

# Dissemination of Methicillin-Resistant *Staphylococcus aureus* USA300 Sequence Type 8 Lineage in Latin America

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**Background.** Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important nosocomial and community-associated (CA) pathogen. Recently, a variant of the MRSA USA300 clone emerged and disseminated in South America, causing important clinical problems.

**Methods.** *S. aureus* isolates were prospectively collected (2006–2008) from 32 tertiary hospitals in Colombia, Ecuador, Peru, and Venezuela. MRSA isolates were subjected to antimicrobial susceptibility testing and pulsed-field gel electrophoresis and were categorized as health care–associated (HA)–like or CA-like clones on the basis of genotypic characteristics and detection of genes encoding Panton-Valentine leukocidin and staphylococcal cassette chromosome (SCC) mec IV. In addition, multilocus sequence typing of representative isolates of each major CA-MRSA pulsotype was performed, and the presence of USA300-associated toxins and the *arcA* gene was investigated for all isolates categorized as CA-MRSA.

**Results.** A total of 1570 *S. aureus* were included; 651 were MRSA (41%)—with the highest rate of MRSA isolation in Peru (62%) and the lowest in Venezuela (26%)—and 71%, 27%, and 2% were classified as HA-like, CA-like, and non-CA/HA-like clones, respectively. Only 9 MRSA isolates were confirmed to have reduced susceptibility to glycopeptides (glycopeptide-intermediate *S. aureus* phenotype). The most common pulsotype (designated ComA) among the CA-like MRSA strains was found in 96% of isolates, with the majority (81%) having a ≤6-band difference with the USA300–0114 strain. Representative isolates of this clone were sequence type 8; however, unlike the USA300–0114 strain, they harbored a different SCCmec IV subtype and lacked *arcA* (an indicator of the arginine catabolic mobile element).

**Conclusion.** A variant CA-MRSA USA300 clone has become established in South America and, in some countries, is endemic in hospital settings.

Methicillin-resistant *Staphylococcus aureus* (MRSA) has been recognized as a major cause of infections world-

wide. Although initially recognized as an important nosocomial pathogen, MRSA is now endemic in the community outside hospitals [1]. Community-associated MRSA (CA-MRSA) infections are caused by highly virulent strains of *S. aureus*, which can affect healthy individuals [2]; most worrisome, CA-MRSA strains have been increasingly reported as an important cause of nosocomial infections, indicating that they may become endemic in hospital settings [3]. Another important issue related to the treatment of MRSA infections is the emergence of resistance to vancomycin [4] and the observation that the effectiveness of vancomycin for the treatment of severe infections may be compromised [5].

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Diverse molecular typing tools have established that the worldwide dissemination of MRSA is mainly due to a few successful clones [6] with a rather specific geographical pattern [7]. Health care-associated MRSA (HA-MRSA) clones detected in South America have typically belonged to 2 major genotypes: (1) the Brazilian sequence type (ST) 239, staphylococcal cassette chromosome (SCC) mec III (MRSA-ST239-III) [8, 9], and (2) the Chilean clone (MRSA-ST5-I) [8–12]. The later appears to have replaced the Brazilian clone on the continent. Regarding CA-MRSA, 2 major clones also have been identified in South America: (1) MRSA-ST30-IV, which is mainly present in the southern part of the continent [13, 14], and (2) MRSA-ST8-IV (and its single-locus variant [SLV], MRSA-ST923-IV), which is genetically related to MRSA USA300 and was recently reported for the first time as the predominant and exclusive genetic lineage in Colombia [15]. In the present work, we report the results of the first prospective multicenter study of the molecular epidemiology of MRSA recovered from 4 Latin American countries during 2006–2008.

