MAJOR ARTICLE

Are Community-Associated Methicillin-Resistant *Staphylococcus aureus* (MRSA) Strains Replacing Traditional Nosocomial MRSA Strains?

Kyle J. Popovich, Robert A. Weinstein, and Bala Hota

Division of Infectious Disease, Department of Medicine, Rush University Medical Center, and Division of Infectious Disease, Department of Medicine, Stroger Hospital of Cook County, Chicago, Illinois

(See the editorial commentary by Boyce on pages 795–8)

Background. Recent studies have suggested that community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) infection is encroaching on health care settings. We describe the epidemiology of hospital-onset community-associated MRSA bloodstream infections using phenotypic and genotypic analysis.

Methods. Using an update of an established rule derived from antibiotic susceptibilities, we inferred genotypes (i.e., community [CG] or hospital [HG]) for 208 MRSA isolates from hospital-onset (>72 h after hospital admission) bloodstream infections during 2000–2006. We compared demographic characteristics, risk factors, and outcomes of patients infected with CG or HG strains.

Results. Total hospital-onset MRSA bloodstream infection incidence density rates for the periods January 2000–June 2003 and July 2003–December 2006 (0.215 cases per 1000 patient-days and 0.207 cases per 1000 patient-days, respectively) were stable (risk ratio, 1.0; 95% confidence interval, 0.7–1.3; $P = .79$, period 2 vs. period 1). However, the risk that these bloodstream infections were due to CG strains doubled (risk ratio, 1.9; 95% confidence interval, 1.2–3.1; $P = .01$), whereas the risk due to HG strains decreased (risk ratio, 0.7; 95% confidence interval, 0.46–0.93; $P = .02$). After adjustment for comorbidities in multivariate analysis, no significant risk factors for or outcomes of infections due to CG versus HG strains were detected. Patients infected with HG strains showed a trend toward later day of acquisition of a positive blood culture, and those infected with CG strains showed trend toward greater risk of intensive care unit admission.

Conclusion. Although total hospital-onset MRSA bloodstream infection rates were relatively stable during 2000–2006, CG strains were responsible for an increasing proportion of cases (from 24% to 49%), suggesting replacement of traditional hospital-associated strains. For most risk factors and outcomes, patients infected with CG and HG strains were similar, suggesting that, thus far, CG strains are behaving like their traditional hospital-associated counterparts.

Methicillin-resistant *Staphylococcus aureus* (MRSA) was once thought to be primarily a hospital-associated pathogen; however, a clone of MRSA—predominantly, strain type USA300—has emerged in the community [1, 2]. Community-associated (CA) methicillin-resistant (MRSA) infection is increasingly common in outpatient clinics and emergency departments [3]; has caused outbreaks among athletes [4], children [1], prisoners [5], aboriginal populations [6], military personnel [7], Native Americans [8], and men who have sex with men [9]; and produces clinical syndromes that range from minor skin and soft-tissue infections [10] to severe systemic infections, including necrotizing fasciitis [11] and pneumonia [12].

Epidemiologic and molecular typing methods exist for classifying CA MRSA infections. Epidemiologic definitions have been used to distinguish CA MRSA from hospital-associated MRSA among inpatients (e.g., occurrence within the first 3 days of hospitalization for CA MRSA infection or, thereafter, for hospital-associated MRSA infection) [2]. In addition, specific health care exposures among patients with MRSA infections that arise in the community—dialysis, surgery, hospi-

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Reprints or correspondence: Dr. Kyle Popovich, Division of Infectious Disease, Department of Medicine, Stroger Hospital of Cook County, 637 S. Wood St., Chicago, IL 60612 (kyle_popovich@rush.edu).

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talization, residence in a long-term care facility, or surgery during the prior year; presence of an in-dwelling catheter or percutaneous medical device; or history of MRSA infection [13]—identify a third potential epidemiologic category, termed health care–associated MRSA [14].

Molecular methods that have been used to describe MRSA strains include PFGE [15], testing for presence of the Panton-Valentine leukocidin gene (PVL) [16], and staphylococcal cassette chromosome *mec* (SCC*mec*) typing [17], multilocus sequence typing [18], and *spa* typing [19]. In addition, phenotypic rules (e.g., using antibiotic susceptibility) can be used to infer MRSA strain type [20]. Because USA300 isolates are typically susceptible to a greater number of non–β-lactam antibiotics than are traditional hospital MRSA strains, combinations of antibiotic susceptibility may provide useful information for studying the epidemiology—for example, trends over time—of CA MRSA infections [13].

