

# Microbiological and Molecular Characterization of *Staphylococcus hominis* Isolates from Blood

Soraya Mendoza-Olazarán<sup>1</sup>, Rayo Morfin-Otero<sup>2</sup>, Eduardo Rodríguez-Noriega<sup>2</sup>, Jorge Llaca-Díaz<sup>3</sup>, Samantha Flores-Treviño<sup>1</sup>, Gloria Ma González-González<sup>1</sup>, Licet Villarreal-Treviño<sup>4</sup>, Elvira Garza-González<sup>3,5\*</sup>

**1** Departamento de Microbiología, Facultad de Medicina, Universidad Autónoma de Nuevo León. Monterrey Nuevo León, México, **2** Hospital Civil de Guadalajara, Fray Antonio Alcalde, and Instituto de Patología Infecciosa y Experimental, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara. Guadalajara, Jalisco México, **3** Departamento de Patología Clínica, Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León. Monterrey Nuevo León, México, **4** Departamento de Microbiología e Inmunología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León. Monterrey Nuevo León, México, **5** Servicio de Gastroenterología Universidad Autónoma de Nuevo León. Monterrey Nuevo León, México

## Abstract

**Background:** Among Coagulase-Negative Staphylococci (CoNS), *Staphylococcus hominis* represents the third most common organism recoverable from the blood of immunocompromised patients. The aim of this study was to characterize biofilm formation, antibiotic resistance, define the SCCmec (Staphylococcal Chromosomal Cassette mec) type, and genetic relatedness of clinical *S. hominis* isolates.

**Methodology:** *S. hominis* blood isolates (n = 21) were screened for biofilm formation using crystal violet staining. Methicillin resistance was evaluated using the cefoxitin disk test and the *mecA* gene was detected by PCR. Antibiotic resistance was determined by the broth microdilution method. Genetic relatedness was determined by pulsed-field gel electrophoresis (PFGE) and SCCmec typed by multiplex PCR using two different methodologies described for *Staphylococcus aureus*.

**Results:** Of the *S. hominis* isolates screened, 47.6% (10/21) were categorized as strong biofilm producers and 23.8% (5/21) as weak producers. Furthermore, 81% (17/21) of the isolates were methicillin resistant and *mecA* gene carriers. Resistance to ampicillin, erythromycin, and trimethoprim was observed in >70% of isolates screened. Each isolate showed a different PFGE macrorestriction pattern with similarity ranging between 0–95%. Among *mecA*-positive isolates, 14 (82%) harbored a non-typeable SCCmec type: eight isolates were not positive for any *ccr* complex; four contained the *mec* complex A *ccrAB1* and *ccrC*, one isolate contained *mec* complex A, *ccrAB4* and *ccrC*, and one isolate contained the *mec* complex A, *ccrAB1*, *ccrAB4*, and *ccrC*. Two isolates harbored the association: *mec* complex A and *ccrAB1*. Only one strain was typeable as SCCmec III.

**Conclusions:** The *S. hominis* isolates analyzed were variable biofilm producers had a high prevalence of methicillin resistance and resistance to other antibiotics, and high genetic diversity. The results of this study strongly suggested that *S. hominis* isolates harbor new SCCmec structural elements and might be reservoirs of *ccrC1* in addition to *ccrAB1* and *mec* complex A.

**Citation:** Mendoza-Olazarán S, Morfin-Otero R, Rodríguez-Noriega E, Llaca-Díaz J, Flores-Treviño S, et al. (2013) Microbiological and Molecular Characterization of *Staphylococcus hominis* Isolates from Blood. PLoS ONE 8(4): e61161. doi:10.1371/journal.pone.0061161

**Editor:** Herminia de Lencastre, Rockefeller University, United States of America

**Received:** October 12, 2012; **Accepted:** March 6, 2013; **Published:** April 9, 2013

**Copyright:** © 2013 Mendoza-Olazarán et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Funding:** The authors have no support or funding to report.

**Competing Interests:** The authors have declared that no competing interests exist.

\* E-mail: [elvira\\_garza\\_gzz@yahoo.com](mailto:elvira_garza_gzz@yahoo.com)

## Introduction

Coagulase-negative staphylococci (CoNS) represent a group of opportunistic microorganisms commonly associated with infections of immunocompromised patients [1]. Among CoNS, *Staphylococcus hominis* is one of the three most frequently identified isolates recoverable from the blood of neonates and immunosuppressed patients [2,3] and has been associated as a causal agent of bacteremia, septicemia, and endocarditis [3–7]. Nosocomial infections caused by CoNS are associated with the use of indwelling medical devices in combination with biofilm-forming potential of respective isolates [8–10]. However, among the CoNS,

