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Prevalence of Methicillin-Resistant *Staphylococcus aureus* Nasal Colonization among Taiwanese Children in 2005 and 2006[▽]

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From July 2005 to October 2006, a total of 3,046 children, of ages between 2 months and 5 years, presented for a well-child health care visit to one of three medical centers, which are located in the northern, central, and southern parts of Taiwan, and were surveyed for nasal carriage of methicillin-resistant *Staphylococcus aureus* (MRSA). The overall prevalences of *S. aureus* and MRSA nasal carriage among the children were 23% and 7.3%, respectively (18% and 4.8% in the central region, 25% and 6.7% in the southern region, and 27% and 9.5% in the northern region). Of the 212 MRSA isolates (96%) available for analysis, a total of 10 pulsed-field gel electrophoresis (PFGE) patterns with two major patterns (C [61%] and D [28%]) were identified. One hundred forty-nine isolates (70%) contained type IV staphylococcal cassette chromosome *mec* (SCC*mec*) DNA, and 55 isolates (26%) contained SCC*mec* V_T. The presence of Panton-Valentine Leukocidin (PVL) genes was detected in 60 isolates (28%). Most MRSA isolates belonged to one of two major clones, characterized as sequence type 59 (ST59)/PFGE C/SCC*mec* IV/absence of PVL genes (59%) and ST59/PFGE D/SCC*mec* V_T/presence of PVL genes (25%). We concluded that between 2005 and 2006, 7.3% of healthy Taiwanese children were colonized by MRSA in nares. MRSA harbored in healthy children indicates an accelerated spread in the community.

Recent reports indicate that community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) infections are increasing worldwide and may now involve persons without risk factors predisposing them for acquisition (2, 11–14, 20, 24). Asymptomatic CA-MRSA colonization has been documented in healthy children attending the emergency departments and outpatient clinics of children's hospitals (6, 19, 25, 27, 28).

Carriage of *S. aureus*, including MRSA, is well known to be a significant risk factor for subsequent infection (7, 29), and the anterior nares are the most consistent sites of colonization. The presence of *S. aureus* nasal colonization can provide an indication of a high risk for subsequent infection.

In Taiwan, previous reports (1, 3, 9, 15, 17, 23, 31) have indicated that during the period from 1997 to 2003, MRSA accounted for 9.8% to 36% of CA *S. aureus* infections in children without risk factors and the MRSA colonization rate in the general population ranged from 1.9% to ~3.3% for school children and 5.3% for healthy children presented for health care visits to 10.8% for health care workers and 13.6% for contacts of CA-MRSA infection. It is noteworthy, however, that most of these studies were conducted in the northern part of Taiwan and no island-wide survey has yet been conducted to elucidate this issue. To estimate the extent of MRSA in the community in Taiwan and to assess if there is an increasing trend of MRSA nasal colonization in healthy children during the past 5 years, we conducted this island-wide survey between 2005 and 2006. All collected MRSA isolates were also further characterized by molecular methods.

MATERIALS AND METHODS

This study was approved by the Institutional Review Board of the Chang Gung Memorial Hospital. From July 2005 to October 2006, all children of ages between 2 months and 5 years who presented for a well-child health care visit to any one of three medical centers in Taiwan were invited to participate in this study. The three medical centers involved were the Chang Gung Children's Hospitals at Linko (hospital A) and Kaohsiung (hospital C) and Taichung Veterans General Hospital (hospital B), which are situated, respectively, in northern, southern, and central parts of Taiwan. In each hospital, around 80 subjects were recruited for study for each month, and the ages of the subjects were evenly distributed in seven separate age ranges, which included >2 to 6 months, >6 to 12 months, >12 to 18 months, >18 to 24 months, >2 to 3 years, >3 to 4 years, and >4 to 5 years. A culture from the anterior nares for the detection of MRSA was obtained from each subject after written consent was obtained from their parents/guardians.

Survey specimens for culture were obtained with a cotton swab, placed in the transport medium (Venturi Transystem; Copan Innovation Ltd., Limerick, Ireland), and then brought to and processed in the microbiological laboratories within 4 hours of the sampling. All *S. aureus* isolates were sent to Chang Gung Memorial Hospital at Linko for microbiological characterization. Identification of MRSA was confirmed according to Clinical and Laboratory Standards Institute 2005 guidelines (5). Pulsed-field gel electrophoresis (PFGE) with SmaI digestion was used in this study to fingerprint the MRSA isolates and was performed according to procedures described previously (3, 16, 18). The genotypes were designated in alphabetical order, as in our previous studies (3, 15–18); any new genotype, if identified, was designated consecutively. PFGE patterns with fewer than four band differences from an existing genotype were defined as subtypes of that genotype.

