

Differences in Methicillin-Resistant *Staphylococcus aureus* Strains Isolated from Pediatric and Adult Patients from Hospitals in a Large County in California

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Studies of U.S. epidemics of community- and health care-associated methicillin-resistant *Staphylococcus aureus* (MRSA) suggested differences in MRSA strains in adults and those in children. Comprehensive population-based studies exploring these differences are lacking. We conducted a prospective cohort study of inpatients in Orange County, CA, collecting clinical MRSA isolates from 30 of 31 Orange County hospitals, to characterize differences in MRSA strains isolated from children compared to those isolated from adults. All isolates were characterized by *spa* typing. We collected 1,124 MRSA isolates from adults and 159 from children. Annual Orange County population estimates of MRSA inpatient clinical cultures were 119/100,000 adults and 22/100,000 children. *spa* types t008, t242, and t002 accounted for 83% of all isolates. The distribution of these three *spa* types among adults was significantly different from that among children ($\chi^2 = 52.29$; $P < 0.001$). Forty-one percent of adult isolates were of t008 (USA300), compared to 69% of pediatric isolates. In multivariate analyses, specimens from pediatric patients, wounds, non-intensive care unit (ICU) wards, and hospitals with a high proportion of Medicaid-insured patients were significantly associated with the detection of t008 strains. While community- and health care-associated MRSA reservoirs have begun to merge, significant differences remain in pediatric and adult patient populations. Community-associated MRSA *spa* type t008 is significantly more common in pediatric patients.

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major global cause of morbidity and mortality, imposing serious economic costs on patients and hospitals (1, 6, 7, 13, 26, 53). Prior to the mid-1990s, MRSA was largely a health care-associated pathogen, causing infection predominantly in people with frequent or recent contact with health care facilities (health care-associated MRSA [HA-MRSA]). In the United States, the rates of MRSA carriage (both asymptomatic and symptomatic) are estimated to be 6 to 12% in general hospital patient populations and 9 to 24% in intensive care unit populations (ICUs) (23, 32, 50). Although HA-MRSA has long been the primary cause of MRSA infections, community-associated MRSA (CA-MRSA), which often causes infections among healthy children and young adults with no exposure to the health care setting, is becoming increasingly prevalent. The first reports of MRSA isolated from patients with no identifiable risk factors came from Australia and the United States in the 1990s (5, 21, 56). Since then, the prevalence of CA-MRSA has rapidly increased, with reports of CA-MRSA infection from virtually every geographic region of the world (55, 59). The incidence of life-threatening invasive infections owing to CA-MRSA is increasing, and CA-MRSA appears to be particularly virulent among children (38). Moreover, CA-MRSA has caused outbreaks in the hospital setting (4, 41, 51), with some reports suggesting that it may be replacing HA-MRSA (8, 46, 49, 52).

In the United States, the predominant community-associated MRSA clone is now USA300 (defined by *spa* typing and multilocus sequence typing [MLST] as t008 and ST8, respectively), having rapidly disseminated and replaced USA400 (t128/ST1) since its appearance in 2000. USA300 has several characteristics that may

offer a selective advantage over other MRSA clones, both community associated (e.g., USA400) and health care associated (e.g., USA100 [t002/ST5]). These advantages include (i) a smaller staphylococcal cassette chromosome *mec* (SCC*mec*) element (usually type IV) than those of health care-associated strains (usually SCC*mec* types I to III), which is more readily transmissible and may be an advantage in terms of the DNA replication speed; (ii) fewer antibiotic resistance genes than health care-associated strains, resulting in a fitness benefit due to the carriage of smaller or fewer genes; and (iii) a higher growth rate, which may lead to successful colonization by outcompeting health care-associated strains (8, 43). Furthermore, the linkage of an arginine catabolic mobile element with SCC*mec* type IV in USA300 likely confers increased fitness and/or pathogenicity (11). Finally, high levels of expression of regulatory genes associated with the virulence factors Pantone-Valentine leukocidin and alpha-toxin have been shown for USA300 versus USA400 isolates, which may contribute to the invasiveness of USA300 (39).