## METHODS

**Study design.** The participating centers included 32 high-level care hospitals, which were distributed as follows: 22 hospitals in Colombia (located in 6 cities), 5 hospitals in Ecuador (located in 1 city), 3 hospitals in Peru (located in 1 city), and 2 hospitals in Venezuela (located in 1 city). The *S. aureus* isolates included in the present study were collected prospectively from individual patients (repeated isolates from the same patient were excluded). Each hospital collected 50–150 consecutive isolates, which were recovered from January 2006 through January 2008 according to a specific protocol that was monitored by the local coordinator in each country. Clinical specimens included blood, cerebrospinal fluid, urine, secretions from complicated skin and soft-tissue infections (SSTIs) and from post-surgical wound infections (after clinical evaluation), pleural fluid, bronchoalveolar lavage fluid, pericardial collection, intraabdominal or intracerebral abscess, bone tissue from suspected osteomyelitis, arthritis aspirates (in the setting of septic arthritis), and peritoneal fluid (in the setting of peritonitis, including that associated with peritoneal dialysis). Isolates recovered from catheters and sputum and those labeled as being recovered from skin without clinical justification were excluded. The organisms were identified in the local hospital and, once included in the protocol, were sent to the reference laboratory (Bogota, Colombia) in transport medium (BBL Amies with Charcoal; Becton Dickinson). On arrival, the isolates were re-identified (see below) and preserved in soy trypticase broth with 10% glycerol at  $-70^{\circ}\text{C}$ .

**Bacterial isolates and antimicrobial susceptibility testing.** Identification of all *S. aureus* isolates was confirmed at the species level by a multiplex polymerase chain reaction (PCR)

assay [16]. The antimicrobial susceptibility profiles of all isolates were determined by the agar dilution method, in accordance with the Clinical Laboratory Standards Institute (CLSI) guidelines [17]. Screening for reduced susceptibility to vancomycin was performed on all MRSA isolates, in accordance with the CLSI guidelines [17]. In addition, all MRSA isolates with a vancomycin minimum inhibitory concentration (MIC) of 1 or 2  $\mu\text{g}/\text{mL}$  were further screened by 2 additional agar methods (Mueller-Hinton agar supplemented with 5  $\mu\text{g}/\text{mL}$  teicoplanin, and brain-heart infusion agar supplemented with 4  $\mu\text{g}/\text{mL}$  vancomycin), as described elsewhere [18, 19]. MRSA isolates that were positive by at least 1 of the screening tests were additionally tested by the Etest macromethod [20]; subsequently, isolates identified as positive by the Etest were further evaluated by the new Etest glycopeptide-resistance detection strip (vancomycin, 32–0.5  $\mu\text{g}/\text{mL}$ ; teicoplanin, 32–0.5  $\mu\text{g}/\text{mL}$ ; AB bioMérieux) [21]. The following reference organisms were used as controls for susceptibility testing and for the evaluation of low-level glycopeptide resistance (glycopeptide-intermediate *S. aureus* [GISA]) and heterogeneous glycopeptide resistance (heterogeneous GISA [hGISA]): *S. aureus* ATCC 29213, ATCC 700698 (Mu3; hGISA), and ATCC 700699 (Mu50; GISA).

**Molecular typing and detection of genes associated with virulence.** The SCCmec types (I–IV) and subtypes were evaluated for all MRSA isolates by multiplex PCR, using assays that have been reported elsewhere [22–24]. The MRSA strains USA300–0114 (SCCmec type IVa), USA300 (SCCmec type IVb), MR108 (SCCmec type IVc) [25], JCSC4469 (SCCmec type IVd) [23], and HAR22 (SCCmec IVh) [24] were used as controls for the PCR assays. Pulsed-field gel electrophoresis (PFGE) was performed on all MRSA isolates, using a method that has been described elsewhere with some modifications [26]. Banding patterns were interpreted according to standard criteria [27]. *S. aureus* NCTC8325 was used as a molecular-size control, and representatives of MRSA strains belonging to the Chilean, Brazilian, and pediatric clones [12]; MRSA NRS 382 (New York/Japan clone); NRS 123 (MRSA USA400); USA300–0114; and USA300 (carrying the SCCmec IVb) were used as controls for comparisons of PFGE banding patterns. Multilocus sequence typing (MLST) [28] was performed with representative isolates of each PFGE type, and the presence of 6 CA-MRSA virulence-associated genes (*lukS-PV*, *lukF-PV*, *arcA*, *sek*, *seq*, and *bsaA*) previously reported in the USA300 (ST8) strain was investigated in all CA-MRSA isolates, using PCR assays and primers that have been described elsewhere [29, 30]. The USA300–0114 strain was used as a positive control for the PCR amplifications.