Multiple studies have described outbreaks of CA MRSA in the community or within 72 h after admission to a hospital [2, 3, 10, 21]. Recent studies have suggested that CA MRSA strains may be encroaching on nosocomial settings [22, 23], causing infections that have onset >72 h after hospital admission. In this study, we examined whether changes in the epidemiology and rates of MRSA bloodstream infection (BSI) occurred over a 7-year period, whether prevalence of CA MRSA isolates increased among hospital-onset BSIs, and whether the outcomes of patients with hospital-onset BSIs caused by CA MRSA strains were different from those of patients infected with traditional hospital-associated strains of MRSA.

METHODS

Phenotype rule. We updated an established algorithm that used PFGE results and antibiotic susceptibilities (MicroScan; Dade Behring) to derive phenotypic rules for predicting genotype [20]. The prior rule was based on an analysis of all genotyped MRSA BSI isolates at Stroger (formerly Cook County) Hospital (Chicago, IL). The updated phenotypic rule was derived from hospital-onset (defined as onset >72 h after hospital admission) MRSA BSI isolates that were the subject of our study. Gentoypic analyses—PFGE, PVL, and SCC*mec* typing—were performed, as described elsewhere [17, 24, 25], on hospital-onset BSI isolates during 2004–2006. The phenotypic rule was applied retrospectively to all hospital-onset MRSA BSIs from January 2000 through December 2006, to infer genotype (inferred community genotype [CG] or inferred hospital genotype [HG]).

Surveillance of hospital-onset MRSA BSIs. We retrospectively studied patients hospitalized at Stroger Hospital, a 464-bed inner-city safety-net hospital in Chicago. Using electronic data, we identified patients with hospital-onset MRSA BSIs during January 2000–December 2006. The first blood culture (if obtained after 72 h into the hospitalization) was studied; any second blood culture $\geq$30 days after the first culture, during a single hospitalization, also was studied.

MRSA BSI incidence density rates for all strains, CG strains, and HG strains were measured using hospital-wide patient-days as the denominator. Intensive care unit (ICU) and non-ICU incidence density rates were measured using combined patient-days for all 7 ICUs at Stroger Hospital or non-ICU patient-days as the denominator, respectively. Patient-days for 6 months in 2003 were not available and were imputed on the basis of the patient-days in the prior and subsequent 6 months. Using all hospital-onset MRSA BSIs, we derived a yearly MRSA antibiogram to examine temporal trends in clindamycin, ciprofloxacin, and gentamicin susceptibility.

Cohort study. We evaluated risk of hospital-onset MRSA BSI due to HG strains versus CG strains. Using electronic data and chart review, we collected patient-level information, including demographic characteristics, use of immunosuppressive medications, presence of HIV infection, Charlson comorbidity score [26], health care exposures, prior surgery, prior MRSA infection, illicit drug use, and presence of a vascular catheter. A central venous catheter was recorded as being present if it was in site any time from 3 days before until 1 day after the positive MRSA blood culture collection date; central venous catheters were classified as being "upper line" (internal jugular, subclavian, peripherally inserted central catheter) or "lower line" (femoral). BSIs were classified as being primary or secondary, as determined by established definitions; additional sites for which results of culture were positive were identified for BSIs categorized as secondary [27]. Individuals without central venous catheters but with BSIs identified as primary infections were further evaluated for the diagnosis of thrombophlebitis related to peripheral intravenous catheters.

Outcomes of all-cause in-hospital mortality, duration of bacteremia, and ICU admission were examined. Appropriate therapy was included in the analysis and was defined as treatment (if an isolate was susceptible) with vancomycin, linezolid, daptomycin, trimethoprim-sulfamethoxazole, or clindamycin. For each patient, admission to an ICU was documented both at the time of and in the week after the date the positive culture specimen was collected. Persistent BSI was defined as bacteremia for $\geq$7 days while the patient received appropriate therapy [28].

