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Differences in prevalence of community-associated MRSA and MSSA among U.S. and non-U.S. born populations in Six New York Community Health Centers

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Abstract

Background—*Staphylococcus aureus* is the most common cause of Skin and Soft Tissue Infections (SSTIs) in the community in the United States of America. Community Health Centers (CHC) serve as primary care providers for thousands of immigrants in New York.

Methods—As part of a research collaborative, 6 New York City-area CHCs recruited patients with SSTIs. Characterization was performed in all *S. aureus* isolates from wounds and nasal swabs collected from patients. Statistical analysis examined the differences in wound and nasal cultures among immigrant compared to native-born patients.

Results—Wound and nasal specimens were recovered from 129 patients and tested for antibiotic susceptibility. 40 patients were immigrants from 15 different countries. Although not statistically

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CONFLICTING AND COMPETING INTERESTS

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significant, immigrants had lower rates of MRSA infections (n=15) than did native-born participants, and immigrants showed significantly higher rates of MSSA wound cultures (n=11) (OR=3.5, 95% CI: 1.3, 9.7).

Conclusions—In our study, immigrants were more likely to present with SSTIs caused by MSSA than US-born patients. This suggests that antibiotic resistance may vary regionally and that immigrants presenting with SSTIs may benefit from a broader range of antibiotics. Immigrants also reported lower frequencies of antibiotic prescription or consumption in the months prior to SSTI infection.

Keywords

Skin and Soft Tissue Infection (SSTI); *Staphylococcus aureus*; Antibiotic Resistance; Foreign Born; Federally Qualified Health Centers (FQHCs); Practice-Based Research Network (PBRN)

INTRODUCTION

Skin and soft tissue infections (SSTIs) such as abscesses are commonly seen in the primary care setting, and their incidence is dramatically increasing [1]. Community-acquired Methicillin-Resistant *Staphylococcus aureus* (CA-MRSA) emerged in the community in the 1990s, and is now the leading cause of skin and soft tissue infections (SSTIs) in out-patient settings in the United States of America [2]. Nonetheless, methicillin-susceptible *S. aureus* (MSSA) still remains an important cause of *S. aureus* infections [3,4].

The high frequency of global travel and migration in the 21st century influences the spread of infections. Pathogens and their microbial resistance to antibiotics are no longer confined to specific regions of the world [5]. There have been a number of studies reporting the global spread of prevalent MRSA clones via international travel, including that of immigrant populations [6–8]. In contrast, fewer studies focus on the molecular epidemiology of MSSA in the community, where its presence can be underestimated[9]. In hospitals, MSSA is more often associated with bacteremia, endocarditis and sepsis than MRSA[10]. But MSSA strains do not show the clonal clustering often seen in MRSA, so their epidemics are less understood [11–13].

Community Health Centers (CHCs) are private, nonprofit organizations in the USA that provide preventive and primary health care services to residents of areas that are medically under-served [14]. CHCs serve a high proportion of racial and ethnic minorities and uninsured people, including immigrant and migrant populations and their goal to reduce disparities and improve health status in these communities [15]. There are over 1,400 health centers, operating over 10,000 delivery sites and providing care to over 23 million patients. CHCs are increasingly participating in research projects as part of practice-based research networks (PBRNs). These research projects offer the centers and their patients the benefit of addressing primary care clinical questions that historically, given their resource limitations, were not investigated in the settings where care was provided. The goal of this study was to assess the prevalence of CA-MRSA/MSSA among patients with SSTIs in CHCs in New York City and the surrounding area, and to identify risk factors and clinical outcomes, including recurrence, of CA-MRSA/MSSA infection. This report examines the differences

in MRSA and MSSA prevalence on confirmed *S. aureus* infections in a cohort of patients who presented at CHCs with SSTIs.

METHODS

Patient recruitment

Six New York City area CHCs collaborated with Clinical Directors Network (CDN, www.CDNetwork.org), a primary care Practice Based Research Network (PBRN), The Rockefeller University Center for Clinical and Translational Science, and the Laboratory of Microbiology and Infectious Diseases at The Rockefeller University. From November 15, 2011 to March 26, 2013, 174 patients who presented at these six CHCs with SSTIs compatible with *S. aureus* infections based on Infectious Disease Society of America (IDSA) clinical practice guidelines [14] were asked by participating clinicians to take part in the study, and 129 patients consented. Inclusion criteria were: age between 7–70 years old; ii) fluency in English or Spanish; iii) plans on receiving care at the same health center during the next year; iv) signs and symptoms of SSTI present at the time of recruitment. Exclusion criteria were: i) signs of active illness (crying, wheezing, bleeding, screaming or shaken) and ii) inability to understand the information shared about the study or to participate in a discussion about the study. This study was approved by the IRBs at The Rockefeller University and CDN and all patients consented to participate after the study was described in a language they understood.

