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Characterization of *Staphylococcus aureus* Isolates from Nasal Cultures Collected from Individuals in the United States in 2001 to 2004[▽]

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This study characterizes methicillin-susceptible *Staphylococcus aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) isolates recovered from nasal cultures of noninstitutionalized individuals in the United States obtained in 2001 to 2004 as part of the National Health and Nutrition Examination Survey. Every tenth MSSA isolate and all MRSA isolates were typed by pulsed-field gel electrophoresis (PFGE), screened for multiple toxin genes, and tested for susceptibility to 14 antimicrobial agents. USA200, USA600, and USA900 were the predominant PFGE types among MSSA isolates in both the 2001 to 2002 and the 2003 to 2004 time periods, although they accounted for only 51.3% of 316 MSSA isolates typed in 2001 and 2002 and only 43.4% of 237 MSSA isolates typed in 2003 and 2004. In contrast, USA100, USA800, and USA700 accounted for 80.0% of the 75 MRSA isolates typed in 2001 and 2002, while USA100, USA800, and USA300 accounted for 78.4% of 134 MRSA isolates typed in 2003 and 2004. The proportion of MRSA isolates that were USA300 increased significantly from the first to the second time period ($P = 0.03$). Most USA200 isolates (both MSSA and MRSA) carried the gene for toxic shock syndrome toxin; however, carriage of the genes encoding Panton-Valentine leukocidin, while common among MRSA of PFGE type USA300, was rare among MSSA USA300 in both time periods. Most MSSA isolates remained susceptible to all antimicrobial agents except erythromycin (79.1 and 76.0% susceptibilities in the 2001 to 2002 and the 2003 to 2004 periods, respectively). In contrast, the proportions of MRSA isolates that were susceptible to chloramphenicol, clindamycin, and erythromycin were lower in 2003 and 2004 than in 2001 and 2002, although none of these differences was statistically significant.

Infections caused by *Staphylococcus aureus* are frequently preceded by colonization of body sites, particularly the nares (16). Population-based data on *S. aureus* nasal colonization in healthy, noninstitutionalized adults in the United States were collected from 2001 to 2004 as part of the National Health and Nutrition Examination Survey (NHANES). A report describing the results of this survey for 2001 and 2002 was published by Kuehnert et al. in 2005 (12). In that report, Kuehnert et al. noted that 32.4% (95% confidence interval [CI] 30.7 to 34.1%) of the population surveyed were colonized with *S. aureus* (including methicillin-susceptible *S. aureus* [MSSA] and methicillin-resistant *S. aureus* [MRSA]) and that *S. aureus* colonization was more common among young males. Only 0.8% (95% CI = 0.4 to 1.4%) of the study population carried MRSA in their nares, and MRSA colonization was associated with age >65 years and female sex. The pulsed-field gel electrophoresis (PFGE) types of the MSSA isolates were more diverse than the MRSA PFGE types. Recently, Gorwitz et al. reported the results of the second NHANES nasal colonization study conducted in 2003 and 2004 (6). Compared to 2001 to 2002, the prevalence of *S. aureus* colonization among the noninstitutionalized people surveyed in 2003 to 2004 decreased significantly to 28.6% (95% CI = 27.2 to 30.0; $P < 0.01$), while the prevalence of MRSA colonization increased to 1.5% (95% CI = 1.2 to 1.8%; $P < 0.05$). In the present report, we describe the PFGE types, toxin profiles, and antimicrobial susceptibility patterns of MSSA and MRSA isolates recovered during the NHANES surveys in the 2003 to 2004 period and compare them to the results of the 2001 to 2002 survey isolates.

