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Nosocomial spread of ST72-MRSA-IV methicillin-resistant *Staphylococcus aureus* in a neonatal intensive care unit at a university hospital in Daejeon, Korea

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Introduction and Purpose

Methicillin-resistant *Staphylococcus aureus* (MRSA) is the most common causes of hospital-acquired infection. Recently the emergence and increasing prevalence of community-associated Methicillin-resistant *Staphylococcus aureus* (CA-MRSA) in hospitals have been reported worldwide.

In Korea, the established representative CA-MRSA clone (sequence type 72-MRSA-SCC*mec* type IV [ST72-MRSA-IV]) has been increasingly isolated in various healthcare settings, emerging as a significant cause of HA infections. However, little information is available regarding the epidemiology of *S. aureus* in NICUs in Korea.

In this study, we investigated the molecular epidemiology of MRSA isolated in a neonatal intensive care unit (NICU) and conducted surveillance cultures.

Material and Methods

1. Collection and classification of MRSA isolates

All MRSA isolates from NICU were consecutively collected from August 2014 to March 2015. Thye were classified either HA-MRSA or CA-MRSA based on the 48-hour interval between patient admission and initial sample collection. The Vitek 2 automated system (bioMerieux, Marcy l'Etoile, France) was used for microbiological identification and antimicrobial susceptibility testing. The presence of MRSA was confirmed by detecting the *mec*A gene.

2. Surveillance of healthcare workers and the environment

Fifty-seven healthcare workers were screened for MRSA after obtaining hand and nasal swabs. Extensive environmental screening was carried out with all surfaces. Microbiological identification and antimicrobial susceptibility testing were performed using the Vitek2 automated system. Molecular characterization was performed in cases where the isolates were positive for MRSA.

3. Molecular characterization

Staphylococcal cassette chromosome *mec* (SCC*mec*) typing, Panton-Valentine leukocidin (PVL) gene detection, multilocus sequence typing (MLST), *spa* typing, and pulsed field gel electrophoresis (PFGE) were performed.

Results

1. Clinical characteristics of patients and antimicrobial susceptibilities

Seventy four MRSA clinical isolates were collected and confirmed by *mec*A gene PCR amplification. Eighteen isolates (24%) were found to be CA-MRSA and 56 isolates (76%) were HA-MRSA. A comparison of the patient characteristics and antimicrobial susceptibility results of CA-MRSA and HA-MRSA is shown in Table 1.

2. Surveillance of healthcare workers and the environment

A total of 242 environmental samples and 114 samples collected from 57 healthcare workers were included. MRSA was detected in 23 surveillance cultures. Susceptibility testing results are shown in Table 1.

	CA-MRSA (n = 18)	HA-MRSA (n = 56)	Surveillance culture (n=23)
Gestational age (weeks)	38.1 ± 1.7	32.7 ± 5.3	NA
Birth weight (g)	3286.7 ± 601	1968.8 ± 1090	NA
Caesarian section (n, %)	6 (33.3%)	47 (82.5%)	NA
Outborns (n, %)	18 (100%)	12 (21.4%)	NA
t324	6 (33.3%)	41 (73.2%)	19 (82.6%)
t2431	3 (16.7%)	9 (16.1%)	3 (13.0%)
t664	7 (38.9%)	4 (7.1%)	0
t452	0	0	1 (4.4%)
Nontypeable	2 (11.1%)	2 (3.6%)	0
Ciprofloxacin	0	0	0
Clindamycin	0	0	0
TMP-SMX	0	0	0
Erythromycin	6 (33.3%)	4 (7.1%)	1
Gentamicin	2 (11.1%)	26 (46.4%)	17
Mupirocin	3 (16.7%)	34 (60.7%)	18
Rifampin	0	0	0
Tetracycline	3 (16.7%)	8 (14.3%)	1

Table 1. Comparison of patient characteristics and antimicrobial susceptibility among isolates from CA-MRSA, HA-MRSA and surveillance culture.

3. Molecular characterization

All clinical isolates and isolates from surveillance culture were identified as ST72, SCC*mec* type IV and PVL negative. The distribution of *spa* types was shown in Table 1. Differences between HA-MRSA and CA-MRSA were found in terms of their *spa*-type distributions (Table 2). And the distributions of *spa* types of surveillance culture were similar to those in HA-MRSA isolates ($P > 0.05$). PFGE showed 3 major pulsotypes, of which pulsotype A included the majority of HA-MRSA isolates (45/56), CA-MRSA isolates (15/18) and surveillance culture isolates (14/23).

Number of isolates resistant to antimicrobial	spa type			
	t324 (n = 66)	t2431 (n = 15)	t664 (n = 11)	P value (t324 vs. t664)
Ciprofloxacin	0	0	0	NS
Clindamycin	0	0	0	NS
TMP-SMX	0	0	0	NS
Erythromycin	1 (1.5)	1 (6.7)	8 (72.7)	<0.05
Gentamicin	42 (63.6)	3 (20.0)	0	<0.05
Mupirocin	45 (68.2)	9 (60.0)	0	<0.05
Rifampin	0	0	0	NS
Tetracycline	1 (1.5)	10 (66.7)	0	<0.05

Table 2. Antimicrobial susceptibility results according to *spa* types

Discussions

We demonstrated ST72-SCC*mec* IV without the PVL gene predominated in NICU and that person-to-person and environment-to-person transmission appeared to be the reason for predominance of a single MRSA clone. Among the several molecular typing methods, spa typing was the most simple and useful tool in our hospital where a single predominant seqeunce type is present. As colonization of MRSA in neonates imposes a risk of infection, stronger infection control measures including strict hand washing and implementation of active surveillance should be enforced to eradicate nosocomial MRSA colonization or infection.