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Edward Stenehjem, *Emory University*
David Rimland, *Emory University*

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MRSA nasal colonization burden and risk of MRSA infection

Edward Stenehjem, MD, MSc[a,b,*] and **David Rimland, MD**[a,b]
[a]Atlanta Veterans Affairs Medical Center, Decatur, GA
[b]Division of Infectious Diseases, Emory University School of Medicine, Atlanta, GA

Abstract

Background—*Staphylococcus aureus* nasal colonization burden has been identified as a risk factor for infection. This study evaluates methicillin-resistant *S aureus* (MRSA) nasal burden, as defined by the cycle threshold (C_t) and risk of subsequent infection.

Methods—In a retrospective cohort study, United States veterans were classified into 3 MRSA nasal colonization groups: noncarriers, low burden (C_t > 24 cycles), and high burden ($C_t \leq 24$ cycles). MRSA infections were identified prospectively, and clinical information was obtained by chart review. Multivariate logistic regression assessed the association of MRSA nasal burden and risk of MRSA infection.

Results—During 4-years of follow-up, 4.3% of noncarriers, 18.5% of low burden, and 17.2% of high burden developed a MRSA infection. In multivariate analysis, MRSA nasal colonization was a risk factor for MRSA infection (*P* = .008) with low burden (risk ratio [RR], 3.62; 95% confidence interval [CI]: 1.47–8.93) and high burden (RR, 2.71; 95% CI: 0.95–7.72) associated with subsequent MRSA infection when compared with noncarriers. When compared with low burden, high burden nasal carriers were not at increased risk of infection (RR, 0.75; 95% CI 0.36–1.55).

Conclusion—MRSA nasal colonization was a risk factor for MRSA infection. High nasal burden of MRSA did not increase the risk of infection.

Keywords

Staphylococcus aureus; Carriage quantification; Cycle threshold

The association of *Staphylococcus aureus* nasal colonization and staphylococcal infection was first described in the 1930s.[1] Since 1930, the epidemiology of *S aureus* has changed dramatically, and methicillin-resistant *S aureus* (MRSA) has reached epidemic levels in both hospitals and community settings.[2–6] With the changing epidemiology of MRSA, multiple studies have confirmed nasal colonization as a risk factor for subsequent infection,[7–10] with most infections caused by the colonizing strain.[11,12]

Longitudinal studies clearly identify 3 patterns of *S aureus* carriage: persistent carriage, intermittent carriage, and non-carriage.[13–16] Persistent nasal carriage, defined as ≥80% of weekly nasal swabs positive, is associated with a higher colonization burden when compared

*Address correspondence to Edward Stenehjem, MD, MSc, Department of Clinical Epidemiology and Infectious Diseases, Intermountain Medical Center, 5121 S. Cottonwood St, Gardner Women and Newborn Center LL2, Murray, UT 84157. eddie.stenehjem@imail.org (E. Stenehjem).

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with intermittent carriage.[17–19] In high-risk patients (postsurgical or peritoneal dialysis), increased nasal colonization burden and/or the persistently colonized state are associated with an increased infection risk when compared with intermittent or noncarriers.[20–22] The clinical implications of *S aureus* nasal burden have yet to be defined, and comparative effectiveness research is needed utilizing quantitative colonization data.

In response to the United States MRSA epidemic, the Veterans Health Administration (VHA) implemented active surveillance of MRSA colonization for all patients admitted to acute care facilities. To reduce the time needed to identify MRSA from surveillance cultures, molecular tests have now become standard in identification of patients with MRSA colonization. Molecular methods utilize polymerase chain reaction (PCR) technology to detect and amplify regions of MRSA-specific DNA. These tests can detect the presence of MRSA DNA within 2 hours and dramatically reduce the time to result in surveillance testing. In addition to time saved, PCR-based tests can be used for quantification of bacteria. The number of cycles the test completes before target DNA is detected (cycle threshold [C_t]) is inversely proportional to the amount of DNA in the sample. The C_t from Cepheid's Xpert MRSA Assay (Cepheid, Sunnyvale, CA) has recently been shown to be an excellent quantitative measure of MRSA on nasal swabs.[23]

Standard quantitative culture techniques are burdensome and labor intensive, whereas the C_t from MRSA nasal surveillance swabs is readily accessible and routinely collected in active surveillance programs. Using data from the VHA MRSA surveillance program and the C_t to define MRSA nasal burden, we performed a retrospective cohort study to assess the affect of nasal MRSA colonization burden on the risk of subsequent MRSA infection among veterans in Atlanta.

