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REVIEW ARTICLE
Staphylococcal cassette chromosome *mec* (SCC*mec*) in methicillin-resistant coagulase-negative staphylococci. A review and the experience in a tertiary-care setting

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SUMMARY

Coagulase-negative staphylococci (CNS) are increasingly recognized to cause clinically significant infections, with *S. epidermidis* often cited as the third most common cause of nosocomial sepsis. Among CNS, there is a high prevalence of methicillin resistance associated with staphylococcal cassette chromosome (SCC*mec*) elements. Although identical SCC*mec* types can exist in *S. aureus* and CNS, some novel classes of SCC*mec* may be unique to CNS. Differences in the accuracy of identification of CNS species and use of non-standardized methods for the detection of methicillin resistance have led to confusing data in the literature. In addition to the review of SCC*mec* in CNS, in this paper we report a 2-year surveillance of methicillin-resistant CNS in a tertiary-care hospital in Guadalajara, Mexico.

Key words: Methicillin-resistant coagulase-negative staphylococci, PFGE, SCC*mec*.

Clinical importance of coagulase-negative staphylococci (CNS)

CNS are differentiated from the closely related but more virulent *Staphylococcus aureus* by their inability to produce free coagulase enzyme [1]. There are currently more than 40 recognized species in the group [2], many of which form part of the normal flora of healthy human skin and mucus membranes; those most frequently associated with infections in humans are *S. epidermidis*, *S. haemolyticus* and *S. saprophyticus*. Other species occasionally isolated from clinical specimens include *S. hominis*, *S. warneri*, *S. capitis*, *S. simulans*, *S. cohnii*, *S. xylosus*, *S. saccharolyticus* and *S. lugdunensis* [3–5].

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Within the last few years, CNS have been increasingly recognized to cause clinically significant infections and are particularly associated with the use of medical devices such as intravascular and peritoneal dialysis catheters, cerebrospinal fluid shunts, prosthetic heart valves, and other plastic indwelling devices. Most infections result from the inoculation of organisms on the skin at the time of device implantation in the hospital [3–5]. The ability to infect patients carrying medical devices is primarily related to the capacity of some CNS to form biofilms where the bacteria adhere to the inert surface of the plastic devices, triggering a change in microbial behaviour such as by quorum sensing, in which the outer layer of cells protect the interior community [6] and confer increased resistance to antimicrobial agents [7].

S. epidermidis is the most commonly isolated CNS and was first identified in microbiological cultures in

Table 1. *Distribution of* SCC*mec types found in coagulase-negative staphylococci, both in animals and in humans*

Species	Source	SCC*mec* type	Reference
S. epidermidis	Human	I, IIa, IIb, III, IV, IVa, IVb, IVc, IVd, V, (III variant), (I and III), (III and IV), (II and V), (III and V) NT	[36–40], this study
	Cats, dogs, chicken	IV, IVb	[47, 48]
S. haemolyticus	Human	I, II, III, IV, V, III variant, (II and V) New, NT	[36, 37, 39, 40, 42], this study
S. warneri	Human	IVE	[40]
	Dogs	IVb	[47]
S. lentus	Sheep, goat, cattle	III	[48]
S. sciuri	Human	III	[36]
	Sheep, goat, cattle, pigs	I, V	[48]
S. xylosus	Cattle	III	[48]
S. saprophyticus	Human	III (Similar to II/III)	[44, 45]
S. hominis	Human	III, NT, New	[36, 39], this study
S. capitis	Human	I, IA, II, III, IV, V, NT, New	[36, 39]

NT, Non-typable; SCC*mec* types in parentheses amplified for both elements.

1880. In contrast to *S. aureus*, which is often a cause of serious and fatal infections, *S. epidermidis* has a predisposition to cause chronic and recurring infections [3, 4, 8, 9]. The identification of this species as an aetiological agent of infection is sometimes difficult as most infections associated with it are characterized by non-specific clinical manifestations and as part of the normal skin flora it is frequently found as a contaminant in cultures. Nevertheless, *S. epidermidis* is today recognized as an important cause of nosocomial infections and has been ranked the third most common cause of nosocomial sepsis in some studies [10, 11].

The second most commonly isolated species of CNS, *S. haemolyticus* is part of the resident flora in the axilla, perineum, and inguinal areas of humans. It is sometimes a cause of sepsis and has been repeatedly implicated in bloodstream infections, peritonitis, and infections of the urinary tract, wounds, bone, and joints [10, 11]. Most strains of *S. haemolyticus* exhibit a highly antibiotic-resistant phenotype [12].