Patient visits schedule

At the first visit, the clinicians examined the SSTIs and enrolled the patients into the study. A digital photo with a measuring scale was taken of each wound (Figure 1). Patients were treated with incision and drainage (I&D) of abscesses, antibiotics, or both, depending on clinical criteria, following the IDSA guidelines [16] and swabs of both the wound and the nares were collected. To reduce clinician burden, telephone interviewers followed up with the patients within the next 48 hours to obtain exhaustive data regarding demographics, co-morbidity, environmental exposures (occupational; comorbidities; household structure and healthcare services utilization in the past six months (Table 1).

One month later, follow-up phone interviews were conducted to collect data on the patients' clinical responses and medication adherence. At that time, patients were also asked either to return to the CHC or to send a second digital photograph showing the lesion in its current state (Figure 1).

Three months after the first visit, study staff completed patient chart reviews to assess patient follow-up visits, including reinfection and subsequent treatments.

S. aureus molecular characterization

At the first visit, specimens (swabs) from the wound and nares were sent to a commercial laboratory (BioReference Laboratories, Inc, Elmwood Park, NJ, US) for speciation and antibiotic sensitivity determination. When *S. aureus* was identified in the wound or nasal cultures, the purified subcultures were prepared by the commercial laboratory and sent to the

Laboratory of Microbiology and Infectious Diseases at The Rockefeller University. Molecular characterization of the *S. aureus* isolates that was performed at The Rockefeller University included: 1. s*pa* typing – based on the sequence of a polymorphic region of the *S. aureus*-specific staphylococcal protein A (*spa*). 2. Multi-locus Sequence Typing (MLST) — based on the sequences of seven housekeeping genes of *S. aureus.* 3. Pulsed-field Gel Electrophoresis (PFGE) —which identifies bacterial clones by partial digestion of their DNA and migration of the particular fragments generated on a gel by electrophoresis. 4. The Arginine Catabolic Mobile Element (ACME) and the Panton-Valentine Leukocidin (PVL), screens for two virulence genetic determinants strongly associated to CA-MRSA. All molecular techniques were performed as previously described [17–28].

Statistical Methods

Application of statistical methods assessed potential risk factors of CA-MRSA/MSSA infection in the studied population. First, a bivariate analysis using the Fishers exact test was carried out to assess differences between immigrants and native-born patients in their demographics, clinical covariates, and dermatologic characteristics of the infection. Odds Ratios (OR) for each demographic covariate as a potential risk factor, were estimated by the median unbiased estimator, and 95% exact confidence intervals (95% CIs) were computed. As a secondary analysis, two multivariate logistic regression analyses, including the set of demographic covariates as predictors, were fitted by iterative weighted least squares to CA-MRSA and CA-MSSA wound infections, respectively. From the logistic regression analysis, it was possible to re-estimate odds ratio and 95% CIs after adjusting for demographics covariates. No adjustments for multiple comparisons were made in this exploratory study.

RESULTS

Of the 174 patients who were approached to participate in the study, 129 (74.1%) were enrolled, with the consent rate ranging from 54% to 85% across the six sites. Enrollment across the six sites ranged from 2 to 50 participants. From the 129 patients who enrolled in the study, data on birthplace were collected from 117 patients. Of those whose birthplace was known, 40 (34.2%) were born outside of the USA, most in Latin-American countries (87.5%, Figure 2) and therefore, of Hispanic ethnicity (p-value 0.0058) (Table 1). Compared to USA-born patients, those who were foreign-born were more likely to be uninsured (p=0.0038) (Table 1).

Wound and nasal specimens from the patients were cultured, screened for *S. aureus* and tested for antibiotic sensitivity. The most common body sites for skin infections were: axilla (18.8%), buttocks (12.8%), head and neck (10.3%) and lower leg (10.3%) (Table 2). Foreign-born patients were more likely to have lesions located on the thigh than native-born patients (p=0.03), and more likely to have a wound characterized by draining pus (p=0.06) (Table 2). The most common type of SSTI was abscess (70.5%). Among the total study population, 41.6% of patients had methicillin-resistant *Staphylococcus aureus* (MRSA) in their wound culture, and 18.4% had methicillin-susceptible *S. aureus* (MSSA). MRSA was identified in 16.3% of nasal cultures, and MSSA was identified in 24.2% of nasal cultures

(Table 2). Nasal carriage of MRSA or MSSA was a highly significant risk factor for having the same type of *S. aureus* in the wound culture [29].

Molecular epidemiologic findings showed that among all *S. aureus* infection*s*, including both MRSA and MSSA strains, the USA300 clone (CC8/ACME+) was the most common genetic background, accounting for 88% of MRSA strains, and 39% of MSSA strains ($p<0.0001$). The second most common clone was USA1100 (CC30/ACME−), accounting for 5.1% of MRSA strains (wound and nasal isolates), and 19.5% of all MSSA strains ($p=0.25$).