*S. hominis* strains are not typically categorized as a major biofilm producers [9,11]. It has been reported that some *S. hominis* isolates are resistant to methicillin that is conferred by protein PBP2a encoded by the *mecA* gene that resides within a mobile genetic element called the Staphylococcal Cassette Chromosome *mec* (SCC*mec*) [12]. At present, eleven SCC*mec* types (I–XI) of have been assigned for *S. aureus* based on the classes of the *mec* gene complex (A–E) and the *ccr* gene complex (1–8) ([http://www.sccmec.org/Pages/SCC\\_TypesEN.html](http://www.sccmec.org/Pages/SCC_TypesEN.html)). Some studies have reported that SCC*mec* elements are more diverse in methicillin-resistant CoNS, with new variants of *ccr* genes continually being identified [13–20].

A recent molecular epidemiologic study of *S. hominis* isolates conducted by Bouchami *et al.*, 2011 demonstrated low clonality between isolates and the identification of isolates harboring the SCC $_{mec}$  type VI, VIII, and the new SCC $_{mec}$  type composed of *mec* complex A (in combination with *ccrABI*). In addition, some isolates harbored the non-typeable SCC $_{mec}$  in the absence of the *ccr* complex and others expressed two *ccr* types (in the same isolate). Additionally, *ccrB1* and *ccrB4* were identified in *mecA*-negative and *mecA*-positive isolates with high nucleotide sequence homology to genes present in *S. aureus* isolates expressing SCC $_{mec}$  I, VI, or VIII, respectively (>95%) [21].

In agreement with a report by Hanssen *et al.*, 2004 staphylococcal strains from the same geographical region possess identical *ccr* genes that differ from sequences of strains from other regions. There is evidence of horizontal SCC $_{mec}$  gene transfer between CoNS and *S. aureus* [22,23]; therefore, characterization of SCC $_{mec}$  of *S. hominis* can provide useful information regarding the evolution and mobilization of this element from this species. The aim of this study was to characterize biofilm formation potential, antibiotic resistance, SCC $_{mec}$  type, and genetic relatedness of 21 *S. hominis* clinical isolates obtained from blood cultures.

## Materials and Methods

### Ethics Statement

This study was performed with the approval of the Local Ethics Committee of the School of Medicine of the Universidad Autónoma de Nuevo León (Approval MB11-006). Informed consent was not required since bacterial isolates were the subject of this study. Isolates, not human beings were studied. Thus, informed consent was not required by the local Ethics Committee.

### Clinical isolates

*S. hominis* clinical isolates (n=21) were collected between January 2006 and December 2011 from blood cultures from two hospitals in Mexico: Hospital Civil Fray Antonio Alcalde and Hospital Universitario Dr. José Eleuterio González. All isolates were causative agents of Laboratory-Confirmed Bloodstream Infection (LCBI) according to CDC criteria ([http://www.cdc.gov/nhsn/pdfs/psmanual/17pscnsinfdef\\_current.pdf](http://www.cdc.gov/nhsn/pdfs/psmanual/17pscnsinfdef_current.pdf)). Isolates examined met at least one of the following criteria: a) Patient had a recognized pathogen cultured from two or more blood cultures and organisms cultured from blood were not related to an infection at another site, b) Patient had at least one of the following signs or symptoms: fever (>38°C), chills, or hypotension and positive laboratory results not related to an infection at another site. Isolates were kept frozen in *Brucella* broth containing 15% glycerol at -70°C. Only one isolate per patient was included in this study.

**Identification of isolates.** Isolates were identified at the species level using API Staph galleries (bioMérieux, Inc., Durham, NC) according to the manufacturer's instructions. Species identification was confirmed by partial sequencing of the 16S rRNA and the *tuf* genes as previously described [24]. Sequencing was performed at the Instituto de Biotecnología, Universidad Nacional Autónoma de México. DNA sequences were compared to gene sequences at the National Center for Biotechnology Information (NCBI) GenBank using the BLAST algorithm (<http://www.ncbi.nlm.nih.gov/BLAST>).

**Phenotypic biofilm assay.** Semi quantitative determination of biofilm formation was performed by crystal violet staining as previously described [10,25]. All isolates were tested in quadruplicate in two different experiments conducted on different days. These assays were conducted on polystyrene 96-well flat bottom,

untreated plates with a low evaporation lid. Biofilm-forming capacity of all isolates was tested under two different growth conditions: in trypticase soy broth (TSB) supplemented with 1% glucose (TSBglu) or in TSB supplemented with 3% NaCl (TSB NaCl). Briefly, biofilm samples stained with crystal violet were dissolved in an ethanol-acetone mixture (70:30). The optical density of these solutions was subsequently measured at 550 nm. To simplify the data we used the ordinal classification for the level of biofilm production proposed by Christensen *et al.* Isolates with optical densities OD  $\geq$ 0.25 were considered strong biofilm producers and isolates with optical densities between 0.15 and 0.24 were considered weak biofilm producers.