Methicillin resistance and SCC*mec*

Methicillin-resistant *S. aureus* (MRSA) isolates were first reported in 1961 [13], and by the mid-1980s it was recognized as a significant problem in the USA, with several outbreaks documented in tertiary-care teaching hospitals [14, 15]. Today, MRSA strains are widespread in all parts of the world and represent a serious burden of infection in many countries, not only in hospitals but also in the wider community. Intrinsic methicillin resistance in staphylococci is due to the expression of a modified penicillin-binding protein PBP2a (PBP2′) encoded by the *mecA* gene and located on the mobile element staphylococcal cassette chromosome (SCC*mec*), a genomic island of variable size (range 21–67 kb) [16] integrated at the 3′ end of the *orfX* [17] gene located near the chromosomal origin of replication. For *S. aureus*, the element includes the repressor genes *mec1* and *mecR1* [18–21].

Eight different SCC*mec* types (I–VIII) have been identified and are classified according to different sets of *ccr* (chromosome cassette recombinase) (*ccrAB1*, *ccrAB2*, *ccrAB3*, *ccrAB4*, *ccrC*), which are genes that are responsible for both its chromosomal integration and excision [16, 22]. Several SCC*mec* subtypes IIA–E [23], IVa–g [24–26], and SCC non-*mec* types have been reported [27–31]. In addition, differences in the *mec* gene complex (classes A–E) [27, 32–35] have been described. It should be noted that the majority of the work on the characterization of *mec*A and its vector, SCC, has centred on MRSA, but this element is not exclusive to *S. aureus* as it has been found in other species of the genus.

The prevalence of methicillin resistance has been reported to be higher in CNS than in *S. aureus*, with rates ranging globally from 75% to 90% during the 1990s [12]. *S. epidermidis* is the most frequently isolated of the methicillin-resistant (MR)-CNS [36–40], which mirrors the frequency of both methicillin susceptible and resistant isolates in CNS species. Among human isolates, SCC*mec* has been described in *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. capitis*, *S. sciuri*, *S. warneri*, and *S. saprophyticus* [36–45] (Table 1).

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It soon became evident that novel classes of the SCC*mec* element may exist in CNS as many reports described strains lacking the elements present in *S. aureus* or reported strains that amplified two elements, suggesting the presence of different elements of SCC*mec* [36, 37, 39, 40]. As reported for MRSA, high levels of resistance to oxacillin or cefoxitin were linked to the presence of SCC*mec* type III in CNS [36, 37]. Nevertheless, additionally to SCC*mec* type III, other types and subtypes have been described for CNS. For example, for *S. epidermidis*, types I, II (subtypes a, b), III, IV, (subtypes a, b, c, d) and V have been described as well as other putative different SCC*mec* elements characterized by amplification for two elements: for I and III, for III and IV, for II and V, and for III and V (Table 1).

For *S. haemolyticus* SCC*mec* types I, II, III, IV, V and, as described for *S. epidermidis*, new proposed elements (III variant, amplification for II and V). Additionally to *S. epidermidis* and *S. haemolyticus*, SCC*mec* types have been described for *S. warneri, S. lentus, S. sciuri, S. xylosus, S. saprophyticus, S. hominis* and *S. capitis* (Table 1).

MR-CNS in animals

MR-CNS has been reported in several species of animals, such as cattle, sheep, goat, pigs, chickens, dogs, cats, horses and Cope's grey treefrogs where a prevalence as high as 59% has been found [46–50]. In several of these studies, some SCC*mec* elements have been reported (Table 1). It has been suggested that the diversity of CNS species and the SCC*mec* elements found in isolates from several species of animals, some of them domestic or so-called food animals, and the demonstrated capacity of these bacterial species to cause suppurative disease in these animals (which undoubtedly increases the shed of microorganisms) render them a potential threat to humans and constitutes a potential risk from the consumption of foods of animal origin [51, 52].

Clonal diversity of MR-CNS

The classification of CNS in relation to the SCC*mec* elements has been achieved primarily by the use of the same strategies used for MRSA. However, as CNS can harbour SCC*mec* elements different from those in MRSA, the high diversity of these mobile elements poses a significant challenge for researchers. CNS are highly clonally diverse, the most noteworthy example being *S. epidermidis*, in which a high degree of genetic diversity has been described for the SCC*mec* element IVa [38]. Moreover, epidemiological studies using multilocus sequence typing (MLST) suggest that *S. epidermidis* isolates prevalent in the hospital environment differ from those causing community-acquired disease [53]. Lancastre *et al.* proposed that *S. epidermidis* clones could be defined by the combination of a carefully standardized pulsed-field gel electrophoresis (PFGE) protocol and identification of the SCC*mec* type [54].