Regarding antibiotic resistance, some strains were resistant to clindamycin (8 MRSA (13.8%), 10 MSSA (21.8%)), erythromycin (48 MRSA (82.7%, 19 MSSA (41.3%)), levofloxacin (27 MRSA 46.5%), 4 MSSA (8.7%)), tetracycline (4 MRSA (6.9%), 4 MSSA (8.7%)) and trimethoprim/sulfamethoxazole (1 MRSA (1.7%), 1 MSSA) (2.2%). No *S. aureus* isolates in this study were resistant to gentamycin, vancomycin, or linezolid. All 129 patients recovered clinically from their SSTIs. Those born outside of the USA were more likely to experience a first-time infection ($p=0.0005$) than native-born patients: the latter were more likely to experience a recurrent infection ($p=0.0631$) and to seek additional treatment for the same lesion ($p=0.02$) (Table 1). Foreign-born patients were less likely than native-born patients to receive an antibiotic prescription for the lesion ($p=0.10$) or to have taken antibiotics in the month prior to seeking treatment ($p=0.05$) (Table 1). Examining clinical and demographic risk factors, we did not find any co-morbidity related to having a MRSA positive wound culture. (Table 3).

When comparing the immigrant and native-born populations, both had similar rates of MRSA wound infections (44.6% in native-born, 36.5% in foreign-born, $p=0.56$). However, rates of MSSA wound cultures were significantly different between the two groups: 28.2% of foreign-born participants had MSSA in their wounds compared to 10.8% of native-born participants ($p=0.03$) Table 2). The two populations had similar rates of MSSA nasal carriage (21.9% in native-born, 28.2% in foreign-born, $p=0.49$).

Table 4 shows the parameter estimates from a logistic regression that assesses the multivariate association between the presence of CA-MRSA or CA-MSSA wound infection (75 positive individuals) and a set of potential risk factors from demographic covariates. By using the package lme4 in R software, a random intercept was included for each site accounting for heterogeneity and missing data could be handled properly under the mixed-effects model approach. Odds ratios derived from the coefficients estimates indicated higher odds for the USA/Hispanic group to show wound infection compared to USA/Non-Hispanic group ($p=0.011$). The other demographics (owner of insurance, education and income) showed no significant association with the presence of wound infection.

DISCUSSION

We observed significant differences in rates of MRSA and MSSA infection between participants who were born in the USA and those born outside of the USA. Furthermore, we noted that those born outside the USA were more likely to be uninsured, less likely to have

received prior treatment for the same lesion, and less likely to have received antibiotics or to have taken antibiotics in the past month. These differences may suggest variations in the patterns of medical care received, both in their country of origin as well as the USA, with lower frequency of antibiotic use among immigrants. This lower antibiotic exposure may have resulted in a protective benefit with a lower likelihood of MRSA infection and a higher likelihood of MSSA infection (Table 1).

The clonal distribution of *Staphylococcus aureus* has an important geographic correlation, but this is more evident among MRSA clones than among MSSA isolates, as described in previous studies [9, 29]. Some strains are pandemic, while other clones remain endemic in certain areas. For example, ST80 is mostly European, while ST59 is also called the 'Taiwan clone' because of its predominance in that country [5,30–32]. USA300 was first detected in the USA in 1999 among inmates in Mississippi [33], and it soon became endemic nationwide as the most common CA-MRSA clone. It is the primary cause of SSTIs among patients seen in primary care settings such as CHCs. The USA300 strain of CA-MRSA has also spread internationally, and is now being reported on all continents except Antarctica [2]. The strains identified from the patients enrolled in this study have been reported primarily in the United States, though they have also been identified in the countries of origin of the participants. In this study, USA300 was the most prevalent clone, accounting for more than 87% of all MRSA isolates; its MSSA variant, however, was identified among fewer than 40% of MSSA isolates. MRSA wound isolates in this study belonged to up to five different clonal complexes (CC8, CC30, CC5, ST72, CC88) while MSSA strains belonged to eight different clonal complexes (CC8, CC30, CC5, CC15, CC121, CC45, CC152, CC398) [29]. The small numbers of isolates belonging to each clone didn't allow us to analyze any association by country of birth. The one exception was that of a patient from Ghana, whose strain, ST398, has not been reported in Africa, suggesting acquisition may have occurred in the USA.