The phenotypic and genotypic differences between HA- and

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CA-MRSA strains have been well documented (2, 10, 12, 33, 43), yet there are few studies that have directly explored the differences in MRSA strains isolated from adults and those isolated from children. Park et al. (44) previously compared a small number of adult and pediatric MRSA isolates in a South Korean hospital and found a predominance of CA-MRSA isolates among children. A better understanding of the frequency of community- versus health care-associated MRSA clones among adults and children, and in particular the USA300 clone, may inform strategies to prevent transmission and disease.

Children may have different exposures to MRSA, as they constitute a largely healthy population that is most likely to incur MRSA infection through skin and soft tissue injuries related to sports and other play activities (16). This is in contrast to the chronically and critically ill adult population, which frequents hospitals and may encounter health care-associated MRSA strains more readily. Furthermore, children may experience different antimicrobial drug selection pressure compared to that of adults due to differences in common disease syndromes and different guidance on antibiotic therapy (9, 44).

Defining the characteristics of MRSA strains in adults and children would provide insight into the spread of MRSA strains, particularly since there is growing evidence that community and health care MRSA reservoirs are mixing (28, 30, 34, 49, 52). Furthermore, few studies of adult or pediatric MRSA strains have involved a population-based sample of strains. We conducted a prospective cohort study of inpatients in a large metropolitan county to characterize differences in pediatric and adult MRSA strains.

MATERIALS AND METHODS

Study. We conducted a population-based, prospective collection of clinical isolates of MRSA from 30 of 31 hospitals in Orange County, CA. This study was approved by the Institutional Review Board of the University of California Regents.

Isolate collection. Clinical (nonscreening) isolates of MRSA from unique adult patients (≥ 18 years of age) and unique pediatric patients (< 18 years of age) were collected from hospital microbiology laboratories. Hospitals were instructed to collect MRSA isolates from unique patients up to a total of 100 isolates or for a duration of 12 months, whichever came first. In order to have a representative sample of Orange County MRSA isolates, we limited isolates in this study to those collected for a uniform duration of time from adult hospitals. Since the largest adult hospitals reached 100 isolates over a 5-month period, we restricted the period of all adult isolate collections to 5 months. All pediatric hospitals required a 12-month collection period. Nearly all adult isolates were collected between December 2008 and April 2009. Pediatric isolates were collected between October 2008 and September 2009. Isolates from patients not admitted to hospitals were excluded from the study. Samples were batched and delivered to the Orange County Public Health Laboratory using soy agar slants. For the repeated confirmation of MRSA, isolates were plated onto selective medium for MRSA (BD CHROMagar). MRSA strains were stored at -65°C in 15% glycerol Brucella broth.

Specimen data and hospital characteristics. Specimen data, including patient age in years, specimen source (wound, blood, urine, sputum, or other), specimen location (ICU or non-ICU), and time of specimen collection with respect to admission date (hospital onset [HO], ≥ 3 days after admission; community onset [CO], < 3 days after admission), were collected. Hospital characteristics were obtained from a California hospital data set (42), which included annual admissions, hospital type (acute care versus long-term acute care [LTAC] facility), percentage of Medicaid-insured patients, and percentage of Hispanic patients. Popula-

tion estimates of adults and children in Orange County were obtained from the 2010 U.S. Census (57).

