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ARTICLE

Molecular epidemiology of hospital-onset methicillin-resistant *Staphylococcus aureus* infections in Southern Chile

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Abstract Methicillin-resistant *Staphylococcus aureus* (MRSA) is a pathogen of public health importance. In Chile, the Cordobes/Chilean clone was the predominant healthcare-associated MRSA (HA-MRSA) clone in 1998. Since then, the molecular epidemiological surveillance of MRSA has not been performed in Southern Chile. We aimed to investigate the molecular epidemiology of HA-MRSA infections in Southern Chile to identify the MRSA clones involved, and their evolutionary relationships with epidemic international MRSA lineages. A total of 303 single inpatient isolates of *S. aureus* were collected in the Valdivia County Hospital (2007–2008), revealing 33 % (100 MRSA/303) prevalence for HA-MRSA infections. The SCC*mec* types I and IV were identified in 97 % and 3 % of HA-MRSA, respectively. All isolates lacked the *pvl* genes. A random sample ($n = 29$) of all MRSA was studied by pulsed-field gel electrophoresis (PFGE), multilocus sequence typing (MLST), SCC*mec* subtyping, *agr* and *spa* typing, and virulence genes profiling. PFGE analysis revealed the predominance (89 %, 26/29) of pulsotype A and three additional pulsotypes, designated H1, I33, and G1. Pulsotype A (ST5-SCC*mec*I-*spa*-t149) is clonally related to the Cordobes/Chilean clone. Pulsotype H1 (ST5-SCC *mec*IVNT-*spa*-t002) is genetically related to the Pediatric clone (ST5-SCC*mec*IV). Pulsotype I33 (ST5-SCC*mec*IVc-*spa*-t002) is clonally related by PFGE to the community-associated MRSA (CA-MRSA) clone spread in Argentina, I-ST5-IVa-PVL$^+$. The G1 pulsotype (ST8-SCC*mec*IVc-*spa*-t024) is clonally related to the epidemic USA300 CA-MRSA. Here, we demonstrate the stability of the Cordobes/Chilean clone over time as the major HA-MRSA clone in Southern Chile. The identification of two CA-MRSA clones might suggest that these clones have entered into the healthcare setting from the community. These results emphasize the importance of the local surveillance of MRSA infections in the community and hospital settings.

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Introduction

Over the past 50 years, *Staphylococcus aureus* has overcome all the therapeutic agents developed against it, proving to be a great stumbling block for antimicrobial chemotherapy. An example of this phenomenon is the emergence of methicillin-resistant *S. aureus* (MRSA) strains in 1961. Over the next several decades, hospital-associated MRSA (HA-MRSA) clones were spread throughout the world [1, 2].

More recently, in the 1990s, virulent community-associated MRSA (CA-MRSA) clones, harboring the toxin Panton–Valentine leukocidin (PVL) and the staphylococcal cassette chromosome *mec* (SCC*mec*) type IV (2B) or V (5C2), spread worldwide, first in restricted communities but later into healthcare facilities. These epidemic clones were associated to major genetic lineages designated by their multilocus sequence type (ST) or by their pulsed-field gel electrophoresis (PFGE) pattern (ST1, ST8-USA300, ST30, ST59, ST93, and ST80) [3].

Most of the HA-MRSA clones detected in South America typically belong to two major lineages, designated as clonal complexes (CC) 8 and CC5 [4]. Importantly, the most

frequently identified genotypes within these CCs in Latin America were the Cordobes/Chilean clone characterized as sequence type (ST) 5, SCC*mec* I (MRSA-ST5-I) and the Brazilian clone (MRSA-ST239-IIIA) [4–9].

Early reports have described the predominance of the Brazilian clone in hospitals in Brazil, Uruguay, Chile, and Argentina [4, 10–13]. In 2002, the first report about the Cordobes/Chilean clone was published, which was coexisting with the Brazilian clone in the second largest city in Argentina [11]. Other subsequent studies have shown the replacement of the Brazilian clone by this new clone, which has predominantly been isolated in Argentina, Chile, and Paraguay [4–6, 14] and, recently, in Venezuela, Colombia, and Perú [7, 8].