## RESULTS

**Phenotypic characteristics of MRSA in Latin American hospitals.** A total of 1890 consecutive *S. aureus* isolates were

collected from 32 hospitals in 4 countries. Overall, 320 isolates were not included in the study because of protocol violations, which most frequently were the result of contamination, isolates being from the same patient, a source not being included in the protocol, or misidentification. Of the included isolates (1570 in total), Colombian hospitals contributed 707 (45%); Ecuador, 309 (20%); Peru, 287 (18%); and Venezuela, 267 (17%). Blood, secretions from surgical wounds, and complicated SSTIs were the most common sources of *S. aureus* isolates, accounting for 27%, 26%, and 8%, respectively.

Methicillin resistance in *S. aureus* was found in 41% of isolates, with geographic variations (Peru, 62%; Colombia, 45%; Ecuador, 28%; Venezuela, 26%). Table 1 shows the percentage of resistance to each class of antibiotic in the region and by country among *S. aureus* isolates and among the subset of MRSA isolates. Overall, MRSA isolates demonstrated high rates of resistance to erythromycin (75%), clindamycin (72%), ciprofloxacin (72%), and gentamicin (69%). The lowest rates of resistance were found to trimethoprim-sulfamethoxazole (5%), rifampin (5%), and minocycline (1%). All isolates were susceptible to linezolid and vancomycin (MIC<sub>90</sub> [value for which 90% of isolates are susceptible], 1 µg/mL; MIC range, 0.5–2 µg/mL) by the agar dilution method. Of 651 MRSA isolates evaluated, only 9 (6 from Peru, 2 from Colombia, and 1 from Ecuador) were found to be GISA after the screening and confirmatory methods were used.

#### HA-MRSA versus CA-MRSA in the Andean region.

To differentiate the South American MRSA isolates with a typical HA pulsotype (HA-like) from those with a CA type (CA-like), the PFGE banding pattern of all isolates was compared with that of representative isolates of the most common HA clones previously described in South America (eg, Chilean, Bra-

zilian, pediatric, and New York/Japan). Isolates that were not genetically related to any of these clones (>6-band difference) were tested for the presence of *lukF-lukS* genes (encoding Panton-Valentine leukocidin [PVL]) and SCCmec IV; organisms that yielded a positive result for both were designated as CA-like strains, and their PFGE patterns were compared with those of representatives of the USA300–0114 strain (SCCmec IVa), a USA300 strain carrying the SCCmec cassette IVb, and a representative of USA400 (NRS 123). On the basis of these genotypic criteria, 3 groups of isolates were clearly identified: (1) 461 isolates (71%) were categorized as having a HA-like MRSA type; (2) 174 isolates (27%) were likely to be CA-MRSA (CA-like MRSA); and (3) 16 isolates (2%) showed patterns that were not related to the circulating HA or CA clones previously characterized in the region and lacked the genes encoding PVL. All MRSA isolates recovered in Peru had genotypic characteristics (see below) of HA-like MRSA, and we were unable to identify any isolate with a CA-like profile. Conversely, 74% of MRSA isolates submitted from Ecuadorian centers had a CA-like genotype. In Venezuela and Colombia, 14% and 31% of MRSA isolates recovered in hospitals had characteristics that were compatible with CA-like MRSA, respectively (Table 2).