METHODS

The study population consisted of US veterans at the Atlanta VA Medical Center (AVAMC). The AVAMC is a large, integrated health care system with approximately 200 inpatient beds, 8 community-based outpatient clinics, and 1 nursing home care unit. Approximately 82,000 veterans receive care through the AVAMC and account for over 30,000 annual bed-days of care at the acute care facility. All AVAMC medical facilities utilize the VA's computerized patient records system to access medical information. The AVAMC uses 1 central microbiology laboratory that receives specimens from the surrounding VA outpatient clinics, nursing home, and acute care facility. Most veterans at the AVAMC do not have private insurance coverage and rely solely on the VA for their medical needs. The Emory University Institutional Review Board and the VA Research and Development Committee approved this study.

In an attempt to reduce nosocomial MRSA transmission, the VHA issued a directive in 2007 mandating the use of a MRSA bundle in all acute care settings. The MRSA bundle utilized, in addition to other measures, active surveillance for MRSA nasal colonization in all patients admitted to the hospital, transferred between units, and upon discharge from the hospital. At the AVAMC, MRSA admission screening is performed using a Liquid Stuart double swab (Copan, Murrieta, CA) inserted 1 cm into each nasal vestibule and rotated 4 revolutions while maintaining even contact with the nasal mucosa. Nursing staff collects all nasal surveillance specimens within 12 to 24 hours of admission. All nursing staff has undergone training on appropriate collection techniques, but no system is in place to ensure adequate collection techniques are utilized. Colonization results were obtained from the electronic medical record via a Web-based hospital surveillance system (TheraDoc; Hospira, Lake Forest, IL).

Admission nasal swabs are sent directly to the microbiology laboratory for testing using the Xpert MRSA assay. The Xpert MRSA assay is performed according to the manufacturer's instructions with a C_t of 15 to 36 cycles considered positive for MRSA. All C_t data are archived and easily extracted from the Xpert system. Patients with a $C_t > 24$ cycles were considered to have low nasal MRSA burden, and those ≤24 cycles were considered to have high MRSA nasal burden. The decision to dichotomize the C_t was based on previous work from our laboratory that demonstrated the logarithmic association of quantitative cultures and C_t.[23] Extranasal sites are not routinely screened for MRSA, and decolonization strategies are not routinely recommended for colonized patients.

At the AVAMC, surveillance of MRSA-positive clinical cultures from all body sites began October 1, 2005. All positive cultures were identified prospectively on a monthly basis by utilizing the microbiology option for specific organisms in the electronic medical record (Veterans Health Information Systems and Technology [VISTA]). All clinical MRSA cultures and corresponding clinical data (anatomic site of culture, radiographic studies, laboratory results, and physician notes) were reviewed by the same experienced infectious disease physician on a monthly basis to identify true infections and exclude cultures representing colonization.

Infections were classified according to the Centers for Disease Control and Prevention criteria.[24] Cultures not associated with a true infection were excluded. The infections were categorized according to primary site of infection into the following categories: skin and soft tissue, bone and joint, bloodstream, genitourinary, lower respiratory tract, surgical site, and other.

Patient selection

All patients admitted to the AVAMC acute care medical facility from October 1, 2007, through February 1, 2008 (4 months), were eligible to be included in the study population. This allowed for at least 4 years of follow-up. All patients with positive admission nasal MRSA surveillance results were included in the study. A random sample of patients from the same time period with negative admission nasal MRSA surveillance results was also included. Patients sent to the AVAMC for a surgical procedure with no prior or subsequent follow-up within the AVAMC system were excluded. The inpatient psychiatric department does not perform MRSA nasal surveillance routinely and thus were excluded from the study population.