In 1981, the first isolation of MRSA was reported in Chile [15]. Since then, MRSA has spread to healthcare centers, with an isolation frequency ranging from 30 to 80 % [16]. Aires de Sousa et al. [10] detected a variant of the Brazilian clone, coexisting with the newly discovered Cordobes/Chilean clone mentioned above. Recent data (2004 and 2005) indicate that the Cordobes/Chilean clone has become the predominant clone in Chile [4]. Regarding CA-MRSA, three major clones encoding *pvl* genes have been identified in South America: (i) MRSA-ST30-IV clone [17–19, Sola C, Egea AL, et al. 52nd ICAAC (Slide Sessions, Presentation C2-1910), San Francisco, CA, September 9–12, 2012], (ii) MRSA-ST5-IV clone [6, 18, 20], and (iii) MRSA-ST8- IV or USA300 clone [8, 18, 21]. The first two were detected in southern areas of South America and the third was identified as the predominant CA-MRSA clone in the north [8] and a minor CA-MRSA clone in the south [18] of the continent.

A few studies have shown the continuous predominance of a small number of clones in some geographic regions, while other longitudinal studies suggest that the epidemiology of MRSA can evolve rapidly [2]. Therefore, the continuous epidemiologic surveillance of MRSA is important in order to obtain a better understanding of the dynamics of these microorganisms. Unfortunately, since 1998 [10], there has not been a search for new potential nosocomial MRSA epidemic clones in Southern Chile. The goal of the current study is to identify the possible MRSA clones present in Southern Chile, and their evolutionary relationships with epidemic international MRSA lineages and with other epidemic MRSA clones distributed in South America. In addition, we compare our results to previous data evaluating the molecular epidemiology of MRSA in Chile [10] to examine the stability of MRSA clones over time.

Materials and methods

Bacterial isolates and antimicrobial susceptibility testing

A total of 303 isolates of *S. aureus* were collected from inpatients in the County Hospital of Valdivia, Southern Chile, between June 2007 and June 2008. The overall prevalence of MRSA was 33 % (100/303 isolates).

This hospital is a tertiary-care medical center, one of the most complex hospitals in Southern Chile, with 507 inpatient beds and 2,043 annual admissions. It includes an outpatient care facility with 151,904 annual visits.

The Centers for Disease Control and Prevention (CDC) definitions for nosocomial or community-acquired infections was used for suspected MRSA infections [22, 23]. Therefore, we considered an infection to be healthcare-associated–hospital onset (HA-MRSA-HO) if the MRSA culture was obtained >48 h after a patient was admitted to the hospital, regardless of whether they had healthcare risk factors or not. Invasive infections and sepsis were defined as previously described [18].

S. aureus was identified by standard microbiological procedures. Confirmation of the methicillin-resistant phenotype of the isolates was performed by the cefoxitin disc diffusion test according to the recommendations of the Clinical and Laboratory Standards Institute (CLSI) [24]. Susceptibility to different antibiotics was performed using the MicroScan® Dried Gram Positive semi-automated system. The following antibiotics were tested: β-lactams (cephradine, oxacillin, and penicillin), ciprofloxacin, clindamycin, erythromycin, gentamicin, linezolid, rifampicin, trimethoprim–sulfamethoxazole (SXT), and tetracycline. Vancomycin minimum inhibitory concentrations (MICs) were determined by the agar dilution method for all isolates [24].

Molecular typing

The SCC*mec* types were evaluated for all MRSA isolates by multiplex polymerase chain reaction (PCR) using assays that have been reported elsewhere [25, 26]. The presence of PVL-encoding genes (*luk*S-PV and *luk*F-PV) was investigated in all MRSA isolates, using PCR primers previously described [18].

After this initial molecular characterization (SCC*mec* typing and detection of *pvl* genes) of all MRSA isolates in Chile, a random sample (n = 29) representative of isolates of each antibiotype of MRSA was received at the Departamento de Bioquímica Clínica, Universidad Nacional de Córdoba, Argentina, for further test analyses, which included DNA restriction pattern by pulsed-field gel electrophoresis (PFGE), SCC*mec* subtyping by allotyping using conventional PCR [18, 27, 28], multilocus sequence typing (MLST) and *spa*A typing, and the detection of the virulence gene profiles by PCR [18].

The PFGE analysis of *Sma*I digests of chromosomal DNA was performed and interpreted as previously described [6]. *S. aureus* NCTC8325 was used as a molecular size control, and representatives of MRSA strains belonging to the Cordobes/Chilean, Brazilian, and Pediatric (in Argentina: ST100-IVNv) clones [5, 6, 11, 18] USA300-0114 (ST8-IVa-t008-ACME^{+}) and South American USA300 clone [(ST8-IVc-

t008-ACME⁻) detected in Argentina] [18] were used as controls for comparisons of PFGE banding patterns.