SCC*mec* typing of isolates was done using a multiplex PCR strategy described previously (26). Control strains for SCC*mec* types I, II, III, and IVa, kindly provided by Keiichi Hiramatsu, were as follows: type I, NCTC10442; type II, N315; type III, 85/2082; and type IVa, JCSC4744. SCC*mec* typing for type V_T was determined by using a particular primer described elsewhere (1), and strain TSGH-17, kindly provided by Chi-Chien Wang, was used as a control. However, the SCC*mec* typing method for type V_T yielded inconsistent results; thus, an

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TABLE 1. Nasal carriage of MRSA among infants and children presented for a well-child health care visit in Taiwan

Area of Taiwan	No. of subjects	No. (%) with *S. aureus*[a]	No. (%) with MRSA[b]
Northern	1,279	344 (26.9)	121 (9.5)
Central	1,011	180 (17.8)	49 (4.8)
Southern	756	189 (25)	51 (6.7)
Total	3,046	713 (23.4)	221 (7.3)

[a] The rate of carriage of *S. aureus* among children in the central region was significantly lower than those among children in the northern and southern regions ($P < 0.001$).

[b] The rate of carriage of MRSA among children in the northern region was significantly higher than those among children in the central ($P < 0.001$) and southern ($P = 0.039$) regions.

alternative method was used. The appearance of an isolate with only two bands (414 bp and 243 bp) in the multiplex PCR analysis may have indicated that the isolate contained SCC*mec* V_T. To confirm their identities, a novel pair of primers, ccrC-5F (5′-CAC TTA ATC CAT TGA CAC AG-3′) and ccrC-5R (5′-AAA GAT TGA GGG ATA AGA CT-3′), was designed according to the published sequence (GenBank accession no. AY894416) of the *ccrC* gene of a Taiwanese strain, *S. aureus* TSGH-17. Amplification of a specific 1,081-bp DNA fragment, which was subjected to further sequence analysis for some representative isolates in preliminary experiments, confirmed that the isolates contained SCC*mec* V_T.

The presence of Panton-Valentine leukocidin (PVL) genes was determined by a PCR strategy described previously (22). Some isolates of representative PFGE patterns were selected and underwent multilocus sequence typing (MLST) as described elsewhere (8). The allelic profiles were assigned through comparison of the sequences at each locus with those of the known alleles in the *S. aureus* MLST database and were defined as sequence types accordingly.

RESULTS

During the study period, 1,279 subjects were recruited from hospital A, 1,011 subjects from hospital B (from July 2005 to June 2006), and 756 subjects from hospital C (from October 2005 to June 2006). All the children enrolled are Taiwanese. The number of subjects enrolled in each age group ranged from 430 for children of ages >6 to 12 months to 443 for children of ages >2 to 3 years. Of the total of 3,046 subjects enrolled in this study, 713 (23%) were colonized with *S. aureus*. Of the 713 isolates, 221 (31%) were demonstrated to be MRSA. The details of the nasal MRSA colonization prevalence for subjects in the different parts of Taiwan are shown in Table 1. The MRSA colonization rate in northern Taiwan was significantly higher than that in the central ($P < 0.001$) and southern ($P < 0.039$) parts of Taiwan. The nasal MRSA colonization prevalences for the subjects in each age group were 8.4% for the children of ages >2 to 6 months and 6.3%, 3.2%, 3.9%, 9.0%, 9.5%, and 10.1% for children of ages >6 to 12 months, >12 to 18 months, >18 to 24 months, >2 to 3 years, >3 to 4 years, and >4 to 5 years, respectively. For those less than 18 months of age, the carriage rate decreased with increasing age ($P = 0.0011$; Mantel-Haenszel test for trend), while for those older than 12 months of age, the carriage rate increased with increasing age ($P < 0.0001$).

Of the 221 MRSA isolates, 212 isolates were available for analysis. All of these 212 isolates were sensitive to vancomycin and teicoplanin. All but two of the isolates identified from hospital A were resistant to penicillin. Most isolates were resistant to erythromycin and clindamycin but sensitive to trimethoprim-sulfamethoxazole (SXT) and doxycycline. The detailed susceptibility distribution of various antibiotics for the isolates is shown in Table 2. No significant difference in antibiotic susceptibility patterns was noted among the isolates from the three different regions of Taiwan.