HA-like MRSA isolates were mostly recovered from blood (30%), and PFGE analysis revealed that the majority (92%) were clonally related to a major PFGE pulsotype (designated pulsotype A in this work) that is related to the pattern previously observed for the Chilean clone, which harbors SCCmec type I and belongs to ST5 by MLST. SCCmec typing of 23 representative isolates of this clone recovered in different countries confirmed the presence of SCCmec I, and MLST of a representative isolate yielded ST5, confirming the genetic relatedness with the Chilean clone. In addition, minor pulsotypes

**Table 1. Phenotypic Characteristics of *Staphylococcus aureus* in the Andean Region of South America**

Organism, country (no. of isolates)	No. (%) of resistant isolates									
	OXA	ERY	CLI	CIP	GEN	CHL	RIF	TET	MIN	SXT
<i>S. aureus</i> (n = 1570)										
Colombia (n = 707)	318 (45)	288 (41)	227 (32)	240 (34)	225 (32)	5 (1)	11 (1)	147 (21)	1 (0.1)	5 (1)
Peru (n = 287)	177 (62)	200 (70)	178 (62)	180 (63)	189 (66)	69 (24)	11(4)	34 (12)	7 (2)	17 (6)
Ecuador (n = 309)	87 (28)	61 (20)	20 (6)	32 (10)	37 (12)	7 (2)	15 (5)	75 (24)	1 (0.3)	16 (5)
Venezuela (n = 267)	69 (26)	98 (37)	54 (20)	66 (25)	52 (19)	0 (0)	11 (4)	50 (19)	0 (0)	3 (1)
Total	651 (41)	647 (41)	479 (30)	518 (33)	503 (32)	81 (5)	48 (3)	306(19)	8 (0.5)	41(3)
MRSA (n = 651)										
Colombia (n = 318)	...	227 (71)	221 (69)	217 (68)	204 (64)	3 (1)	9 (3)	58 (18)	0 (0)	2 (1)
Peru (n = 177)	...	175 (99)	174 (98)	176 (99)	171 (97)	62 (35)	10 (6)	23 (13)	7 (4)	16 (9)
Ecuador (n = 87)	...	27 (31)	18 (21)	25 (29)	23 (26)	6 (7)	12 (14)	39 (45)	1 (1)	16 (18)
Venezuela (n = 69)	...	60 (87)	53 (77)	53 (77)	49 (71)	0 (0)	5 (7)	6 (9)	0 (0)	1 (1)
Total	...	489 (75)	466 (72)	471 (72)	447 (69)	71 (11)	36 (5)	126 (19)	8 (1)	35 (5)

**NOTE.** CIP, ciprofloxacin; CHL, chloramphenicol; CLI, clindamycin; ERY, erythromycin; GEN, gentamicin; MIN, minocycline; MRSA, methicillin-resistant *S. aureus*; OXA, oxacillin; RIF, rifampin; TET, tetracycline; SXT, trimethoprim-sulfamethoxazole.

**Table 2. Distribution of Health Care–Associated (HA)–Like and Community–Associated (CA)–Like Methicillin–Resistant *Staphylococcus aureus* (MRSA) Pulsotypes in the Andean Region of South America**

Country	% (no.)		
	HA-like	CA-like	Non–HA/CA-like
Colombia	68 (216)	31 (100)	1 (2)
Peru	97 (171)	0 (0)	3 (6)
Ecuador	24 (21)	74 (64)	2 (2)
Venezuela	77 (53)	14 (10)	9 (6)
Total	71 (461)	27 (174)	2 (16)

were identified. Pulsotype B, which corresponds to the Brazilian clone, was detected in 20 isolates (4%), was the predominant HA-like clone found in Ecuadorian hospitals (62%), and was identified in 4% of the HA-like MRSA isolates from Peru. Of isolates belonging to the Brazilian clone ( $n = 20$ ), 90% harbored the SCCmec type III and were resistant to trimethoprim-sulfamethoxazole, whereas 10% harbored the SCCmec I and were susceptible to trimethoprim-sulfamethoxazole. Pulsotype C, which corresponds to the New York/Japan clone, was detected in 18 isolates (4%). Most (72%) of the pulsotype C isolates were associated with SCCmec type II, and the remaining isolates carried the SCCmec type IV.