MSSA tends to be more clonally diverse than MRSA, and this seems to be conditioned by two factors: the lack of an antibiotic pressure and the longer time these clones have to spread before they are detected and treated. It is important to control the spread of the different MSSA clonal types between countries and continents, as MSSA may provide the genetic reservoir for the emergence of MRSA [29]. In our study, we found a significant association between MSSA infection and immigrant status (Table 3). The impact of travel and migration on MSSA and MRSA geographic variation will undoubtedly become more evident as surveillance networks capture these differences, such as the studies performed in the Caribbean by the Etienne-Tristan group from Lyon, France [34,35] and the Uhlemann-Lowy team from New York, US [34,35].

This analysis was exploratory in nature, and conducted as part of a pilot study in which a convenience sample was collected in busy urban practices serving large numbers of immigrants. No adjustments were made for multiple comparisons. Our study did not permit a precise determination whether the resistance patterns were imported or acquired in the USA by non USA-born participants. This was limited, in part, by insufficient data regarding length of time in the USA, and thus by the heterogeneity of the non-USA born group. The results of this study are insufficient to determine whether the bacteria came from the

patients' countries of origin or whether they acquired in the USA. Detailed demographic data, however, permitted a stronger characterization of the differences between the USA-born and non-USA born groups. Furthermore, we were unable to evaluate in any detail the possibility of differential selection bias, or the impact of the well-recognized "healthy immigrants effect," where mostly healthy individuals are both more likely to emigrate, and less likely to have received prior antibiotics to treat infections [36]. Future studies should examine the prevalence and distribution of MRSA/MSSA strains in both their home countries and in the USA.

CONCLUSIONS

While MRSA was similarly distributed among patients regardless of their origin, MSSA strains were more prevalent among subpopulations from other countries.

MSSA infections involving SSTIs, because they involve organisms broadly sensitive to antibiotics, are likely to be more responsive to recommended treatment [36]. The variability among MSSA strains, however, is wider than among MRSA clones, this may complicate the epidemiological control of *S. aureus* infections.

The challenge of treating *S. aureus* infections, given the threat of emerging multi-resistance, makes the analysis of antimicrobial susceptibilities and the study of the genetic determinants of resistance paramount to appropriate care, and to a better epidemiologic understanding.

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Manhattan's Physician Group 125th Street, New York, NY

Open Door Family Health Center, Ossining, NY

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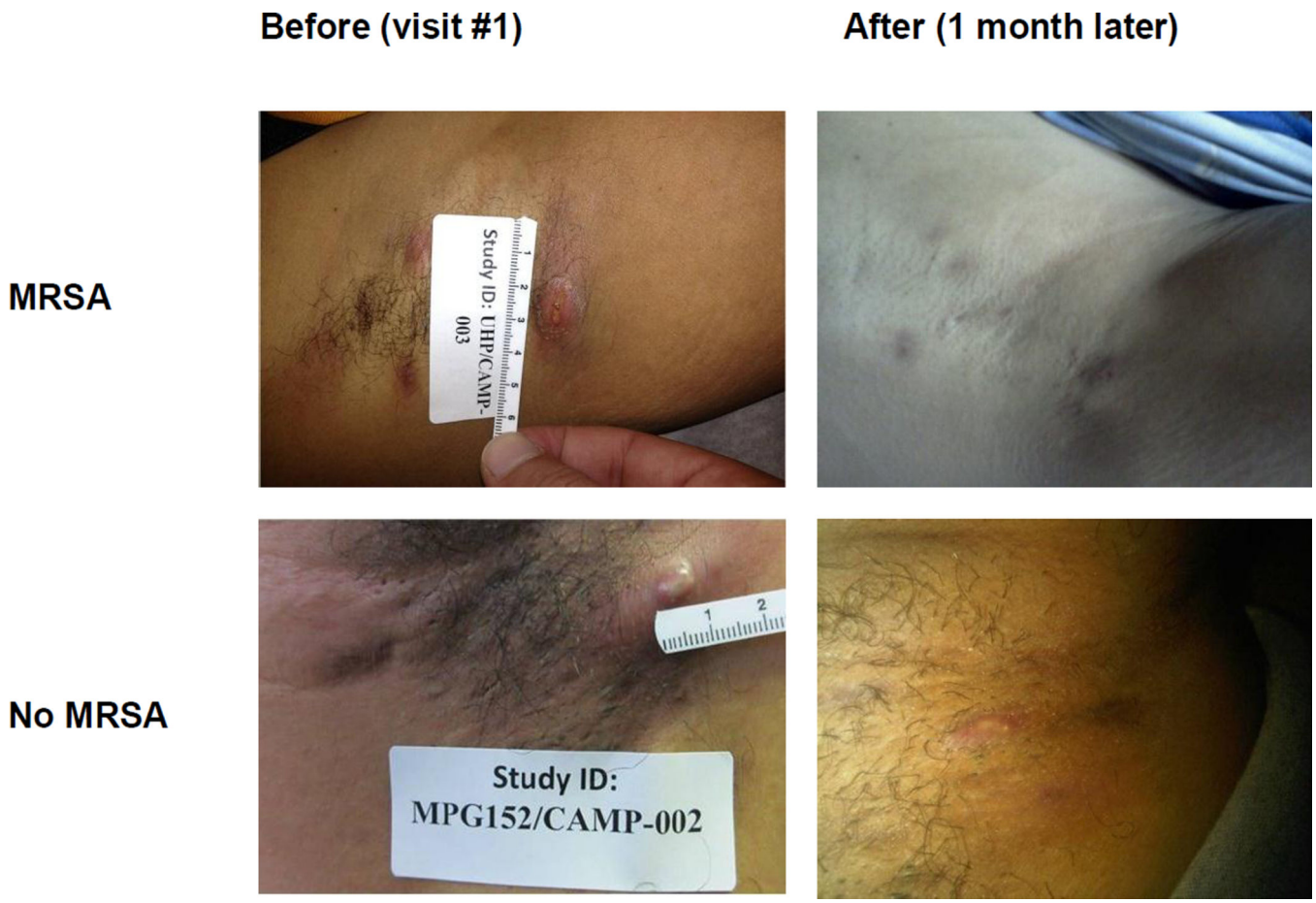