MATERIALS AND METHODS

Sampling methods. A total of 19,412 nasal samples were collected from both anterior nares from 19,412 noninstitutionalized patients (i.e., not in hospitals, long-term care facilities, or prisons) using culturette swabs (BD Diagnostics [BDD], Sparks, MD) and plated on mannitol salt agar (BDDS). After overnight incubation at 35°C, each distinctive colony morphotype that fermented mannitol was selected from the mannitol salt agar plate and subcultured on a Trypticase soy agar plate containing 5% sheep blood (BAP; BDD). After overnight incubation, colonies were screened by using tube coagulase tests and Staphaurex agglutination assays (Remel, Lenexa, KS).

Strain characterization. *S. aureus* isolates were screened for oxacillin resistance by using the Clinical Laboratory Standards Institute (CLSI) disk diffusion method (3). Organisms growing on BAP were suspended in Mueller-Hinton broth to the turbidity of a 0.5 McFarland standard and plated on Mueller-Hinton agar (BDD). A 1-μg oxacillin disk was placed within the inoculum. Zone diameters were measured and recorded after 24 h of incubation at 35°C. A subset of isolates was screened by using a 30-μg cefoxitin disk test according to CLSI standards (3), but no additional isolates of MRSA were identified. All isolates that were categorized as intermediate or resistant to oxacillin by disk diffusion were tested by the CLSI broth microdilution reference method (see below). All MRSA and every tenth MSSA isolate received sequentially were further characterized with PCR assays for the genes encoding toxic shock syndrome toxin 1 (TSST-1) (*tst*), the Panton-Valentine leukocidin (PVL) genes (i.e., *lukF-PV* and *lukS-PV*), and the genes encoding staphylococcal enterotoxins A through E and H (i.e., *sea*, *seb*, *sec*, *sed*, *see*, and *seh*) as previously described (14). For MRSA, staphylococcal cassette chromosome *mec* (SCC*mec*) types I through IV were determined as previously described (15). PFGE was performed as described by McDougal et al. (13). The PFGE patterns were analyzed by using Bionumerics

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TABLE 1. Most common pulsed-field types among MSSA and MRSA isolates from nasal colonization studies

Methicillin status	*S. aureus* pulsed-field type; no. (%) of isolates in:	
	2001 to 2002	2003 to 2004
Methicillin susceptible[a]	USA200; 92 (29.1)	USA200; 59 (24.9)
	USA600; 40 (12.7)	USA600; 33 (13.9)
	USA900; 29 (9.2)	USA900; 10 (4.2)
	USA800; 21 (6.6)	Group A; 10 (4.2)
	Group A; 18 (5.7)	USA500; 9 (3.8)
	USA300; 14 (4.4)	Group D; 9 (3.8)
	Other types; 102 (32.3)	Other types; 107 (45.1)
Methicillin resistant[b]	USA100; 36 (48.0)	USA100; 60 (44.8)
	USA800; 17 (22.7)	USA800; 23 (17.2)
	USA700; 7 (9.3)	USA300; 23 (17.2)
	USA300; 6 (8.0)	USA400; 8 (6.0)
	USA1000; 2 (2.7)	USA200; 6 (4.5)
	USA400; 1 (1.3)	USA700; 3 (2.2)
	Other types; 6 (8)	Other types; 11 (8.1)

[a] Every tenth MSSA isolate was characterized. For 2001 to 2002, $n = 316$; for 2003 to 2004, $n = 237$.
[b] All MRSA isolates were characterized. For 2001 to 2002, $n = 75$; for 2003 to 2004, $n = 134$.

version 4.1 (Applied Maths, Austin, TX), and isolates were grouped into PFGE types by using Dice coefficients and >80% relatedness. Multilocus sequence typing was not performed on the isolates in the present study; however, multilocus sequence types (STs) were inferred based on prior studies (13).