Another study analysed representative isolates of *S. epidermidis* from diverse geographic and clinical origins, characterized by SCC*mec* and MLST, and reported the finding that nine epidemic clonal lineages are disseminated worldwide with one single clonal lineage comprising 74% of the isolates. They concluded that *S. epidermidis* has a population with an epidemic structure, in which clones have emerged as a result of high levels of recombination and evolved through the transfer of genetic mobile elements, including SCC*mec* [55].

Origin of methicillin resistance

Evidence suggests that acquisition of SCC*mec* elements in *S. aureus* by susceptible ancestors has taken place at different times and at different locations. The first MRSA strain emerged when a SCC*mec* element was integrated into the chromosome of a susceptible *S. aureus* strain, but the donor remains unidentified. The mechanisms may involve the action of recombinases, which are capable of striking and incorporating the element into the bacterial chromosome [16]. Although the *mec* origin remains unknown, it has been suggested that SCC*mec* can shift between both coagulase-positive and coagulase-negative staphylococci and *mecA*-positive CNS may act as potential SCC*mec* donors accounting for the rise in new MRSA clones [56, 57].

In general, CNS are thought to comprise a reservoir of resistance genes for *S. aureus* and some features that support this hypothesis are:

(i) the higher frequency of SCC*mec* elements in CNS than in *S. aureus*;
(ii) the evidenced horizontal transfer of resistance genes from CNS to *S. aureus* [58–64];
(iii) genome flexibility in *S. epidermidis* which may lead to the acquisition of some transferable resistance elements [65];

(iv) the species-independent conservation of some *ccr* elements [66];
(v) CNS are more likely to contain different *ccr* complexes [66];
(vi) the great diversity of SCC elements found in CNS (Table 1),
(vii) the high variation in the prevalence of MRSA according to geographic region and the high prevalence of MR-CNS regardless of the geographic area [12].

New SCC*mec* types or elements are being continuously discovered around the world in different species and it will be necessary to determine if these diverse elements have been present for a long time or if new clones continue to arise in a microevolutionary process.

Detection of methicillin resistance

Detection of methicillin resistance in CNS is problematic, as expression of the *mec* gene is heterotypic, being constitutive in many strains, whereas in others it is inducible. Phenotypic methods have been used to detect MR-CNS because they can be readily performed in most laboratories. According to the Clinical and Laboratory Standards Institute (CLSI), the cefoxitin diffusion disk is the preferred method for detection of *mec*A-mediated resistance in CNS (except for *S. lugdunensis*); cefoxitin is used as a surrogate for detection of oxacillin resistance [67]. When compared to the molecular detection of methicillin resistance, the sensitivity and specificity of the phenotypic tests for cefoxitin disk diffusion is 94·9% and 97%, respectively, with detection of resistance dependent on species [68].

The performance of the automated Vitek 2 system for identifying *mec*A-positive staphylococci was comparable to PCR and the CLSI disk diffusion method (sensitivity and specificity of 94·6% and 93·5%, respectively). However, its performance was species dependent as results were poor in tests with *S. cohnii*, *S. hominis* and S. *saprophyticus* [68].