The type and subtype were designated according to the order of identification in the database at the CIBICI, Córdoba, Argentina.

Virulence genes were detected by PCR as described above [18]. They included the following genes: enterotoxin: *sea*, *seb*, *sec*, *sed*, *see*, *seg*, *seh*, *sei*, *sej*, *sen*, *seo*, *sem*; TSST-1: *tst*; exfoliative toxin: *eta* and *etb*; leukocidin: *lukE-lukD* and the class F leukocidin: *lukM*; bacteriocin (*bsa*); adhesins for collagen (*cna*) and bone sialoprotein (*bpp*); K enterotoxin (*sek*); and the *agr* group (*agr* 1–4). The detection of ACME clusters (arginine-catabolic-mobile-element) was analyzed with previously described primers [18]. All isolates were characterized by *spa*A typing, as described above [18]. The sequences obtained by *spa*A typing were compared to those held on the SpaServer (http://spaserver.ridom.de). Representative isolates of each subtype (defined by PFGE) were also characterized by MLST, as previously described [5, 6]. The sequence types (STs) were determined with the MLST database (http://www.mlst.net) and were compared by using the BURST algorithm to assign isolates to clonal complexes (CCs).

Results

Demographic and clinical features of the patients

Of all MRSA isolates (n = 100), 59 % were obtained from males. The median age among all patients was 57.5 years (range 0.6–84 years) and 55 % (n = 55) were 30–69 years of age.

Isolates were most commonly obtained from skin and soft tissue infections (50 %), followed by bloodstream infections (16 %), respiratory tract infections (15 %), urinary tract infections (9 %), bone and joint infections (4 %), and other infections (6 %), including peritoneal fluid and biliary secretion, among others. Using the CDC criteria [22, 23], all isolates were classified as healthcare-associated and hospital-onset infections. Table 1 shows the demographic and clinical characteristics of the 29 patients from whom MRSA strains selected for molecular typing were recovered.

Table 1 Demographic and clinical characteristics of patients from whom methicillin-resistant *Staphylococcus aureus* (MRSA) strains selected for the molecular analysis were isolated

Characteristic (n=29)	No.	Percentage (%)
Gender		
Female	10	34
Age group (years)		
Children (0–14)	1	3
Young adults (15–30)	3	10
Adults (31–69)	16	55
Elderly (>69)	9	31
Infection type		
Skin and soft tissue (SSTI)	7	24
Abscesses	3	
Wound	4	
Surgical site	6	20
Bloodstream	4	14
Sepsis	4	
Bone and joint	3	10
Osteomyelitis	2	
Arthritis	1	
Respiratory tract	5	17
Ventilator-associated pneumonia	4	
Pneumonia	1	
Urinary tract	2	7
Other	2	7
Invasive	14	48

Microbiological features

Antimicrobial susceptibility testing

From all MRSA isolates (n = 100), the percentages of resistance to ciprofloxacin, clindamycin, erythromycin, gentamicin, and rifampicin were 99 %, 96 %, 97 %, 92 %, and 2 %, respectively. No strains were resistant to linezolid, SXT, and tetracycline. All isolates were susceptible to vancomycin by the agar dilution method (MIC_{90}, 1 μg/ml; MIC range, 0.25–2 μg/ml).

The resistance patterns of the 29 isolates selected for molecular analysis are shown in Fig. 1.

Molecular characterization of MRSA strains

From all MRSA (n = 100), SCC*mec* type I and SCC*mec* type IV were identified in 97 % and 3 % of strains, respectively. All isolates lacked the *pvl* genes.

The ST, SCC*mec* type, *spa*A type, virulence genes profile, *agr* type, and drug resistance of the 29 MRSA isolates selected for further molecular typing are shown in the Fig. 1.

PFGE analysis of the 29 MRSA isolates revealed a predominant major pulsotype (89 %, 26/29 isolates), designated pulsotype A in this work, as well as in the database of the CIBICI, Córdoba, Argentina, and three additional pulsotypes, G (G1), H (H1), and I (I33), with one isolate each (Fig. 1).