Antimicrobial susceptibility testing. All isolates that underwent characterization were tested using the CLSI broth microdilution reference method (2) for susceptibility to chloramphenicol, clindamycin, erythromycin, gentamicin, levofloxacin, linezolid, mupirocin, penicillin, oxacillin, quinupristin-dalfopristin, rifampin, tetracycline, trimethoprim-sulfamethoxazole, and vancomycin using MIC plates prepared at the Centers for Disease Control and Prevention. Cation-adjusted Mueller-Hinton broth was obtained from BDD. MIC plates were incubated in ambient air at 35°C for 18 to 24 h as described by the CLSI. Isolates for which the oxacillin MICs were 1 to 8 μg/ml were tested for the presence of *mecA* by PCR as described by Killgore et al. (10). The D-zone test was performed to screen for inducible clindamycin resistance as described by the CLSI (3). The following quality control organisms were included on each day of susceptibility testing: *S. aureus* ATCC 25923, *S. aureus* ATCC 29213, and *Enterococcus faecalis* ATCC 29212 (4).

Statistical methods. Statistics were performed using SAS v.9.1 (The SAS Institute, Inc., Cary, NC). We report the unweighted proportions of isolates possessing various characteristics. Because NHANES oversamples certain age and racial or ethnic groups (e.g., Mexican Americans and non-Hispanic black persons), the findings of unweighted analyses should not be generalized to the U.S. civilian, noninstitutionalized population. Associations of specific strain characteristics between the two time periods were assessed using a general chi-square test or the Fisher exact test when categorical variable cells were <10. Trends were assessed using a chi-square for linear trend test. CIs were calculated as previously described (6).

RESULTS

Pulsed-field types of MSSA and MRSA. The descriptions of the individuals from whom the MSSA and MRSA isolates were obtained in 2003 to 2004 are presented elsewhere (6). The most common PFGE types of MSSA and MRSA isolates recovered during the two study periods are shown in Table 1. Among the 316 MSSA isolates collected from 2001 to 2002, there were 148 PFGE banding patterns observed that clustered into 11 USA types, 5 additional PFGE groups (A through E), and an additional 42 unique patterns that did not cluster into any of these groups (Table 2). Among the 237 MSSA isolates from 2003 to 2004, there were 207 isolates whose PFGE patterns were among the same 128 patterns that clustered into the USA types and groups (A through E) seen in 2001 to 2002. Thirty additional isolates each had a unique banding pattern, only three of which were observed in the first 2-year period (i.e., there were 27 novel PFGE banding patterns not observed in 2001 to 2002) (Table 2). The most common PFGE types among MSSA isolates were USA200 (typically multilocus ST30), USA600 (typically ST45), and USA900 (ST15). These three PFGE types accounted for 51.3% of the MSSA isolates in 2001 to 2002 but only 43.4% of MSSA isolates in 2003 to 2004. This change was not statistically significant (χ^2 test, $P = 0.069$). Only a small percentage of MSSA isolates were PFGE

TABLE 2. Key MSSA resistance and toxin profiles by PFGE type

Type	2001 to 2002[a]				2003 to 2004[b]			
	No. of isolates ($n = 316$)	% Resistant to:		%PVL$^+$/%TSST$^+$	No. of isolates ($n = 237$)	% Resistant to:		%PVL$^+$/%TSST$^+$
		Erythromycin	Levofloxacin			Erythromycin	Levofloxacin	
USA200	92	28.3	1.1	0/87.0	59	33.9	0	0/84.7
USA300	14	28.6	0	7.1/7.1	6	33.3	0	0/0
USA400	5	40.0	0	0/0	7	0	0	0/0
USA500	3	33.3	0	0/0	9	33.3	22.2	0/0
USA600	40	2.5	0	0/2.5	33	6.1	0	0/6.1
USA700	7	14.3	0	0/0	4	50.0	0	0/0
USA800	21	9.5	0	0/14.3	25	40.0	8.0	0/0
USA900	29	24.1	0	0/0	10	20.0	0	0/0
USA1000	7	0	0	0/0	7	28.6	0	0/0
USA1100	1	0	0	100/0	1	0	0	100/0
USA1200	6	16.7	0	0/0	9	11.1	0	0/0
Group A	18	72.2	0	0/0	10	60.0	0	0/0
Group B	10	0	0	0/0	7	14.3	0	0/0
Group C	6	16.7	0	0/0	2	0	0	0/0
Group D	11	9.1	0	0/0	9	11.1	0	0/0
Group E	4	0	0	0/0	9	0	0	0/0

[a] These values do not include 42 isolates, each with a unique PFGE pattern.
[b] These values do not include 30 isolates, each with a unique PFGE pattern.

