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Major article

Methicillin-resistant *Staphylococcus aureus* in Rio de Janeiro hospitals: Dissemination of the USA400/ST1 and USA800/ST5 SCC*mec* type IV and USA100/ST5 SCC*mec* type II lineages in a public institution and polyclonal presence in a private one

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Key Words:
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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) infections have changed since certain non-multiresistant MRSA lineages have emerged in hospitals. In this study, 99 MRSA isolates, 77 from a public and 22 from a private hospital, were characterized.

Methods: Isolates were tested for antimicrobial susceptibility, whereas staphylococcal chromosomal cassette *mec* (SCC*mec*) typing and Panton-Valentine leukocidin genes were assessed by polymerase chain reaction. Pulsed-field gel electrophoresis and multilocus sequence typing analyses were carried out to determine the MRSA lineages.

Results: High rates of resistance were found to erythromycin (96%), ciprofloxacin (93%), and clindamycin (90%). The SCC*mec* types found were as follows: type II (14.2%), III (62.6%), and IV (23.2%). Approximately 85% of type III isolates was related to the Brazilian epidemic clone in both hospitals. For type IV isolates, 94.4% were related to both USA400/ sequence type (ST) 1 and USA800/ST5 lineages in the public hospital, whereas the USA400/ST1, USA800/ST5, USA1100/ST30, and EMRSA (Epidemic MRSA)-15/ST22 lineages were detected in the private hospital. Among the SCC*mec* II isolates, approximately 85% were related to the USA100/ST5 lineage. Three MRSA isolates were positive to Panton-Valentine leukocidin genes.

Conclusion: The study showed that there was an emergence of USA400/ST1, USA800/ST5 SCC*mec* IV, and USA100/ST5 SCC*mec* II MRSA lineages in both hospitals. There was a dissemination of them in the public hospital and a polyclonal presence of the MRSA isolates in the private hospital. The spread of these lineages can be facilitated by the characteristics of the health institution.

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Staphylococcus aureus continues to be a major cause of health care-associated infections (HCAI) worldwide. Methicillin-resistant *S aureus* (MRSA) presents an additional penicillin-binding protein, PBP2a, coded by the *mec*A gene that is in a genetic mobile element called "staphylococcal chromosomal cassette *mec*" (SCC*mec*).[1] Eleven types (I-XI) of SCC*mec* have been assigned to *S aureus* based on the classes of the *mec* gene complex and the types of the *ccr* gene complex.[2] The SCC*mec* types II and III MRSA isolates are commonly associated with HCAI and are usually multiresistant. On the other hand, community-acquired MRSA isolates that are

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non-multiresistant normally carry the SCC*mec* types IV or V and are related to the patients without traditional risk factors for MRSA.[3,4]

In recent years, type IV isolates have emerged in hospital settings and have become a common type of MRSA found in inpatients worldwide.[5,6] In Brazil, MRSA accounts for approximately 31% of all *S aureus* isolates recovered from hospital settings,[7] and the Brazilian epidemic clone (BEC) carrying the SCC*mec* III has been considered responsible for the majority of these infections.[8] However, some studies have already found infections caused by isolates harboring SCC*mec* IV, belonging to different sequence types (STs), such as the pediatric clone (USA800/ST5),[9-11] the USA400/ST1,[10-12] and the Ocean Southwest Pacific clone (USA1100/ST30).[12] The New York/Japan clone (USA100/ST5) carrying the SCC*mec* type II has also been detected in Brazilian hospitals but related to less than 5% of isolates.[9]

The health system in Brazil is made up of a large public sector that covers 75% of the population and a private sector that attends the remaining 25%. The public sector is organized around the Brazilian Unified National Health System, which is financed with general taxes and social contributions collected by the 3 levels of government (federal, state, and municipal).[13] The private sector includes individual insurance plans and a system of insurance schemes known as "Supplementary Health," which is financed by employers and/or households. The private sector also includes clinics, hospitals, and laboratories offering services on an out-of-pocket basis that are mostly used by the high-income population.[13,14]

Characteristics associated with MRSA isolates from Brazilian public hospitals have already been described.[7-12] However, studies that characterize isolates from private health institutions have never been reported before. Therefore, this study aimed to characterize and compare MRSA isolates obtained from 2 tertiary care hospitals, 1 private and 1 public, in Rio de Janeiro, in relation to their antimicrobial susceptibility, SCC*mec* types, and Panton-Valentine leukocidin (PVL) genes and clonal diversity by pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST).

