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Prevalence of and Risk Factors for Colonization by Methicillin-Resistant *Staphylococcus aureus* among Adults in Community Settings in Taiwan[▽]

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In order to determine the prevalence of methicillin (meticillin)-resistant *Staphylococcus aureus* (MRSA) colonization among adults in community settings in Taiwan and identify its risk factors, we conducted the present study. For a 3-month period, we enrolled all adults who attended mandatory health examinations at three medical centers and signed the informed consent. Nasal swabs were taken for the isolation of *S. aureus*. For each MRSA isolate, we performed multilocus sequence typing, identification of the staphylococcal cassette chromosome *mec*, tests for the presence of the Panton-Valentine leukocidin gene, and tests for drug susceptibilities. Risk factors for MRSA colonization were determined. The results indicated that the MRSA colonization rate among adults in the community settings in Taiwan was 3.8% (119/3,098). Most MRSA isolates belonged to sequence type 59 (84.0%). Independent risk factors for MRSA colonization included the presence of household members less than 7 years old ($P < 0.0001$) and the use of antibiotics within the past year ($P = 0.0031$). Smoking appeared to be protective against MRSA colonization ($P < 0.0001$).

Before the late 1990s, nearly all methicillin (meticillin)-resistant *Staphylococcus aureus* (MRSA) infections occurred in patients with specific risk factors who were in health care facilities (31). However, the emergence of MRSA infections among previously healthy persons in community settings (without exposure to health care facilities) was noted thereafter (6, 31). Therefore, MRSA infections are now classified as health care-associated MRSA (HA-MRSA) infections and community-associated MRSA (CA-MRSA) infections (38).

Strains responsible for CA-MRSA infections differ from those for HA-MRSA infections in several phenotypic and genetic features (1, 28). CA-MRSA strains carry type IV or V staphylococcal cassette chromosome *mec* (SCC*mec*) elements, are usually Panton-Valentine leukocidin (PVL) producing, and are not multidrug resistant; HA-MRSA strains carry type I, II, or III SCC*mec* elements, are usually not PVL producing, and are multidrug resistant (15, 22, 28).

Initially, CA-MRSA infections were mostly reported in young children (36). However, as CA-MRSA infections became more common, infections were reported among people of all ages and contributed to the increase of community-associated *S. aureus* infections with significance (25, 29, 36). MRSA colonization is an important risk factor for subsequent MRSA infection (30), so several studies in the United States have characterized the MRSA colonization rate in a community setting (13, 16). These studies demonstrated that the nasal colonization rates among healthy children increased from 0.8% in 2001 to 9.2% in 2004 (13). The colonization rate was 0.84% among people participating in the 2001 to 2002 National Health and Nutrition Examination Survey (NHANES) (16).

In Taiwan, MRSA strains of sequence type 59 (ST59), determined by multilocus sequence typing (MLST) and carrying type IV or V SCC*mec* elements, were recently found to be the major strains of CA-MRSA (5, 7, 27). Other studies demonstrated that these CA-MRSA strains were responsible for the rapid increase in the number of CA-MRSA infections among children and adults in Taiwan (7, 37). The MRSA colonization rates among Taiwanese children increased from 1.5% from 2001 to 2002 to 7.2% from 2005 to 2006 (18, 19). However, the MRSA colonization rate among adults in community settings in Taiwan is unclear. This study was conducted to determine the prevalence and risk factors for the colonization of MRSA among adults in community settings in Taiwan.

MATERIALS AND METHODS

Study population. From 1 October 2007 to 31 December 2007, all adults (ages, >18 years) who attended mandatory health examinations (as a part of the workplace health promotion program) at three medical centers located in northern Taiwan and signed the informed consent were enrolled in this study. Three well-trained study assistants took a nasal swab from each enrolled person. The swabs were sent to the central laboratory located at National Taiwan University Hospital (a major teaching hospital in Taiwan with a total capacity of 2,200 beds) and were cultured within 6 h. When an enrolled person was found to be a MRSA carrier, his or her household members were invited to participate in the study. After the informed consent was signed, nasal swabs from these household members were also taken and sent to be cultured. This study has been approved by the institute review boards of the three medical centers.