The electronic medical record for each study participant was reviewed. Admission history and physical, discharge summaries, operative notes, last primary care note, progress notes within 30 days of admission, and pertinent laboratory values were reviewed. Problem lists were not used as a source of clinical information. External devices were considered anything foreign that entered the body and had an externalized segment (ie, urinary catheter, central vascular access, suprapubic urinary catheter, tracheostomy, feeding tube). End stage renal disease (ESRD) included only those patients on renal replacement therapy. Patients not known to be HIV positive were assumed to be negative. Wounds were considered anything that caused the integrity of the skin to be compromised and included severe psoriasis, decubitus ulcers, chronic diabetic wounds, surgical wounds not yet healed, and burns. Chronic liver disease was defined as cirrhosis or chronic liver failure and did not include hepatitis A, hepatitis B, or hepatitis C without liver failure of acute liver failure. Malignancies were considered active if the patient was actively being treated with chemotherapy, was under hospice care secondary to malignancy, had metastatic disease, or had active disease in which treatment was recommended. Localized prostate cancer was not considered an active malignancy. All other comorbidities were obtained from the medical record.

Statistical analysis

Sample size was determined by the known distribution of the admission C_t of Atlanta veterans[23] and an estimated risk of subsequent infection of 2.5% for noncolonized, 10% with low burden ($C_t > 24$ cycles), and 30% with high burden ($C_t \leq 24$ cycles).

Descriptive statistics were used to compare the study population stratified by colonization status (negative, low burden, high burden) to identify potential factors that are associated with colonization status. Differences in categorical variables were tested using χ^2. If expected cell counts were less than 5, Fisher exact test was utilized. Continuous variables were analyzed with a 1-way analysis of variance to compare means or 2-sample *t* test. A *P* value of ≤.05 was considered significant unless otherwise stated.

Unadjusted risk ratios were obtained for all covariates and the outcome (infection). Because of the limited published clinical data on nasal colonization burden, an exploratory analysis for potential interaction terms was performed. In this analysis, the study population was stratified on individual covariate levels and risk ratios for each level of the exposure variable (colonization status) were compared with the Breslow-Day test. A *P* value ≤.10 was considered significant in addition to biologically plausible interaction terms.

A multivariate logistic regression model was used to analyze the relationship between MRSA nasal colonization burden and subsequent infection. All covariates significant in bivariate analysis ($P < .10$) and those considered clinically or epidemiologically relevant were evaluated in the initial model. Variables classified as collinear were not used in combination in the model. Model selection was based on a purposeful selection of covariates and not on statistical algorithms (backward, forward, or stepwise). Confounding was evaluated by assessing the effect covariates had on the parameter estimate for nasal colonization. Interaction terms with nasal colonization status were evaluated using the likelihood ratio test to compare models with and without interaction terms.

Data were analyzed using SAS software, version 9.3 (SAS Institute Inc, Cary, NC). Proc Genmod was used for model building and analysis assuming a binary distribution with the log link function. A Poisson distribution was used if models failed to converge.

RESULTS

From October 1, 2007, to February 1, 2008, 205 patients were admitted to the AVAMC with positive MRSA nasal colonization. Of those colonized, 141 of 205 (68.8%) had a $C_t > 24$ cycles, and 64 of 205 (31.2%) had a $C_t \leq 24$ cycles (Fig 1). One hundred fifty patients with negative MRSA nasal colonization were randomly selected during the same time period, and 9 patients were excluded because of lack of follow-up data (n = 141). The study cohort was predominately white (53.5%) or African American (43.9%), and the majority was male (95.1%). The mean age was 63.4 years (standard deviation = 12.8).

Table 1 shows the baseline demographics and covariates of the 3 colonization groups (noncarriers, low burden, and high burden). Noncarriers were more likely to be admitted to the intensive care unit ($P = .03$). Patients with either low or high burden were more likely to have a wound or device present on admission ($P < .0001$), a previous or concurrent MRSA infection ($P < .0001$), received an antibiotic within 30 days of admission ($P = .05$), or were diagnosed with ESRD ($P = .003$) or HIV ($P = .05$) when compared with those without nasal colonization. When restricting the comparison of demographics and covariates to patients with low or high burden only, ESRD and having a device present on admission were more common in those with high burden ($P = .004$ and $P = .004$, respectively), whereas patients with low burden were more likely to have 3 or more comorbidities on admission ($P = .06$).