Statistical methods. SPSS software, version 10 (SPSS), was used for statistical analysis. Categorical variables were examined with χ^2 analysis, with Fisher's exact test used for small samples (i.e., if counts in $\geq$2 cells in a contingency table were <10; continuous variables were analyzed with the Student's independent-samples *t* test; changes over time were evaluated with the χ^2 test for trend; and logistic regression analysis was used for multivariate analysis. For risk-factor analysis, the outcome variable was the inferred genotype (CG or HG). For outcomes

Table 1. Distribution of PFGE, Panton-Valentine leukocidin (PVL) gene detection, and staphylococcal cassette chromosome *mec* typing (SCC*mec*) for available hospital-onset methicillin-resistant *Staphylococcus aureus* bloodstream isolates, 2004–2006.

	No. of isolates				
PFGE type	Total	PVL positive	PVL negative	SCC*mec* II	SCC*mec* IV[a]
USA100	27	0	27	24	3
USA500	5	2	3	1	3
USA800	4	0	4	0	4
USA300[b]	23	21	1	1	19
USA300–0114[c]	16	15	0	1	13
USA400	1	1	0	0	1
USA600	1	0	1	NT	NT
Other[d]	5	0	5	2	3

NOTE. NT, not tested.

[a] SCC*mec* analysis was not performed for 1 USA500 isolate, 3 USA300 isolates, and 1 USA600 isolate.

[b] PVL analysis was not performed for 1 isolate.

[c] USA300–0114 represents the strain described by Tenover et al. [16], and the 16 isolates listed comprise the major subset of all 23 USA300 strains in our study.

[d] These isolates did not conform to the standard PFGE designations, as described by McDougal et al. [15], and were not used to derive our prediction rule.

analysis, each outcome of interest was modeled in a separate logistic regression model, and the inferred genotype was included as the main covariate of interest in each model. Statistically important (i.e., $P < .2$) factors on univariate analysis, including comorbidities, demographic characteristics, days until positive culture result, and secondary sites of infection, were included in each model. Variables were removed using backward elimination of covariates with P values >.15.

RESULTS

Phenotype rule. PFGE was performed for 66 hospital-onset MRSA BSI isolates during 2004–2006, which included a subset of 47 isolates previously studied [20]. A CA MRSA strain was identified by PFGE for 24 isolates: USA300 (23) and USA400 (1); of the USA300 isolates, 16 had the prevalent USA300–0114 PFGE pattern [16]. We classified 36 isolates as being hospital-associated MRSA strains: USA100 (27), USA500 (5), and USA800 (4) (table 1). Six isolates (1 USA600 and 5 with genotypes of indeterminate origin) were not used to derive the prediction rule; the 6 isolates were dispersed over time.

For these 60 isolates, phenotypic analysis revealed that 2 susceptibility patterns—clindamycin susceptible and clindamycin or ciprofloxacin susceptible—were better than other phenotypic combinations at predicting a CA MRSA strain (likelihood ratio, 5.75; 95% CI, 3.39–6.89). In our subsequent analyses, we used the "clindamycin- or ciprofloxacin-susceptible rule" because of potential increased applicability.

PVL and SCC*mec* analyses were performed for 65 and 61

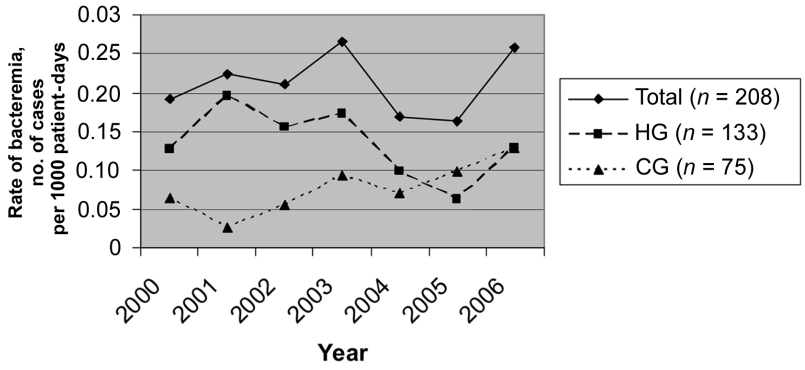

Figure 1. Overall rate of hospital-onset methicillin-resistant *Staphylococcus aureus* bacteremia for the period 2000–2006. Rates of infection with community genotype (CG) and hospital genotype (HG) strains, as inferred by the phenotypic rule (see Methods), are shown.