Figure 1. Examples of Lesions from Digital Library
Both lesions pictured above were located on the axilla.

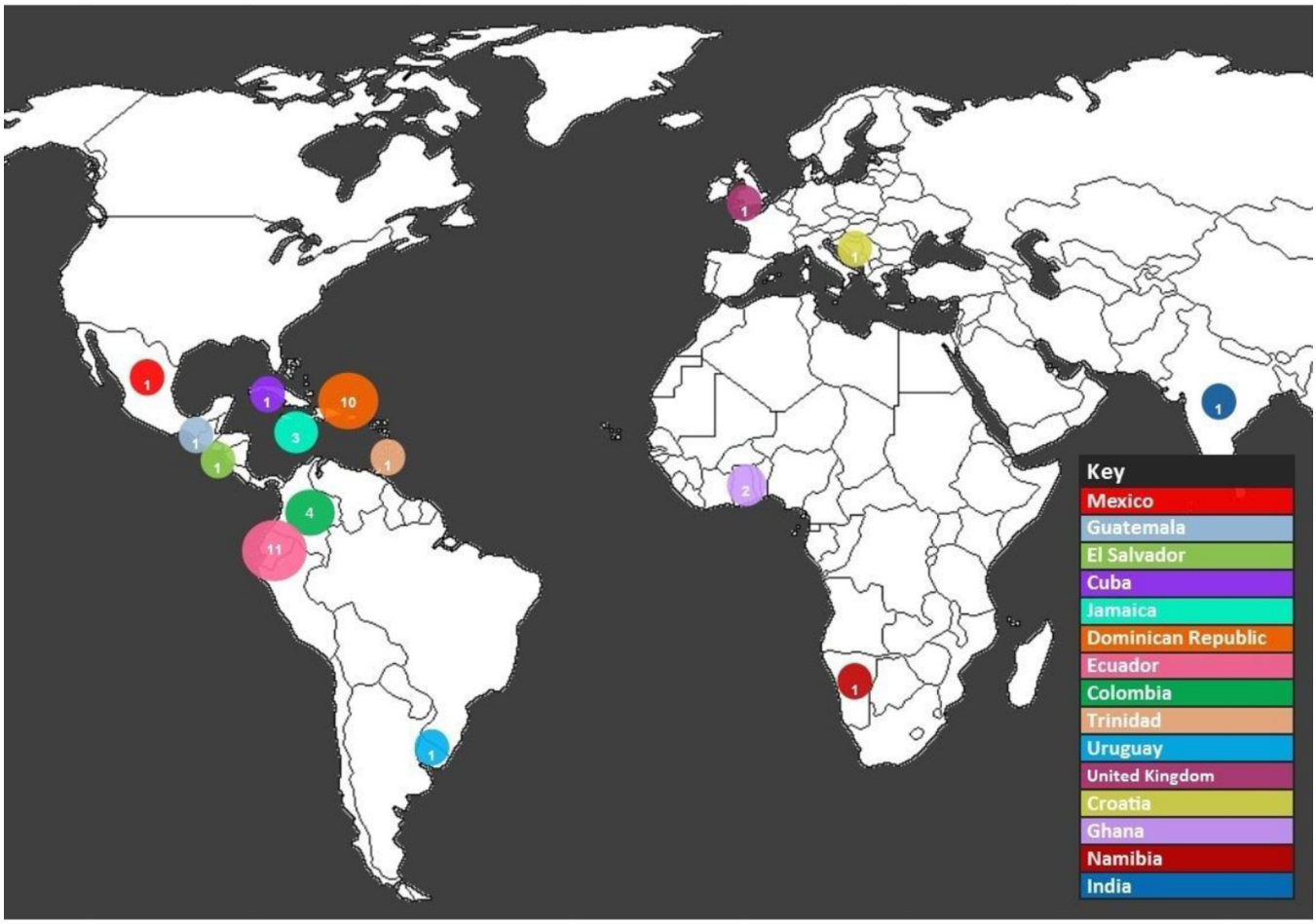

Figure 2. Country of Origin for Non-USA Born Participants (n=40)

