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RESEARCH BRIEFS

Methicillin-Resistant *Staphylococcus aureus* (MRSA) Carriage in 10 Nursing Homes in Orange County, California

Nursing home residents have multiple risk factors for acquiring methicillin-resistant *Staphylococcus aureus* (MRSA), including diabetes, hemodialysis, frequent hospitalization, and sharing rooms and common areas.[1,2] Previous studies showed MRSA prevalence ranged 5%–40%, but few studied entire regions or explained this variation.[1,3-6] We measured MRSA prevalence among nursing homes within 1 county and identified factors predicting carriage.

We measured MRSA carriage in residents of 10 nursing homes in Orange County, California, from October 2008 through November 2009. At each facility, we obtained nares swab samples from 100 residents during point prevalence screening and 50 consecutive residents on admission. The Institutional Review Board of the University of California Regents approved this study.

Bilateral nares swab samples (BD Culture Swabs; Fisher Scientific) were cultured for MRSA. Isolates were tested for susceptibility to oxacillin, vancomycin, linezolid, quinupristin-dalfopristin, rifampin, tetracycline, trimethoprim-sulfamethoxazole, gentamicin, clindamycin, erythromycin, levofloxacin, and mupirocin.

Nursing home characteristics were derived from public sources, including the proportion of residents who were male, less than 65 years old, of Hispanic ethnicity, or Medicaid-insured.[7] For each swabbed resident, we recorded the nursing home day of swab collection, whether residents shared a room, and whether residents had a history of MRSA.

We tested the correlation between MRSA admission and point prevalence using the Pearson coefficient. We performed paired *t* tests comparing mean MRSA admission in relation to point prevalence, length of stay for MRSA-positive residents compared with length of stay for MRSA-negative residents, and facility proportions of isolates nonsusceptible to specific antibiotics at admission and corresponding proportions at point prevalence. We tested associations of resident and facility-level characteristics with individual MRSA carriage at point prevalence. We performed χ^2 tests on several variables: admission prevalence, annual admissions, residence in shared rooms, MRSA history, nursing home day of swab collection, and the proportion of residents who were male, less than 65 years old, nonwhite, Hispanic, Medicaid-insured, or resident for more than 3 months. Variables with $P < .1$ entered an individual-level generalized linear mixed model clustered by facility (ProcGLIMMIX; SAS, version 9.2; SAS Institute). For multiple-occupant rooms, we included the first 2 swabbed residents per room in multivariate analyses.

We obtained 500 admission and 1,000 point prevalence nares swab samples from 10 nursing homes. Facility characteristics, including MRSA admission and point prevalence, varied substantially (Table 1). Overall, MRSA admission prevalence correlated well with MRSA point prevalence (coefficient, 0.6). However, even when facilities had similar admission prevalence, MRSA point prevalence differed significantly

TABLE 1. Facility Characteristics and Methicillin-Resistant *Staphylococcus aureus* (MRSA) Prevalence for 10 Orange County Nursing Homes

	Nursing home, by identifier									
Variable	1	2	3	4	5	6	7	8	9	10
Characteristic										
No. of beds	145	24	198	255	80	138	99	182	99	143
No. of annual admissions	1803	392	1071	443	393	323	350	759	390	723
LOS, mean, days	387	29	554	429	292	678	689	277	331	362
Residents with characteristic, %										
Age <65 y	41	4	2	62	0	39	0	1	27	40
Male sex	46	35	25	49	25	34	26	32	37	46
Nonwhite race	34	4	10	40	4	30	1	15	31	42
Hispanic ethnicity	20	0	3	23	0	12	0	9	18	24
History of MRSA on admission	12	9	12	15	18	3	10	16	26	16
Sharing room	100	0	100	95	69	100	85	99	100	99
LOS >3 mo	87	97	90	91	92	77	87	54	82	88
Medicaid insurance	33	0	42	86	<1	NA	0	60	80	75
MRSA admission prevalence, %	8	11	12	12	13	22	21	25	29	31
MRSA point prevalence, %	30	7	22	42	25	30	16	39	44	52
Point prevalence − admission prevalence, %	22	−4	10	30	12	8	−5	14	15	21

NOTE. LOS, length of stay; NA, not applicable.