*Staphylococcus saprophyticus* ATCC 15305 (biofilm producer) and *S. hominis* ATCC 27844 (biofilm non-producer) were used as control organisms.

**Methicillin resistance and susceptibility testing.** Methicillin resistance was evaluated using the cefoxitin disk test and the *mecA* gene was detected by polymerase chain reaction (PCR) [26,27]. During the cefoxitin disk evaluation, isolates were considered resistant if measurements were  $\geq$ 24 mm and susceptible if measurements were  $\leq$ 25 mm [27]. Susceptibility testing was performed using the broth microdilution method as recommended by the Clinical and Laboratory Standards Institute (CLSI) [27]. The antibiotics tested were penicillin, ampicillin, amoxicillin-clavulanic acid, cefotaxime, vancomycin, daptomycin, gentamicin, erythromycin, tetracycline, ciprofloxacin, nitrofurantoin, trimethoprim, chloramphenicol, rifampin, and linezolid (Sigma Aldrich, Toluca, Mexico).

**SCC $_{mec}$  and PFGE typing.** SCC $_{mec}$ , *ccr*, and *mec* class typing was performed as previously described by Zhang *et al.* [26] and Kondo *et al.* [28] with modification to three primers as previously described Ruppe *et al.* [29]. All SCC $_{mec}$  typing experiments were performed in duplicate. As control strains we used for all PCR reactions isolates previously typed by Garza-González *et al.*, 2010: *Staphylococcus epidermidis* JC-5, JC-6, JC-28, JC-30, JC-488, JC-1439 and *Staphylococcus haemolyticus* JC-2165 [14,30]. PFGE was performed as described for *S. aureus* [31] with modifications to the restriction enzymes used and running conditions were as previously described by Bouchami *et al.* [21]. *S. hominis* DNA samples were digested with the *XhoI* endonuclease and bands were separated using a CHEF-DRIII instrument (Bio-Rad Laboratories, Hercules, CA). Band patterns were generated by visual analysis using Labworks 4.5 software with 1% of tolerance. The similarity coefficients were generated from a similarity matrix calculated using the Jaccard coefficient (SPSS 20.0 software).

## Results

### Biofilm formation

By assay with TBSglu, 47.6% (10/21) of the *S. hominis* isolates were categorized as strong biofilm producers (defined by the cut-off values used in this study). Weak biofilm production was observed in 23.8% (5/21) of the isolates and 28.6% (6/21) were non-producers. Whereas by assay with TBS NaCl, 33.3% (7/21) were strong biofilm producers, 23.8% (5/21) weak producers, and 42.9 (9/21) non-producers (Table 1).

### Methicillin resistance and susceptibility testing

Most isolates, 81% (17/21), showed methicillin resistance by the cefoxitin disk test, and all isolates tested positive for the *mecA* gene (Table 1). All *S. hominis* isolates were resistant to at least one of the non- $\beta$ -lactam antibiotics tested. Resistance rates for penicillin, ampicillin, amoxicillin-clavulanic acid, erythromycin, trimethoprim, ciprofloxacin, tetracycline, chloramphenicol, gentamicin,