Laboratory methods and molecular typing. All strains were shipped to Imperial College London in the United Kingdom for *spa* typing and stored at -80°C . Cells were harvested on blood agar plates (Oxoid) and incubated at 37°C overnight. DNA was extracted by using a Qiagen DNeasy Blood & Tissue kit. DNA samples were eluted in 200 μl of elution buffer (10 mM Tris-Cl, 0.5 mM EDTA [pH 9.0]) and stored at -20°C . Following the sequencing of the *spa* region, *spa* types were determined by using Ridom StaphType v2.1 (Ridom GmbH, Würzburg, Germany) (20). To assess *spa* type diversity and relatedness, cluster analysis of *spa* types was performed separately for adult and pediatric isolates by using the Based upon Repeat Pattern (BURP) algorithm, a built-in feature of the StaphType software (35). MLST and SmaI pulsed-field gel electrophoresis (PFGE) were performed on a subset of the isolates ($n = 171$), to confirm MRSA strain types, according to methods described previously (14, 48). This subset included one isolate of each *spa* type and, for the 10 most common *spa* types, one isolate from each of the hospitals in which these *spa* types were present. Isolates were selected by using a random number generator. For PFGE, DNA profiles were analyzed by using BioNumerics software (version 5.0, 2007; Applied Maths). PFGE types were defined using a similarity coefficient of 78%, and USA100 to USA800 strains were used as references.

Statistical analyses. Annual adult and pediatric population estimates of hospitalized patients with clinical MRSA cultures were calculated by *spa* type, accounting for the duration of countywide collection. We further calculated the percentage of MRSA strains from adult versus pediatric patients that were due to the most common *spa* types (t008, t242, and t002) and compared them by using χ^2 tests. Specimen data for t008, t242, and t002 isolates were compared by using χ^2 or Fisher's exact tests and, for patient age, the Wilcoxon Mann-Whitney test. Simpson's index of diversity ($1 - D$) was used to compare the genetic diversities of MRSA strains among adults and children. $1 - D$ gives an unbiased measure of the probability of drawing two different *spa* types given the distribution of *spa* types in a sample (19). The 95% confidence intervals (CIs) were calculated as described previously (18). We conducted bivariate tests to evaluate the association of *spa* type t008 with individual variables, including age (adult/pediatric), specimen source (particularly wound and blood), time of specimen collection (community or hospital onset), and ward type (non-ICU/ICU). We also tested hospital-level variables, including annual admissions (greater or less than 10,000), LTAC facility, percentage of Hispanic patients, and percentage of Medicaid-insured patients. For multivariate analyses, variables with a P value of < 0.1 were entered into a generalized linear mixed model clustered by hospital and were retained at an α value of ≤ 0.05 (xtmelogit, STATA release 11, 2009; Stata Corp.).

RESULTS

A total of 1,124 adult and 159 pediatric MRSA isolates were collected over the 5- and 12-month periods, respectively. A summary of the characteristics of the clinical MRSA strains collected is shown in Table 1. The median age of adults was 67 years (interquartile range [IQR], 50 to 81 years), and that of children was 2 years (IQR, 1 to 9 years).

t008, t242, and t002 were the predominant *spa* types in Orange County, accounting for 83% of all isolates (Table 2). The distribution of these *spa* types among adults (t008, 41%; t242, 23%; t002, 19%) was significantly different from that among children (t008, 69%; t242, 9%; t002, 6%) ($\chi^2 = 52.29$; $P < 0.001$). Annual population estimates of clinical inpatient MRSA infections were 119/100,000 adults and 22/100,000 children. Annual estimates by *spa* type were 48/100,000 adults and 15/100,000 children for t008, 27/100,000 adults and 2/100,000 children for t242, and 22/100,000 adults and 1/100,000 children for t002.