Bacterial culture and identification of MRSA. Each swab was plated onto a sheep blood agar plate. All plates were incubated at 35°C ambient air for 48 h. Isolates suspected of being *S. aureus* from sheep blood agar were first checked by

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catalase and Gram stain if deemed necessary, and all *S. aureus* isolates were confirmed by coagulase latex agglutination. *S. aureus* isolates were spotted onto ChromAgar MRSA to check for methicillin resistance. All isolates were preserved.

Drug susceptibility tests. The MICs of all MRSA isolates were determined for gentamicin, clindamycin, erythromycin, ciprofloxacin, minocycline, rifampin (rifampicin), trimethoprim-sulfamethoxazole, and vancomycin using the agar dilution method proposed by the Clinical and Laboratory Standards Institute (CLSI) (10). In brief, a Steers' replicator was used to apply 10^4 CFU of bacteria onto Mueller-Hinton agar containing serial twofold dilutions of each antimicrobial agent (256 to 0.03 mg/liter). The agar plates were incubated at 35°C for 18 h before reading. The MIC was defined as the lowest concentration of antimicrobial agents completely inhibiting the growth of bacteria. *S. aureus* ATCC 25923 was used as the internal control in each run of the test. The breakpoints used to determine susceptibility were as defined by the CLSI (11).

Molecular typing and detection of the PVL gene. Chromosomal DNA was prepared as described previously (17). The presence of the PVL gene *lukF-lukS* was determined by PCR with the use of a primer as described elsewhere (26). Typing of the SCC*mec* elements (I to V) and the *mecA* gene was performed by methods described by Ito et al. (22, 23). MLST was performed as described by Enright et al. (14).

Data collection. A standardized questionnaire was used to collect information on the risk factors for CA-MRSA colonization. The data collected were age; sex; educational degree; marital status; whether the subject was living in a dormitory or not; the number of household members; the presence of any household member who was a health care worker; the presence of any household member who was less than 7 years old; the presence of any household member who was bedridden; the presence of chronic diseases; smoking habits; hospitalizations within the previous year; a history of caring for inpatients within the past year; outpatient clinic visits within the past year; the use of antibiotics within the previous year; tattoos, acupuncture treatments, parenteral drug use, and/or dialysis treatments within the previous year; a history of skin and soft-tissue infection within the previous year; whether the subject takes a shower every day; a history of visiting public places (e.g., hot-spring baths, swimming pools, sauna baths, gymnasiums, and dancing saloons) within the previous year; and economic status.

Statistics. Continuous variables were given as means ± standard deviations and compared using Student's *t* test. The categorical variables were compared with a chi-square test or Fisher's exact test if the expected values were below 5. The prevalence of MRSA colonization was determined. To analyze the risk factors for carrying MRSA, we used polytomous logistic regression to compare people with MRSA to those without *S. aureus* and people with MRSA to those with methicillin-susceptible *S. aureus* (MSSA). All parameters were initially tested by univariate analysis; those with a *P* value of <0.05 and those being biologically meaningful were used for the multivariate analysis. However, parameters with colinearity, tested by correlation matrices, were not simultaneously considered in the final model. In the multivariate analysis, stepwise model comparison was used to determine the best model. Statistical analyses were performed using SAS 9.1.3 (SAS Institute, Inc., Cary, NC). All tests were two-tailed, and a *P* value of <0.05 was considered statistically significant.

RESULTS

During the 3-month study period, there were 3,098 people enrolled. Among them, 686 people were found to carry *S. aureus*. A total of 119 of these 686 people carried MRSA and 567 had MSSA. The comparisons of demographics and other parameters of the enrolled people are shown in Table 1. There were statistically significant differences between these three groups in the parameters of sex, educational degree, the presence of any household member who was a health care worker, the presence of any household member less than 7 years old, smoking habits, and the use of antibiotics within the past year. Based on a post-hoc analysis, we found that people with MRSA (i) tended to have less education than those with MSSA or without *S. aureus* colonization ($P = 0.0875$ and 0.0650, respectively), (ii) were more likely to have household members who were less than 7 years old than the other two groups (both $P < 0.0001$), (iii) were less likely to be smokers than those without *S. aureus* colonization ($P = 0.0077$), and (iv) were more likely to have used antibiotics during the past year than the two other groups ($P = 0.0012$ and 0.0004, respectively).