Dots mark the geographic location of the countries of origin of foreign-born patients in the study: Different colors mark different countries and both the size of dots and the number inside the dots correlate with the number of patients from each country. Mexico, Central and South America, and the Caribbean were categorized as Latin America.

Table 1

Demographic and Clinical Covariates by Place of Birth

	Non-USA Born		USA Born		Total**		p-value
Demographic Covariates	**40**	**% (row)**	**77**	**%(row)**	**117**	**%(row)**	
Sex							
Female	17	42.5%	42	54.5%	59	50.4%	0.2459
Male	23	57.5%	35	45.5%	58	49.6%	
Age							
Under 18	1	2.5%	6	7.8%	7	6.0%	0.2797
19–40	16	40.0%	41	53.2%	57	48.7%	
41–64	20	50.0%	26	33.8%	46	39.3%	
Over 65	3	7.5%	4	5.2%	7	6.0%	
Ethnicity							
Hispanic	28	70.0%	31	40.3%	59	50.4%	0.0058
Not Hispanic	12	30.0%	44	57.1%	56	47.9%	
NR	0	0.0%	2	2.6%	2	1.7%	
Region of Origin (if Foreign Born)			–				
North/Central America	3	7.5%	–				
Caribbean	15	37.5%	–				
South America	16	40.0%	–				
Europe	2	5.0%	–				
Africa	3	7.5%	–				
Asia	1	2.5%	–				
Income			–				
Less than $10,000	10	25.0%	36	46.8%	46	39.3%	0.1854
More than $10,000	19	47.5%	35	45.5%	54	46.2%	

	Non-USA Born		USA Born		Total**		p-value
Demographic Covariates	**40**	**% (row)**	**77**	**%(row)**	**117**	**%(row)**	
NR	11	27.5%	6	7.8%	17	14.5%	
Education Level			–				
Below High School	24	60.0%	57	74.0%	81	69.2%	0.8102
High School or over	9	22.5%	18	23.4%	27	23.1%	
NR	7	17.5%	2	2.6%	9	7.7%	
Insurance							
None	15	37.5%	10	13.0%	25	21.4%	0.0176
Medicaid	14	35.0%	30	39.0%	44	37.6%	
Medicare	1	2.5%	6	7.8%	7	6.0%	
Private or Other	10	25.0%	31	40.3%	41	35.0%	
Clinical Covariates							
BMI							
Underweight (<18.5)	2	5.0%	2	2.6%	4	3.4%	0.4392
Normal weight (18.6–24.9)	8	20.0%	14	18.2%	22	18.8%	
Overweight (25–29.9)	12	30.0%	24	31.2%	36	30.8%	
Obese (<30)	9	22.5%	31	40.3%	40	34.2%	
NR	9	22.5%	6	7.8%	15	12.8%	
Medical History *							
First time infection	31	77.5%	41	53.2%	72	61.5%	0.0157
Recurrent infection	7	17.5%	32	41.6%	39	33.3%	0.0125
Prior Treatment for the Same Lesion	5	12.5%	27	35.1%	32	27.4%	0.0093
Family/Friends with Same Lesion	12	30.0%	17	22.1%	29	24.8%	0.3727
Had Lesion While in School	3	7.5%	10	13.0%	13	11.1%	0.5382
Had Lesion While Working	5	12.5%	18	23.4%	23	19.7%	0.2212

	Non-USA Born		USA Born		Total**		p-value
Demographic Covariates	**40**	**% (row)**	**77**	**%(row)**	**117**	**%(row)**	
Antibiotics *							
Receive Prescription	30	75.0%	73	94.8%	103	88.0%	0.0047
Taken Antibiotics Last Month	22	55.0%	63	81.8%	85	72.6%	0.0040
Co-morbidities *							
Influenza	6	15.0%	7	9.1%	13	11.1%	0.3631
Drug Use (Marijuana or Cocaine)	3	7.5%	12	15.6%	15	12.8%	0.2576