According to MLST, the t008 isolates in our study were of the

TABLE 1 Characteristics of clinical MRSA strains isolated from adult and pediatric patients

Characteristic	No. (%) of isolates		
	Adult ^a	Pediatric ^b	Total/overall
Total MRSA isolates	1,124 (87.6)	159 (12.4)	1,283 (100)
Specimen source of ^c :			
Wound/abscess	488 (43.4)	81 (55.9)	569 (44.8)
Sputum	331 (29.4)	27 (18.6)	358 (28.2)
Urine	109 (9.7)	4 (2.8)	113 (8.9)
Blood	104 (9.3)	7 (4.8)	111 (8.8)
Other ^d	92 (8.2)	26 (17.9)	118 (9.3)
Intensive care unit collection ^e	187 (16.7)	17 (11.8)	204 (16.1)
Hospital onset	399 (35.5)	40 (25.2)	439 (34.2)

^a Collected for 5 months from hospitals serving adults.

^b Collected for 12 months from hospitals serving children.

^c Fourteen missing pediatric entries.

^d According to brief notes in the data set, "other" specimen sources included the following anatomical locations or types of specimens: 5 ear; 5 eye; 3 buttock; 2 each of finger, leg, pleural, and skin; and 1 each of gastrointestinal, sinus, perineum, spleen, and umbilical for pediatric specimen sources and 8 leg; 7 foot, knee, and medical device related; 6 groin; 5 abdominal, spinal, and stool; 4 gastric; 4 hand; 3 back, pleural, and tissue; 2 each of ankle, body fluid, buttock, ear, eye, stump, synovial fluid, and unknown; and 1 each of drainage, gallbladder, hip, humerus, ileal crest, lung, pancreatic fluid, skin, and stoma.

^e Nineteen missing entries (4 adult and 15 pediatric).

prototypic community clone USA300 (t008/ST8), and the t002 isolates were of the prototypic hospital clone USA100 (t002/ST5), with t242 isolates being identified as ST5 (Table 2). Comparison of t242 and t002 isolates for the following parameters revealed no significant difference: the proportion from each specimen source, the proportion of hospital and community onset, the proportion collected in ICU and non-ICU wards, and the age distribution of patients (all $P > 0.05$). Conversely, t008 isolates were significantly different from t242 and t002 isolates in the same tests ($P < 0.001$). t242 and t002 isolates shared the most common specimen source, sputum (34% and 38%, respectively), whereas wounds were the most common specimen source of t008 isolates (56%). PFGE of a sample of t242 and t002 isolates showed them to be predominantly USA100 isolates (data not shown).

BURP analysis of the *spa* types clustered the majority of adult isolates (97%) into three *spa* clonal complexes (*spa*-CCs) and

most pediatric isolates (96%) into two *spa*-CCs (Fig. 1). *spa* types were clustered with either t008 (*spa*-CC008; community-associated strains) or t002 (*spa*-CC002; health care-associated strains), but in adults, a further *spa*-CC with founder t324 was identified (*spa*-CC324). Isolates in this *spa*-CC were characterized as ST72 isolates. For both adult and pediatric MRSA isolates, MLST results showed that all isolates in *spa*-CC008 were of ST8 and that all isolates in *spa*-CC002 were of either ST5 or a single-locus variant, ST105 (*spa* types t045, t088, and t1791 for the latter). According to the BURP algorithm, *spa* types that differ from all other *spa* types in the sample by more than 4 repeats, and thus which cannot be clustered into a *spa*-CC, are termed singletons. For adults, 10 (11.2%) *spa* types (40 [3.6%] isolates) were classified as singletons, and for children, 4 (18.2%) *spa* types (6 [3.8%] isolates) were classified as singletons. *spa* types of less than 5 repeats in length were excluded from the BURP analysis because no reliable evolutionary history can be inferred from "short" *spa* types (35). For adults, 2 (2.2%) *spa* types (2 [0.2%] isolates) were excluded, and for children, 1 (4.5%) *spa* type (1 [0.6%] isolate) was excluded. The estimated genetic diversity of MRSA isolates was significantly higher among adults than among children ($1-D = 75\%$ versus 51%) (Table 2).