**Table 1.** Molecular and phenotypic characterization of *S. hominis* blood isolates.

Isolate	Biofilm <sup>1</sup>		FOX <sup>2</sup>		Zhang <sup>4</sup>		Kondo <sup>4</sup>		SCCmec type <sup>5</sup>	Resistance profile <sup>6</sup>	
	Glu	NaCl	meCA <sup>3</sup>	meC	meC	ccr	meC	ccr			
397	Strong	Strong	R	Pos	A	1+5	A	1+5	UT1	PEN, AMP, AUG, GEN, ERY, TET, TMP, RIF	
501	Weak	Neg	S	Neg	Neg	Neg	Neg	Neg	Neg	PEN, AMP, AUG, ERY, CIP	
1786	Neg	Neg	R	Pos	B	Neg	B	Neg	UT	PEN, AMP, AUG, CTX, GEN, ERY, TET, CIP, NIT, TMP, CHL, RIF DAP*	
8115	Neg	Neg	R	Pos	A	1+5	A	1+5	UT1	PEN, AMP, AUG, ERY, CIP, TMP, CHL	
8122	Neg	Neg	R	Pos	A	1+5	A	1+4+5	UT2	PEN, AMP, AUG, ERY, TET, CIP, TMP, CHL	
8125	Neg	Neg	S	Neg	Neg	Neg	Neg	Neg	Neg	PEN, AMP, AUG, ERY, TMP	
8127	Weak	Neg	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, ERY, TET, TMP DAP*	
8129	Weak	Weak	R	Pos	A	1	A	1	New	PEN, AMP, AUG, GEN, ERY, TET	
8144	Neg	Neg	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, ERY, TET, CIP, TMP	
8179	Neg	Neg	R	Pos	A	3	A	3	III	PEN, AMP, AUG, TMP, CHL DAP*	
9241	Strong	Weak	S	Neg	Neg	Neg	Neg	Neg	Neg	ERY	
9989	Strong	Strong	R	Pos	A	1	A	1	New	PEN, AMP, AUG, ERY, CIP, TMP, CHL	
9994	Strong	Weak	R	Pos	A	5	A	4+5	UT3	PEN, AMP, AUG, GEN, ERY, TMP, CHL	
10866	Weak	Neg	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, ERY, CIP, TMP DAP*	
11200	Strong	Weak	R	Pos	B	Neg	B	Neg	UT	PEN, AMP, AUG, ERY, TET, CIP, NIT, TMP, RIF DAP*	
11477	Strong	Strong	S	Neg	Neg	Neg	Neg	Neg	Neg	PEN, AMP, AUG, ERY DAP*	
11621	Strong	Strong	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, ERY, TMP, CHL DAP*	
11628	Strong	Strong	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, GEN, ERY, CIP, TMP DAP*	
11630	Strong	Strong	R	Pos	A	1+5	A	1+5	UT1	PEN, AMP, AUG, GEN, ERY, TET, CIP, TMP	
11631	Strong	Strong	R	Pos	A	1+5	A	1+5	UT1	PEN, AMP, AUG, CTX, GEN, ERY, TET, CIP, TMP, CHL, RIF DAP*	
11634	Weak	Weak	R	Pos	A	Neg	A	Neg	UT	PEN, AMP, AUG, ERY DAP*	

<sup>1</sup>Neg: biofilm non-producer; Glu: media with 1% glucose; NaCl: media with 3% NaCl.

<sup>2</sup>FOX: ceftoxitin test; R: resistant; S: susceptible.

<sup>3</sup>Pos: meCA gene present; Neg: meCA absent.

<sup>4</sup>Neg: not amplified.

<sup>5</sup>SCCmec type III was assigned for *S. aureus* according to [http://www.sccmec.org/Pages/SCC\\_TypesEN.html](http://www.sccmec.org/Pages/SCC_TypesEN.html).

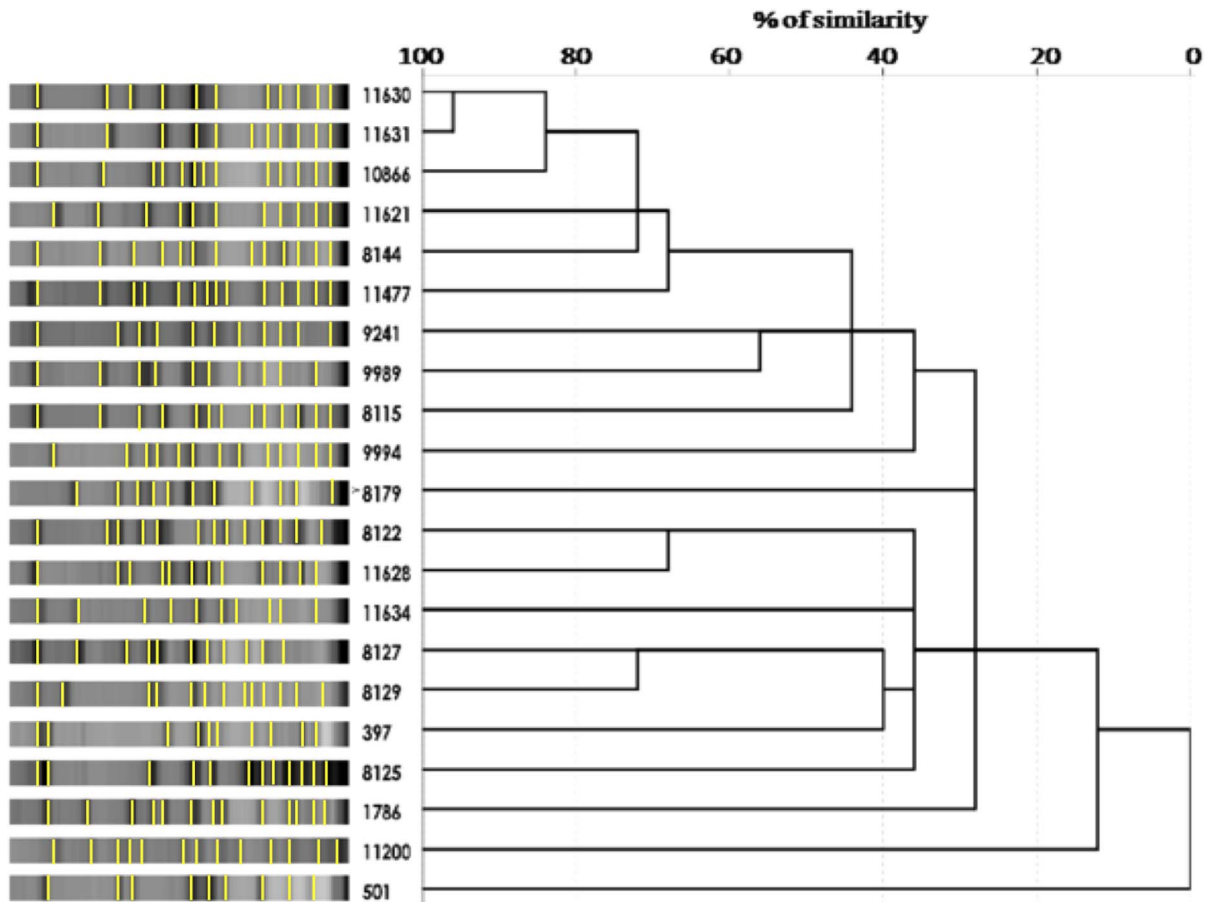
Neg: not amplified; UT: untyped; UT1, UT2 and UT3 types are assigned in this study.