MATERIALS AND METHODS

Settings

This study was conducted at 2 tertiary care hospitals in Rio de Janeiro, Brazil: the Marcilio Dias public hospital and the Copa D'Or private hospital. The public hospital is a military institution located in a suburb where the population is predominately low income. It has 532 beds, and 35 of them are in an intensive care unit (ICU). The private hospital is an institution with 188 beds: 47 of them are in an ICU, and it is located in a wealthy area of the city. There are also public hospitals in these wealthy areas, but the population in general tends to use the paid health services.

Bacterial isolates

A total of 99 *S aureus* isolates was obtained consecutively from both infected and colonized patients from the public hospital (77 isolates) between June 2004 and October 2005 and from the private hospital (22 isolates) between October 2006 and August 2007. One patient from the public hospital presented 2 types of infection of isolates with different characteristics; both isolates were included in this study. The strains were isolated from blood (30.3%), tracheal secretion (26.3%), cutaneous secretion (13.1%), surgical site secretion (7%), bronchoalveolar lavage (6.1%), urine (6.1%), nasal swabs (5%), and other sites that comprised 6.1% of isolates (cerebrospinal fluid, peritoneal liquid, and pleural fluid). MRSA isolates were identified by the automated systems in the hospitals. All isolates were confirmed as *S aureus* by the detection of coagulase and catalase enzyme production.[15] As controls, the strains of *S aureus* ATCC 25923 and ATCC 29213 (for susceptibility tests), μ50 (SCC*mec* type II),[16] and clinical strains (SCC*mec* types III and IV; PVL genes positive)[11] were used.

*Antimicrobial susceptibility and SCC*mec *typing*

S aureus isolates were evaluated by the disk diffusion test[17] and by the oxacillin (Sigma-Aldrich, St. Louis, MO) and vancomycin (Sigma-Aldrich) agar dilution methods.[18] Susceptibility was tested against the antimicrobial agents chloramphenicol, ciprofloxacin, clindamycin, erythromycin, gentamicin, penicillin, rifampin, teicoplanin, tetracycline, and trimethoprim-sulfamethoxazole (Cecon, São Paulo, Brazil) and cefoxitin, linezolid, and mupirocin (Oxoid, Cambridge, UK). All results were analyzed according to Clinical Laboratory Standards Institute,[19] except for mupirocin.[20] SCC*mec* typing was performed using the polymerase chain reaction (PCR) multiplex assay, as described previously by Milheiriço et al.[21]

Characterization of genotypes and STs and presence of PVL genes

All MRSA isolates were typed by PFGE after digestion of whole-cell DNA with *Sma*I in a CHEF-DRIII system (Bio-Rad, Richmond, CA), as previously described.[22] Cluster analysis was assessed using the unweighted pair group methodology based on the Dice coefficient. PFGE type clusters were defined using a coefficient of similarity of 80%, and the visual interpretation was done using the criteria of Van Belkum et al.[23] The clonality of the isolates was obtained by comparisons with previously published pictures.[24]

One isolate representative of each PFGE profile was chosen for multilocus sequence typing (MLST) that was carried out according to the protocol described by Enright et al.[25] The PCR products were sequenced bi-directionally at the Multidisciplinary Genomic Unit of Carlos Chagas Filho Biophysics Institute of the Federal University of Rio de Janeiro. STs were determined using the MLST database (http://www.mlst.net) and characterized as singletons or members of a clonal complex (CC) by the eBURST algorithm (accessible at http://eburst.mlst.net). The presence of the *lukS-PV* and *lukF-PV* genes that encoded the PVL was detected by PCR, according to Lina et al.[26]

Statistical analysis

All comparisons were performed using the software EpiInfo version 3.5.2 (Centers for Disease Control and Prevention, Atlanta, GA). Differences were considered statistically significant when the value of $P < .05$.