In bivariate analyses, pediatric patients, wound specimens, isolation in a non-ICU ward, community-onset timing of collection, and isolation from a hospital with >10,000 annual admissions were associated with t008 (USA300) isolates (Table 3). In addition, admission to a hospital with a high proportion of Medicaid-insured patients or a high proportion of Hispanic patients was linearly associated with the recovery of t008 isolates. In multivariate analyses, isolates from pediatric patients, wounds, non-ICU wards, and hospitals with a high proportion of Medicaid-insured patients remained significantly associated with *spa* type t008 (Table 4). Isolates from hospitals with a high proportion of Hispanic patients were significantly more likely to be t008 isolates (20% higher odds of being a *spa* type t008 isolate per 10% increase in numbers of Hispanic patients). However, this finding was collinear with hospitals with a high proportion of Medicaid-insured patients and thus was removed from the multivariate model.

DISCUSSION

We conducted a prospective cohort study of inpatients in a large metropolitan county in Californian, collecting all clinical MRSA

TABLE 2 Ten most frequently found *spa* types among adult and pediatric patients in Orange County, CA^a

Rank	Adult patients					Pediatric patients				
	<i>spa</i> type	MLST	No. of isolates	% of isolates	Cumulative %	<i>spa</i> type	MLST	No. of isolates	% of isolates	Cumulative %
1	t008	8	457	40.7	40.7	t008	8	110	69.2	69.2
2	t242	5	260	23.1	63.8	t242	5	14	8.8	78
3	t002	5	211	18.8	82.6	t002	5	9	5.7	83.7
4	t024	8	19	1.7	84.3	t024	8	3	1.9	85.5
5	t037	8	15	1.3	85.6	t045	5	2	1.3	86.8
6	t127	1	14	1.3	86.8	t068	8	2	1.3	88.1
7	t088	105	12	1.1	87.9	t2689	8	2	1.3	89.3
8	t1737	5	11	1	88.9	t324	72	2	1.3	90.6
9	t306	5	6	0.5	89.4	t622	8	2	1.3	91.8
10	t126	72	5	0.4	89.9	13 others		1 each	0.6 each	100

^a The total numbers of *spa* types were 89 for adult patients and 22 for pediatric patients. Simpson's index of diversity ($1-D$) values were 75% (95% CI, 73%, 76%) for adult patients and 51% (95% CI, 41%, 60%) for pediatric patients. MLST, multilocus sequence type.