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(eg, nursing home 3 vs nursing home 4: 22% vs 42%; $P = .004$). Overall, MRSA point prevalence significantly exceeded admission prevalence (31% vs 18%; $P = .006$, paired t test). This finding was not attributable to differential mean length of stay among MRSA-positive patients (373 days) versus MRSA-negative patients (423 days) ($P = .4$, paired t test).

Across facilities, median proportions of isolates nonsusceptible to antibiotics were as follows: gentamicin, 11% (facility range, 0–35%); vancomycin, 0%; linezolid, 0% (0–1%); quinupristin-dalfopristin, 0% (0–1%); mupirocin, 10% (0–17%); clindamycin, 74% (38%–83%); erythromycin, 95% (84%–100%); levofloxacin, 98% (94%–100%); rifampin, 0% (0–14%); tetracycline, 3% (0–17%); and trimethoprim-sulfamethoxazole, 3% (0–17%). Paired t tests revealed no significant differences between mean facility proportions of nonsusceptible isolates at admission versus point prevalence.

In multivariate models, predictors of MRSA carriage at point prevalence included MRSA history (odds ratio [OR], 2.7; $P < .001$); residence in facilities with high MRSA admission prevalence (30% higher odds of MRSA carriage per 10% increase in facility MRSA admission prevalence; $P = .05$); and residence in facilities with high proportions of Medicaid-insured residents (20% higher odds of MRSA carriage per 10% increase in percentage of Medicaid-insured residents; $P < .001$). Proportions of nonwhite (OR, 1.3; $P < .001$), Hispanic (OR, 1.5; $P < .001$), and Medicaid-insured residents were colinear.

MRSA carriage varied substantially across 10 nursing homes. Overall point prevalence was 31% (range, 7%–52%) versus 6% in hospitals and 9%–24% in intensive care units.[8,9] Although variability arose partly from differences in MRSA admission prevalence, evidence of transmission remained. Often, nursing homes with similar admission prevalence differed in MRSA point prevalence, suggesting some facilities cannot contain MRSA from spreading.

Overall, MRSA point prevalence was 67% higher than admission prevalence, which was not attributable to differential length of stay for MRSA-positive versus MRSA-negative residents. MRSA acquisition may relate to congregating in common areas or having roommates. Additionally, nursing homes lack standard contact isolation policies, and much variability exists.[10] More research is needed to understand whether specific infection control and/or cleaning policies affect transmission.

Our study provides insight into risk factors associated with MRSA carriage. Residence in nursing homes with high MRSA importation predicted MRSA carriage at point prevalence, even after accounting for an individual's MRSA history. Plausibly, living in nursing homes with many MRSA carriers increases individuals' chances of exposure. MRSA carriage was also associated with residence in facilities with high proportions of Medicaid-insured residents. This predictor was interchangeable with proportions of nonwhite and Hispanic residents. Thus, race may be a proxy for economic disadvantage or residence in resource-poor facilities. Limited resources may impact patient care and cleaning staff ratios, availability of single rooms, and cleaning and infection control practices. Nevertheless, we cannot exclude the possibility that cultural factors may affect transmission.

Limitations include small sample size and point prevalence design, reflecting MRSA carriage at one time. We did not culture samples from multiple sites for MRSA, but nares screening detects the majority of carriers. We primarily used facility-level risk factors and did not measure several patient-specific factors, including wounds, devices, and antibiotic use.

MRSA carriage in 10 Orange County nursing homes varied greatly, reaching 50% in some. MRSA burden was associated with importation, but transmission was evident and may relate to facility resources. More research is needed to evaluate the contribution of nursing homes to regional MRSA transmission and ways to adapt infection control to this unique setting.