*Non-mutually exclusive responses

**12 Non-responses in immigrant status

NR: Non-response

Table 2

Dermatologic and Clinical Characteristics by Place of Birth

	Non-USA Born		USA Born		total **		p-value
Dermatologic Characteristics	**40**	**% (row)**	**77**	**% (row)**	**117**	**% (row)**	
Wound *							
MRSA+	15	37.5%	33	42.9%	48	41.0%	0.6925
MSSA+	11	27.5%	8	10.4%	19	16.2%	0.0320
Nasal *							
MRSA+	4	10.0%	15	19.5%	19	16.2%	0.2903
MSSA+	11	27.5%	16	20.8%	27	23.1%	0.4892
Lesion Location *							
Axilla	6	15.0%	16	20.8%	22	18.8%	0.6187
Buttock	3	7.5%	12	15.6%	15	12.8%	0.2577
Head/Neck	3	7.5%	9	11.7%	12	10.3%	0.7491
Lower Leg	5	12.5%	7	9.1%	12	10.3%	0.5411
Chest/Abdomen	4	10.0%	7	9.1%	11	9.4%	1.0000
Thigh	7	17.5%	3	3.9%	10	8.5%	0.0304
Back	3	7.5%	5	6.5%	8	6.8%	1.0000
Hand/Finger	0	0.0%	8	10.4%	8	6.8%	0.0495
Arm	4	10.0%	3	3.9%	7	6.0%	0.2284
Groin	2	5.0%	5	6.5%	7	6.0%	1.0000
Foot/Ankle	3	7.5%	2	2.6%	5	4.3%	0.3364
Lesion Region *							
Lower Limbs	20	50.0%	29	37.7%	49	41.9%	0.2378
Upper Limbs	10	25.0%	27	35.1%	37	31.6%	0.3009

	Non-USA Born		USA Born		total **		p-value
Dermatologic Characteristics	**40**	**% (row)**	**77**	**% (row)**	**117**	**% (row)**	
Torso	7	17.5%	12	15.6%	19	16.2%	0.7963
Head/Neck	3	7.5%	9	11.7%	12	10.3%	0.7491
Lesion Type*							
Abscess	29	72.5%	52	67.5%	81	69.2%	0.6753
Boil/Furuncle	6	15.0%	13	16.9%	19	16.2%	1.0000
Cellulitis	4	10.0%	13	16.9%	17	14.5%	0.4123
Folliculitis	3	7.5%	10	13.0%	13	11.1%	0.5382
Carbuncle	2	5.0%	3	3.9%	5	4.3%	1.0000
Size							
0–5 cm	23	57.5%	54	70.1%	77	65.8%	0.2033
5–10 cm	4	10.0%	6	7.8%	10	8.5%	
10–15 cm	0	0.0%	1	1.3%	1	0.9%	
Over 15 cm	3	7.5%	1	1.3%	4	3.4%	
NR	10	25.0%	15	19.5%	25	21.4%	
Signs/Symptoms*							
Redness	33	82.5%	62	80.5%	95	81.2%	1.0000
Swelling	38	95.0%	69	89.6%	107	91.5%	0.4907
Warmth	19	47.5%	35	45.5%	54	46.2%	0.8475
Pain/Tenderness	33	82.5%	71	92.2%	104	88.9%	0.1298
Complaint of “spider bite”	2	5.0%	1	1.3%	3	2.6%	0.2689
Purulence*							
Fluctuance	25	62.5%	51	66.2%	76	65.0%	0.6887
Yellow/white center	16	40.0%	34	44.2%	50	42.7%	0.6979
Central point or head	15	37.5%	30	39.0%	45	38.5%	1.0000

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	Non-USA Born		USA Born		total**		p-value
Dermatologic Characteristics	**40**	**% (row)**	**77**	**% (row)**	**117**	**% (row)**	
Draining pus	18	45.0%	20	26.0%	38	32.5%	0.0601
Possible to aspirate with needle and syringe	2	5.0%	4	5.2%	6	5.1%	1.0000