Table 2. Rates of hospital-onset bloodstream infections caused by inferred community genotype (CG) and hospital genotype (HG), 2000–2006.

Patient location and genotype	Incidence density rates		Risk ratio (95% CI)	*P*
	Period 1	Period 2		
Hospital[a]				
Total	0.215	0.207	0.96 (0.73–1.27)	.79
CG	0.05	0.1	1.93 (1.2–3.1)	.01
HG	0.16	0.11	0.66 (0.46–0.93)	.02
Intensive care unit[b]				
Total	0.29	0.31	1.08 (0.67–1.74)	.86
CG	0.05	0.17	3.12 (1.25–7.81)	.02
HG	0.23	0.14	0.61 (0.33–1.13)	.15
Non–intensive care unit[c]				
Total	0.19	0.18	0.91 (0.65–1.27)	.63
CG	0.05	0.08	1.55 (0.88–2.73)	.16
HG	0.14	0.1	0.68 (0.44–1.03)	.08

NOTE. The study period was divided into 2 study periods: period 1 (January 2000–June 2003) and period 2 (July 2003–December 2006). The bacteremia rates are shown with a risk ratio with period 1 as reference.

[a] Hospital incidence density rates are per 1000 patient-days.

[b] Intensive care unit incidence density rates are per 1000 intensive care unit patient-days.

[c] Non–intensive care unit incidence density rates are per 1000 non–intensive care unit patient-days.

isolates, respectively. CA MRSA strains typically carried PVL and SCC*mec*-IV, whereas hospital-associated MRSA strains did not (table 1).

Surveillance of MRSA BSIs. Clindamycin or ciprofloxacin susceptibility was used to infer genotype of all hospital-onset MRSA BSIs from January 2000 through December 2006 (i.e., isolates susceptible to either clindamycin or ciprofloxacin were identified as CG; isolates resistant to both antibiotics were classified as HG). During this period, there were 208 isolates for 199 patients; 75 isolates were classified, using the phenotypic rule, as being CG, and 133 isolates were classified as being HG.

Over the 7 years of the study, hospital-onset MRSA BSI rates were relatively stable. When the study period was divided in half, the January 2000–June 2003 (period 1) and July 2003–December 2006 (period 2) total hospital-onset MRSA BSI incidence density rates (0.215 cases per 1000 patient-days and 0.207 cases per 1000 patient-days, respectively) were similar (risk ratio, 1.0; 95% CI, 0.7–1.3; $P = .79$, for period 2 vs. period 1) (figure 1). However, the risk for hospital-onset MRSA BSIs due to CG strains increased (risk ratio, 1.9; 95% CI, 1.2–3.1; $P = .01$), whereas the risk for a BSI due to HG strains decreased (risk ratio, 0.7 95% CI, 0.46–0.93; $P = .02$) (table 2). The proportion of cases due to CG doubled between the 2 time periods (24% vs. 49%). Similarly, the proportion of patients infected with CG strains in an ICU or non-ICU setting increased from period 1 to period 2 (19% to 54% and 27% to 45%, respectively).

The antibiogram for MRSA reflected the increasing number of hospital-onset MRSA BSIs due to CG strains during the study period; over time, there was a statistically significant decrease in the number of strains with clindamycin ($P < .001$), ciprofloxacin ($P = .037$), or gentamicin ($P < .001$) resistance (figure 2).

Cohort study. In univariate analysis (table 3), variables associated with hospital-onset MRSA BSIs due to HG strains included day of acquisition of positive blood culture, residence in a long-term care facility, and exposure to clindamycin, ciprofloxacin, or any antibiotic in the prior 3 months. There were no statistically significant differences between patients infected with CG and HG strains with regard to demographic characteristics, Charlson comorbidity score, other health care exposures, type of BSI (primary or secondary), or presence in the ICU when the culture was performed.

Vascular catheter use (i.e., peripheral intravenous catheter or central venous catheter) was not statistically different between patients infected with CG and HG strains. Additionally, among patients with central venous catheters, the location of the line was unimportant in assessing risk.

