Multilocus sequence typing (ST) was carried out on 120 representative strains.

Result

1. Distribution of SCCmec type and Spa type (Table 1)

Five major SCCmec types were found in this study. The most prevalent type through the study period was SCCmec type III (166, 40.6%), followed by IV (82, 20.0%) and II (74, 18.1%), VT (43, 10.5%) and V (23, 5.6%), respectively. Spa typing of 409 isolates revealed 33 different types. The five most common spa types were SCCmec II-t002 (n=71), SCCmec III-t037 (n=136), SCCmec IV-t437 (n=38), SCCmec V-t1081 (n=19) and SCCmec VT-t437 (n=33), respectively.

2. Sequence type and the presence of PVL and sasX gene (Table 2)

The most common sequence types for each SCCmec category were ST5-II (18%), ST239-III (32%) and ST59-V/VT (28%). Two ST30 and another two ST8 strains were identified in this study. Moreover, one ST9-UT-t2922 strain, isolated from an elder man with left knee septic arthritis and bacteremia, is a well-known livestock associated MRSA strain in Asia.

PVL gene was carried by SCCmec VT MRSA (81.4%, p<0.001) and ST 59 MRSA (51.7%). The sasX gene was mainly identified in the SCCmec III MRSA (91.6%, p<0.001) and ST 239 MRSA (100%)

Table 1

SCCmec type	N	Major Spa type (%)	Other Spa type (%)	PVL N (%)	sasX N (%)
II	74	t002 (73, 98.7%)	t001 (1), 1.3%	0	0
III	166	t037 (136, 81.9%)	t032 (4, 2.4%), t031 (1), 0.6%, t030 (1), 0.6%, t028 (1), 0.6%, t027 (1), 0.6%, t026 (1), 0.6%	5 (3.0%)	152 (91.6%)
IV	82	t437 (38, 46.3%)	t008 (3), 3.7%, t009 (1), 1.2%, t010 (1), 1.2%, t011 (1), 1.2%, t012 (1), 1.2%, t013 (1), 1.2%, t014 (1), 1.2%, t015 (1), 1.2%, t016 (1), 1.2%, t017 (1), 1.2%, t018 (1), 1.2%, t019 (1), 1.2%, t020 (1), 1.2%, t021 (1), 1.2%, t022 (1), 1.2%, t023 (1), 1.2%, t024 (1), 1.2%, t025 (1), 1.2%	17 (20.7%)	0
V	23	t1081 (19, 82.7%)	t1082 (1), 4.3%, t1083 (1), 4.3%, t1084 (1), 4.3%, t1085 (1), 4.3%	1 (4.3%)	1 (4.3%)
VT	43	t437 (33, 76.7%)	t438 (1), 2.3%, t439 (1), 2.3%, t440 (1), 2.3%, t441 (1), 2.3%, t442 (1), 2.3%, t443 (1), 2.3%, t444 (1), 2.3%, t445 (1), 2.3%	35 (81.4%)	0
UT	21	t037 (6, 28.6%)	t038 (1), 4.8%, t039 (1), 4.8%, t040 (1), 4.8%, t041 (1), 4.8%, t042 (1), 4.8%, t043 (1), 4.8%, t044 (1), 4.8%, t045 (1), 4.8%	1 (4.8%)	8 (38.1%)

Table 2

Sequence type	N	SCCmec type	Spa type	PVL	sasX
ST5	21	II (18)	t002 (18)	0%	0%
ST239	39	III (32)	t037 (32)	2.0%	100%
ST59	8	V (28)	t437 (8)	0%	12.5%
ST30	2	IV (20)	t008 (2)	0%	0%
ST8	4	III (32)	t037 (4)	0%	0%
ST3	4	III (32)	t037 (4)	0%	0%
ST10	3	III (32)	t037 (3)	0%	0%
ST13	2	III (32)	t037 (2)	0%	0%
ST14	2	III (32)	t037 (2)	0%	0%
ST17	1	III (32)	t037 (1)	0%	0%
ST24	1	III (32)	t037 (1)	0%	0%
ST28	1	III (32)	t037 (1)	0%	0%
ST31	1	III (32)	t037 (1)	0%	0%
ST32	1	III (32)	t037 (1)	0%	0%
ST33	1	III (32)	t037 (1)	0%	0%
ST34	1	III (32)	t037 (1)	0%	0%
ST35	1	III (32)	t037 (1)	0%	0%
ST36	1	III (32)	t037 (1)	0%	0%
ST37	1	III (32)	t037 (1)	0%	0%
ST38	1	III (32)	t037 (1)	0%	0%

Table 3

Hospital setting and Antibiotic use	Antibiotic use susceptibility rate					
	CC	EM	SM	LVX	CM	PA
Hospital A	84.1%	82.1%	78%	83.2%	83.1%	82.1%
Hospital B	84.2%	82.2%	80.2%	89%	87.4%	79.6%
Total	84.1%	82.1%	79.1%	83.2%	83.1%	80.8%

SCCmec type and Antibiotic use	Antibiotic use susceptibility rate					
	CC	EM	SM	LVX	CM	PA
II	100%	100%	91.4%	100%	98.6%	100%
III	97.6%	92.1%	91.6%	92.5%	96.4%	96.4%
IV	72.8%	85.6%	81.7%	41.2%	78.7%	2.4%
V	65.8%	73.3%	82.4%	82.4%	73.3%	73.3%
VT	93.9%	97.7%	91.2%	92.4%	88.4%	7.6%
UT	66.7%	71.4%	81.4%	47.6%	71.4%	27.8%

3. Antibiotic non-susceptibility test

The antimicrobial resistance rate was more higher seen in hospital A than hospital B except fusidic acid (p<0.05). The rate of resistance to other drugs varied from fusidic acid (22%) to erythromycin (93.8%). It is noteworthy that resistance rate to more than 3 different class antimicrobials was as high as 86.3%. The lowest multi-drug resistance rate was seen in SCCmec IV-MRSA (62.2%, p<0.05).

4. Change in epidemiology of MRSA over time

There was a significant decrease in trend for detecting MRSA in hospital B (p = 0.031) but not in hospital A (p=0.34) from 2010. In addition, the proportion of hospital associated and community associated MRSA (HA-MRSA vs CA-MRSA) was significantly different between these 2 hospitals (67.5% vs 37.5% for hospital A and 50.0% vs 41.7% for hospital B, p<0.001). Moreover, CA-MRSA has become the predominant MRSA strains in hospital B since 2011 (p=0.031) but HA-MRSA strains continuously remained stable in hospital A (p=0.06).



Conclusions

MRSA genotypes, ST239-III-sasX positive and ST59-VT-PVL positive, were the two major MRSA strains in central Taiwan. CA-MRSA (ST59) supplanted as the predominant MRSA strain in a certain hospital. In addition, livestock-associated MRSA (ST9) invasive infection was identified in this study. Our study described the epidemiological changes of MRSA in Taiwan and pointed out the potential threats of certain MRSA genotypes.

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