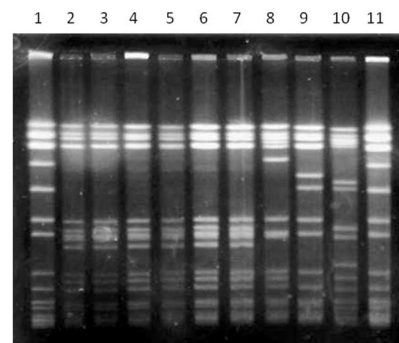
Among the CA-like MRSA group (174 isolates), secretions from SSTIs, surgical wound infections, and blood were the most common sources, accounting for 26%, 25% and 18%, respectively; we were able to identify 4 pulsotypes among these 174 CA-MRSA isolates. The major pulsotype (designated ComA) (Figure 1) was detected in 167 isolates (96%) (Table 3) and was the most common type in the 4 countries of the region, being found in 100%, 98%, and 50% of the CA-like MRSA isolates from Ecuador, Colombia, and Venezuela, respectively. The majority (81%) of CA-like MRSA isolates corresponding to the ComA pulsotype were clonally related ( $\leq 6$ -band difference) to the USA300 MRSA-ST8-IV epidemic strain, and representative isolates were shown to belong to ST8. However, unlike the USA300–0114 strain, the vast majority of these isolates (158 of 167) carried a SCCmec subtype other than IVa; when a different set of primers for SCCmec typing [24] was used that included primers specific for the J1 region, a band corresponding to subtypes IVc and IVE was found in the majority of these isolates (93%), suggesting that a different SCCmec IV variant was present in CA-MRSA from South America. The subtype IVa, typical of USA300–0114, was detected in only 9 isolates (5%), and we were unable to determine a subtype (1%) in 2 isolates. MLST of representative isolates from the pulsotype ComA confirmed that they belonged to ST8 (Table 3), and we detected *bsaA*, *sek*, and *seq* in 99%, 95%, and 91% of these isolates, respectively. Conversely, the majority of CA-like MRSA from the ComA clone lacked the *arcA* gene

(only present in 4% of the isolates), which is an indicator of the presence of the arginine catabolic mobile element (ACME) typical of the USA300–0114 strain. An important characteristic of these CA-like MRSA isolates was the observed high rate of resistance to tetracycline (41%) but not to minocycline, typical of the *tet(K)* determinant. Rates of resistance to erythromycin (10%), clindamycin (4%), ciprofloxacin (5%), gentamicin (2%), trimethoprim-sulfamethoxazole (4%), chloramphenicol (1%), and rifampin (1%) were low. Of note, the highest rates of resistance to antibiotics were found in CA-like MRSA isolates from Ecuador (Table 3). Four minor pulsotypes that differed from the patterns of USA300 MRSA-ST8-IV isolates by  $\geq 7$  bands were found among the rest of the isolates exhibiting CA-like characteristics; these were designated ComB (ST6), ComC (SLV of ST5), ComD (ST22), and ComE (ST923), which had been described previously only in Colombia [15].

Among the remaining 16 isolates, whose PFGE pattern was unrelated to the HA or CA pattern and which lacked the gene encoding PVL, we identified 12 pulsotypes (designated DifA to DifL). Among these isolates, high rates of resistance to quinolones (69%), erythromycin (62%), clindamycin (50%), and gentamicin (62%) were observed, and SCCmec types III and IV were found in most.