*Non-mutually exclusive responses

**12 Non-responses in immigrant status

NR: Non-response

Table 3

MRSA/MSSA Correlates

Demographic and Clinical Covariates	Total	% (row)	MRSA+	% (row)	MSSA+	%(row MSSA+ (23)	MRSA+ OR (95%CI)	MSSA+ OR (95%CI)
	129		**52**		**23**			
BIRTHPLACE/ETHNICITY								
Non-USA/Hispanic	28	21.7%	11	21.2%	8	34.8%	1.160 (0.433,3.109)	4.105 (1.097,15.361)
USA/Hispanic	31	24.0%	17	32.7%	4	17.4%	2.391 (0.912,6.266)	1.560 (0.357,6.812)
Non-USA/Non-Hispanic	12	9.3%	4	7.7%	3	13.0%	0.844 (0.219,3.255)	3.250 (0.616,17.147)
USA/Non-Hispanic (Ref.)	44	34.1%	16	30.8%	4	17.4%	-	-
NR	14	10.9%	4	7.7%	4	17.4%		
BIRTHPLACE								
Non-USA	40	31.0%	15	28.8%	11.00	47.8%	0.777 (0.351,1.713)	3.241 (1.178,8.919)
USA (Ref.)	77	59.7%	33	63.5%	8.00	34.8%	-	-
NR	12	9.3%	4	7.7%	4	17.4%		
ETHNICITY								
Hispanic or Latino	68	52.7%	32	61.5%	14.00	60.9%	1.745 (0.840,3.628)	1.647 (0.635,4.275)
Not Hispanic or (Ref.)	57	44.2%	20	38.5%	8.00	34.8%	-	-
NR	4	3.1%	0	0.0%	1	4.3%		
EDUCATION								
Below high school	28	21.7%	16	30.8%	3.00	13.0%	2.022 (0.843,4.850)	0.600 (0.158,2.286)
High school or over (Ref.)	81	62.8%	31	59.6%	13.00	56.5%	-	-
NR	20	15.5%	5	9.6%	7	30.4%		

Demographic and Clinical Covariates	Total	% (row)	MRSA+	% (row)	MSSA+	%(row MSSA+ (23)	MRSA+ OR (95%CI)	MSSA+ OR (95%CI)
	129		52		23			
INCOME								
Less than $10,000/year	47	36.4%	22	42.3%	5	21.7%	1.304 (0.584,2.911)	0.525 (0.165,1.671)
Over $10,000/year (Ref.)	54	41.9%	22	42.3%	10	43.5%	-	-
NR	28	21.7%	8	15.4%	8	34.8%		
INSURANCE								
None	26	20.2%	9	17.3%	6	26.1%	0.818 (0.303,2.208)	1.4 (0.442,4.434)
Medicaid	44	34.1%	16	30.8%	7	30.4%	0.808 (0.353,1.849)	0.817 (0.282,2.365)
Medicare	6	4.7%	5	9.6%	0	0.0%	6.818182 (0.743,62.551)	- -
Private or Other (Ref.)	53	41.1%	22	42.3%	10	43.5%	-	-
ANTIBIOTICS PRESCRIPTION RECEIVED								
No	8	6.2%	3	5.8%	2	8.7%	0.764 (0.173,3.371)	1.889 (0.348,10.255)
Yes (Ref.)	104	80.6%	44	84.6%	15	65.2%		
NR	17	13.2%	5	9.6%	6	26.1%		
ANTIBIOTICS TAKEN IN THE LAST MONTH								
No	25	19.4%	10	19.2%	6	26.1%	0.852 (0.342,2.119)	2.038 (0.668,6.223)
Yes (Ref.)	86	66.7%	36	69.2%	11	47.8%		
NR	18	14.0%	6	11.5%	6	26.1%		
INFLUENZA								
No	97	75.2%	40	76.9%	15	65.2%	1.575 0.491,5.047)	0.439 (0.053,3.632)

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Demographic and Clinical Covariates	Total	% (row)	MRSA+	% (row)	MSSA+	% (row	MRSA+ OR (95%CI)	MSSA+ OR (95%CI)
	129		52		23	MSSA+ (23)		
Yes (Ref.)	13	10.1%	7	13.5%	1	4.3%		
NR	19	14.7%	5	9.6%	7	30.4%		
OTHER DRUG (MARIJUANA OR COCAINE)								
No	96	74.4%	39	75.0%	15	65.2%	1.88 (0.604,5.851)	0.878 (0.178,4.328)
Yes (Ref.)	15	11.6%	8	15.4%	2	8.7%		
NR	18	0.14	5	0.10	6	0.26		

NR: Non-response

Table 4

Multiple Logistic Regression for Wound Infection (MRSA or MSSA)

	Estimate	Std.Error	Z value	P-value	Odds.Ratio	Odds.Ratio(Lower 95% C.I.)	Odds.Ratio(Upper 95% C.I)
(Intercept)	−0.200	0.397	−0.504	0.614			
Non-USA/Hispanic+	1.033	0.640	1.614	0.107	2.809	0.781	10.102
USA/Hispanic+	1.464	0.576	2.540	0.011	4.324	1.365	13.693
Non-USA/Not Hispanic+	0.393	0.803	0.489	0.625	1.481	0.297	7.373
Below High School*	0.916	0.601	1.524	0.127	2.500	0.751	8.315
Non-insured**	0.205	0.630	0.325	0.745	1.227	0.348	4.321
Less than U$10,000***	−0.479	0.506	−0.947	0.344	0.619	0.225	1.704

Ref.Categories	
USA/Not Hispanic	+
Above High School	*
Insured (Medicaid, Medicare, Private or Other)	**
More than U$10,000	***

obs: A Random intercept was estimated for each Site