On multivariate analysis, only greater number of days between

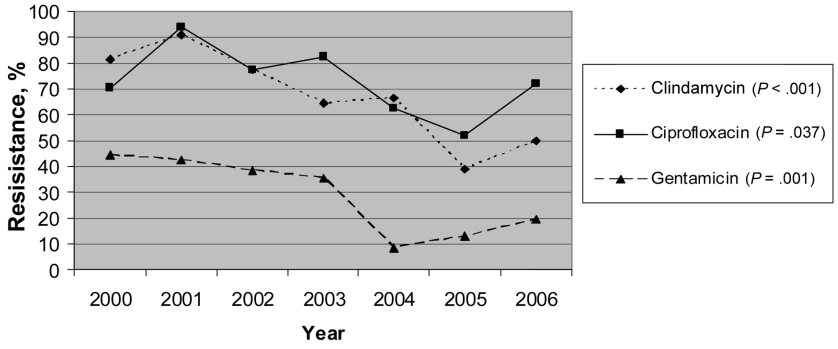

Figure 2. Resistance of hospital-onset methicillin-resistant *Staphylococcus aureus* bloodstream isolates to clindamycin, ciprofloxacin, and gentamicin. Associated *P* values were calculated by the χ^2 test for trend.

Table 3. Univariate analysis of risk factors and outcomes for patients with hospital-onset methicillin-resistant *Staphylococcus aureus* bloodstream isolates, 2000–2006.

Characteristic	CG (n = 75)	HG (n = 133)	P
Age, mean years ± SD	49 ± 17.5	50 ± 20.2	.816
Sex			.333
Male	48 (64)	76 (57)	
Female	27 (36)	57 (43)	
Ethnicity			.438
White	11 (15)	11 (8)	
Black	50 (67)	94 (71)	
Hispanic	10 (13)	23 (17)	
Other	4 (5)	5 (4)	
Charlson comorbidity score, mean ± SD	1.8 ± 2.8	2.6 ± 3	.063
Hemodialysis treatment	5 (7)	8 (6)	.852
Prior surgery	5 (7)	21 (16)	.056
Prior MRSA infection	1 (1)	10 (8)	.056
Prior hospitalization	37 (49)	81 (61)	.106
Resident of long-term care facility	0	7 (5)	.043
Diabetes	37 (49)	57 (43)	.368
HIV infection	7 (9)	15 (11)	.661
Use of immunosuppressive medications	11 (15)	19 (14)	.94
In ICU at time of culture	41 (55)	72 (54)	.941
Illicit drug use	13 (17)	23 (17)	.994
Vascular catheter use[a]			.91
Secondary bacteremia	37 (49)	68 (51)	
Primary bacteremia, catheter related	25 (33)	45 (34)	
Primary bacteremia, not catheter related	13 (17)	20 (15)	
Central venous catheter, upper line[b]	30 (70)	60 (66)	.659
Antibiotic exposure[c]	22 (29)	62 (47)	.015
Clindamycin	0	16 (12)	.002
Ciprofloxacin[d]	9 (12)	34 (26)	.02
Trimethoprim-sulfamethoxazole	3 (4)	11 (8)	.238
Tetracycline	0	1 (1)	.452
Penicillin	4 (5)	14 (11)	.201
Oxa β-lactamase	18 (24)	38 (29)	.475
Linezolid	1 (1)	0	.182
Vancomycin	9 (12)	26 (20)	.162
Erythromycin	4 (5)	14 (11)	.201
Time to culture, mean days ± SD	13.8 ± 15.9	24.5 ± 42.3	.01
Persistent bacteremia	9 (12)	26 (20)	.162
Duration of hospital stay, mean days ± SD	34.7 ± 30.2	42.4 ± 59.2	.295
Hospital readmission at 3 months	20 (27)	45 (34)	.284
In ICU 72 h after culture was performed	32 (43)	42 (32)	.109
In ICU 1 week after culture was performed	38 (51)	55 (41)	.195
ICU during hospitalization	49 (65)	77 (58)	.292
All-cause in-hospital mortality	12 (16)	31 (23)	.211

NOTE. Data are no. (%) of patients, unless otherwise indicated. ICU, intensive care unit. CG, inferred community genotype; HG, inferred hospital genotype.