RESULTS

*Antimicrobial susceptibility and SCC*mec *typing*

All MRSA isolates were susceptible to linezolid and teicoplanin and resistant to penicillin and cefoxitin by the disk diffusion test. The highest resistance rates were found for erythromycin (96%), ciprofloxacin (93%), and clindamycin (90%). The lowest resistance rate was found for mupirocin (25.2%). Except for mupirocin ($P = .006$) and chloramphenicol ($P = .003$), no statistically significant difference was found in relation to bacterial antimicrobial resistance between the 2 hospitals evaluated (Table 1).

Among the 99 MRSA isolates evaluated in this study, 62 (62.6%) harbored the SCC*mec* III, 23 (23.2%) the SCC*mec* IV, and 14 (14.2%) the SCC*mec* II. In the public hospital where 77 MRSA isolates were

Table 1
Antimicrobial resistance evaluated for 99 methicillin-resistant *Staphylococcus aureus* isolates from a public and a private hospital in Rio de Janeiro, between September 2004 and August 2007

Antimicrobial	No. (%) of resistant isolates		
	Public hospital (N = 77)	Private hospital (N = 22)	*P* value*
Chloramphenicol	51 (66.2)	7 (31.8)	.003†
Ciprofloxacin	73 (94.8)	19 (86.4)	.139
Clindamycin	71 (92.2)	18 (81.8)	.111
Erythromycin	75 (97.4)	20 (90.9)	.179
Gentamycin	52 (67.5)	17 (77.3)	.148
Mupirocin	24 (31.2)	1 (4.5)	.006†
Rifampin	43 (55.8)	12 (54.5)	.190
Tetracycline	46 (59.7)	15 (68.2)	.155
TMP/STX	46 (59.7)	15 (68.2)	.155

TMP/STX, Trimethoprim/sulfamethoxazole.
NOTE. All isolates were resistant to cefoxitin and penicillin and susceptible to linezolid and teicoplanin.
*Fisher exact test.
†Statistically significant difference ($P < .05$).

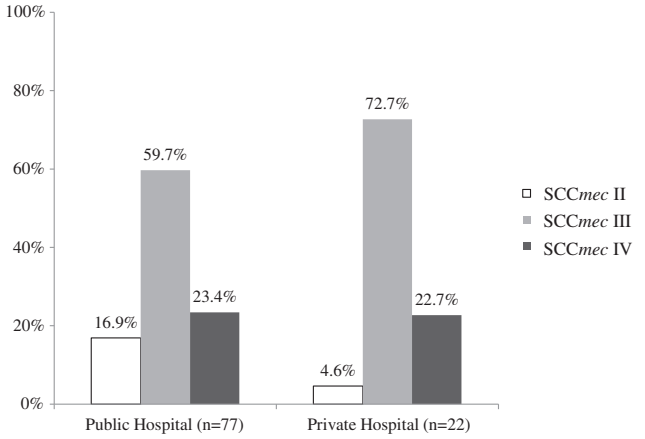

Fig 1. Distribution in percentage of SCC*mec* types among 99 MRSA isolates recovered from patients in a public and a private hospital in Rio de Janeiro.

obtained, the SCC*mec* III was found in 46 (59.7%) of the isolates, the SCC*mec* IV in 18 (23.4%), and the SCC*mec* II in 13 (16.9%) (Fig 1). In the private hospital, among the 22 MRSA isolates, 16 (72.7%) carried the SCC*mec* III, 5 (22.7%) the SCC*mec* IV, and only 1 (4.6%) isolate harbored the SCC*mec* II. No statistically significant difference was observed in relation to the SCC*mec* types found for MRSA isolates for the 2 hospitals evaluated.