## DISCUSSION

The present multicenter study evaluated prospectively and systematically the phenotypic characteristics and population genetics of MRSA in 4 Latin American countries of the Andean region. The protocol was designed to include patient isolates consecutively submitted to the clinical laboratory in each hospital under specific guidelines and clinical criteria for collection



**Figure 1.** Pulsed-field gel electrophoresis of community-associated–like methicillin-resistant *Staphylococcus aureus* isolates representative of the ComA pulsotype from different countries. Lane 1, *S. aureus* NCTC 8325; lane 2, Col-177 (Colombia); lane 3, HUV-01 (Colombia); lane 4, CA-12 (Colombia); lane 5, C609 (Colombia); lane 6, V2125 (Venezuela); lane 7, E403 (Ecuador); lane 8, USA300–0114; lane 9, USA300 carrying staphylococcal cassette chromosome mec IVb (Nebraska); lane 10, USA400 (North Dakota); lane 11, *S. aureus* NCTC 8325.

**Table 3. Molecular and Phenotypic Characteristics of Community-Associated Methicillin-Resistant *Staphylococcus aureus* Clones from Hospital Laboratories in the Andean Region of South America**

Country (no. of isolates)	PFGE pulsotype/clone (% of isolates)	ST	SCCmec IV subtype <sup>a</sup> (% of isolates)	Virulence genes (% of isolates)	Resistance profile (% of isolates <sup>b</sup> )
Colombia (n = 100)	ComA (98)	8	IVc-E (98)	<i>bsaA</i> (99)	TET (43), ERY (9), CLI (6), CIP (4), SXT (2), GEN (1)
			IVa (1)	<i>sek</i> (93)	
			IVNT (1)	<i>seq</i> (89)	
	ComB (1)	6	IVb (100)	<i>bsaA</i> (100)	None
			IVa (100)	Negative	GEN (100), CHL (100)
Ecuador (n = 64)	ComA (100)	8	IVc-E (87)	<i>bsaA</i> (100)	TET (39), ERY (9), CIP (5), GEN (5), SXT (6), CHL (2) RIF (2)
			IVa (11)	<i>sek</i> (98)	
			IVNT (2)	<i>seq</i> (95)	
	ComD (10)	22	IVa (100)	Negative	GEN (100)
			IVa (100)	<i>bsaA</i> (100)	ERY (100), TET (100)
Venezuela (n = 10)	ComA (50)	8	IVc-E (80)	<i>bsaA</i> (100)	TET (20), ERY (20), CLI (20), CIP (20)
			IVa (20)	<i>sek</i> (80)	
				<i>seq</i> (80)	
	ComE (40)	923	IVa (100)	<i>bsaA</i> (100)	ERY (100), TET (100)
				<i>sek</i> (100)	
			<i>seq</i> (100)		

**NOTE.** IVNT, nontypeable SCCmec IV; PFGE, pulsed-field gel electrophoresis; SCC, staphylococcal cassette chromosome; SLV, single-locus variant; ST, sequence type.

<sup>a</sup> SCC mec IV subtyping by multiplex polymerase chain reaction, as described by Milheirico et al [24].

<sup>b</sup> Percentage of isolates resistant to erythromycin (ERY), clindamycin (CLI), ciprofloxacin (CIP), gentamicin (GEN), chloramphenicol (CHL), rifampin (RIF), tetracycline (TET), trimethoprim-sulfamethoxazole (SXT), and minocycline (MIN).

to avoid the recovery of isolates that were likely to represent colonization. The overall rate of isolation of MRSA was 41%, with important differences between countries. In Colombia, the rate of MRSA in the participating 22 hospitals (from 6 cities across the country) was 45%; this value is similar to that from a previous multicenter surveillance study (rate of 51%) [31], indicating that the prevalence of MRSA in Colombia remains high. In contrast, there were fewer participating centers and cities in the other countries, making generalizations regarding rates of MRSA in those countries more difficult and raising the possibility that the molecular epidemiology of the organisms recovered may be skewed by the predominance of a particular strain in a given hospital. In Ecuador, for example (unlike in the other countries of the region), the local hospital clinical laboratories also receive and process clinical samples from ambulatory services and outpatient clinics, which likely influenced the type of isolates that were collected. In fact, the majority of clinical samples from Ecuador originated from SSTIs and were likely from patients who were not admitted the hospital. Therefore, the rates of MRSA and the proportions of HA-like versus CA-like MRSA circulating in the Ecuadorian hospitals are difficult to estimate. Nonetheless, our aim was to determine the

population genetics of consecutive isolates submitted to a hospital clinical laboratory, and the findings indicate high circulation of CA-like MRSA in Ecuador. Moreover, the limitations specified above are common in this type of study, which included centers from different countries with heterogeneous populations and varied antibiotic-prescribing policies.