Among the 119 MRSA isolates from the 119 people (henceforth the "index people"), 100 were classified as ST59, 11 as ST508, 5 as ST89, 2 as ST239, and 1 as ST6. Of the 100 isolates of ST59, 65 carried the type IV SCC*mec* element (ST59-IV) and 35 carried the type V SCC*mec* element (ST59-V). Of the 65 ST59-IV MRSA isolates, only 10 (15.4%) were positive for the PVL gene. All 35 of the ST59-V isolates were positive for the PVL gene. All isolates of ST6 and ST508 carried the type IV SCC*mec* element, all isolates of ST89 carried the type II SCC*mec* element, and both isolates of ST239 carried the type III SCC*mec* element (Table 2). All isolates, except two of ST508, that belonged to ST6, ST89, ST239, and ST508 were negative for the PVL gene. The overall prevalence of MRSA was 3.8% (119/3,098; 95% confidence interval, 3.1% to 4.5%). However, when those isolates carrying type IV and V SCC*mec* elements were taken into consideration as CA-MRSA strains, the prevalence of CA-MRSA carriage among healthy adults in Taiwan was found to be 3.6% (112/3,098; 95% confidence interval, 2.9% to 4.3%).

We also screened household members of 70 of the 119 index people. In total, there were 242 household members screened. Among these 242 people, 64 people (47 adults and 17 children) from 39 families carried MRSA. Of these 64 MRSA isolates, 47 were classified as ST59, 11 as ST508, 2 as ST30, 2 as ST89, 1 as ST182, and 1 as ST342. Of the 47 isolates of ST59, 31 carried the type IV SCC*mec* element and the other 16 carried the type V SCC*mec* element. Of the 31 ST59-IV MRSA isolates from household members, 11 (35.5%) were positive for the PVL gene. All 16 ST59-V isolates from household members were positive for the PVL gene. All isolates of ST30, ST182, ST342, and ST508 carried the type IV SCC*mec* element, and both isolates of ST89 carried the type II SCC*mec* element (Table 2). Of the 11 ST508-IV MRSA isolates from household members, one (9.1%) was positive for the PVL gene. All isolates of ST30 and ST182 were positive for the PVL gene. None of the ST89 and ST342 isolates was positive for the PVL gene.

A comparison of genotypes of the MRSA isolates from household members and their associated index people indicated that there were 16 (41.0%) families in which the MRSA isolates from all household members and index people belonged to the same genotypes (same results from MLST typing, same SCC*mec* element, and identical presence/absence of the PVL gene). There were six (15.4%) families in which MRSA isolates from some (but not all) household members were of the same genotypes as those of the index people. There were five (12.8%) families in which MRSA isolates from household members were of the same MLST type and the same types of SCC*mec* elements as those of the index people but different in the presence/absence of the PVL gene. There were four (10.3%) families in which MRSA isolates from household members were of the same MLST type as those of the index people but different in the types of SCC*mec* elements (despite the presence/absence of the PVL gene). And there were eight (20.5%) families in which MRSA isolates from household members differed from those of the index people in MLST type.

TABLE 1. Characteristics of people with MRSA, MSSA, and no *S. aureus* colonization (n = 3,098)[a]