<sup>6</sup>PEN: penicillin; AMP: ampicillin; AUG: amoxicillin-clavulanic acid; ERY: erythromycin; TMP: trimethoprim; CIP: ciprofloxacin; TET: tetracycline; CHL: chloramphenicol; GEN: gentamicin; RIF: rifampin; NIT: nitrofurantoin; CTX: cefotaxime; DAP: daptomycin.

\*Non-susceptible.

All isolates were susceptible to vancomycin and linezolid.

doi:10.1371/journal.pone.0061161.t001



**Figure 1. PFGE dendrogram of *S. hominis* isolates.** Similarity coefficients were generated from a similarity matrix calculated with the Jaccard coefficient using SPSS 20.0 software.  
doi:10.1371/journal.pone.0061161.g001

rifampin, nitrofurantoin, and cefotaxime for all isolates were 95%, 95%, 95%, 95%, 76%, 52%, 43%, 38%, 33%, 19%, 10%, and 10%, respectively. Furthermore, 48% of isolates were daptomycin-non susceptible. None of the 21 isolates tested in this study were found to be resistant to vancomycin or linezolid. The 4 *mecA*-negative isolates showed resistance to at least one of the  $\beta$ -lactam antibiotics tested. No correlation was found between the level of biofilm production and the resistance phenotype.

### SCC*mec* and PFGE typing

A high frequency of *mec* complex class A (88.2%), *ccrAB1* (41.1%), and *ccrC* (35.3%) was observed among *mecA*-positive *S. hominis* isolates (Table 1).

Among the 17 *mecA*-positive isolates a high proportion were non-typeable (82%), eight were negative for *ccr* complex tested by both methods (UT); four isolates had a *mec* complex *AccrAB1* and *ccrC* (UT1), one isolate had the *mec* complex A, *ccrAB4* and *ccrC* (UT2), and; one isolate had the *mec* complex A, *ccrAB1*, *ccrAB4* and *ccrC* (UT3). Two isolates carried association *mec* complex A and *ccrAB1*. One strain had SCC*mec* type III described for *S. aureus* (Table 1) (*mec* complex A, *ccr* 3, and isolate 8179).

PFGE analysis of *S. hominis* isolates identified 21 different restriction patterns with at least 3 band differences between each isolate (Figure 1). Although a 100% similarity was not observed between isolates, two isolates had 95% similarity (11630 and 11631) and were categorized as strong biofilm producers, *mecA*-

positive, *mec* class A, *ccrAB1+ccrC*, and only differed in their susceptibility pattern.