[a] Patients were classified as having secondary bacteremia, having primary bacteremia with a vascular catheter as the source (i.e., either a peripheral intravenous catheter causing thrombophlebitis [6 patients] or a central venous catheter infection [64 patients]), or having primary bacteremia with no obvious vascular catheter source. Central venous catheter data were missing for 17 patients (CG, 3 patients; HG, 14 patients).

[b] Upper lines included internal jugular, subclavian, or peripherally inserted central catheter lines. Remaining central catheter lines were femoral. For the analysis of location of central catheter line, data were missing for 5 cases.

[c] Antibiotic exposures were within the 3 months before culture was performed (OR for HG, 2.1; 95% CI, 1.16–3.83).

[d] OR for HG, 2.52; 95% CI, 1.15–5.5.

Table 4. Multivariate analysis of risk factors and outcomes for patients with hospital-onset methicillin-resistant *Staphylococcus aureus* bloodstream infection, 2000–2006.

Risk factor[a]	OR (95% CI)	*P*
Increased risk of inferred hospital genotype strain for each additional day into length of stay[b]	1.02 (0.998–1.041)	.08
Increased risk of admission to the intensive care unit within 72 h after admission with inferred community genotype strain	1.8 (0.91–3.55)	.09

[a] Each represents a separate multivariate model; other variables were not statistically significant.

[b] Length of stay refers to days from hospital admission until acquisition of the positive blood culture.

hospital admission and blood culture sample collection showed a trend toward association with HG, but the difference did not reach statistical significance (table 4). Clinical outcomes—bacteremia duration, length of hospital stay, and hospital readmission within 3 months—were similar for patients infected with CG and HG strains. Frequency of receiving vancomycin as initial therapy was not statistically different between patients infected with CG and HG strains. Even after adjustment for comorbidities, there was no all-cause in-hospital mortality difference noted between patients infected with CG and HG strains. Patients infected with CG strains, however, did show a nonsignificant trend toward greater risk of ICU admission within 72 h after culture specimen acquisition (table 4).

For hospital-onset MRSA BSI strains that were classified as causing secondary infections, positive primary sites were most commonly the respiratory tract (73% for CG strains and 60% for HG strains; $P = .194$), followed by skin and soft tissue (32% for CG strains and 41% for HG strains; $P = .378$).

DISCUSSION

To establish the epidemiology of hospital-onset MRSA BSIs at our institution, we used a phenotypic prediction rule that was based on antibiotic susceptibility results during 2000–2006. We found that the proportion of hospital-onset BSIs attributable to CG strains increased over this period (from 24% [January 2000–June 2003] to 49% [July 2003–December 2006]), whereas the overall hospital-onset MRSA BSI rate was stable. Furthermore, there does not appear to be a clustering attributable to CG strains in a particular hospital location (e.g., the proportion of infections due to CG strains increased in ICUs and in non–ICU wards). The statistically significant decrease in resistance to clindamycin, ciprofloxacin, and gentamicin among hospital-onset MRSA BSI isolates parallels the increase in number of BSIs due to CG strains.

On univariate analysis, time to culture, residence in a long-term care facility, and antibiotic exposure in the prior 3 months were predictors of infections with HG strains. After multivariate analysis, increased time to culture showed a nonsignificant trend toward association with HG isolates, suggesting exogenous infection with hospital-associated flora, whereas CG infections presenting earlier during hospitalization may reflect nosocomial infection due to endogenous CA MRSA. Although outcomes for individuals infected with CG and HG isolates were largely similar, there was a nonsignificant trend toward infections with CG strains being associated with earlier ICU admission. Cases of fulminant infections due to CA MRSA have been described [11, 29]. Although there were no mortality differences detected in our study, our ICU admission data suggest that a subset of CA MRSA strains may be more virulent than traditional hospital-associated MRSA strains.