TABLE 3. Key MRSA resistance and toxin profiles by PFGE type

Type	2001 to 2002[a]					2003 to 2004[b]				
	No. of isolates (n = 75)	No. of PFGE patterns	% Resistant to:		%PVL$^+$/%TSST$^+$	No. of isolates (n = 134)	No. of PFGE patterns	% Resistant to:		%PVL$^+$/%TSST$^+$
			Erythromycin	Levofloxacin				Erythromycin	Levofloxacin	
USA100	36	21	94.4	91.7	0/0	60	15	100	91.7	0/0
USA200	1	1	100	100	0/100	6	5	66.7	50	0/66.7
USA300	6	3	83.3	33.3	83.3/0	23	5	91.3	34.8	87.0/0
USA400	1	1	100	0	100/0	8	3	50.0	25.0	62.5/0
USA500	1	1	0	100	0/0	0				
USA600	1	1	0	0	0/0	3	3	100	100	0/0
USA700	7	3	85.7	0	0/0	3	2	33.3	0	0/0
USA800	17	6	29.4	5.9	0/17.6	23	6	52.2	4.3	0/30.4
USA1000	2	1	50	50	0/0	1	1	100	0	0/0
USA1100	0					1	1	100	0	0/0
Iberian	1	1	100	100	0/0	0				

[a] These values do not include two isolates, each with a unique PFGE pattern.
[b] These values do not include six isolates, each with a unique PFGE pattern.

type USA300 in both time periods (4.4 and 1.9% in the periods from 2001 to 2002 and from 2003 to 2004, respectively; note that the 2003-2004 data are within the "Other types" given in Table 1). Among the 553 MSSA isolates, 12 PFGE patterns within seven PFGE types were recognized in all 4 years; 3 USA200, 1 USA500 (ST8), 3 USA600, 1 USA700 (ST72), 1 USA800 (ST5), 2 USA900, and 1 USA1200 (ST unknown). PFGE pattern USA200-0007 was the most common pattern observed in the NHANES database, representing 14.1% of all MSSA isolates; however, while there were 27 isolates of USA200-0007 in 2001 and 29 in 2002, there were only 12 in 2003 and 3 in 2004 ($P < 0.001$ [χ^2 test for linear trend]). There were no other apparent trends regarding changes in the MSSA strain types. None of the MSSA isolates that were characterized corresponded to PFGE type USA100.

In contrast to the MSSA isolates, the diversity of the PFGE patterns of the MRSA isolates was more limited. A total of 41 different PFGE patterns were observed among nine USA types (plus the Iberian type) for the 75 MRSA samples isolated in 2001 to 2002 compared to 45 different patterns in eight USA types among the 134 MRSA samples from 2003 to 2004. There were only two PFGE patterns observed in 2001 to 2002 and six observed in 2003 to 2004 that did not fall into a known USA or Iberian type. USA100 (ST5), USA800 (also ST5), and USA700 (ST72) accounted for 80% of the MRSA isolates in 2001 to 2002, while USA100, USA800, and USA300 (ST8) accounted for 79.2% of isolates in 2003 to 2004 (Table 1). The remaining MRSA isolates recovered in 2001 to 2002 included two USA1000 (ST59), and a single isolate each of USA200, USA400 (ST1), USA500 (ST8), USA600, and the Iberian type (ST237). In contrast, in 2003 to 2004 the isolates included multiple USA200, USA400, and USA600 isolates and single isolates of USA1000 and USA1100 (ST30).