All SCC*mec* III isolates presented resistance rates higher than 90% for ciprofloxacin, clindamycin, erythromycin, gentamicin, trimethoprim/sulfamethoxazole, and tetracycline. Among the SCC*mec* II isolates, almost 100% were also resistant to ciprofloxacin, clindamycin, erythromycin, and mupirocin. On the other hand, MRSA SCC*mec* IV isolates presented resistance rates less than 83% for erythromycin (83%), ciprofloxacin (70%), chloramphenicol (61%), and clindamycin (56%). All SCC*mec* types II and IV isolates were susceptible to trimethoprim/sulfamethoxazole and tetracycline (Data not shown).

An oxacillin minimum inhibitory concentration $(MIC)_{90}$ of 256 μg/mL was found for MRSA type III isolates, whereas, for SCC*mec* types II and IV isolates, the values were 128 μg/mL and 32 μg/mL, respectively. The vancomycin MIC_{90} was 1 μg/mL, but 2 isolates with SCC*mec* IV presented MIC of 2 μg/mL (Data not shown).

Characterization of genotypes and STs and presence of PVL genes

Among the 28 MRSA SCC*mec* III isolates selected for PFGE analysis, 14 pulsotypes included in 4 lineages were found. However, all isolates showed the allelic profile 2-3-1-1-4-4-3 by MLST, compatible to ST239. In addition, 85.7% of them presented a PFGE profile related to BEC, which was the majority of the SCC*mec* III isolates from both hospitals (Data not shown).

The 23 isolates that carried the SCC*mec* IV cassette belonged to 5 lineages, but the majority was related to the USA400/ST1 (13; 56.5%) and the USA800/ST5 (6; 26%). In the public hospital, 94.4% of the SCC*mec* IV isolates were related to USA400/ST1 (12; 66.7%) or USA800/ST5 (5, 27.8%) lineages (Table 2). One isolate showed the allelic profile 1-2-2-2-6-3-2, compatible to ST714, a single locus variant of ST30. In the private hospital, among the 5 SCC*mec* IV isolates, the polyclonal presence of USA400/ST1, USA800/ST5, USA1100/ST30, and EMRSA (Epidemic MRSA)-15/ST22 lineages was observed. Among the 14 SCC*mec* II isolates, 3 lineages were found: USA100/ST5 (12, 85.7%), detected in both the public and private hospitals, and USA200/ST36 and USA600/ST45 associated with 2 isolates obtained in the public hospital (Table 2).

Three MRSA type IV isolates were positive for PVL genes (Table 2). Two isolates were recovered from community-acquired wounds, 1 of them from the private hospital was associated to the ST30 lineage, and the other from the public hospital was related to the ST714 lineage. The third isolate was recovered from peritoneal liquid at the public hospital and belonged to the USA800/ST5 lineage.

Over the study period, there was a variation in the occurrence of MRSA isolates related to the USA100, USA400, and USA800 lineages in the public hospital. Figure 2 shows that this temporal variation occurred between July 2004 and October 2005, highlighting an initial dissemination of USA100 followed by an increased spread of USA400 among the patients.

DISCUSSION

Some studies have evaluated the epidemiology of MRSA in Brazil and found that a great number of lineages once known to be restricted to other continents are emerging in Brazilian hospitals.[9,11,27] However, in Brazil there are differences between the public and the private hospitals in terms of the economic profile of the patients and the number of patients per ward.[14] In this study, for the first time, the molecular and phenotypic characteristics associated with MRSA isolates were evaluated and compared between a public and a private hospital located in Rio de Janeiro city.

The antimicrobial susceptibility and the distribution of cassette *mec* types among the isolates were balanced between the 2 hospitals. Similar resistance rates were found, except for mupirocin and chloramphenicol, which had significantly higher rates in the public hospital. Mupirocin is used in decolonization schemes for patients colonized by MRSA only in the public hospital. Therefore, the high rates of resistance may be a reflection of the antimicrobial policy used in the different institutions. Concerning the *mec* cassettes, SCC*mec* III was the most common in both institutions, and the isolates were characterized as ST239, and approximately 85% of them were related to BEC. Pacheco et al[28] analyzed 67 MRSA isolates from a public hospital in São Paulo city and verified that all SCC*mec* type III isolates belonged to the ST239 lineage, and the same was found for all SCC*mec* III isolates analyzed by Silva-Carvalho et al[12] and Schuenck et al[11] in hospitals in Rio de Janeiro, confirming our findings.