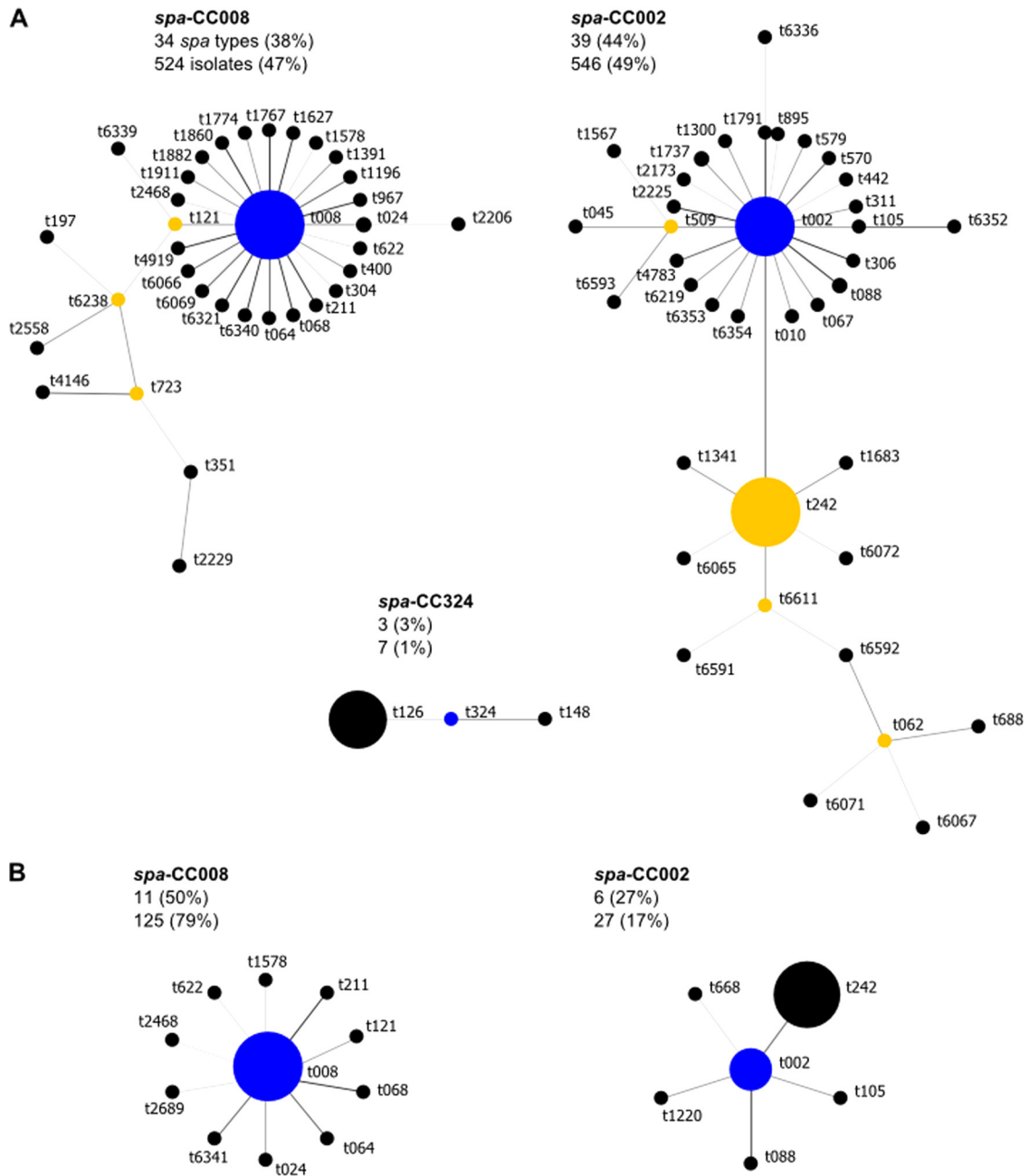


FIG 1 Relatedness of *spa* types among adult (A) and pediatric (B) MRSA isolates according to the Based upon Repeat Pattern (BURP) algorithm. Clusters of linked *spa* types correspond to *spa* clonal complexes (*spa*-CCs). *spa* types are clustered into a *spa*-CC when their repeat patterns differ by no more than 4 repeats. The BURP algorithm sums up “costs” (a measure of relatedness based on the repeat pattern) to define a founder score for each *spa* type in a *spa*-CC. The founder (blue node) is the *spa* type with the highest founder score in its *spa*-CC, and the subfounder (yellow node) is the *spa* type with the second highest founder score. *spa*-CC008 has founder t008. Each node represents a *spa* type. The node size represents the number of clustered strains that belong to that *spa* type. The shading of the branches represents the costs (similarities in repeat patterns) between two *spa* types; the darker the branch, the lower the cost (more similar repeat patterns).

isolates from 30 of 31 hospitals in order to characterize differences in pediatric and adult MRSA strains. To our knowledge, this is the first study to assess adult and pediatric MRSA isolates from a population-based sample across a large region.