Pulsotype A is clonally related to the pattern previously observed for the Cordobes/Chilean clone (Fig. 1). Among the isolates with pulsotype A, two predominant subtypes were identified: A23, 5/26 isolates (19 %) and A3, 3/26 isolates (12 %). Six subtypes, A59, A39, A1, A21, A11, and A5, all with two isolates and accounting for 8 % each, and the remaining PFGE subtypes were single isolates. All

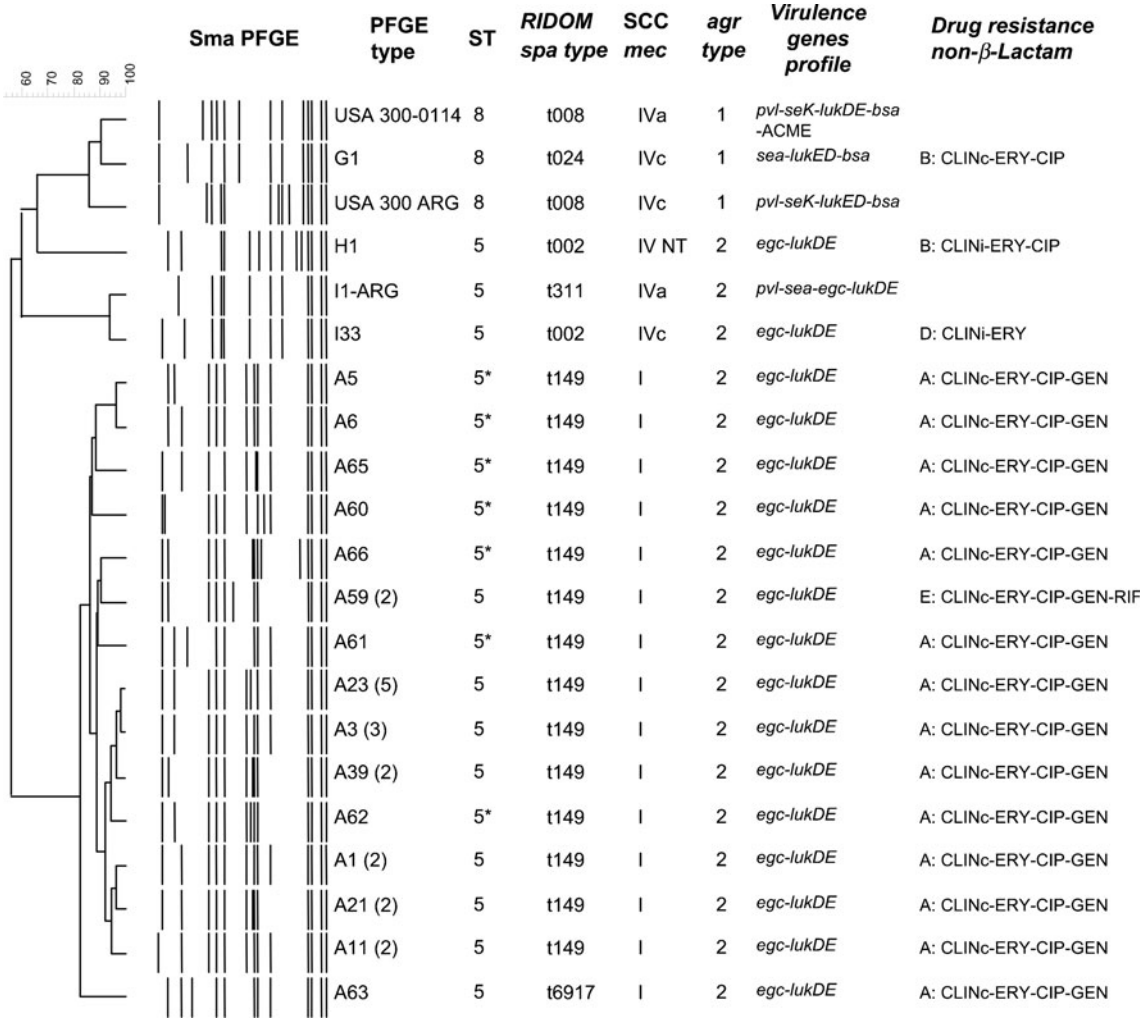

Fig. 1 Characteristics of 29 MRSA strains, representative of all MRSA cases isolated from the County Hospital of Valdivia, Southern Chile, during the period from June 2007 to June 2008. *Sma*I restriction patterns from MRSA strains were digitally schematized (*middle*) and analyzed to calculate the Dice coefficient of correlation and to generate a dendrogram (*left*) by the unweighted pair-group method using average linkage clustering. Isolates differing by up to six fragments were considered to be subtypes of a given clonal type and the similarity cut-off was set at 80 %. The genotypic [subtype (PFGE), sequence type (ST by MLST), RIDOM *spa* type, SCC*mec* type, *agr* type (type of accessory gene regulator allotype), and virulence genes profiles] and phenotypic (drug resistance non-β-lactams) characteristics of these strains (*right*) are shown. The number of strains within each pulsotype by PFGE is indicated when more than one isolate was detected. The PFGE patterns of the most frequent subtype (I1) of the epidemic CA-MRSA-ST5-IVa clone from Argentina and two USA300 strains, USA300-0114 (ST8-IVa-t008-ACME^{+}) and USA300-ARG [CA-MRSA (ST8-IVc-t008-ACME^{-}) detected in Argentina [18]] are shown for comparison purposes. ST*: predictive ST according *spa* type (*t*149) and PFGE type (A); ST: ST experimentally assigned. The virulence genes profile was analyzed and the genes which were detected are indicated. Drug resistance to non-β-lactams is indicated as follows: gentamicin (GEN), ciprofloxacin (CIP), erythromycin (ERY), clindamycin (CLINc and CLINi: constitutive and inducible resistance to macrolides, lincosamide, and streptogramin B, respectively), and rifampin (RIF)

these isolates contained SCC*mec* type I and were associated to *spa* type t149, except for one isolate (*spa* type t6917) and *agr* type 2. MLST of a representative isolate for each subtype by PFGE yielded ST5, confirming the genetic relatedness with the Cordobes/Chilean clone [5, 11].

Two of three remaining pulsotypes belong to ST5 and they are associated with SCC*mec* type IV, but pulsotype I33 carries the SCC*mec* subtype IVa and the pulsotype H1 carries the IVNT subtype (non-typable). In this case, ccrB2 and the *mec* gene complex class B were positive but amplifications by PCR with specific primers to the J1 regions a, b, c, d, g, and h were negative.