MRSA type IV had a similar result of antimicrobial susceptibility for the isolates from both hospitals. However, differences in PFGE

Table 2
Characteristics of 37 MRSA isolates carrying SCC*mec* II or IV recovered from a public and a private hospital in Rio de Janeiro, between September 2004 and August 2007

Hospital (No. of isolates)	Isolate number	Isolation date (mo/day/yr)	Clinical source	Unit or floor	Resistance profile*	MIC oxacillin (μg/mL)	SCC*mec* type	Genotype†	Clonality‡	ST§/CC
Public (31)	649	9/08/04	Blood	10th	CIP/CLI/ERY/MUP	128	II	A1	NY/Japan	5/5
	557	9/10/04	SS	8th	CIP/CLI/ERY/MUP	128	II	A1	NY/Japan	5
	655	10/27/04	Blood	ICU	CIP/CLI/CHL/ERY/MUP	128	II	A2	NY/Japan	5
	659	11/10/04	TS	ICU	CIP/CLI/ERY/MUP	128	II	A2	NY/Japan	5
	555	11/19/04	Urine	9th	CIP/CLI/ERY/MUP	128	II	A1	NY/Japan	5
	663	12/01/04	Blood	9th	CIP/CLI/ERY/MUP	128	II	A1	NY/Japan	5
	554	12/02/04	Wound	ICU	CIP/CLI/ERY/MUP	256	II	A4	NY/Japan	5
	670	1/11/05	SS	8th	CIP/CLI/ERY/GEN//MUP	128	II	A1	NY/Japan	5
	840	1/15/05	TS	ICU	CIP/CLI/ERY/MUP	128	II	E	USA200	36/30
	913	2/14/05	SS	ER	CIP/CLI/CHL/ERY/MUP	128	II	A1	NY/Japan	5
	769	4/22/05	Blood	9th	CIP/CLI/ERY/MUP	128	II	A3	NY/Japan	5
	843	5/18/05	TS	ICU	CIP/CLI/CHL/ERY	256	II	F	USA600	45/45
	881	6/24/05	SS	PSU	CIP/CLI/CHL/ERY/GEN/ MUP	128	II	A1	NY/Japan	5
	584‖	7/15/04	Wound	8th	GEN	8	IV	G	ND	714/30
	559‖	7/22/04	PL	dialysis	CHL/ERY	16	IV	C1	USA800	5
	833	9/13/04	Urine	10th	CIP/CLI/ CHL/ERY/GEN/ MUP	32	IV	B2	USA400	1/1
	677	3/10/05	SS	8th	CIP/ERY/RIF	8	IV	C2	USA800	5
	771	4/25/05	Blood	8th	CIP/CLI/CHL/ERY/MUP	32	IV	B1	USA400	1
	780	5/07/05	TS	9th	CHL/ERY	16	IV	C1	USA800	5
	772	5/19/05	Blood	IMU	CIP/CLI/ERY/MUP	32	IV	B1	USA400	1
	773	5/22/05	TS	ICU	CIP/CLI/CHL/ERY	8	IV	C1	USA800	5
	852	7/05/05	TS	CICU	CIP/CLI/CHL/ERY/MUP	32	IV	B1	USA400	1
	856	8/10/05	Blood	ICU	CIP/CLI/CHL/ERY	32	IV	B1	USA400	1
	859	8/15/05	SS	6th	ERY/GEN/RIF	32	IV	C1	USA800	5
	861	8/30/05	Blood	10th	CIP/CLI/CHL/ERY/MUP	32	IV	B1	USA400	1
	862	8/31/05	Blood	ICU	CIP/CLI/CHL/ERY/GEN	32	IV	B1	USA400	1
	922	9/03/05	Blood	ICU	CIP/CLI/CHL/ERY	32	IV	B1	USA400	1
	923	9/06/05	SS	9th	CIP/CLI/CHL/ERY/GEN	32	IV	B2	USA400	1
	919	9/21/05	Urine	10th	CIP/CLI/CHL/ERY	32	IV	B1	USA400	1
	920	9/28/05	PL	CICU	CHL/CIP	32	IV	B3	USA400	1
	915	10/24/05	Urine	10th	CIP/CLI/CHL/ERY	32	IV	B3	USA400	1
Private (6)	838	10/22/06	BAL	ICU	CIP/CLI/ERY/GEN/MUP	128	II	A3	NY/Japan	5
	1003	3/28/07	Nares	CICU	CIP/CHL/ERY	8	IV	B1	USA400	1
	969	4/25/07	BAL	PSU	ERY	8	IV	I	ND	30/30
	1007	7/27/07	TS	CICU	CIP/ERY	64	IV	H	EMRSA-15	22/22
	1008	8/04/07	BAL	10th	(-)	32	IV	C3	USA800	5
	1013‖	8/24/07	Wound	PSU	(-)	8	IV	D	OSPC	30