The most striking finding of our study was that the highly virulent USA300 MRSA-ST8-IV lineage (which includes MRSA-ST923-IV, a SLV of ST8) was the predominant and almost-exclusive CA-like clone in this region of Latin America, accounting for ~21% of MRSA isolates. We had previously reported the emergence and dissemination of this USA300 clone variant in Colombia, which caused severe SSTIs in outpatients with important morbidity and mortality [15]. In the present study, we confirmed that the same strain (exhibiting the PFGE banding pattern ComA) has now been established in other Colombian hospitals (accounting for 31% of their MRSA isolates) and has also been identified in Ecuador and Venezuela (100% and 50% of CA-like MRSA isolates, respectively). The South American USA300 MRSA-ST8-IV clone has unique characteristics compared with the USA300-0114 strain: it has a different SCCmec subtype cassette, it appears to lack

the ACME island, and 41% of isolates exhibited resistance to tetracycline (although minocycline remained active), whereas the rates of resistance to erythromycin were low. Our findings confirm that a USA300-ST8 derivative genetic lineage has now been established in Latin America and support the hypothesis that a highly virulent ancestral USA300-ST8 methicillin-susceptible *S. aureus* strain related to USA300-0114 was likely present in this region of the continent and subsequently acquired the SCCmec independently. Recently, it has been shown that the USA300 lineage is a derivative of a progenitor strain, USA500 [32], and it is tempting to speculate that the South American USA300 variant may also be a sublineage derivative of USA500. Our results also indicate that the CA-MRSA lineage prevalent in this area of the continent differs substantially from that of isolates found in the southern cone of South America, where MRSA-ST30-IV and MRSA-ST5-IV derivatives appear to predominate [13, 14, 33]. A single MRSA-ST22-IV isolate found in Venezuela (with the ComD pattern) (Table 3) belongs to one of the pandemic MRSA clones (referred to as EMRSA-15 [7]), which is predominant in UK hospitals and is characterized by a low frequency of multidrug resistance and the presence of SCCmec IV; this clone was also recently identified in isolates from nonhospitalized patients in Europe [34]. Our results also indicate an important variation in the molecular epidemiology of HA-MRSA in the Andean region. The HA Chilean clone (MRSA-ST5-I) has now been successfully established in Colombia, Peru, and Venezuela. This clone was first identified in Chile in the late 1990s [9], replaced the previously predominant pediatric clone in Colombian hospitals over a span of 2 years [12], and is now spreading to the rest of the continent [8–11]. Of note, a few MRSA isolates (3%) from the region were determined to be of the New York/Japan (MRSA-ST5-II) clone, and this is the first time that the presence of this clone has been reported in Latin America.

The vancomycin MIC<sub>90</sub> of the MRSA isolates in this study was 1 µg/mL, which is identical to that previously reported in Colombia [31], indicating that an obvious “MIC creep” [35] has not occurred among MRSA from this region of Latin America. We also report, for the first time, the emergence of GISA isolates in the northern area of Latin America (isolates with reduced susceptibility to vancomycin have been reported in Brazil), following a very strict methodology that included 3 different methods of screening. Of interest, 1 of the 9 VISA isolates exhibited a CA genotype, supporting the finding that this phenotype may also be present in MRSA USA300, as has been described previously [36].

In conclusion, we present evidence that a MRSA USA300 genetic lineage has been established as the almost-exclusive CA-like clone in the northern region of South America and has entered nosocomial settings in some countries.

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