The proportion of patients who had a history of MRSA infection or a concurrent MRSA infection on admission did not differ between low and high nasal burden patients (18.4% vs 21.9%, respectively, $P = .57$).

During 4 years of follow-up, 43 subsequent MRSA infections were identified. Six infections occurred in noncolonized patients (6/141, 4.3%), 26 infections occurred in low burden patients (26/141, 18.5%), and 11 occurred in high burden patients (11/64, 17.2%). The distribution of infection types was not significantly different in each colonization strata (Table 2). Time to subsequent MRSA infection did not differ between colonization categories ($P = .80$). Death during follow-up was more common in patients with any MRSA nasal colonization (>50% mortality) when compared with those without MRSA nasal colonization (34% mortality). Patients with high burden nasal MRSA were most likely to remain colonized with MRSA on readmission to the AVAMC (Table 2).

Table 3 shows demographic variables and statistically significant results from bivariate and multivariate analysis of factors associated with subsequent MRSA infection among our cohort. Factors associated with subsequent MRSA infection in the unadjusted analysis included MRSA nasal colonization (either low or high burden vs noncarriers), wounds present on admission, device present on admission, previous or concurrent MRSA infection, hospital admission in the year prior to index admission, antibiotics within 30 days of admission, diabetes, and HIV infection. All other variables did not reach the prespecified level of significance ($P \leq .10$).

A purposeful selection strategy including assessment of confounding and interaction was used to select the covariates for multivariate analysis from among those significant in bivariate analysis. No evidence of interaction with colonization status was observed with the following interaction terms: wounds, antibiotic use within 30 days, HIV, diabetes, ESRD, device present on admission, race, or previous/concurrent MRSA infection. The final model included colonization status, wounds, and device present on admission (goodness-of-fit test, $P = .30$). MRSA colonization status was a significant risk factor for subsequent MRSA infection ($P = .008$). After adjustment for confounding variables, low colonization burden (compared with no colonization) was associated with increased risk of subsequent infection (risk ratio, 3.62; 95% confidence interval: 1.47–8.93), whereas high colonization burden (compared with no colonization) did not reach the predefined level for significance (risk ratio, 2.71; 95% confidence interval: 0.95–7.72, $P = .06$). No variables were added to the final model solely as confounders, and no interaction was detected.

DISCUSSION

In this retrospective cohort study, we evaluate MRSA nasal colonization burden as a risk factor for subsequent MRSA infection using the C_t from the Xpert MRSA assay as a surrogate for colonization burden. MRSA nasal colonization was again found to be a risk factor for subsequent infection; however, patients with high MRSA nasal burden did not have an increased risk for subsequent infection when compared with those with low nasal burden. In addition to MRSA nasal colonization, the presence of wounds and invasive devices were also independent risk factors for the development of MRSA infections.

Colonization with *S aureus* is a well-known risk factor for subsequent staphylococcal infection and is the basis for many infection control interventions. The literature on nasal colonization burden and its clinical consequences is much less robust and based on studies from the 1960s.[17,20,25] More recent studies[21,22] continue to demonstrate the relationship of colonization burden, persistent colonization, and increased infection risk. These studies, assessing the relationship of staphylococcal colonization burden and disease, were

conducted in countries with low levels of MRSA, only included patients at high risk of subsequent staphylococcal infection, and collected nasal culture specimens under strict study protocols.[18,21,22] Our study is the first to assess an easily accessible quantification measure (C_t) obtained through routine infection control surveillance as a risk factor for subsequent MRSA disease among a population of veterans with significant MRSA infection rates.[26,27]