### Discussion

Most studies examining the presence of SCC*mec* among CoNS isolates have included in their respective analyses few *S. hominis* clinical isolates recovered from catheters, the catheter insertion site, pus, wound secretions, cerebral spinal fluid, or blood [11,13,14,21,30,32–34]. *S. hominis* comprises part of the normal flora colonizing the skin and mucous membranes of humans and may be found as a culture contaminant. However, detection of *S. hominis* is indicative of an infection and a probable causative agent of bacteremia. In this study, we analyzed 21 *S. hominis* clinical isolates recovered from blood and were causative agents of Laboratory-Confirmed Bloodstream Infection (LCBI) according to CDC criteria. To our knowledge, this is the first report characterizing *S. hominis* isolates identified as causative agents of bacteremia recovered from the blood at the microbiological and molecular level.

A significant observation associated with the *S. hominis* isolates studied was the ability of almost half of these strains (47.6%) to produce biofilm (since *S. hominis* is not known as a major biofilm producer) [9,11]. This characteristic represents a significant virulence factor since biofilms facilitate bacterial adherence to biomedical surfaces (such as catheters), thereby facilitating their entrance into the bloodstream [8]. However, the polysaccharide or

protein composition of *S. hominis* biofilms (or genes involved on its production) remains unknown to date.

Among the *mecA*-positive isolates (81%), nearly half were carriers of a putative new SCC*mec*. In addition, most expressed the *mec* gene class A, *ccr* type 1, and others *ccr* type 5. This combination of *mec-ccr* complexes has been reported in this bacterial species before [11,14,21,32].

The *mec-ccr* complexes identified in this study were similar to those reported by Bouchami *et al.* that demonstrated that *S. hominis* could serve as a *mec-ccr* reservoir and also serve as a likely donor of *ccrAB1* and *mec* complex A to other bacterial species. Unlike that study, we found a higher proportion of non-typeable isolates (82%) and isolates harboring *ccrC* (29%).

The data regarding SCC*mec* diversity in CoNS presented in this study may be biased due to the typing methodology used that was developed for *S. aureus*, therefore caution should be taken in the interpretation of these data. Therefore, a variety of non-typeable elements in CoNS may be simply an indication that *S. hominis* elements are different enough from those of *S. aureus* that the present typing methods can not be applied to this CoNS.

Data presented in this report also demonstrated that most isolates with new or untypeable SCC*mec* were resistant to at least three antibiotic classes, and some isolates presented with two or three recombinase complexes types, suggesting the presence of multiple SCC*mec* elements in tandem. However, to verify this, the *S. hominis* SCC*mec* cassette should be sequenced completely and compared to the *S. aureus* cassette. This analysis is currently underway in our laboratory.

We found that the 82% of *mecA*-positive isolates were untypeable and neither of the two methods used amplified any of the known recombinases suggesting that these strains are therefore

likely candidates for carrying novel SCC*mec* types. This observation was previously described for *S. hominis* [11,13,21,30,33,34] and may be explained by: a) that this cassette is a carrier of a new recombinase not related to *ccrAB* or *ccrC* genes, b) they represent new *ccr* complex isotypes that cannot be amplified by currently utilized *ccr* primers, or c) *ccr* genes were not present [23].

In this study, we identified a high rate of methicillin resistance (81%) in addition to resistance to other antibiotics among the clinical isolates studied; an observation previously reported for *S. hominis* and other CoNS species [17,21]. All methicillin resistant isolates were also positive for SCC*mec* in addition to displaying resistance to most  $\beta$ -lactams antibiotics tested.

Among the *S. hominis* isolates collected in the present study none were clonal, therefore we concluded that infections caused by these isolates were not caused by dissemination of the same isolate throughout the hospital. Taking into account the fact that *S. hominis* is a component of the normal skin and mucous membrane flora, it is likely that these infections were endogenous.

In conclusion, our results showed that *S. hominis* is a biofilm producer and in combination with its high resistance rate to antibiotics, renders this species a serious threat for infections in immunocompromised patients. Finally, *S. hominis* isolates may possess different SCC*mec* types compared to those present in *S. aureus*.

## Author Contributions

Revised the final version of the manuscript: SMO RMO ERN JLD SFT GMGG LVT EGG. Conceived and designed the experiments: EGG RMO. Performed the experiments: SMO SFT. Contributed reagents/materials/analysis tools: ERN JLD GMGG LVT. Wrote the paper: SMO.