Parameter	No. (%) of people colonized with:			*P* value
	MRSA (n = 119)	MSSA (n = 567)	No_C (n = 2,412)	
Age (mean ± SD)	38.1 ± 12.7	39.5 ± 11.9	39.9 ± 11.6	0.2513
Sex[b]				0.0186
Male	50 (42.0)	275 (48.8)	1014 (42.3)	
Female	69 (58.0)	288 (51.2)	1381 (57.7)	
Education[b]				
Under elementary school	3 (2.6)	3 (0.5)	22 (0.9)	0.0278
Elementary school	8 (6.8)	19 (3.4)	68 (2.9)	
Junior high school	4 (3.4)	11 (2.0)	78 (3.3)	
Senior high school	18 (15.4)	74 (13.3)	376 (15.9)	
University	59 (50.4)	324 (58.2)	1380 (58.4)	
Graduate or beyond	25 (21.4)	126 (22.6)	437 (18.5)	
Status of marriage[b]				
Married	87 (75.7)	359 (65.5)	1568 (66.9)	0.2589
Divorced	1 (0.9)	11 (2.0)	56 (2.4)	
Unmarried	27 (23.5)	178 (32.5)	721 (30.7)	
Working as a HCW[b]				0.1894
Yes	13 (13.3)	40 (8.1)	212 (10.3)	
No	85 (86.7)	453 (91.9)	1844 (89.7)	
Living in a dormitory[b]				0.7715
Yes	1 (1.2)	10 (2.0)	37 (2.2)	
No	85 (98.8)	406 (98.0)	1674 (97.8)	
No. of household members (mean ± SD)	3.0 ± 1.6	3.7 ± 1.5	3.7 ± 1.6	0.0761
Presence of household members who are HCWs[b]				0.0085
Yes	10 (8.7)	54 (9.7)	144 (6.1)	
No	105 (91.3)	504 (90.3)	2209 (93.9)	
Presence of household members less than 7 yr old[b]				<0.0001
Yes	52 (44.8)	121 (21.7)	610 (25.7)	
No	64 (55.2)	437 (78.3)	1759 (74.3)	
Presence of household members who are bedridden[b]				0.7468
Yes	4 (3.4)	18 (3.2)	64 (2.7)	
No	113 (96.6)	541 (96.8)	2299 (97.3)	
Chronically ill[b]				0.4702
Yes	42 (36.5)	180 (32.7)	741 (31.5)	
No	73 (63.5)	370 (67.3)	1614 (68.5)	
Smoking habits[b]				<0.0001
Yes	13 (11.0)	76 (13.5)	505 (21.2)	
No	105 (89.0)	485 (86.5)	1876 (78.8)	
Hospitalization[b]				0.3568
Yes	9 (7.6)	25 (4.5)	128 (5.4)	
No	109 (92.4)	534 (95.5)	2256 (94.6)	
Caring for an inpatient[b]				0.6462
Yes	22 (19.3)	90 (16.2)	416 (17.4)	
No	92 (80.7)	465 (83.8)	1952 (82.6)	
Visiting outpatient clinics[b]				0.5940
Yes	78 (67.8)	364 (64.8)	1587 (66.9)	
No	37 (32.2)	198 (35.2)	784 (33.1)	
Using antibiotics[b]				0.0016
Yes	35 (30.1)	95 (17.1)	409 (17.2)	
No	81 (69.9)	461 (82.9)	1964 (82.8)	
Tattoo or acupuncture or using parenteral drug or dialysis[b]				0.7917
Yes	2 (1.7)	16 (2.8)	64 (2.7)	
No	114 (98.3)	546 (97.2)	2310 (97.3)	
Skin or soft-tissue injury[b]				0.8420
Yes	55 (47.8)	282 (50.8)	1186 (50.4)	
No	60 (52.2)	273 (49.2)	1165 (49.6)	
Showering every day[b]				0.3498
Yes	112 (96.6)	539 (96.3)	2315 (97.4)	
No	4 (3.4)	21 (3.7)	62 (2.6)	
Visiting public amusement places[b]				0.1761
Yes	67 (57.3)	322 (57.5)	1454 (61.4)	
No	50 (42.7)	238 (42.5)	913 (38.6)	
Family income (NTD)[b]				
Less than 20,000	1 (2.4)	1 (0.6)	17 (2.5)	0.4533
20,000-50,000	3 (7.1)	28 (16.3)	108 (15.8)	
50,000-100,000	20 (47.6)	64 (37.2)	244 (35.7)	
100,000-200,000	8 (19.0)	38 (22.1)	123 (18.0)	
200,000-300,000	3 (7.1)	5 (2.9)	31 (4.5)	
Over 300,000	7 (16.7)	36 (20.9)	160 (23.4)	

[a] No_C, no *S. aureus* colonization; SD, standard deviation; M, male; F, female; HCWs, health care workers; NTD, new Taiwan dollar.

[b] There are missing data for some parameters, including the sex category (21 people), education (63), working as a HCW (95), living in a dormitory (885), presence of household members who are HCWs (72), presence of household members under 7 years old (55), presence of household members who are bedridden (59), chronically ill (78), smoking habits (38), hospitalization (37), caring for inpatients (61), visiting outpatient clinics (50), using antibiotics (53), tattoo or acupuncture or using parenteral drug or dialysis (48), skin or soft-tissue injury (77), showering every day (47), visiting public amusement places (54), and family income (2,201).