Identification of CNS

Several commercial kits have been used in diagnostic laboratories with varying success for the identification of CNS species including API Staph ID 32 and Vitek 2 (bioMérieux, France); Staph-Zym test (Rosco, Denmark); Staphylo LA test (Wako, Japan); Sensititre (TEK Diagnostic Systems Inc., USA); MicroScan (Dade Behring, USA); Phoenix and Crystal GP systems (Becton Dickinson, USA). The sensitivity of these systems is often not better than fair, particularly for species other than *S. epidermidis* and *S. haemolyticus*. For example, MicroScan, Vitek 2, and Crystal GP correctly identified 82·5%, 87·5% and 67·5% of CNS, respectively in human clinical isolates in which *S. epidermidis* and *S. haemolyticus* predominated [69]. Furthermore, the new low-inoculum mode of the Phoenix system correctly identified 90·5% of isolates and accuracy was satisfactory for *S. epidermidis, S. saprophyticus* and *S. haemolyticus*, but was notably lower for other species such as *S. hominis* (69·6%) [70]. In general, for most kit systems a lower sensitivity has been reported for the identification of CNS species when *S. epidermidis* and *S. haemolyticus* are infrequent in the sample. For example, API Staph ID 32 correctly identified 41% of the CNS isolates from veterinary sources and showed complete (100%) sensitivity for *S. epidermidis*, but lower values were observed for *S. xylosus* (87%), *S. chromogenes* (37%) and *S. warneri* (15%) [71]. It should be noted that the prevalence and diversity of the SCC*mec* in CNS has been studied mainly by the use of phenotypic systems, mainly by API ID 32 Staph (Table 2). The results obtained using such systems should be interpreted with caution in the light of the sometimes low specificity for species other than *S. epidermidis* and *S. haemolyticus*. As a result many laboratories are increasingly relying on DNA sequencing for species identification [72], while for identification of CNS species, sequence data of housekeeping genes such as *rpoB* [73, 74], *hsp60* [75], *dnaJ* [76], *tuf* [77], *sodA* [78] and 16S RNAr [79] is recommended.

Two-year surveillance of MR-CNS in a tertiary-care hospital in Guadalajara, Mexico

To determine the distribution of the SCC*mec* in MR-CNS and its relation to antimicrobial resistance in a tertiary-care hospital in Guadalajara, Mexico, we studied all the MR-CNS collected from blood samples in 2007 and 2008 ($n=45$). CNS isolates were identified by conventional biochemical tests [1] and via the use of API strips. Resistance to methicillin was determined for all isolates by the cefoxitin disk test [67] and by PCR [80]. MR-CNS with uncertain biochemical patterns, including species other than *S. epidermidis* and *S. haemolyticus* were further examined by amplification and sequencing of the 16S

Table 2. *Distribution of identification of coagulase-negative staphylococci species and the method used for identification*

Method used for identification	Species	SCC*mec* type	Ref.
API ID 32 Staph and *tuf* PCR	*S. epidermidis*	I, III, IV, (I and III), (III and IV), NT	[36]
API ID 32 Staph	*S. haemolyticus*	I, II, NT	[36]
	S. hominis	III, NT	
	S. sciuri	III	
	S. capitis	I, III, NT	
	S. epidermidis	IVb	[47]
	S. hominis	Ib	
	S. haemolyticus	IV, V	
	S. warneri	IVb	
	S. saprophyticus	III, Similar to II/III,	[44, 45]
	S. haemolyticus	V	[42]
	S. epidermidis	IV	[48]
	S. sciuri	I, V	
	S. xylosus	III	
	S. lentus	III	
	S. epidermidis	III, III variant, IVc, IVE, New, NT	[40]
	S. haemolyticus	III variant, NT, New	
	S. warneri		
Conventional biochemical tests or genotype	*S. epidermidis*	I, II, IV, V, NT, New	[39]
	S. haemolyticus	IV	
	S. capitis	IA, II, IV, V, New	
	S. hominis	New	
Sequencing of the *rrs* region	*S, cohnii* and *S. hominis*	NT	
	S. epidermidis	III, IV, V, NT	[37]
	S. haemolyticus	IV, V, NT	
Staphylo LA test	*S. epidermidis*	I, IIa, IIb, III, IVa, IVb, IVc, IVd, V NT	[38]

NT, Non-typable.

rRNA gene using primers F-5′-GGIACTGAGAC-ACIGICCIIACTCCT-3′ and R-5′-TTCCIITACIGI-TACCTTGTTACGACTT-3′ [81].

All sequencing was performed at the Instituto de Biotecnología de la Universidad Nacional Autónoma de México.

Preparation of template DNA and SCC*mec, ccr* and *mec* class typing were performed as previously described [80] and susceptibility testing was performed by broth microdilution using panels from Sensititre (TEK Diagnostic Systems Inc.) according to the manufacturer's instructions. For all assays, the control organism (*S. aureus* ATCC 29213) was used and susceptibility breakpoints were as recommended by CLSI [67].

As expected, the most frequently identified MR-CNS species was *S. epidermidis* ($n=34$) followed by *S. haemolyticus* ($n=7$) and *S. hominis* ($n=4$) (Table 3).