## References

- Hidron AI, Edwards JR, Patel J, Horan TC, Sievert DM, et al. (2008) NHSN annual update: antimicrobial-resistant pathogens associated with healthcare-associated infections: annual summary of data reported to the National Healthcare Safety Network at the Centers for Disease Control and Prevention, 2006–2007. *Infect Control Hosp Epidemiol* 29: 996–1011.
- Al Wohoush I, Rivera J, Cairo J, Hachem R, Raad I (2011) Comparing clinical and microbiological methods for the diagnosis of true bacteraemia among patients with multiple blood cultures positive for coagulase-negative staphylococci. *Clin Microbiol Infect* 17: 569–571.
- Chaves F, Garcia-Alvarez M, Sanz F, Alba C, Otero JR (2005) Nosocomial spread of a *Staphylococcus hominis* subsp. novobiosepticus strain causing sepsis in a neonatal intensive care unit. *J Clin Microbiol* 43: 4877–4879.
- Palazzo IC, d'Azevedo PA, Secchi C, Pignatari AC, Darini AL (2008) *Staphylococcus hominis* subsp. novobiosepticus strains causing nosocomial bloodstream infection in Brazil. *J Antimicrob Chemother* 62: 1222–1226.
- Sunbul M, Demirag MK, Yilmaz O, Yilmaz H, Ozturk R, et al. (2006) Pacemaker lead endocarditis caused by *Staphylococcus hominis*. *Pacing Clin Electrophysiol* 29: 543–545.
- Cunha BA, Esrick MD, Lorusso M (2007) *Staphylococcus hominis* native mitral valve bacterial endocarditis (SBE) in a patient with hypertrophic obstructive cardiomyopathy. *Heart Lung* 36: 380–382.
- d'Azevedo PA, Trancesi R, Sales T, Monteiro J, Gales AC, et al. (2008) Outbreak of *Staphylococcus hominis* subsp. novobiosepticus bloodstream infections in Sao Paulo city, Brazil. *J Med Microbiol* 57: 256–257.
- Fredheim EG, Klingenberg C, Rohde H, Frankenberger S, Gaustad P, et al. (2009) Biofilm formation by *Staphylococcus haemolyticus*. *J Clin Microbiol* 47: 1172–1180.
- de Allori MC, Jure MA, Romero C, de Castillo ME (2006) Antimicrobial resistance and production of biofilms in clinical isolates of coagulase-negative *Staphylococcus* strains. *Biol Pharm Bull* 29: 1592–1596.
- Christensen GD, Simpson WA, Younger JJ, Baddour LM, Barrett FF, et al. (1985) Adherence of coagulase-negative staphylococci to plastic tissue culture plates: a quantitative model for the adherence of staphylococci to medical devices. *J Clin Microbiol* 22: 996–1006.
- Garza-Gonzalez E, Morfin-Otero R, Mart Nez VZMA, Gonzalez-Diaz E, Gonz Lez-Santiago O, et al. (2011) Microbiological and molecular characterization of human clinical isolates of *Staphylococcus cohnii*, *Staphylococcus hominis*, and *Staphylococcus sciuri*. *Scand J Infect Dis* 43: 930–936.
- Katayama Y, Ito T, Hiramatsu K (2000) A new class of genetic element, staphylococcus cassette chromosome *mec*, encodes methicillin resistance in *Staphylococcus aureus*. *Antimicrob Agents Chemother* 44: 1549–1555.
- Mombach Pinheiro Machado AB, Reiter KC, Paiva RM, Barth AL (2007) Distribution of staphylococcal cassette chromosome *mec* (SCC*mec*) types I, II, III and IV in coagulase-negative staphylococci from patients attending a tertiary hospital in southern Brazil. *J Med Microbiol* 56: 1328–1333.
- Garza-Gonzalez E, Lopez D, Pezina C, Muruet W, Bocanegra-Garcia V, et al. (2010) Diversity of staphylococcal cassette chromosome *mec* structures in coagulase-negative staphylococci and relationship to drug resistance. *J Med Microbiol* 59: 323–329.
- Pi B, Yu M, Chen Y, Yu Y, Li L (2009) Distribution of the ACME-arcA gene among methicillin-resistant *Staphylococcus haemolyticus* and identification of a novel *ccr* allotype in ACME-arcA-positive isolates. *J Med Microbiol* 58: 731–736.
- Zong Z, Lu X (2010) Characterization of a new SCC*mec* element in *Staphylococcus cohnii*. *PLoS One* 5: e14016.
- Zong Z, Peng C, Lu X (2011) Diversity of SCC*mec* elements in methicillin-resistant coagulase-negative staphylococci clinical isolates. *PLoS One* 6: e20191.
- Soderquist B, Berglund C (2009) Methicillin-resistant *Staphylococcus saprophyticus* in Sweden carries various types of staphylococcal cassette chromosome *mec* (SCC*mec*). *Clin Microbiol Infect* 15: 1176–1178.
- Bouchami O, Ben Hassen A, de Lencastre H, Miragaia M (2011) High prevalence of *mec* complex C and *ccrC* is independent of SCC*mec* type V in *Staphylococcus haemolyticus*. *Eur J Clin Microbiol Infect Dis*.
- Urushibara N, Paul SK, Hossain MA, Kawaguchiya M, Kobayashi N (2011) Analysis of *Staphylococcal cassette chromosome mec* in *Staphylococcus haemolyticus* and *Staphylococcus sciuri*: identification of a novel *ccr* gene complex with a newly identified *ccrA* allotype (*ccrA7*). *Microb Drug Resist* 17: 291–297.
- Bouchami O, Ben Hassen A, de Lencastre H, Miragaia M (2011) Molecular epidemiology of methicillin-resistant *Staphylococcus hominis* (MRSHo): low clonality and reservoirs of SCC*mec* structural elements. *PLoS One* 6: e21940.
- Hanssen AM, Kjeldsen G, Sollid JU (2004) Local variants of *Staphylococcal cassette chromosome mec* in sporadic methicillin-resistant *Staphylococcus aureus* and methicillin-resistant coagulase-negative *Staphylococci*: evidence of horizontal gene transfer? *Antimicrob Agents Chemother* 48: 285–296.
- Hanssen AM, Ericson Sollid JU (2006) SCC*mec* in staphylococci: genes on the move. *FEMS Immunol Med Microbiol* 46: 8–20.