Our study did not find high colonization burden, as defined by the C_t of ≤24, to be a significant risk factor for subsequent MRSA infection when compared with low colonization burden. This null finding may be due to a number of factors. As discussed in several publications, attempting to define the persistently colonized state (and also colonization burden) is dependent on repeatability of the nasal sampling method to adequately quantify the bacterial burden.[18,28] In our study, screening nasal swabs are collected on admission to the AVAMC by nursing staff throughout the hospital and not under strict study protocols. This collection, although intended to be standardized by the VHA directive, is likely plagued by variable nasal swabbing technique because of the large number of nurses collecting specimens throughout the hospital. For example, one patient had 9 admission or transfer MRSA nasal screens performed over the course of 6 months. Of these 9 tests, 4 had a $C_t \leq 24$ cycles and 5 had a $C_t > 24$ cycles without systemic antibiotics or nasal decolonization being prescribed. This variability may be due to normal fluctuation of MRSA burden or may reflect, more likely, different collection techniques and not actual changes in the nasal burden of MRSA. Because of this variability of collection that occurs in routine clinical surveillance programs, our study likely suffers from measurement error and resultant misclassification bias. In a previous study, we validated the C_t as a measure of bacterial burden on nasal swabs in a sample of US veterans.[23] The study, however, did not evaluate whether nasal swabs collected during routine infection control surveillance accurately reflect the true nasal burden of MRSA in the patient. To effectively use the C_t as quantitative measure of nasal MRSA burden, one must ensure that health care workers follow strict collection procedures to ensure reliability of results.

Also, potentially contributing to our null findings, we evaluated the risk of subsequent MRSA infection among a heterogeneous cohort of veterans; we did not limit our evaluation to 1 specific high-risk subgroup. This selection process was in an attempt to determine if, in a highly colonized population, a simple screening test could identify patients who could potentially benefit from decolonization or other preventative measures. Colonization burden may play a greater role in infection pathogenesis in those with altered skin integrity (ESRD with hemodialysis catheters, postoperative surgical wounds, external devices present, ulcers), and an evaluation of nasal burden and infection risk is warranted in this high-risk population.

Finally, studies evaluating *S aureus* burden have largely been conducted in geographic regions without a high prevalence of MRSA. Outcomes of MRSA and methicillin-senstive *S aureus* (MSSA) colonization and clinical infection are distinct.[29] Only 2 studies have begun to explore MRSA colonization burden in the United States,[30,31] and no study has compared differences between MRSA and MSSA colonization burden. Our study, in concordance with the study by Mermel et al,[30] did not find a positive association between MRSA burden and previous/concurrent MRSA infection, calling into question the role nasal burden of MRSA has in pathogenesis of infection. Whether results of studies evaluating MSSA nasal burden can be extrapolated to MRSA colonization is unclear.

Our study has several strengths and limitations. In our study, all MRSA infections during the 4 years of follow-up were analyzed prospectively using a consistent clinical and microbiologic definition and reviewed by the same experienced infectious disease physician, a major strength of our study. In addition, most veterans do not have outside medical

insurance coverage and do not seek care outside of the local VA system. Because of this, we are confident our study captured the majority of subsequent MRSA infections within our cohort and data obtained on comorbidities and preadmission characteristics were accurate.

The power of our study was limited by estimates of infection risk that were based on minimal prior data, resulting in a small calculated sample size needed in the high burden population. Because of these faulty estimates, our final model failed to demonstrate a statistically significant risk ratio when comparing high colonization burden to negative colonization ($P = .06$). Even though it did not reach our predefined level of significance, the risk ratio and confidence intervals are similar to that of low colonization burden and would likely reach significance if the sample size were increased. In addition, colonization burden was dichotomized based on our previous work demonstrating a logarithmic relationship between C_t and quantitative cultures. Exploring the C_t as a continuous, time-dependent, variable among colonized individuals may be more appropriate. Last, the association between nasal colonization and community-associated MRSA infection has been called into question.[32] Relying only on nasal colonization burden results may not be adequate to assess risk of community-associated disease.

In addition to better defining MRSA colonization as a risk factor for infection, our study further identifies important characteristics of colonization and infection. We demonstrate the effect external devices (urinary catheters, central lines, tracheostomy, and others) and wounds have on MRSA infections. Wounds and external devices both disrupt the natural barrier of the skin and allow a portal of entry for bacteria. Our findings add to the literature demonstrating similar findings in hospitalized patients.[33–35] The mortality rate seen in our study also highlights the complex patient population seen at the AVAMC. Interestingly, the death rate among MRSA colonized patients was considerably greater than those without nasal colonization (53% vs 34%, respectively). This finding has not been well studied and deserves further evaluation.