Importantly, the I33 subtype (ST5-SCC*mec*IVc-*spa*-t002) is clonally related by PFGE to the epidemic CA-MRSA clone spread in Argentina during the period 2001–2008: I-ST5-IVa-PVL^{+} (Fig. 1), but in this case, it is a PVL-negative variant (PVL^{-}) with SCC*mec* IVc.

On the other hand, the G1 pulsotype is clonally related by PFGE to the epidemic USA300 CA-MRSA (Fig. 1). It is associated to *spa*-t024 and carries the *sea*, *lukE-lukD*, and *bsa* genes.

Discussion

Molecular epidemiology studies have highlighted the continuing global evolution and spread of different MRSA clones worldwide [2]. This is the first systematic prospective study analyzing the molecular background and exotoxin equipment of MRSA isolates in the hospital setting in Southern Chile.

Nosocomial MRSA is a growing problem in Latin America [29]. According to the last Epidemiological Surveillance Report of Nosocomial Infections published in 2007 by the Ministry of Health, Government of Chile (http://www.minsal.cl), the prevalence of MRSA, considering the total *S. aureus* isolated in Chile during the years 1991–2007, shows a persistent increase. In fact, the prevalence of MRSA doubled between the years 1991–2007, reaching values above 60 % (Table 2).

In Southern Chile, specifically in the County Hospital of Valdivia, the prevalence of MRSA in 1995 was 9.1 % in hospitalized patients. This value increased to 33.3 % in 1999 and remained stable until 2005 (data published in 2008) [30]. In our research, we report an MRSA prevalence of 33 % during the period from June 2007 to June 2008. It is, therefore, likely that this value has remained stable from 1999 to 2007. Furthermore, considering other studies showing a decrease in MRSA infections, especially in the hospital setting over the last few years [2, 31, 32], and the absence of data on trends in the prevalence of MRSA in this hospital, we are unable to rule out an increase and subsequent decrease in MRSA infections over this period. Different factors may have contributed to either of these two possible situations (either stability over time at low levels of MRSA prevalence or its decline in recent years), including the implementation and enforcement of MRSA prevention practices and restrictions in antibiotic use in the County Hospital Valdivia. These recommendations are supported by studies that have shown decreases in the rates of MRSA infections following the implementation of MRSA prevention practices, usually at individual institutions or in small groups of facilities [32, 33].