BAL, bronchoalveolar lavage; *CC*, clonal complex; *CHL*, chloramphenicol; *CICU*, cardiac intensive care unit; *CIP*, ciprofloxacin; *CLI*, clindamycin; *ER*, emergency room; *ERY*, erythromycin; *GEN*, gentamycin; *ICU*, intensive care unit; *IMU*, immunocompromised unit; *MUP*, mupirocin; *ND*, not determined; *PL*, peritoneal liquid; *PSU*, postsurgical unit; *RIF*, rifampin; *SS*, surgical site; *TS*, tracheal secretion.
*β-lactams not included.
†Defined by pulsed-field gel electrophoresis.
‡According to McDougal et al, 2003.
§ST, sequence type obtained by MLST.
‖PVL-positive isolates.

profiles were observed. Whereas, for the private hospital, the profile of a few isolates was polyclonal, in the public hospital, the great majority of isolates belonged to a few lineages, and 94.5% were related to the USA400/ST1 (66.7%) and USA800/ST5 (27.8%). These latter findings allowed us to confirm important changes that have occurred to the epidemiology of MRSA infections in Brazilian public hospitals. In the initial period of the past decade, the BEC/typeIII/ST239 was the main lineage in Brazilian hospitals, although SCC*mec* IV isolates were already circulating in hospitals with rates of approximately 10%.[8,11] However, in the middle of 2000s, Silva-Carvalho et al[12] evaluated 150 MRSA isolates from 2 public hospitals in Rio de Janeiro and verified that SCC*mec* IV isolates were responsible for 69.3% of them. Likewise, Schuenck et al[11] found 57.1% of MRSA SCC*mec* IV isolates, between 2005 and 2007, from a public orthopedic hospital in Rio de Janeiro. In both studies, the main lineages found were USA400/ST1 followed by USA800/ST5. Our study, which found 23.2% of MRSA SCC*mec* IV isolates, recovered between 2004 and 2007, probably reflects the period when these isolates became establishment, especially in public hospital. In the private hospital, where only 5 SCC*mec* IV isolates were detected, the low occurrence of them could be related to the shorter study period (11 months vs 17 months, respectively), fewer beds, and the success of the infection control policies.

Our findings suggest that, in Brazil, USA400 isolates of community origin have gradually replaced BEC/type III in the hospital environment because that type IV isolates have shown antimicrobial resistance rates higher than other SCC*mec* IV isolates, such as ST5 or ST30.[8,12] Moreover, it is possibly that this type IV lineage has achieved a balance between virulence and resistance that allowed it to spread, leading to outbreaks as observed in our study, where 9 strains from the same genotypic profile were recovered in a period of 3 months. The constant presence of USA800/ST5 isolates in Brazilian hospitals may indicate that this lineage is also able to maintain itself in our health institutions.