The most notable change in MRSA PFGE types between 2001 to 2002 and 2003 to 2004 was the increase in the percentage of USA300 isolates from 8.0% of MRSA isolates in 2001 to 2002 to 17.2% in 2003 to 2004. The proportion of MRSA isolates that were USA300 was significantly higher in 2003 to 2004 compared to 2001 to 2002 ($P = 0.031$; Fisher exact test). The unique USA300-0114 strain (a subset of all USA300 isolates) appeared only once in 2001, but there were three USA300-0114 isolates in 2002, seven in 2003, and nine in 2004 ($P = 0.0017$, Fisher exact test). Another pattern that increased in prevalence among MRSA isolates was USA100-0022. There were no USA100-0022 isolates in 2001, 1 in 2002, 4 in 2003, and 14 isolates in 2004. This change was statistically significant ($P = 0.0017$, Fisher exact test). Only two PFGE patterns, USA300-0114 and USA800-0179, were observed in all 4 years.

Characteristics of MSSA isolates. The key toxin and antimicrobial resistance patterns of the MSSA isolates (and those that were most variable among different PFGE types), stratified by PFGE type, are shown in Table 2. Approximately, 87 and 85% of USA200 isolates carried the TSST-1 gene in 2001 to 2002 and in 2003 to 2004, respectively, while a smaller percentage (60 and 52%, respectively) carried *sea* (data not shown). Several isolates also carried a second enterotoxin gene (either *seb* [1 isolate], *sec* [10 isolates], *sed* [5 isolates], or *seh* [9 isolates]) in addition to *tst*. USA600 isolates did not consistently carry either enterotoxin or PVL genes, although enterotoxin C was present in approximately 10 isolates in each period. Rare isolates of USA600 contained *tst*. None of the USA900 isolates harbored genes encoding PVL, TSST-1, or any of the enterotoxins for which we tested. The remaining 45 to 55% of the MSSA isolates recovered from nasal swabs represented at least 10 other PFGE types and varied considerably in their enterotoxin gene profiles, although rarely did an isolates carry more than one enterotoxin gene. Two of the USA1100 isolates (one in 2001 to 2002 and one in 2003 to 2004) carried the genes encoding PVL. Overall, PVL gene carriage was rare among MSSA isolates. USA300 MSSA isolates, with one exception, did not harbor the PVL genes.

Characteristics of MRSA isolates. The key toxin and antimicrobial resistance patterns of the MRSA isolates stratified by PFGE type are shown in Table 3. None of the USA100 isolates contained the genes for either PVL or TSST-1 in either study period, but 88.9 and 71.7% of USA100 isolates in 2001 to 2002 and 2003 to 2004, respectively, contained the genes for *sed* (data not shown). Although 91.6% of the USA100 isolates carried SCC*mec* type II in 2001 to 2002 (three isolates carried SCC*mec* type IV), all of the USA100 isolates carried SCC*mec* type II in 2003 to 2004. USA800 was the next most common PFGE type recognized in both time periods; 88.2 and 100% of