Regarding the demographic and clinical features of inpatients and in agreement with several reports, the results of this work showed that most (48 %) HA-MRSA infections were invasive (mainly lungs and bloodstream infections) and occurred with a higher frequency in older populations (>30-years of age) and in males (59 %), characteristics which are common to HA-MRSA disease [34]. Moreover, 26 % of HA-MRSA isolates were obtained from surgical site infections.

Table 2 Prevalence of MRSA isolated in Chile during the period 1991–2007. Epidemiological Surveillance Report of Nosocomial Infections (Ministry of Health, Government of Chile)

Oxacillin	Resistant/total isolates	Percentage resistant (%)
1991–1993	1,153/3,439	33.5
1994–1996	1,215/2,512	48.4
1997–2000	817/1,409	58.0
2001–2004	1,568/2,544	61.6
2005–2007	583/927	62.9

The percentages of resistance to ciprofloxacin, clindamycin, erythromycin, and gentamicin are higher than those reported previously by Otth et al. [30]. Nonetheless, those investigators calculated the percentages of resistance by considering the total number of *S. aureus* cases. Conversely, we calculated the percentages of resistance by only taking into consideration the total number of MRSA cases.

In addition, we did not detect MRSA strains resistant to vancomycin or resistant to SXT and tetracycline. Susceptibility to these antibiotics allows a broader range of possible treatments, which directly benefits the patient.

Referring to the resistance patterns of isolates selected for molecular typing, most of the strains were classified as pattern A (resistant to β-lactams, ciprofloxacin, erythromycin, clindamycin, and gentamicin). This resistance pattern has been detected since 2004 in the County Hospital of Valdivia, with a prevalence of approximately 80 % [30, 35]. Epidemiologically, it is important to note that patterns A and E are consistent with the pattern described for the Cordobes/Chilean clone, which is resistant to erythromycin, clindamycin (constitutive resistance), gentamicin and ciprofloxacin, variable resistance to rifampicin (susceptible or resistant) and susceptible to tetracycline, SXT, and vancomycin [5, 6, 11, 18]. The molecular characteristics shared by the isolates belonging to this major clone corresponded largely to those reported in our previous studies [5, 6, 11], namely, *agr*2, ST5, *spa*-t149, and one related to *spa*-t6917 and SCC*mec* I. In addition, all these isolates carried *egc* and *lukE-lukD* genes. This clone has been spread from the south to the north of Latin America through the Andean region (Perú, Ecuador, Venezuela, and Colombia), as well as in Paraguay and Brazil [5–11, 14]. The biodiversity of MRSA in the hospital setting in Southern Chile appears to be rather limited. The vast majority of isolates belong to the Cordobes/Chilean clone. Apparently, this strain was already the predominant strain in Chile 10 years ago [10]. Therefore, in this study, we demonstrate its stability over time as the major HA-MRSA clone in Southern Chile.

On the other hand, after the emergence of virulent CA-MRSA strains around the world, since 2003, many reports have documented the spread of SCC*mec* type IV-harboring CA-MRSA strains in hospital settings, primarily in Europe and the United States, and in some countries of Latin America [9, 18, 37–39].

As far as we know, the molecular epidemiology of CA-MRSA infections in Chile has not been reported or published. A few isolated cases of CA-MRSA infections have

been reported, but some of these were in people returning from cities in Uruguay or Brazil with a higher incidence of CA-MRSA [29]. In this study, CA-MRSA infections were not detected, but we demonstrated three isolates harboring SCC*mec* type IV in the hospital setting, one of which belonged to ST8 (CC8) and the others to ST5 (CC5).

Although both isolates belonging to ST5 are genetically related to the international HA-MRSA "classical" Pediatric clone (ST5-SCC*mec*IV), one of these was clonally related by PFGE to the CA-MRSA clone (ST5-SCC*mec*IVa-t311) spreading in many regions of Argentina during the period 2001–2008. This isolate, which is only resistant to erythromycin and clindamycin (inducible), was considered to be a variant PVL$^-$ of this CA-MRSA clone associated to SCC*mec* IVc and *spa*-t002, also described in Argentina [18]. This isolate illustrates the cross-border spread of CA-MRSA from Argentina to Chile.

