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Comparison of Genomic DNA Fingerprinting Using Pulsed-Field Gel Electrophoresis and Antibiotic Susceptibility of Clinical Isolates of Methicillin-Resistant *Staphylococcus aureus* between Chiang Mai and Tokyo

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major nosocomial pathogen in both Thailand and Japan (1-3). Genomic DNA fingerprinting using pulsed-field gel electrophoresis (PFGE) is a powerful tool to investigate the source, transmission, and spread of MRSA infection (4).

Nine and sixteen MRSA isolates obtained respectively from patients in a university hospital in Chiang Mai, Thailand (January to February 2000) and from patients in a hospital (with about 900 beds) in Tokyo (February 1999 to February 2000) were analyzed for chromosomal DNA type (contour-clamped homogeneous electric field system; CHEF Mapper™:

Bio-Rad Laboratories, Hercules, Calif., USA), antibiotic resistance (WalkAway™, Dade Behring, Deerfield, Ill., USA), enterotoxin serotype (SET-RPLA: Denka Seiken Co., Tokyo), toxic shock syndrome toxin-1 (TSST-1) production (TST-RPLA: Denka Seiken), and coagulase serotype (Denka Seiken).

Isolates from Chiang Mai showed 5 different PFGE patterns and 7 different antibiotic patterns (Fig. 1 and Table 1). Band-based cluster analysis of PFGE patterns (Molecular Analyst™: Bio-Rad) revealed a more than 94% similarity among the five isolates (Fig. 2). Chiang Mai isolates with PFGE pattern A,

Table 1. Antibiotic pattern classified by MIC pattern of 16 antibiotics against MRSA

Antibiotic pattern	Antibiotics listed in footnote [#]	MIC (μg/ml) of:							
		EM	GM	MINO	VCM	CLDM	ST	FOM	
Ta(Ja)	R	R	R	S	S	S	S	S	
Tb	R	R	S	S	S	R	S	S	
Tc	R	R	R	S	S	R	R	S	
Td	R	R	R	S	S	I	S	S	
Te	R	I	R	S	S	S	S	S	
Tf	R	I	R	S	S	S	R	S	
Tg	R	R	S	S	S	I	R	S	
Ja(Ta)	R	R	R	S	S	S	S	S	
Jb	R	R	S	S	S	R	S	R	
Jc	R	R	R	I	S	R	S	R	
Jd	R	R	R	I	S	R	S	I	
Je	R	R	S	I	S	R	S	R	
Jf	R	R	R	S	S	R	S	R	
Jg	R	R	S	I	S	R	S	I	
Jh	R	R	R	S	S	R	S	S	

PCG: benzyl-penicillin, MIPIC: oxacillin, ABPC: ampicillin, PIPC:piperacillin, CEZ: cefazolin, CMZ: cefmetazole, CTM: cefotiam, IPM: imipenem/cilastatin, EM: erythromycin, GM: gentamicin, OFLX: ofloxacin, MINO: minocycline, VCM: vancomycin, CLDM: clindamycin, ST: streptomycin, FOM: fosfomicin, R: resistant, S: susceptible, I:intermediate

Antibiotic pattern Ta is the same as pattern Ja.

[#]PCG, MIPIC, ABPC, PIPC, CEZ, CMZ, CTM, IPM, OFLX

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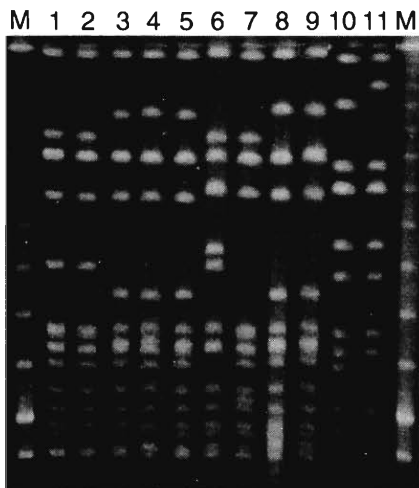


Fig. 1. Pulsed-field electrophoresis of *Sma*I-digested genomic DNA from MRSA isolates. Lanes 1-9: MRSA isolates from Chiang Mai, patterns A, A, D, E, D, B, C, D, and D, respectively. Lanes 10 and 11: two Tokyo isolates with patterns O and T.

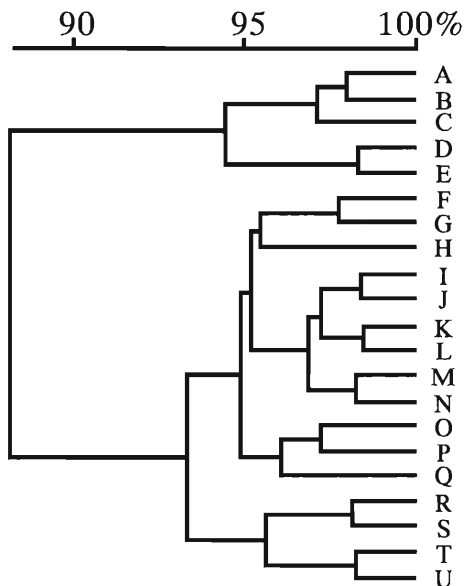


Fig. 2. Cluster analysis of MRSA isolates based on PFGE patterns.

but not those with other PFGE patterns, produced enterotoxin (Table 2). The produced enterotoxin was type A. All the isolates produced coagulase type IV, but not TSST-1.

All the 16 isolates from Tokyo showed different PFGE patterns, yet the similarity was more than 94%. Eight different antibiotic patterns were revealed (Fig. 2 and Table 1). Most Tokyo isolates produced enterotoxin type C, coagulase type II, and TSST-1. The cluster analysis of PFGE pattern revealed that similarity within individual hospitals was high while similarity between Chiang Mai and Tokyo isolates was low (Fig. 2). Antibiotic patterns were different between Chiang

Table 2. Phenotypic and genotypic characterization of the *S. aureus* isolates

PFGE pattern	Antibiotic pattern	Enterotoxin				TSST-1	Coagulase type
		A	B	C	D		
A	Tb,Tc	+	-	-	-	-	IV
B	Tf	-	-	-	-	-	IV
C	Tg	-	-	-	-	-	IV
D	Ta,Td,Te	-	-	-	-	-	IV
E	Te	-	-	-	-	-	IV
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F	Jc	-	-	-	-	+	II
G	Je	-	+	+	-	+	II
H	Jf	-	-	+	-	+	II
I	Ja	-	-	+	-	+	II
J	Jh	-	-	+	-	+	II
K	Je	-	-	+	-	+	II
L	Je	-	-	+	-	+	II
M	Jc	-	-	+	-	+	II
N	Jc	-	-	+	-	+	II
O	Je	-	-	+	-	+	II
P	Jc	-	-	+	-	+	II
Q	Jc	-	-	+	-	+	II
R	Jg	-	-	+	-	+	II
S	Jd	-	-	+	-	+	II
T	Jd	-	-	+	-	+	II
U	Jb	-	-	+	-	+	II

Mai and Tokyo isolates except for pattern Ta (Ja). MRSAs isolated in Thailand and those isolated in Japan were thus quite different in terms of their biological and genomic properties.

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