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Epidemiological Analysis of a Methicillin-Resistant *Staphylococcus aureus* Outbreak in a Surgery Ward by Genomic DNA Fingerprinting Using Pulsed-Field Gel Electrophoresis

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Nosocomial infection, especially postoperative infection, caused by methicillin-resistant *Staphylococcus aureus* (MRSA), is a major problem in surgical wards (1). Genomic DNA fingerprinting using pulsed-field gel electrophoresis (PFGE) is a powerful tool to investigate the source, transmission, and spread of MRSA infection (2).

In a surgery ward in a hospital in Tokyo, three patients successively contracted severe sepsis. MRSA was isolated from the patients' blood. The isolates and isolates from carriers in the same ward during the same period were tested 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).

PFGE profile of *Sma*I DNA digests (Fig. 1) and antibiotic resistance patterns (Tables 1, 2) differed among the three sepsis isolates (No. 57, 63, and 66). This indicates that, though the sepsis occurred apparently in a form of outbreak, these incidences were due to infection by different MRSA strains resulting solely from contamination of the ward by multiple MRSA strains. However, band-based cluster analyses of PFGE profiles (Molecular Analyst™: Bio-Rad) indicated a

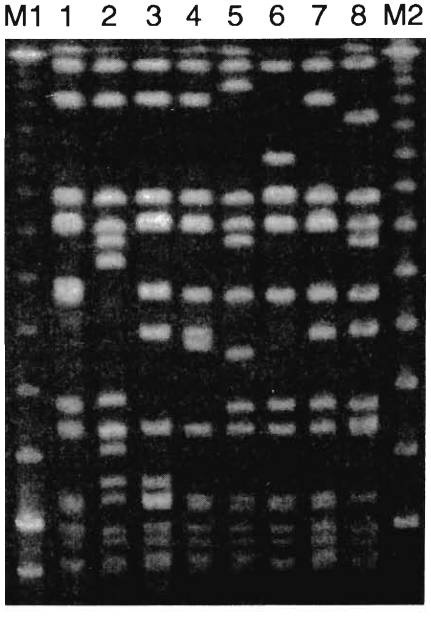

Fig. 1. Pulsed-field electrophoresis of *Sma*I-digested genomic DNA from MRSA isolates.
Lane 1: isolate No.57 (pattern D), lane 2: No. 63 (B), lane 3: No. 66 (G), lane 4: No. 67 (H), lane 5: No. 69 (C), lane 6: No. 70 (E), lane 7: No. 73 (F), lane 8: No. 74 (A), M1: low range PFG Marker, M2: lamda ladder PFG Marker.

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

Antibiotic pattern	MIC (μg/ml) of:															
	PCG	MPIPC	ABPC	PIPC	CEZ	CMZ	CTM	IPM	EM	GM	OFLX	MINO	VCM	CLDM	ST	FOM
a	R	R	R	R	R	R	R	R	R	R	R	I	S	R	S	R
b	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R
c	R	R	R	R	R	R	R	R	R	R	R	I	S	R	S	I
d	R	R	R	R	R	R	R	R	R	S	R	I	S	R	S	I
e	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	S

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

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

Ward	Isolation month (1999)	symptom	Isolation No.	PFGE pattern	Antibiotic pattern	Enterotoxin				TSST-1	Coagulase type
						A	B	C	D		
cardiac	Nov.	sepsis	57	D	a	–	–	+	–	+	II
surgery	Nov.		63	B	b	–	–	+	–	+	II
	Nov.		66	G	c	–	–	+	–	+	II
	Dec.	colonization	67	H	d	–	–	+	–	+	II
	Dec.		69	C	e	–	–	+	–	+	II
	Nov.		70	E	a	–	–	+	–	+	II
	Dec.		73	F	a	–	–	+	–	+	II
	Nov.		74	A	a	–	–	+	–	+	II

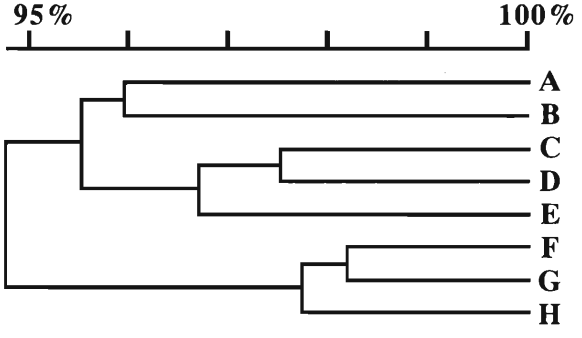

Fig. 2. Cluster analysis of MRSA isolates based on PFGE patterns.

more than 98% similarity among all the strains tested (Fig. 2). This may indicate that MRSA of the same origin may have persisted in the ward with continuous mutations. All the isolates produced enterotoxin type C, TSST-1 and coagulase Type II (Table 2).

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