TABLE 2. MLST types and SCC*mec* elements in the 183 MRSA isolates (119 index people and 64 household members)

MLST type	No. of isolates for indicated type of SCC*mec* element									
	Index people					Household members				
	II	III	IV	V	Subtotal	II	III	IV	V	Subtotal
ST6	0	0	1	0	1					0
ST30					0	0	0	2	0	2
ST59	0	0	65	35	100	0	0	31	16	47
ST89	5	0	0	0	5	2	0	0	0	2
ST182					0	0	0	1	0	1
ST239	0	2	0	0	2					0
ST342					0	0	0	1	0	1
ST508	0	0	11	0	11	0	0	11	0	11
Total	5	2	77	35	119	2	0	46	16	64

We used polytomous logistic regression to identify risk factors for MRSA colonization by comparing people with MRSA to those with MSSA and people with MRSA to those without carriage of *S. aureus*. Univariate analysis indicated that the female gender, the presence of health care workers in the household, the presence of household members less than 7 years old, being a nonsmoker, and the use of antibiotics during the past year were risk factors for MRSA colonization (Table 3). Using a multivariate analysis, the presence of household members less than 7 years old, being a nonsmoker, and the use of antibiotics during the past year were independent risk factors for MRSA colonization compared to those without carriage of *S. aureus*. However, the presence of household members less than 7 years old and the use of antibiotics during the past year were the only two independent risk factors for MRSA colonization compared to those for carriage of MSSA (Table 4).

Table 5 shows the drug susceptibilities of all 183 MRSA isolates (from the index people and their families) stratified by MLST types. The overall susceptibilities were 25.1% for clindamycin, 16.9% for erythromycin, 99.5% for trimethoprim-sulfamethoxazole, 78.1% for gentamicin, 99.5% for minocycline, 98.9% for ciprofloxacin, 100% for rifampin, and 100% for vancomycin.

DISCUSSION

Several reports from the United States indicated that community-associated *S. aureus* infections have increased rapidly in recent years and that MRSA (not MSSA) accounts for most of this increase (24, 29). Studies from Taiwan have demonstrated similar findings among children and adults (7, 37). Therefore, it is increasingly important to characterize the MRSA colonization pool among people in communities. The prevalence of MRSA colonization among children in communities has been extensively studied in Taiwan and the United States (5, 13, 18, 19, 21, 32–34), but there are only a few studies of MRSA colonization among adults in communities (16, 39). Our study showed that the MRSA colonization rate among adults in community settings in Taiwan who attended mandatory health examinations as a part of workplace health promotion was 3.8% (95% confidence interval, 3.1% to 4.5%).

A previous population-based study showed that the MRSA colonization rate among people attending the 2001 to 2002 NHANES was 0.84% (16). A study in The Netherlands from 1999 to 2000 indicated that the MRSA colonization rate among the general Dutch population was 0.03% (39). The MRSA colonization rate in this study was about 5- to 10-fold higher than reported in these prior studies. There may be several reasons for this difference. First, the colonization by MRSA among adults in communities may be more prevalent in Taiwan than in the United States and The Netherlands. Second, our study was conducted 5 to 7 years after those studies, so the difference may be due to an overall increase of MRSA

TABLE 3. Risk factors for people colonized with MRSA compared to those colonized with MSSA and those not colonized with *S. aureus* by univariate analysis using polytomous logistic regression[a]

