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Abstract

Background: Coagulase negative staphylococci (CoNS) are important reservoirs of antibiotic resistance genes and associated mobile genetic elements and are believed to contribute to the emergence of successful methicillin resistant *Staphylococcus aureus* (MRSA) clones. Although, these bacteria have been linked to various ecological niches, little is known about the dissemination and genetic diversity of antibiotic resistant CoNS in general public settings.

Methods: Four hundred seventy-nine samples were collected from different non-healthcare/general public settings in various locations \((n = 355)\) and from the hands of volunteers \((n = 124)\) in London UK between April 2013 and Nov 2014.

Results: Six hundred forty-three staphylococcal isolates belonging to 19 staphylococcal species were identified. Five hundred seventy-two (94%) isolates were resistant to at least one antibiotic, and only 34 isolates were fully susceptible. Sixty-eight (11%) *mecA* positive staphylococcal isolates were determined in this study. SCC\(\text{mec}\) types were fully determined for forty-six isolates. Thirteen staphylococci (19%) carried SCC\(\text{mec}\) V, followed by 8 isolates carrying SCC\(\text{mec}\) type I (2%), 5 SCC\(\text{mec}\) type IV (7%), 4 SCC\(\text{mec}\) type II (6%), 1 SCC\(\text{mec}\) type III (2%), 1 SCC\(\text{mec}\) type VI (2%), and 1 SCC\(\text{mec}\) type VIII (2%). In addition, three isolates harboured a new SCC\(\text{mec}\) type 1A, which carried combination of class A mec complex and ccr type 1.

MLST typing revealed that all *S. epidermidis* strains possess new MLST types and were assigned the following new sequence types: ST599, ST600, ST600, ST600, ST601, ST602, ST602, ST602, ST603, ST604, ST605, ST606, ST607 and ST608.

Conclusions: The prevalence of antibiotic resistant staphylococci in general public settings demonstrates that antibiotics in the natural environments contribute to the selection of antibiotic resistant microorganisms. The finding of various SCC\(\text{mec}\) types in non-healthcare associated environments indicates the complexity of SCC\(\text{mec}\). We also report on new MLST types that were assigned for all *S. epidermidis* isolates, which demonstrates the genetic variability of these isolates.

Keywords: CoNS, Antibiotic resistance, SCC\(\text{mec}\), MLST
**Background**

Staphylococci are the most frequently isolated nosocomial pathogens, accounting for 30% of hospital associated infections [1]. Despite, that the high virulence of S. aureus has been evidenced in many studies [2], it is believed that coagulase-negative staphylococci (CoNS) act as an important reservoir of antimicrobial resistance genes and resistance-associated mobile genetic elements, which can transfer between staphylococcal species. Among other CoNS, S. epidermidis, S. hominis and S. haemolyticus are often reported to be resistant to multiple antibiotics [3, 4].

The mecA gene responsible for methicillin resistance was first determined in S. aureus, however, many other staphylococcal species were found to also harbour it [5]. The mecA gene encodes an additional penicillin-binding protein 2a (PBP 2a), which mediates cell wall synthesis in the presence of β-lactam antibiotics [6]. Together with its regulators mecl-mecRI and site specific recombination genes ccrA and ccrB, the mecA gene, is located on a mobile genetic element known as staphylococcal cassette chromosome mec (SCCmec) [7]. A number of studies have demonstrated the transfer of mecA gene from coagulase-negative staphylococcal species to S. aureus in vivo, and thus contributing to more successful S. aureus clones [8]. To date 11 SCCmec types have been reported based on combinations of mec (A, B, C1, C2 and D) and ccr (AB1, AB2, AB3, AB4 and ccrC) complexes and so called J regions (1, 2, 3) [9].

Traditionally recognised as hospital associated pathogens, methicillin resistant coagulase negative staphylococci (MR-CoNS) have recently been linked with a range of ecological niches (community, wildlife and environmental sources) [10–12]. As a result, today increasing attention is being paid to the rapid spread of MR-CoNS and their role in transmission within the community and non-hospital settings [13].

In this study we demonstrate the dissemination of antibiotic resistance in CoNS isolated from various environmental sites in London, UK. The characterization of mecA gene and the SCCmec elements provide insights into the diversity of environmental CoNS clones.