With respect to the clinical data, the pulsotype I33 (ST5-SCC*mec*IVc-*spa*-t002) was isolated from a diabetic foot ulcer in a patient that previously had a surgery to treat chronic osteomyelitis. The pulsotype H1 (ST5-SCC *mec*IVNT-*spa*-t002), resistant to erythromycin, clindamycin (inducible), and ciprofloxacin, was isolated from a maxillary sinus secretion of a patient diagnosed with rhinosinusitis. This patient had multiple clinical episodes of sinusitis, thrombophlebitis, recurrent outpatient's antimicrobial treatments, and two previous surgeries in 2006 and 2007. These patients were not screened for MRSA colonization on admission, so it is difficult to know with certainty the possible sources of acquisition of CA-MRSA. On the other hand, the pulsotype G1 (ST8-SCC*mec*IVc-*spa*-t024) was clonally related by PFGE to the USA300 CA-MRSA clone. This isolate was isolated from a surgical site infection in a patient diagnosed with diabetes.

USA300 comprised of a cluster of closely related PFGE patterns, including one variant, USA300-0114, that has been dominant in the CA-MRSA epidemic in the USA. All variants belong to ST8-MRSA-IV according to MLST and SCC*mec* typing [21]. USA300-0114 and its closely related variants predominantly carry the SCC*mec* type IVa, *spa*-t008, and a number of virulence genes, including *pvl* and *arc*A (coding for the ACME) [1, 21, 40]. The Latin American variant of USA300 recently dubbed "USA300-LV" or the South American USA300 clone was described as the most predominant CA-MRSA in northern areas of South America between 2006 and 2008 [8]. It has the following genetic characteristics: ST8, predominantly SCC*mec* type IVc, *spa*-t008, *pvl* genes present, and absence of ACME [8, 21].

In this study, the isolate belonging to ST8, clonally related by PFGE to the epidemic USA300-0114 CA-MRSA, carried the SCC*mec* type IVc, was associated to *spa*-t024, and carried *lukE-lukD* and *bsa* genes. Unlike the USA300-0114 CA-MRSA, however, this strain lacked the *pvl* and *seK* genes and the locus ACME, and it harbored the *sea* gene. In addition, it was resistant to erythromycin, clindamycin (constitutive), and ciprofloxacin. Thus, it resembles the Latin American variant of USA300, but with PVL$^-$ [8, 21]. Variability within USA300 can involve resistance genes, beta-hemolysin, converting phages, enterotoxin genes, ACME, or even the *pvl* genes. All these elements can be carried on mobile elements (MGE), which facilitate their horizontal transfer between strains of the same or different lineages [1, 41, 42]. On the other hand, according to the results from Colombia [9] and Denmark [42] on the presence of both *spa* types t008 and t024 in strains clonally related by PFGE to the USA300 clone, it is likely that both ST8-IVc *spa* types (t008 and t024) belong to the USA300-LV lineage. Therefore, an important additional issue of this study was the discovery of the first case of CA-MRSA infection caused by this highly virulent CA-MRSA "USA300-LV" clone in Chile, but, in this case, in the hospital setting. Its potential ability to spread could be demonstrated through molecular surveillance over time of MRSA infections, both at the hospital and in the community.

The USA300 clone has become a major international epidemic clone, commonly causing both CO and HO infections, and is now the dominant CA-MRSA strain in five countries (Canada, Samoa, and the Andean countries of Colombia, Ecuador, and Venezuela) outside of the USA. It has also been identified in countries in Europe, Latin American (Argentina, Perú, Brazil, and Trinidad and Tobago), the Western Pacific, and the Caribbean [18, 21]. It is not known from where this strain was introduced to Chile, but there might be a link to other countries of Latin America, particularly Argentina or Perú. Importantly, more recently, in Medellín (Colombia), the Cordobes/Chilean clone is being displaced by this "USA300-LV" in the hospital setting [9].

Finally, it will be epidemiologically relevant to analyze the evolution of these clones during the following years in order to better understand the coexistence and/or the eventual replacement of the Cordobes/Chilean clone by these CA-MRSA clones at the hospital level. Furthermore, the identification of two CA-MRSA clones present in the hospital setting, though indirectly, might suggest that these clones have entered into the healthcare setting from the community. These results, therefore, emphasize the importance of local surveillance, clinical and molecular, of MRSA infections in both the community and the hospital settings, along with the dissemination of findings, in order to ensure that medical personnel are aware of the changing patterns of the MRSA epidemiology within their institutions, thereby, enabling them to choose efficacious empirical treatments and contribute to successful preventative strategies aimed at controlling the dissemination of MRSA infections.

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Conflict of interest The authors declare that they have no conflict of interest.

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