Parameter	Odds ratio		Overall *P* value
	MRSA vs No_C	MRSA vs MSSA	
Age	0.9871	0.9890	0.2510
Sex	0.9869	0.7589	0.0189
Education degree[b]			
Elementary school	0.8628	0.4210	0.5298
Junior high school	0.3761	0.3636	0.4672
Senior high school	0.3511	0.2432	0.2118
University	0.3277	0.1821	0.0996
Graduate or beyond	0.4195	0.1984	0.1602
Marital status[c]			
Married	0.6749	0.6259	0.1452
Divorced	0.3218	0.3751	0.4951
Working as a HCW	1.3303	1.7320	0.1919
Living in a dormitory	0.5325	0.4776	0.7774
No. of household members	1.1071	1.1435	0.0749
Presence of household members who are HCWs	1.4610	0.8889	0.0092
Presence of household members ≤7 yr old	2.3429	2.9344	<0.0001
Presence of household members who are bedridden	1.2716	1.0640	0.7475
Chronically ill	1.2532	1.1827	0.4711
Smoking habits	0.4599	0.7901	<0.0001
Hospitalization within the past year	1.4553	1.7637	0.3609
Cared for inpatients within the past year	1.1221	1.2355	0.6465
Visited outpatient clinics within the past year	1.0414	1.1467	0.5941
Used antibiotics within the past year	2.0749	2.0968	0.0021
Tattoo and/or acupuncture and/or using parenteral drugs and/or dialysis	0.6332	0.5987	0.7948
Skin or soft-tissue injury within the past year	0.9004	0.8875	0.8420
Shower everyday	0.7620	1.0909	0.3533
Visited public amusement places within the past year	0.8414	0.9904	0.1765
Family income (NTD)			
20,000-50,000	0.4722	0.1071	0.2864
50,000-100,000	1.3935	0.3125	0.3454
100,000-200,000	1.1057	0.2105	0.2842
200,000-300,000	1.6451	0.6000	0.6324
Over 300,000	0.7437	0.1944	0.4139

[a] No_C, no *S. aureus* colonization; HCWs, health care workers; NTD, new Taiwan dollar.
[b] Using the under-elementary-school category result as the baseline.
[c] Using the unmarried category result as the baseline.
[d] Using the less-than-20,000 category result as the baseline.

TABLE 4. Risk factors for MRSA colonization compared to MSSA colonization and no *S. aureus* colonization by multivariate analysis using polytomous logistic regression

Risk factor	MRSA vs No_C[a]		MRSA vs MSSA		*P* value of overall model
	Odds ratio (95% confidence interval)	*P* value of coefficient	Odds ratio (95% confidence interval)	*P* value of coefficient	
Presence of household members aged under 7	2.2387 (1.5255–3.2853)	<0.0001	2.9110 (1.9048–4.4488)	<0.0001	<0.0001
Smoking habits	0.4419 (0.2383–0.8195)	0.0096	0.9582 (0.4946–1.8563)	0.8994	<0.0001
Using antibiotics within the past year	2.0530 (1.3544–3.1118)	0.0007	2.0322 (1.2826–3.2198)	0.0025	0.0031

[a] No_C, no *S. aureus* colonization.

during this time. Several previous studies have demonstrated that the MRSA colonization rate of people in communities has increased over time (5, 13). However, we also understand that only adults who attended mandatory health examinations as a part of a workplace health promotion program were enrolled in our study and thus may not be representative of the adult populations in communities. Since these attendees are presumably healthier than average, our results may be biased by the healthy worker effect (2).

Our molecular analysis indicated that most of the MRSA isolates (112/119) from the index people carried the type IV or type V SCC*mec* element, as is typical for CA-MRSA strains (15, 22, 23, 28). Therefore, the colonization rate of CA-MRSA strains was 3.6% in this study. In this study, ST59 isolates were the most common MLST type of isolates. Previous studies from Taiwan have found that ST59 MRSA isolates were the most common MLST type of MRSA causing CA-MRSA infections in different geographic areas all over Taiwan (8). Studies concerning the MRSA colonization in Taiwanese children also found ST59 is the predominant type among MRSA isolates from child carriers in communities all over Taiwan (7, 18). Our study adds additional information about the MRSA carrier rate and bacterial typing in adults in community settings in Taiwan. However, ST59 MRSA isolates were rarely found in other Asian countries according to the findings from a recent large-scale study (9).

Our molecular analysis that compared MRSA isolates from the index people and their associated households identified numerous instances where the genotypes were different. This strongly suggests that, in addition to household transmission (20), the spread of MRSA in community settings occurred via some other routes, such as sport contact, the use of saunas, exposure to a colonized animal, and so on (3, 4, 12, 40).