24. Heikens E, Fleer A, Paauw A, Florijn A, Fluit AC (2005) Comparison of genotypic and phenotypic methods for species-level identification of clinical isolates of coagulase-negative staphylococci. *J Clin Microbiol* 43: 2286–2290.
25. Klingenberg C, Aarag E, Rommestad A, Sollid JJE, Abrahamson TG, et al. (2005) Coagulase-negative staphylococcal sepsis in neonates. Association between antibiotic resistance, biofilm formation and the host inflammatory response. *Pediatr Infect Dis J* 24: 817–822.
26. Zhang K, McClure JA, Elsayed S, Louie T, Conly JM (2005) Novel multiplex PCR assay for characterization and concomitant subtyping of staphylococcal cassette chromosome mec types I to V in methicillin-resistant *Staphylococcus aureus*. *J Clin Microbiol* 43: 5026–5033.
27. CLSI (2012) M100-S22. Performance Standards for Antimicrobial Susceptibility Testing; Twenty-Second Informational Supplement. Wayne, PA: Clinical and Laboratory Standards Institute.
28. Kondo Y, Ito T, Ma XX, Watanabe S, Kreiswirth BN, et al. (2007) Combination of multiplex PCRs for staphylococcal cassette chromosome mec type assignment: rapid identification system for mec, ccr, and major differences in junkyard regions. *Antimicrob Agents Chemother* 51: 264–274.
29. Ruppe E, Barbier F, Mesli Y, Maiga A, Cojocaru R, et al. (2009) Diversity of staphylococcal cassette chromosome mec structures in methicillin-resistant *Staphylococcus epidermidis* and *Staphylococcus haemolyticus* strains among outpatients from four countries. *Antimicrob Agents Chemother* 53: 442–449.
30. Garza-Gonzalez E, Morfin-Otero R, Llaca-Diaz JM, Rodriguez-Noriega E (2010) Staphylococcal cassette chromosome mec (SCC mec) in methicillin-resistant coagulase-negative staphylococci. A review and the experience in a tertiary-care setting. *Epidemiol Infect* 138: 645–654.
31. Murchan S, Kaufmann ME, Deplano A, de Ryck R, Struelens M, et al. (2003) Harmonization of pulsed-field gel electrophoresis protocols for epidemiological typing of strains of methicillin-resistant *Staphylococcus aureus*: a single approach developed by consensus in 10 European laboratories and its application for tracing the spread of related strains. *J Clin Microbiol* 41: 1574–1585.
32. Bouchami O, Achour W, Mekni MA, Rolo J, Ben Hassen A (2011) Antibiotic resistance and molecular characterization of clinical isolates of methicillin-resistant coagulase-negative staphylococci isolated from bacteremic patients in oncohematology. *Folia Microbiol (Praha)* 56: 122–130.
33. Hanssen AM, Sollid JU (2007) Multiple staphylococcal cassette chromosomes and allelic variants of cassette chromosome recombinases in *Staphylococcus aureus* and coagulase-negative staphylococci from Norway. *Antimicrob Agents Chemother* 51: 1671–1677.
34. Ibrahim S, Salmenlinna S, Virolainen A, Kerttula AM, Lyytikäinen O, et al. (2009) Carriage of methicillin-resistant Staphylococci and their SCCmec types in a long-term-care facility. *J Clin Microbiol* 47: 32–37.