Table 3 illustrates the detailed distribution of PFGE patterns, SCC*mec* types, and the presence/absence of PVL genes among these isolates. A total of 10 PFGE patterns were identified. Patterns C and D were the two most common patterns and accounted for 62% and 28% of the isolates analyzed, respectively. The distribution of PFGE patterns among the three regions showed a trend for a difference ($P = 0.09$ by a log-likelihood contingency test). Four types (types II, III, IV, and V_T) of SCC*mec* genes were identified among the isolates, with type IV (70%) being the predominant type, followed by type V_T (26%). The distribution of SCC*mec* types among the three regions was significantly different ($P = 0.03$). Four isolates of the AF PFGE pattern were untypeable by the methods used in this study. PVL genes were present in 60 isolates (28%). Twenty-five isolates underwent MLST, and eight sequence types were identified. Sequence type 59 (ST59) was the most common sequence type and accounted for 9 of 10 PFGE type C isolates, 4 of 6 PFGE type D isolates, and the isolate of PFGE type AN. The other two isolates of PFGE type D were ST338, which is a single-locus variant of ST59 (a single nucleotide difference in the *gmk* locus). The remaining isolate of PFGE type C belonged to a new sequence type, which is a single-locus variant of ST59 (a single nucleotide difference in the *pta* locus). One isolate of PFGE type F also belonged to a new sequence type, which is also a single-locus variant of ST9 (a single nucleotide difference in the *gmk* locus). The detailed association of PFGE patterns with sequence types and SCC*mec* types and the presence of the PVL gene of these isolates are shown in Table 4. The MRSA isolates characterized by ST59/PFGE type C/SCC*mec* IV/absence of PVL genes and ST59/PFGE type D/SCC*mec* V_T/presence of PVL genes were the two most common clones and accounted for 59% and 25% of the isolates analyzed, respectively.

TABLE 2. Antibiotic susceptibility rates of 212 colonizing MRSA isolates from children in Taiwan

Area of Taiwan (n[a])	No. (%) of isolates susceptible to:						
	Penicillin	Erythromycin	Clindamycin	Doxycycline	SXT	Vancomycin	Teicoplanin
Northern (120)	2 (1.7)	10 (8.3)	13 (11)	118 (98)	119 (99)	120 (100)	120 (100)
Central (42)	0	1 (2.4)	3 (7.1)	39 (93)	39 (93)	42 (100)	42 (100)
Southern (50)	0	3 (6)	3 (6)	50 (100)	49 (98)	50 (100)	50 (100)
Total (212)	2 (0.9)	14 (6.6)	19 (9.0)	207 (98)	207 (98)	212 (100)	212 (100)

[a] n, no. of isolates.

TABLE 3. Distribution of PFGE patterns, SCC*mec* types, and presence of PVL genes among 212 colonizing MRSA isolates

Area of Taiwan (n^a)	No. (%) of isolates with characteristic									
	PFGE pattern				SCC*mec* type[b]				Presence of PVL genes	Absence of PVL genes
	A	C	D	Other	II	III	IV	V_T		
Northern (120)	1 (0.8)	66 (55)	40 (33)	13 (11)	0	0	81 (68)	37 (31)	40 (33)	80 (67)
Central (42)	2 (4.8)	28 (67)	10 (24)	2 (4.8)	0	2 (4.8)	32 (76)	8 (19)	11 (26)	31 (74)
Southern (50)	0	37 (74)	9 (18)	4 (8)	2 (4)	0	36 (72)	10 (20)	9 (18)	41 (82)
Total (212)	3 (1.4)	131 (62)	59 (28)	19 (9.0)	2 (0.9)	2 (0.9)	149 (70)	55 (26)	60 (28)	152 (72)

[a] *n*, no. of isolates.
[b] Four isolates were untypeable. The distributions of SCC*mec* types were significantly different among the three regions ($P = 0.03$).

DISCUSSION

Results from this study indicate that the national prevalence of nasal MRSA colonization among otherwise healthy children in Taiwan was 7.3% during the period from July 2005 to October 2006 inclusively, with values ranging from 4.8% in the central region of Taiwan to 9.5% in the northern region of Taiwan. Compared with those among the healthy children during the period of 2001 to 2002 (1, 17, 23) (Table 5), though the study population was different for these studies, the nasal MRSA colonization prevalence among healthy children in Taiwan increased significantly, from 1.9% in 2001 to 9.5% ($P < 0.0001$ by chi-square test) during the period of 2005 to 2006 for northern Taiwan and significantly from 3.3% to 6.7% for southern Taiwan ($P < 0.001$ by chi-square test). This increasing trend of nasal MRSA colonization prevalence might account for the increasing incidence of CA-MRSA infection in children in Taiwan (3, 9, 31). In the United States, where CA-MRSA is also being increasingly reported, the MRSA colonization prevalence for the general population appeared to have been relatively low until the year 2002 (19, 21, 25, 27, 28). In a survey (21) involving 9,622 persons conducted between 2001 and 2002, national *S. aureus* and MRSA nasal colonization prevalence estimates were 32.4% and 0.8%, respectively. For healthy children, the nasal colonization rates ranged from 0.2% to 2.2% (19, 25, 27, 28), as reported in several pediatric studies; however, an increasing trend in this regard has been noted in certain areas of the United States recently (6). Creech et al. (6) reported that the nasal MRSA colonization rate among healthy children in Nashville, TN, increased significantly from 0.8% in 2001 to 9.2% in 2004, a picture not dissimilar to what we show in the present study from Taiwan.