Although the C_t as a quantitative measure of burden in our study was not predictive of subsequent MRSA infection, its utility has yet to be fully defined and studied. A more thorough evaluation of nasal MRSA colonization burden is warranted with a focus on consistent and reliable nasal swabbing techniques. Also, future studies evaluating the C_t as a risk factor for development of MRSA infection among high-risk patients is warranted in an attempt to identify a population that may benefit from MRSA decolonization. High nasal colonization burden has also been associated with colonization at other body sites[30] and increased rates of transmission to the surrounding environment.[36,37] Whether the C_t can be used as an infection control measure to identify patients at high risk of transmission needs further study. Identifying patients at the highest risk of MRSA transmission could potentially lead to a more cost-effect strategy of isolation and better patient care.[38]

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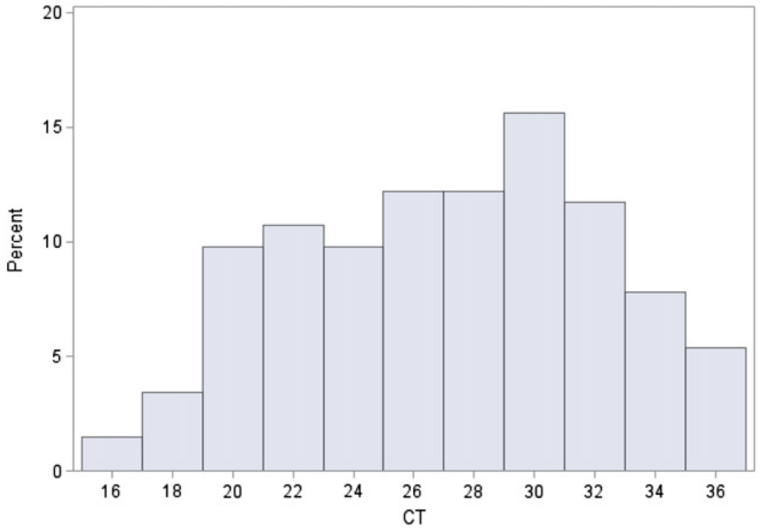

Fig 1.
Distribution of the cycle threshold (CT) among patients with positive admission nasal MRSA screening (Xpert MRSA assay) in Atlanta veterans (n = 205).

Table 1

Baseline patient characteristics among noncarriers, low burden carriers, and high burden carriers of nasal MRSA: N = 346

	Colonization status			
	Negative	Low burden	High burden	
Patient demographics	**n (%)**	**n (%)**	**n (%)**	***P* value***
Total	141	141	64	
C_T	n/a	29.8	21.0	
Age, yr				
Mean (SD)	63.0 (13.3)	62.7 (12.5)	65.5 (12.3)	.34†
>71.7‡	39 (27.7)	33 (23.4)	18 (28.1)	.66
Sex				
Male	130 (92.2)	136 (96.5)	63 (98.4)	.10
Female	11 (7.8)	5 (3.5)	1 (1.8)	
Race				
Black	55 (39.0)	67 (47.5)	30 (46.9)	.35
White	81 (57.4)	70 (49.6)	34 (53.1)	
Other	5 (3.6)	4 (2.9)	0 (0)	
Clinical characteristics				
Admit from other than home	11 (7.8)	17 (12.1)	12 (18.8)	.07
Admission to ICU	44 (31.2)	30 (21.3)	10 (15.6)	.03
Surgery in 12 months prior	35 (24.8)	41 (29.1)	22 (34.4)	.36
Admission in 12 months prior	67 (47.5)	75 (53.2)	40 (62.5)	.14
Antibiotics within 30 days	26 (18.4)	40 (28.4)	21 (32.8)	.05
Comorbidities				
Wound present	10 (7.1)	34 (24.1)	21 (32.8)	<.0001
Device present	8 (5.7)	15 (10.6)	17 (26.7)	<.0001
Previous/concurrent MRSA	1 (0.7)	26 (18.4)	14 (21.9)	<.0001
CAD	55 (39.0)	44 (31.2)	24 (37.5)	.37
CHF	34 (24.1)	43 (30.1)	19 (29.7)	.45
PVD	16 (11.4)	23 (16.3)	15 (23.4)	.08
COPD	26 (18.4)	39 (27.7)	16 (25.0)	.18
DM	60 (42.6)	60 (42.6)	28 (43.8)	.98
Smoker	45 (31.9)	40 (28.4)	12 (18.8)	.15
Advanced liver disease	5 (3.6)	12 (8.5)	3 (4.7)	.19
Active malignancy	31 (22.0)	21 (14.9)	7 (10.9)	.10
ESRD	6 (4.3)	4 (2.9)	9 (14.1)	.003
CVA	18 (12.8)	26 (18.4)	12 (18.8)	.36
HIV	2 (1.4)	10 (7.1)	2 (3.1)	.05
Other	11 (7.8)	18 (12.8)	7 (10.9)	.39
≥3 Comorbidities	58 (41.1)	68 (48.2)	22 (34.4)	.16