In the private hospital, the total number of MRSA isolates was lower than in the public hospital, but a polyclonal occurrence among SCC*mec* IV isolates was seen. The 5 isolates recovered from this institution were associated to 5 PFGE genotypes from 4 different lineages (ST1, 5, 22, and 30), which are well established in hospitals around the world.[6,27,29] Although the EMRSA-15/ST22

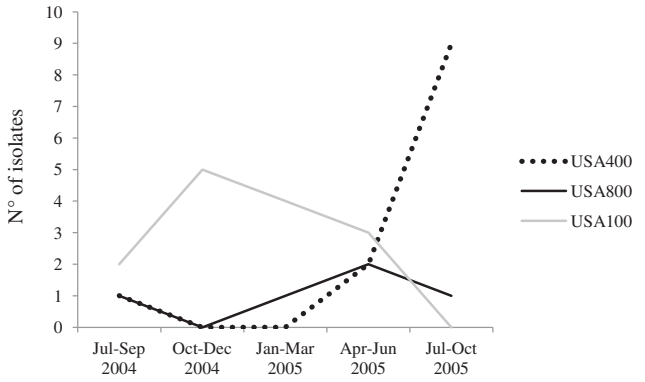

Fig 2. Temporal variation of SCC*mec* IV (USA400 and USA800 lineages) and SCC*mec* II (USA100 lineage) MRSA isolates in a public hospital in Rio de Janeiro.

lineage is common in European hospitals,[30] this is the first report of this ST in Brazil.

The difference in the molecular epidemiology of MRSA infections found between the 2 hospitals evaluated may be closely related to the characteristics of the Brazilian health system. In Brazil, tertiary care public hospitals serve a majority of the population, which is of low income. The patients are accommodated in wards with other patients, contributing to the dissemination of well-adapted lineages and the occurrence of outbreaks. These characteristics could explain the outbreaks related to a few lineages in the public hospital, including the ST1 and ST5/SCC*mec* type IV and the ST5/SCC*mec* type II lineages. Concerning the private hospital, the lineage diversity could be a reflection of fewer outbreaks because of the infection control in the institution. Another important point is that the rooms accommodate only 1 patient, and the number of health care workers per patients is higher than in the public hospitals, which might have contributed to reduction of cross-transmission cases.

In this study, the type II MRSA isolates were mainly identified in the public hospital. Eleven SCC*mec* II isolates belonged to the USA100/ST5 lineage, and 8 (72.7%) were of the same pulsotype. The prevalence of SCC*mec* II isolates in Brazil is very low, and the high occurrence of these isolates in the public hospital evaluated probably reflects an outbreak in this institution. Interestingly, only 1 SCC*mec* II isolate was recovered in the private hospital, and it also belonged to USA100/ST5, suggesting that this lineage is better adapted to our environment than other isolates carrying the SCC*mec* II. In the public hospital, 1 isolate belonging to the USA200/ST36 was detected, which is traditionally found in Ireland and United Kingdom.[30] This is the first report of this SCC*mec* II lineage in Brazil.

In the present study, the PVL genes were found in 3 MRSA type IV isolates: 1 recovered from a HCAI in a public hospital patient and related to the USA800/ST5 lineage and the other 2 isolates from patients presenting community infections that were related to the ST30 lineage. These virulence genes have been commonly found in only a few lineages, such as STs 8, 30, 22, and 59.[31,32] In Brazil, the ST30 and their variants are the main PVL-positive lineages associated with community-acquired infections[10,27] confirming our findings. However, the occurrence of PVL-positive ST5 isolates is not common in hospitals worldwide.

In summary, our results confirm the emergence of MRSA isolates from 2 main SCC*mec* IV lineages, USA400/ST1 and USA800/ST5, and the USA100/ST5 SCC*mec* II lineage in Rio de Janeiro hospitals. The dissemination of these lineages was observed in the public hospital, but, in the private hospital, a polyclonal presence of MRSA isolates was found. These facts indicate the ability of certain MRSA lineages to emerge in Brazilian hospitals, and the characteristics of the health institution could facilitate their dissemination.

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