TABLE 4. Antimicrobial susceptibility profiles for MSSA and MRSA isolates

Antimicrobial agent	No. of susceptible isolates (%) among:			
	MSSA in:		MRSA in:	
	2001 to 2002 (n = 316)	2003 to 2004 (n = 237)	2001 to 2002 (n = 75)	2003 to 2004 (n = 134)
Chloramphenicol	273 (86.4)	197 (83.1)	49 (65.3)	69 (51.9)
Clindamycin[a]	316 (100)	232 (97.9)	51 (68.0)	88 (66.4)
Clindamycin[b]	263 (83.2)	184 (77.6)	34 (45.0)	50 (37.6)
Erythromycin	250 (79.1)	180 (76.0)	19 (25.3)	24 (18.1)
Gentamicin	315 (99.7)	236 (99.6)	75 (100)	12 (99.3)
Levofloxacin	315 (99.7)	233 (98.3)	34 (45.3)	60 (45.1)
Linezolid	316 (100)	237 (100)	75 (100)	133 (100)
Penicillin	39 (12.3)	27 (11.4)	0 (0)	0 (0)
Oxacillin	316 (100)	237 (100)	0 (0)	0 (0)
Quinupristin-Dalfopristin	301 (100)	237 (100)	75 (100)	133 (100)
Rifampin	316 (100)	237 (100)	74 (98.7)	131 (98.5)
Tetracycline	306 (96.8)	230 (97.0)	69 (92.0)	122 (91.7)
Trimethoprim-sulfamethoxazole	316 (100)	235 (99.2)	75 (100)	133 (100)
Vancomycin	316 (100)	237 (100)	75 (100)	133 (100)

[a] Decrease in susceptibility due to constitutive resistance only.
[b] Decrease in susceptibility due to inducible and constitutive resistance.

USA800 isolates carried SCC*mec* type IV in 2001 to 2002 and in 2003 to 2004, respectively. Among USA800 isolates, 17.6% carried *tst* in 2001 to 2002, and 30.4% carried *tst* in 2003 to 2004. None carried PVL genes. None of the USA700 isolates carried enterotoxin, PVL, or TSST-1 genes; all carried SCC*mec* type IV. All USA300 MRSA isolates also contained SCC*mec* type IV, however, 83.3 and 90.9% of USA300 MRSA isolates carried PVL genes in 2001 to 2002 and in 2003 to 2004, respectively. Only one USA300 isolate contained *sed*.

MSSA antimicrobial susceptibility patterns. The MSSA isolates, regardless of USA type, were susceptible to linezolid, rifampin, and vancomycin. Most of the MSSA isolates were susceptible to chloramphenicol, clindamycin, gentamicin, levofloxacin, quinupristin-dalfopristin, tetracycline, and trimethoprim-sulfamethoxazole. Resistance to erythromycin was more variable through all of the USA types (Table 2). The proportion of penicillin susceptibility among MSSA isolates was ca. 12% in both time periods. Only isolates of USA700, USA1200, group A, and group C were uniformly resistant to penicillin (data not shown). The proportion of USA600 isolates that were susceptible to penicillin decreased from 17.1% in 2001 to 2002 to 11.1% in 2003 to 2004 (data not shown). Similarly, the proportion of USA800 isolates that were penicillin susceptible decreased from 33.3% in 2001 to 2002 to 17.4% in 2003 to 2004. Overall, the percentages of MSSA isolates that were susceptible to clindamycin, erythromycin, levofloxacin, and penicillin did not differ significantly between the two time periods (Table 4).

MRSA antimicrobial susceptibility patterns. In general, the susceptibility patterns of the MRSA isolates correlated with their USA types (13). With few exceptions, USA100 isolates were resistant to erythromycin and levofloxacin and susceptible to gentamicin, linezolid, quinupristin-dalfopristin, tetracycline, trimethoprim-sulfamethoxazole, and vancomycin (data not shown). Constitutive resistance to clindamycin among all MRSA isolates increased slightly from 32.0% in 2001 to 2002 to 33.6% in 2003 to 2004, while all clindamycin resistance (inducible plus constitutive) rose from 55.0 to 62.4%. Although there was an apparent decrease in the proportion of MRSA isolates that were susceptible to chloramphenicol, clindamycin, and erythromycin between 2001 to 2002 and 2003 to 2004, the changes were not statistically significant ($P > 0.05$). Five isolates of MRSA showed decreased susceptibility to mupirocin (MIC > 4 μg/ml), but only two of the five, both USA100 isolates from 2001, showed high-level resistance (MIC ≥ 512 μg/ml) (data not shown).