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Prevalence and Risk Factors of Methicillin-Resistant *Staphylococcus aureus* Colonization among Critically Ill Hospitalized Patients in a Tertiary Care Center in Houston, Texas: An Active Surveillance Pilot Project

The Centers for Disease Control and Prevention (CDC) has reported an increase in the number of healthcare-associated infections, with an estimated 1.7 million infections resulting in approximately 99,000 deaths per year in the United States.[1] Every year, more than 126,000 individuals who are hospitalized are infected with methicillin-resistant *Staphylococcus aureus* (MRSA).[2] In 2005, approximately 19,000 people died due to healthcare-associated or community-associated invasive MRSA infection during their hospital stay.[3] Multidrug-resistant organisms, such as MRSA, were associated with increased durations of hospital stays and higher costs.[4] The ongoing increase in the prevalence of MRSA infection has led various agencies to propose recommendations, guidelines, and programs to battle this emerging epidemic.

By implementing CDC and Society for Healthcare Epidemiology of America recommendations for active surveillance of MRSA, Memorial Hermann–Texas Medical Center, an urban tertiary care hospital in Houston, Texas, was able to determine the prevalence of MRSA colonization among non-pediatric patients admitted to intensive care units and evaluate the risk factors associated with colonization. This small, cross-sectional, prospective pilot project involved MRSA screening in the 7 adult intensive care units (ICUs), including neurological trauma, shock trauma, medical, cardiac care, cardiovascular, burn, and transplant units.

Screening criteria included the following: (1) patients newly admitted to the ICU, with the current duration of hospital stay not exceeding 3 days; or (2) patients internally transferred within the hospital to an ICU, with the current duration of ICU stay not exceeding 3 days. Nursing staff were responsible for collecting specimens from patients and for following standard modified contact isolation protocol, which included wearing clear gowns and gloves during the patient's ICU stay. Specimens were collected from the nares with use of dry, unmoistened sterile BBL CultureSwabs Liquid Stuart swabs (BD) and were processed using the BD GeneOhm IDI-MRSA assay in vitro diagnostic test (BD) for rapid MRSA detection.

Statistical analysis was performed using Stata, version 10 (StataCorp); EpiInfo, version 3.3 (CDC); and JavaStat (Ghent University). A descriptive analysis was performed for categorical and risk factor data. Crude odds ratios, 95% confidence intervals, and P values were computed for risk factors. Pearson χ^2 test was used to calculate significance, and the significance level was set at $P < .05$. This study was exempt from review by the Institutional Review Board of the University of Texas Health Science Center at Houston.

From March 1 through May 31, 2007, 1,283 (83.4%) of 1,531 non-pediatric patients admitted to an ICU were screened for nasal MRSA colonization. Of those 1,283 patients screened, demographic and risk factor data were available for 1,260 (98.2%). Nasal MRSA colonization at the time of ICU admission was unresolved for 73 patients because of specimen or a reagent failure during testing. Therefore, a total of 1,187 (77.5%) of the 1,531 patients admitted to an ICU were described in this analysis. Overall, the prevalence of colonization with MRSA among patients in this study population at the time of ICU admission was 12.5% (149 of 1,187 patients).

The patients screened included 717 male patients (60%) and 470 female patients (40%) aged 13–106 years (mean age, 54 years). Univariate analysis demonstrated that 1.4 male patients for each female patient were colonized with MRSA at the time of ICU admission. Ethnic categories represented in the patient population screened included white, African American, Asian or Pacific Islander, all others, and unknown; the highest prevalence of MRSA colonization was found among Asian/Pacific Islander patients (13.3%). Patients aged 41–55 and 56–70 years had the highest prevalence of colonization (15.3% and 13.7%, respectively). The medical ICU had the highest prevalence of MRSA colonization (23.1%) among the 7 ICUs. The prevalence of MRSA colonization among patients hospitalized during the previous 6 or 12 months was double that among patients who were not hos-

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