We used polytomous logistic regression to identify risk factors for MRSA colonization by comparing people with MRSA colonization to those with MSSA colonization and people with MRSA colonization to those without carriage of *S. aureus* at the same time. This allowed us to avoid problems associated with multiple intergroup comparisons. Studies that reported the determinants of MRSA colonization in community settings remained limited (16). Our multivariate analysis indicated that the presence of household members less than 7 years old, being a nonsmoker, and the use of antibiotics within the past year were the independent risk factors for MRSA colonization compared to those without *S. aureus* colonization. The presence of household members less than 7 years old and the use of antibiotics within the past year were the only two independent risk factors for MRSA colonization compared to those for MSSA colonization.

A previous study showed that the MRSA colonization rate of children in community settings in Taiwan was 7.2% from 2005 to 2006 (18), much higher than the adult colonization rate (3.8%) in the present study. In addition, among our 17 pediatric household members who had MRSA, 12 carried MRSA of the same genotype as the associated index person. The hypothesis that transmission from children to their parents through close household contact might play an important role in MRSA colonization among adults is worthy of further study. We also found that the use of antibiotics was associated with the presence of MRSA. This was expected, because antibiotics provide selective pressure and thus facilitated the colonization of drug-resistant pathogens such as MRSA.

TABLE 5. Drug susceptibilities of the 183 MRSA isolates with stratification by MLST type

MLST type (no. of isolates)	% Susceptibility for indicated drug[a]							
	CM	ERM	TXT	GM	MIN	CIP	RIF	VAN
ST6 (1)	100	100	100	100	100	100	100	100
ST30 (2)	50	50	100	100	100	100	100	100
ST59 (147)	14.3	11.6	99.3	74.1	99.3	100	100	100
ST89 (7)	0	0	100	100	100	85.7	100	100
ST182 (1)	100	0	100	100	100	100	100	100
ST239 (2)	50	0	100	50	100	50	100	100
ST342 (1)	100	0	100	100	100	100	100	100
ST508 (22)	90.9	54.5	100	95.4	100	100	100	100
Overall (183)	25.1	16.9	99.5	78.1	99.5	98.9	100	100

[a] CM, clindamycin; ERM, erythromycin; TXT, trimethoprim-sulfamethoxazole; GM, gentamicin; MIN, minocycline; CIP, ciprofloxacin; RIF, rifampin; VAN, vancomycin.

Surprisingly, in a comparison of people with MRSA and those without *S. aureus* colonization, we found that smoking was a protective factor against MRSA colonization. However, a comparison of people with MRSA and those with MSSA found that smoking was not such a factor. In reanalyzing our data, we found that smoking was also an independent protective factor against MSSA and *S. aureus* (pooling MRSA and MSSA together) colonization compared to those without *S. aureus* colonization (odds ratio, 0.4612 and 0.4570, respectively; 95% confidence interval, 0.3480 to 0.6111 and 0.3520 to 0.5940, respectively; $P < 0.0001$ and 0.0001, respectively). Therefore, it seems that smoking is a protective factor against *S. aureus*, not only specifically against MRSA, colonization. To our best knowledge, only a review article described the similar findings based on the results from a Ph.D. thesis (35). Our study therefore provides the important evidence that smoking might be a protective factor against the nasal colonization of *S. aureus*. It might be that smoking creates a microenvironment in the nose that protects against the growth of *S. aureus*. Clearly, the effect of smoking on *S. aureus* colonization requires further study.

The results of our drug susceptibility tests showed that more than 95% of the isolates were susceptible to trimethoprim-sulfamethoxazole, minocycline, and ciprofloxacin; that all isolates were susceptible to rifampin and vancomycin; and that most isolates were resistant to clindamycin and erythromycin. These results differ from those reported from the United States, where the rate of susceptibility to clindamycin of MRSA isolates causing CA-MRSA infection was as high as 95% (29). This may be due to the predominance of different strains in these different geographic regions.

In conclusion, the present study showed that the rate is 3.8%. Most (94.1%) of these MRSA isolates in the present study had typical characteristics of CA-MRSA. Our study also identifies that the presence of household members less than 7 years old as well as the use of antibiotics within the past year were the independent risk factors for MRSA colonization, and smoking appeared to be a protective factor against MRSA colonization. These findings could be helpful for controlling the spread of MRSA in community settings.

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