Of the methicillin-resistant *S. epidermidis* isolates examined, 11-harboured SCC*mec* type III, 12 SCC*mec* type IVa, three showed amplification products for II and V elements and one strain was positive for both V and III SCC*mec* elements. Seven strains were non-typable (Table 3).

Among the *S. haemolyticus* isolates, type III element was detected in two isolates and two others amplified both types II and V. For *S. hominis*, one strain typed for the III SCC*mec* element and three others were non-typable. Multiple *ccr* elements were found in all three species. MRSA clinical isolates that had been previously characterized in this hospital were SCC*mec* type II [82]. Interestingly, the SCC*mec* type II alone was not detected among MR-CNS strains. It should be noted that the MRSA study represented clinical isolates collected from 1999 to 2003.

An extremely high level of drug resistance was found for all isolates (Table 3). Lower resistance rates were observed for cefuroxime, gentamicin, nitrofurantoin and rifampicin; regardless of the SCC*mec* detected (the difference was not statistically significant).

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Table 3. *Distribution of* SSC*mec cassettes among methicillin-resistant isolates from bloodstream infections within a 2-year period and minimal inhibitory concentrations (MIC) of antimicrobials (μg/ml)*

Isolate	Species	*ccr*	*mec* complex	SCC*mec*	Amc	Cfp	Cxm	Mer	Imp	Gm	Clin	Cip	Nor	Nit	Sxt	Clo	Rif	Tet
1	*S. epidermidis*	3	A	III	>8	>16	16	>8	>8	>8	>2	⩽0.5	⩽2	⩽16	⩽1	⩽4	⩽0.5	⩽2
2	*S. epidermidis*	3	A	III	>8	>16	>16	>8	>8	8	>2	>2	>8	⩽16	>2	⩽4	⩽0.5	⩽2
3	*S. epidermidis*	NT	A	III	>8	⩽4	16	>8	>8	⩽2	>2	>2	>8	>64	>2	16	⩽0.5	⩽2
4	*S. epidermidis*	NT	A	III	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
5	*S. epidermidis*	2 & 3	A	III	>8	>16	>16	>8	>8	>8	>2	>2	>8	⩽16	>2	>16	2	⩽2
6	*S. epidermidis*	3 & 4	A & B	III	>8	>16	⩽2	>8	>8	>8	⩽0.25	⩽0.5	⩽2	⩽16	>2	>16	⩽0.5	⩽2
7	*S. epidermidis*	2 & 4	B	III	>8	>16	16	>8	>8	⩽2	>2	>2	>8	⩽16	>2	⩽4	>2	⩽2
8	*S. epidermidis*	2	B	III	>8	>16	⩽2	>8	>8	⩽2	>2	⩽0.5	⩽2	⩽16	⩽1	⩽4	⩽0.5	>8
9	*S. epidermidis*	NT	NT	III	>8	>16	16	>8	>8	8	>2	⩽0.5	⩽2	⩽16	⩽1	>16	>0.5	8
10	*S. epidermidis*	NT	NT	III	>8	>16	>16	>8	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
11	*S. epidermidis*	NT	NT	III	>8	>16	⩽2	>8	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
12	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
13	*S. epidermidis*	2	B	IVa	>8	>16	16	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	16	⩽0.5	⩽2
14	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
15	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	>2	⩽4	>2	⩽2
16	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	>2	⩽4	⩽0.5	⩽2
17	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	>8	>2	2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
18	*S. epidermidis*	2	B	IVa	>8	>16	⩽2	>8	>8	>8	>2	>2	>8	⩽16	⩽1	16	⩽0.5	⩽2
19	*S. epidermidis*	2 & 4	B	IVa	>8	>16	⩽2	>8	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
20	*S. epidermidis*	2 & 4	B	IVa	>8	>16	>16	>8	>8	⩽2	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
21	*S. epidermidis*	2 & 4	B	IVa	>8	>16	⩽2	>8	>8	8	>2	⩽0.5	⩽2	⩽16	>2	⩽4	⩽0.5	>8
22	*S. epidermidis*	2 & 4	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	⩽0.5	⩽2	⩽16	⩽1	⩽4	⩽0.5	⩽2
23	*S. epidermidis*	2 & 4	B	IVa	>8	>16	⩽2	>8	>8	⩽2	>2	⩽0.5	⩽2	⩽16	>2	>16	⩽0.5	>8
24	*S. epidermidis*	2 & 4	NT	II & V	>8	>16	16	>8	>8	⩽2	>2	>2	>8	>64	⩽1	16	⩽0.5	8
25	*S. epidermidis*	2 & 4	NT	II & V	>8	>16	16	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
26	*S. epidermidis*	2 & 4	NT	II & V	⩽2	⩽4	>16	⩽2	⩽2	⩽2	>2	⩽0.5	⩽2	64	⩽1	16	2	⩽2
27	*S. epidermidis*	2 & 4	B	III & V	>8	>16	⩽2	>8	>8	8	>2	>2	>8	⩽16	>2	>16	>2	>8
28	*S. epidermidis*	1	A	NT	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	>2	>16	⩽0.5	>8
29	*S. epidermidis*	3	A	NT	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
30	*S. epidermidis*	4	NT	NT	>8	>16	16	>8	>8	⩽2	>2	>2	>8	⩽16	>2	⩽4	>2	⩽2
31	*S. epidermidis*	NT	NT	NT	>8	>16	⩽2	>8	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
32	*S. epidermidis*	NT	NT	NT	>8	>16	>16	>8	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
33	*S. epidermidis*	NT	NT	NT	>8	>16	⩽2	>8	>8	⩽2	⩽0.25	⩽0.5	⩽2	⩽16	⩽1	⩽4	⩽0.5	⩽2