Countywide, adult and pediatric clinical MRSA isolates were dominated by three *spa* types, two of which were consistent with the prototypic community- and health care-associated clones prevalent in the United States (t008 [USA300] and t002

[USA100]). t008 (USA300) was the most common single clone among both adult and pediatric isolates. Nevertheless, t008 comprised a large majority of pediatric isolates, whereas adult isolates were nearly equally divided among community- and health care-associated clones. Most other *spa* types were shown by BURP to be related to these two dominant clones. The two *spa* clonal complexes *spa*-CC008 and *spa*-CC002 can therefore be thought of as two distinct groups of isolates representing the major

TABLE 3 Bivariate analyses of variables associated with *spa* type t008

Variable	% of t008 isolates		χ^2	P
	Those with characteristic	Those without characteristic		
Individual				
Pediatric	69.81	40.75	47.67	<0.001
Community onset	48.10	37.13	14.09	<0.001
Non-ICU	47.17	27.45	27.00	<0.001
Blood specimen	40.54	44.30	0.58	0.446
Wound specimen	60.04	32.34	96.28	<0.001
LTAC	35.21	44.88	2.54	0.111
Hospital level				
>10,000 annual admissions	38.40	51.52	22.00	<0.001
Medicaid-insured patients ^a			1.34 (1.21–1.48)	<0.001
Hispanic patients ^a			1.29 (1.15–1.44)	<0.001

^a Odds ratio per 10% increase.

community- and health care-associated MRSA strains prevalent in the United States.

Interestingly, t242/ST5 was slightly more common than t002/ST5 among both adult and pediatric isolates, despite the predominance of the t002/ST5 hospital clone in the United States. Given the similarities of t242 and t002 isolates in this study, and the fact that t242 differs from t002 by only one nucleotide (resulting in a different *spa* repeat pattern by one *spa* repeat), t242/ST5 presumably represents a minor variant of USA100 that has become prevalent in Orange County hospitals. t242 has been reported infrequently in the literature (24, 25, 60), with just one study reporting t242 at an endemic level in an Italian hospital (45).

The additional *spa* clonal complex identified among adult isolates included a community-onset isolate identified as a t324/ST72 isolate, an invasive community-associated MRSA clone reported for elderly patients in South Korea from 2006 to 2007, just before our isolate collection began (29). According to the U.S. Census Bureau, 17.9% of the Orange County population is Asian, approximately 2.9% of which is Korean (57).

There was significantly more genetic diversity among adult MRSA isolates than among pediatric isolates. This could simply represent the greater time that health care-associated clones have had to diversify at the *spa* locus than community-associated clones, which have emerged only in the past 2 decades. The greater MRSA diversity among adults could also be due to different degrees of contact; for example, adults may have more diverse MRSA encounters (travel, work, social venues, and health care facilities) than young children (schools and day care centers).

TABLE 4 Multivariate analysis of variables associated with *spa* type t008

Variable	Odds ratio	SE	95% CI	P
Patient/isolate characteristic				
Wound specimen	2.64	0.34	2.06, 3.39	<0.001
Pediatric	2.07	0.52	1.26, 3.40	0.004
Non-ICU	1.77	0.32	1.24, 2.54	0.002
Hospital characteristic				
% Medicaid-insured patients ^a	1.24	0.06	1.13, 1.35	<0.001

^a Odds ratio per 10% increase.

The population estimates of clinical MRSA isolates in Orange County show that there was a 6-fold-higher frequency of inpatient MRSA clinical cultures among adults than among children. This pattern was consistent among the three most common *spa* types, t008, t242, and t002, and is likely a combination of more frequent hospitalizations among adults (many of whom were elderly, with a median age of 67 years) and more frequent MRSA carriage.

In multivariate analyses, community-associated MRSA clone t008 (USA300) was associated with pediatric patients. In contrast to adults, children are often healthier and are more likely to encounter MRSA in the community through exposure to high-density environments, such as schools, day cares, camps, and sporting activities, where close contact may facilitate the spread of community MRSA strains. In agreement with data from previous studies, we found that USA300 was associated with wounds, which is the most common presentation for hospitalization due to community-acquired MRSA infection (2, 17). USA300 was also associated with hospitals that treat a large fraction of Medicaid-insured patients, suggesting that community MRSA infections may be more prevalent among patients from economically disadvantaged or high-density areas.