MRSA, Methicillin-resistant *Staphylococcus aureus; CAD*, coronary artery disease; *CHF*, congestive heart failure; *COPD*, chronic obstructive pulmonary disease; *CT*, cycle threshold; *CVA*, cerebrovascular accident; *DM*, diabetes mellitus; *ESRD*, end stage renal disease; *HIV*, human immunodeficiency virus; *PVD*, peripheral vascular disease.

[*] *P* value for χ^2 or Fisher exact test.

[†] *P* value for 1-way analysis of variance, F test.

[‡] Fourth quartile of age.

Table 2

Subsequent MRSA infection, death, and readmission during 4 years of follow-up stratified by colonization status

Characteristic	Negative colonization (n = 141)	Low colonization burden (n = 141)	High colonization burden (n = 64)	*P* value*
Total subsequent infections, n (%)	6 (4.3)	26 (18.5)	11 (17.2)	.0007
Subsequent infection				
Skin/soft tissue	2	10	4	.20
Bone and joint		4		
Primary bloodstream		7	1	
Genitourinary	2	2	4	
Lower respiratory	2	2	2	
Surgical site		1		
Mean time to infection, days (SD)	310.8 (283.9)	385.8 (398.4)	445.6 (444.9)	.80†
Death, n (%)				
Death during admission	7 (5.0)	9 (6.4)	4 (6.3)	.87
Death during follow up	48 (34.0)	73 (51.8)	35 (54.7)	.003
Readmission during 4 years of follow-up, n (%)				
≥1 Readmission	77 (54.6)	82 (58.2)	41 (64.1)	.44
Admission nasal swab positive on readmission	7 (9.5)	48 (59.3)	28 (70.0)	<.0001

SD, Standard deviation.

*P value for χ^2 test or Fisher exact test.

†P value for 1-way analysis of variance, F test.

Table 3

Demographic characteristics and statistically significant results from bivariate and multivariate analysis of predictors of subsequent MRSA infection among Atlanta veterans

	Bivariate analysis		Multivariate analysis		
Characteristics	**Risk ratio***	**95% CI**	**Risk ratio†**	**95% CI**	***P* value‡**
Male vs female	2.17	0.31–14.83			
Black vs white	1.40	0.79–2.44			
Age: 4th quartile vs other	0.75	0.37–1.50			
Clinical characteristics					
Admission in 12 months prior	1.87	1.02–3.40			
Antibiotics within 30 days	2.14	1.23–3.73			
Comorbidities					
Low vs negative nasal burden	4.33	1.84–10.20	3.62	1.47–8.93	.005
High vs negative nasal burden	4.04	1.56–10.44	2.71	0.95–7.72	.06
High vs low nasal burden	0.93	0.49–1.76	0.75	0.36–1.55	.44
Wound present	2.56	1.46–4.46	1.86	0.98–3.52	.06
Device present	2.63	1.44–4.79	2.12	1.04–4.32	.04
Previous/concurrent MRSA	2.25	1.20–4.22			
DM	1.69	0.96–2.96			
HIV	2.43	1.00–5.85			

DM, Diabetes mellitus; *HIV*, human immunodeficiency virus; *MRSA*, methicillin-resistant *Staphylococcus aureus*.

*Unadjusted risk ratios.

†Adjusted risk ratios.

‡*P* value for χ^2 test.

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