CA MRSA strains are now a prominent cause of skin and soft-tissue infections in the community [3]. Although skin and soft-tissue infections are the predominant presentation of CA MRSA, more-invasive infections also have been seen [2, 30, 31]. In a 7.5-month study period in 2004, BSIs due to the USA300 genotype were found among both health care–associated and nosocomial BSIs in Atlanta [22]. Our study found that CA MRSA is not only an important cause of hospital-onset BSIs but also that CA MRSA has increased over the past 7 years at our hospital as a cause of these infections and may be replacing traditional hospital MRSA strains. Our results support the mathematical model of Bootsma et al. [32] that predicted—on the basis of an assumption of higher growth rate and better fitness in the community—that CA MRSA strains would replace, not add to, traditional hospital-associated MRSA strains. This replacement is in marked contrast to our experience with outpatient infections due to CA MRSA, which are occurring in addition to, rather than replacing, infections with CA methicillin-susceptible *S. aureus* [33].

In addition to encroaching on nosocomial settings, the CA MRSA strains that we studied are behaving largely like their traditional hospital-associated counterparts in terms of demographic characteristics and outcomes. A study by Miller et al. [34] found that clinical and epidemiologic data could not consistently differentiate CA MRSA infection from CA methicillin-susceptible *S. aureus* infection among hospitalized patients. Our study suggests that, among hospital-onset MRSA BSIs, demographic data and risk factors cannot reliably distinguish patients infected with CG strains from those infected with HG strains.

The potential replacement of traditional hospital-associated MRSA strains with CA MRSA strains has several important infection-control implications. First, current guidelines are aimed at decreasing the rate of transmission of MRSA within the hospital [35, 36]; however, the effectiveness of these interventions for controlling CA MRSA is unknown. For example, anitibiotic stewardship of fluoroquinolones has been proposed as a method

for decreasing rates of MRSA infection within hospitals [37]. Although not achieving statistical significance on multivariate analysis, on univariate analysis, ciprofloxacin exposure in the 3 months before infection was a significant risk factor for an infection due to an HG strain. Fluoroquinolone use in our hospital was stable over the 7-year study period (data not shown). Further study is needed to clarify the relationship of fluoroquinolone overuse with infection due to CG strains.

Second, much is unknown regarding the colonization-to-infection pathway of CA MRSA strains. Because CA MRSA may colonize sites different from those colonized by traditional nosocomial MRSA [38], the effectiveness of control of CG strains of interventions using nasal surveillance to identify patients for isolation and to target decolonization is unknown. Furthermore, although MRSA traditionally was thought to be an exogenous pathogen spread person to person in the hospital, it is unclear whether hospital-onset CA MRSA infections are exogenous or endogenous. Cross-transmission of CA MRSA already has been documented in both the hospital [39] and the community [40], but improved understanding of the acquisition and transmission of CA MRSA strains is needed to direct infection-control strategies.

Our findings should be interpreted in light of study limitations. First, the study is retrospective; however, data elements used were collected prospectively in an electronic database, which enhances accuracy and completeness of data and limits recall bias. Second, antibiotic susceptibilities were used to infer genotype. Misclassification of strain type was made less likely, however, by reassessing our previously published prediction rules [20]. The applicability of the rule elsewhere depends on the local antibiogram for CA MRSA. Third, our overall hospital-onset BSI rates may have been relatively low in comparison with those of other institutions [41], which may limit the degree to which our findings can be generalized. In addition, surveillance for nasal colonization of MRSA is not routinely performed at our hospital. Therefore, it is unknown whether changes in hospital-onset MRSA epidemiology resulted from increases in hospital cross-transmission of CA MRSA strains (i.e., exogenous infections) or increases in the number of CA MRSA–colonized patients entering the hospital (i.e., endogenous infections). Finally, although we did not detect differences in risks between patients infected with CG and HG strains, this may reflect less heterogeneity in epidemiologic risks among patients at our institution, the major safety-net hospital in our region.

Our study suggests that CA MRSA infections are encroaching on nosocomial settings and that the demographic characteristics and outcomes of patients with CG- and HG-strain hospital-onset BSIs are largely similar. Our study specifically examined BSIs; assessing whether this shift is occurring among other nosocomial infections is an area for further study. CA MRSA strains may be replacing traditional MRSA strains in the hospital, and differentiating these 2 groups with epidemiologic definitions and risk factors may become increasingly difficult. We did not determine whether CG strains colonized patients before hospital admission or were acquired while in the hospital; prospective surveillance studies will be needed to answer this question. Our findings have important implications for treatment and prevention strategies for MRSA within health care settings.

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