TABLE 4. Association of PFGE patterns with MLST, SCC*mec* types, and presence of PVL genes for 212 MRSA isolates

PFGE pattern (n^a)	No. of subtypes	SCC*mec* type (*n*)	Status of PVL genes (*n*)	Sequence type[b]
A (3)	3	III (2), IV (1)	Absent	ST239
C (131)	25	IV (129), V_T (2)	Absent (129), present (2)	ST59, new*
D (59)	13	V_T (53), IV (6)	Present (57), absent (2)	ST59, ST338*
F (3)	2	II (2), V_T (1)	Absent	ST5, new*
AF (4)	1	Untypeable	Absent	ST89
AK (2)	2	IV	Absent	ST508
AN (3)	2	IV	Absent	ST59
AQ (5)	3	IV	Absent	ST508
AR (1)	1	IV	Absent	ST15
BA (1)	1	IV	Absent	ST5

[a] *n*, no. of isolates.
[b] Each of the three sequence types marked with an asterisk is a single-locus variant of ST59, but they differ from each other.

In the United States, CA-MRSA strains have been recognized as representing a novel pathogen which was genetically different from the nosocomial MRSA strains (14, 24). They have limited antibiotic resistance (except to β-lactams), have two common PFGE patterns (USA 300 and USA 400), possess different exotoxin gene profiles (e.g., PVL), and contain SCC*mec* DNA (10). In contrast, the CA-MRSA clinical isolates in Taiwan were multiresistant and shared two common PFGE patterns (patterns D and C in this study) (1, 3, 4, 30). In the current study, more than 90% of the MRSA colonization isolates were multiresistant to erythromycin and clindamycin but sensitive to SXT and doxycycline. In addition, most colonization isolates shared common molecular characteristics, and more than 80% of the isolates belonged to one of two major clones, characterized by ST59/PFGE type C/SCC*mec* IV/absence of PVL genes or ST59/PFGE type D/SCC*mec* V_T/presence of PVL genes. However, among the clinical isolates, the clone characterized by ST59/PFGE type D/SCC*mec* V_T/presence of PVL genes was the dominant clone (1, 3, 30), while among the colonized isolates, the clone characterized by ST59/PFGE type C/SCC*mec* IV/absence of PVL genes was dominant. It seemed that PVL genes, reported to be a virulence factor associated with necrotizing pneumonia and abscesses (22), may be associated with the ability of a PVL-positive clone to cause infection.

There existed several limitations in the current study. First, the demographic characteristics and the risk factors associated with MRSA acquisition were not analyzed and compared between the children with and without CA-MRSA colonization, though all the children were healthy and presented for health care visits. Living with a family member who works in a hospital or clinic and demographic characteristics (e.g., age and gender) were reported to be associated with an increased risk of MRSA colonization (6, 21, 25). Second, the persistence of MRSA carriage in the subjects could not be determined and the incidence of subsequent MRSA infection in the subjects could not be measured in this cross-sectional analysis of MRSA nasal colonization prevalence.

In summary, 7.3% of healthy children in Taiwan were colonized by MRSA in the nares during the period from 2005 to 2006. MRSA carriage in the children may accelerate the spread in the community. Two major CA-MRSA clones were

TABLE 5. Reported prevalence rates of MRSA nasal colonization for healthy Taiwanese children between 2001 and 2006

Period	Area of Taiwan	Subjects	Age of subjects	No. of subjects	No. (%) with MRSA[b]	Reference
2001	Southern	Schoolchildren	2 yr to ~18 yr	987	33 (3.3)	Lu et al. (23)
2001-2002	Northern	Schoolchildren	3 yr to ~12 yr	262	5 (1.9)	Huang et al. (17)
2003	Northern	Schoolchildren, health care visits	<12 yr	640	48 (7.5)[a]	Boyle-Vavra et al. (1)
2005-2006	Northern	Children for health care visits	2 mo to ~5 yr	1,279	121 (9.5)	This study
	Central	Children for health care visits	2 mo to ~5 yr	1,011	49 (4.8)	This study
	Southern	Children for health care visits	2 mo to ~5 yr	756	51 (6.7)	This study

[a] If restricted to those without risk factors, no. of colonized subjects would be 34 (5.3%).
[b] The prevalence increased significantly in the northern ($P < 0.0001$ by chi-square test) and southern ($P < 0.001$) regions of Taiwan during the period of 2001 to 2006.

identified and would appear to have spread island-wide. Further studies are needed to determine the host factors of colonization and to develop strategies to disrupt transmission of CA-MRSA to susceptible hosts.

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