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Molecular Epidemiology of Methicillin-Resistant *Staphylococcus aureus* in a Hospital in Chiang Mai

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major nosocomial pathogen in Thailand (1). Epidemiological analysis of the MRSA isolates in a hospital, using restriction fragment length polymorphisms of genomic DNA in pulsed-field gel electrophoresis (PFGE), is essential for assessment of hospital infection control (2).

Eighty-two single-patient MRSA isolates were collected during January-February 2001 in a hospital with about 2000 beds in Chiang Mai. These isolates were analyzed for chromosomal DNA typing by using a contour-clamped homogeneous electric field system (CHEF Mapper™, Bio-Rad Laboratories, Hercules, Calif., USA). In the present study, the isolates showing the same PFGE patterns were considered to originate from the same MRSA strain.

Twelve different PFGE patterns of *Sma*I DNA digests were detected (Fig. 1). When PFGE patterns with more than 70% similarity in the band-based cluster analysis (Molecular Analyst™, Bio-Rad) were grouped into the same cluster, four clusters, A to D (Fig. 2A), were identified. Clusters B and C were similar to cluster A by more than 59 and 55 %, respectively. Cluster D shared less similarity with other clusters (Fig. 2A). Figure 2B shows that clusters A1 and C1 were dominant, each occupying 61% and 21% of total isolates. A geographic distribution of MRSA isolates in the hospital is shown in Table 1. The two dominant isolates, belonging to A1 and C1 clusters, spread over most wards in the hospital and were

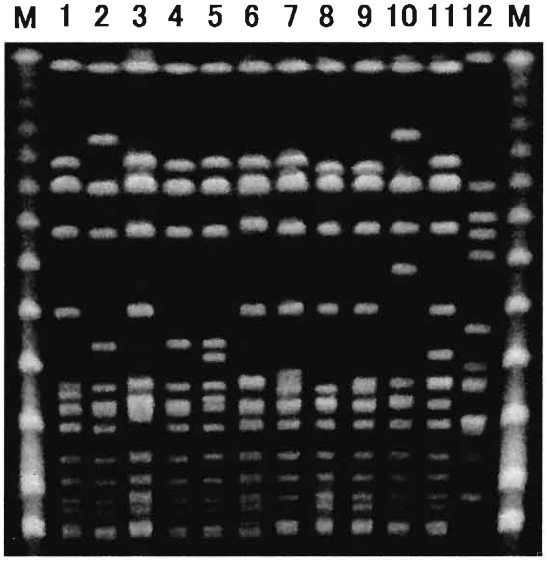

Fig. 1. Pulsed-field gel electrophoresis of *Sma*I-digested genomic DNA from MRSA isolates. Lane 1: PFGE pattern A1, lane 2: C1, lane 3: A2, lane 4: A3, lane 5: A4, lane 6: A5, lane 7: A6, lane 8: A7, lane 9: A8, lane 10: C2, lane 11: B, lane 12: D, M: low range PFG Marker.

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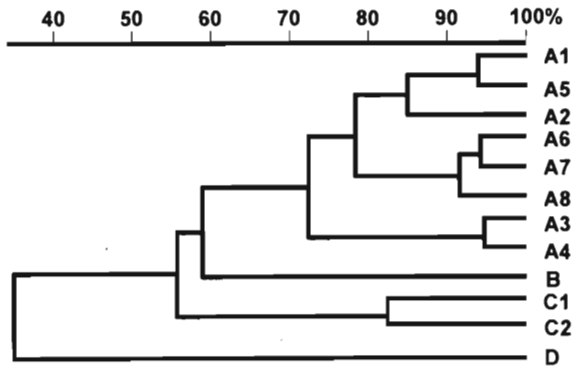

Fig. 2A. Cluster analysis of MRSA isolates based on PFGE patterns of *Sma*I-digested genomic DNA.

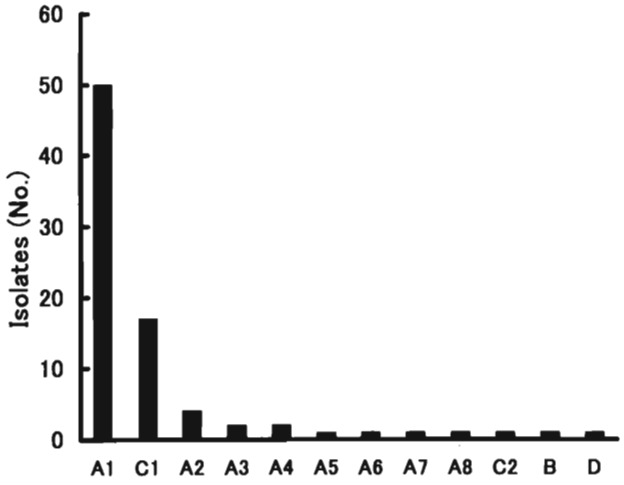

Fig. 2B. Histogram of MRSA isolates based on PFGE patterns.

Table 1. Distribution of MRSA isolates in a hospital

Ward	PFGE pattern											
	A								B	C		D
	1	2	3	4	5	6	7	8		1	2	
a	1									1		
b	1	1					1					
c	5											
d	3									3		
e											1	
f	1											
g	1	1										
h	1											
i	1							1		2		
j	1									1		
k	4			1	1					1		
l	3											
m	3											
n	1					1						
o										2		
p	1											
q	1											
r	2											
s	1											
t	2			1						1		
u	7									1		
v										1		
w	1		1							1		
x	5								1			
y	1		1							1		
z	1											
aa	1	1								1		
ab		1										
ac												1
ad	1									1		

isolated on more than one occasion in the same wards; for example, wards c, d, k, l, m, r, t, u, and x for cluster A1, and wards d, i, and o for cluster C1. These data indicate that there were dominant MRSA strains, which intermittently caused the outbreaks during the study period, in the hospital.

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