DISCUSSION

Our study compared the characteristics of MSSA and MRSA isolates recovered through the NHANES survey of nasal colonization in 2001 to 2002 with those from 2003 to 2004. Kuehnert et al. described the results of the first U.S. population-based survey of *S. aureus* nasal colonization in 2001 to 2002 (12). More recently, the epidemiologic results of the 2003 to 2004 survey were published by Gorwitz et al. (6). As noted previously, MSSA strains recovered from the nares tended to be much more genetically diverse than MRSA strains. The USA 200 PFGE type predominated among the MSSA isolates in both time periods. The organisms typically harbor *tst* but few other toxin genes. They are usually penicillin resistant and have variable rates of resistance to erythromycin (some of which are inducibly clindamycin-resistant) but are susceptible to most other antimicrobial agents. One particular PFGE pattern, designated USA200-0007, was very prominent in 2001 to 2002 (17.7% of all MSSA) but dropped significantly in numbers in 2003 to 2004 (6.3% of all MSSA) for reasons that are not clear.

Interestingly, there were 12 MSSA strains representing seven different USA types that were recovered in all 4 years of the survey, suggesting that there are several widely disseminated strains of MSSA in the United States that are effective colonizers. Unfortunately, we do not have data from studies of invasive MSSA infections to know whether these same strain types commonly cause disease or whether they may be protective against invasive staphylococcal disease. PFGE type USA300 MSSA isolates were uncommon colonizers of the nares in the present study (<5% in both study periods).

The most common MRSA strain type recovered from nasal cultures in both time periods was USA100 (also known as the New York/Tokyo clone; ST5, SCC*mec* type II). This has traditionally been the most common strain type isolated from health care-associated infections in the United States (13). USA100 was also the PFGE type identified most frequently among invasive health care onset MRSA infections from a multistate, population-based surveillance study conducted in 2005 (11).

The statistically significant increase in the proportion of isolates of PFGE type USA300 (ST8, SCC*mec* type IV) causing nasal colonization in 2003 to 2004 compared to 2001 to 2002 is notable. USA300 accounted for 97% of MRSA isolates obtained from purulent skin infections in adult patients presenting to 11 emergency departments across the United States in 2004 (14) and was the most commonly identified cause of community-associated invasive MRSA infections (defined as community-onset MRSA infections in persons that lacked established MRSA risk factors) in the 2005 surveillance study noted above (11). USA300 has also been associated with out-

breaks of disease in community settings among prisoners, children, professional and college athletes, military recruits, and men who had sex with men (1, 5, 8, 9). Our data are consistent with a 2003 study in which 30% of patients with nasal MRSA colonization on admission to an urban public health hospital in Atlanta carried USA300 (7). This increase in MRSA USA300 nasal colonization may help explain the spread of USA300 isolates across the United States.

The MRSA strains from the NHANES colonization study in 2003 to 2004 have toxin profiles and antimicrobial susceptibility patterns similar to the isolates recovered in the Active Bacterial Core Surveillance data of invasive MRSA infections from 2005 (Centers for Disease Control and Prevention, unpublished data). In contrast, the NHANES USA300 MRSA isolates tend to be more susceptible to erythromycin and fluoroquinolones than the strains recovered from the emergency departments across the United States, most of which were USA300 (14). Also, in contrast to the emergency department study reported by Moran et al. (14), where both MSSA and MRSA USA300 isolates carried the genes for PVL, only the USA300 MRSA isolates from nasal carriers tended to carry PVL genes, whereas USA300 MSSA isolates from the NHANES study did not.

In conclusion, the NHANES data from 2003 to 2004 demonstrate a significant increase in nasal colonization in the United States with MRSA isolates of PFGE type USA300. Most of these isolates harbor PVL, but few are multidrug resistant. Nonetheless, USA100 isolates still predominate among the MRSA isolates from this nasal survey and, according to recent data (11), remain the most common cause of invasive MRSA individuals in health care settings.

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