USA300 was also associated with isolation from non-ICU wards, suggesting that this community strain is occurring in healthier hosts or is producing infections that are less severe than those caused by traditional health care-associated strains. Nevertheless, there is ample evidence that community strains are capable of producing fulminant infections (15, 37, 52). An understanding of what component of invasiveness is due to host comorbidities versus pathogen virulence factors is an area of active research.

Interestingly, we did not find that the isolation of t008 was associated with community-onset clinical isolates (clinical culture isolated less than 3 days after admission). This finding is likely due to the fact that the majority of health care-associated carriage or infection is found upon readmission to hospitals (27). It could also be explained by community-associated strains that have become endemic in some hospitals (49, 52).

Community- and health care-associated MRSA strains are becoming increasingly difficult to distinguish epidemiologically as community-associated strains continue to penetrate hospital MRSA reservoirs. Furthermore, it remains unclear whether com-

munity clones are adding to or replacing traditional health care-associated MRSA strains (3, 8, 22, 49). The implication of the blurred line between community- and health care-associated MRSA strains may be that efforts to control MRSA transmission within hospitals will not be effective in controlling community influx into hospitals. Simultaneous community strategies to limit MRSA spread are needed. However, much is still unknown about the acquisition and transmission of CA-MRSA, so improved knowledge is needed to better guide infection control strategies. Further studies are needed to ascertain whether community strategies to reduce transmission in children and young adults would produce benefits across the entire age spectrum.

One limitation of our study is that few individual-level characteristics were available. Also, our study did not account for the different policies in place at each hospital with regard to when to obtain clinical cultures. These differences could affect MRSA detection at each hospital and, possibly, the type of MRSA strains isolated, if clinical cultures were more likely to be obtained for sicker, older patients. Moreover, our results could have been affected by the potential seasonality of MRSA infections and infection types due to the different collection periods for adult and pediatric isolates (largely winter and spring for adult collections, compared to all seasons for pediatric collections). A seasonality of *S. aureus* infections, particularly skin infections, has been observed in pediatric and adult patients in temperate and tropical environments, with a predominance of infections during summer and autumn (31, 36, 54, 58). A recent study in Rhode Island found a 2- to 3-fold-increased incidence of MRSA infections (both CA- and HA-MRSA) in pediatric patients during the second two quarters of the year over the last decade (36). However, in that same study, adult CA-MRSA infections showed less seasonal variation than did pediatric infections, and no variation was observed among adult HA-MRSA infections. Some studies observed no significant seasonality of *S. aureus* infections, but those studies focused on bacteremia (40, 47). The collection of both adult and pediatric MRSA isolates for the same time period, i.e., 12 months, would have accounted for any potential seasonality effects and/or other factors that could affect the type and diversity of MRSA strains isolated.

Mandatory screening of high-risk inpatients was not in place in California until 2009; therefore, our population estimates are likely underestimates. In addition, our estimates should not be construed as measures of MRSA infection among inpatients. Clinical isolates often represent carriage without infection. Finally, our estimates of the index of diversity for adult and pediatric MRSA isolates may have been influenced by differing sample sizes (18).

In conclusion, our study found that in a large county, MRSA isolates from hospitalized children were more likely to be of *spa* type t008 (USA300). This community-associated *spa* type was associated with children, wounds, non-ICU care, and admission to a hospital with a high percentage of Medicaid-insured patients. Despite the association of t008 isolates with children, t008 was still the most common *spa* type among adult patients, suggesting that community-based interventions are needed to stem the influx of t008 isolates into hospitals. We also found evidence for a prevalent variant of the USA100 clone (t242/ST5), which has not been reported elsewhere. While community- and hospital-associated MRSA reservoirs have begun to merge, significant differences remain in pediatric and adult patient populations, which may pro-

vide an impetus for different age-based strategies to reduce transmission and disease.

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