34	*S. epidermidis*	NT	NT	NT	⩽2	⩽4	⩽2	⩽2	⩽2	>2	⩽0.5	⩽2	⩽16	⩽1	⩽4	⩽0.5	⩽2
35	*S. haemolyticus*	NT	NT	III	>8	>16	16	>8	⩽2	>2	>2	>8	>64	>2	16	⩽0.5	⩽2
36	*S. haemolyticus*	NT	NT	III	>8	>16	>16	>8	>8	>2	>2	>8	⩽16	>2	⩽4	>2	⩽2
37	*S. haemolyticus*	NT	NT	II & V	>8	>16	⩽2	>8	⩽2	>2	>2	>8	⩽16	⩽1	⩽4	⩽0.5	⩽2
38	*S. haemolyticus*	NT	NT	II & V	>8	>16	⩽2	>8	⩽2	>2	>2	8	⩽16	⩽1	16	⩽0.5	⩽2
39	*S. haemolyticus*	NT	NT	NT	>8	>16	>16	>8	>8	>2	>2	>8	⩽16	>2	⩽4	2	⩽2
40	*S. haemolyticus*	NT	NT	NT	>8	>16	⩽2	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
41	*S. haemolyticus*	NT	NT	NT	>8	>16	>16	>8	>8	>2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
42	*S. hominis*	1 & 4	A	III	>8	>16	⩽2	>8	>8	>2	2	8	⩽16	>2	⩽4	⩽0.5	>8
43	*S. hominis*	1 & 4	A	NT	>8	>16	⩽2	>8	>8	⩽2	>2	>8	⩽16	>2	>16	⩽0.5	⩽2
44	*S. hominis*	1 & 4	A	NT	>8	>16	⩽2	>8	>8	⩽2	>2	>8	⩽16	>2	⩽4	⩽0.5	8
45	*S. hominis*	NT	A	NT	>8	>16	⩽2	>8	>8	⩽2	>2	8	⩽16	>2	⩽4	⩽0.5	>8

AMC, Amoxicillin-clavulanic acid; Cfp, cefepime; Cxm, cefuroxime; Mer, meropenem; Imp, imipenem; Clin, clindamycin; Cip, ciprofloxacin; Nor, norfloxacin; Nit, nitrofurantoin; Sxt, trimethoprim–sulfamexazole; Clo, chloramphenicol; Rif, rifampicin; Tet, tetracycline; NT, non-typable.
All isolates had a MIC of ⩽4 for teicoplanin, ⩽2 for vancomycin, >32 for cefotaxime, >4 for erythromycin and >16 for cephalothin.

Conclusions

The mechanisms contributing to clonal diversification of MR-CNS remain unidentified. Most available information at the present time has been obtained using the tools designed mainly for MRSA and therefore, new CNS specific strategies are needed for the study of clonal diversity of MR-CNS, the SCC*mec* structure and its potential transmission to *S. aureus*. Although scientific evidence supports horizontal transfer of *mec*A, the shift mechanism has yet to be discovered. Finally, because of the increasing variety of CNS species associated with disease in humans, misidentification can lead to false conclusions in epidemiological studies, particularly in species other than *S. epidermidis* and *S. haemolyticus*.

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DECLARATION OF INTEREST

None.

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