**Methods**

**Isolation**

Four hundred seventy-nine samples were collected from different environmental sites in various locations (n = 355) and from the hands of volunteers (n = 124) in London UK between April 2013 and Nov 2014. Environmental sites included hotels (n = 100), baby care facilities (n = 65), handbags (n = 43), supermarkets (n = 37), restaurants (n = 36), public transport (n = 54), and a public library (n = 20). All specimens were plated on Mannitol Salt Agar (Oxoid, Basingstoke, UK), and then incubated aerobically at 37 °C for 24–72 h. One or two colonies for each site were selected based on staphylococci morphology [4]. The colonies were then purified on Nutrient Agar (Oxoid, Basingstoke, UK).

**Identification**

All isolates were initially screened using Gram staining, catalase and coagulase tests. Those that demonstrated potential staphylococci characteristics were identified by Matrix-assisted laser desorption ionization time flight mass-spectroscopy (MALDI-TOF-MS, Microflex LT, Bruker Daltonics, Coventry, UK) in a positive linear mode (2000–20,000 m/z range) as described previously [12]. The resulting spectra were compared with reference spectra by using the Biotype 3.0 software (Bruker Daltonics, Coventry, UK). *Escherichia. coli* DH5α (Bruker Daltonics, Coventry, UK) was used as a standard for calibration and quality control.

**Antimicrobial susceptibility test**

A panel of 11 antibiotics was used to determine the antibiotic susceptibility of all the isolates. The standard disk diffusion method was used to test AM: amoxicillin (10 µg); CEP: cefepine (30 µg); CHL: chloramphenicol (30 µg); ERY: erythromycin (5 µg); FC: fusidic acid (10 µg); GEN: gentamicin (10 µg); MUP: mupirocin (20 µg); OX: oxacillin (1 µg); PEN: penicillin (1 unit); STR: streptomycin (10 µg); TET: tetracycline (10 µg). The susceptible, intermediate resistant or resistant were determined by the Guidelines for Susceptibility Testing [14]. The Minimum Inhibitory Concentrations (MIC) for oxacillin were additionally evaluated using "M.I.C. evaluators" (Oxoid Ltd., Basingstoke, UK).

**Detection of mecA gene and staphylococcal cassette chromosome mec (SCCmec) typing**

The mecA gene was determined by using PCR method as described previously [15]. For mecA positive isolates, SCCmec types were determined by evaluating mec and ccr complexes [15].

**MLST typing of Staphylococcus epidermidis**

Multi-locus sequence typing (MLST) was used to determine the sequence types of *S. epidermidis* [16]. Sequence types were assigned using the *S. epidermidis* database (www.mlst.net).

**Results**

**Purification of isolates**

A total of 643 staphylococci isolates were recovered in this study, including those from hotels (n = 74), baby care facilities (n = 46), handbags (n = 17), supermarkets (n = 89), restaurants (n = 96), public transport (n = 94), human hands (n = 192) and public libraries (n = 35) (Additional file 1: Table S1).
Species determination
Six hundred forty-three staphylococcal isolates belonging to 19 staphylococcal species were identified in this study. This included: S. epidermidis \((n = 193)\), S. hominis \((n = 161)\), S. capitis \((n = 77)\), S. warneri \((n = 63)\), S. haemolyticus \((n = 45)\), S. pasteuri \((n = 33)\), S. saprophyticus \((n = 20)\), S. aureus \((n = 12)\), S. simiae \((n = 10)\), S. cohnii \((n = 9)\), S. sciuri \((n = 5)\), S. pettenkoferi \((n = 3)\), S. auricularis \((n = 2)\), S. caprae \((n = 2)\), S. equorum \((n = 2)\), S. lugdunensis \((n = 2)\), S. xylosus \((n = 2)\), S. arlettae \((n = 1)\), and S. simulans \((n = 1)\). S. epidermidis was the predominant species, followed by S. hominis, S. capitis, S. warneri, S. haemolyticus, S. pasteuri, and S. saprophyticus. However, the occurrence of the species varied for different sites. S. epidermidis was predominant among the isolates recovered from restaurants, public transport, hands and handbags, whereas S. hominis was predominant among the isolates recovered from supermarkets, baby care facilities and hotels and S. haemolyticus was predominantly isolated from the library (Table 1).

Antibiotic susceptibility test results
The disc diffusion method was used to test 606 isolates against a panel of 11 antibiotics. 572 (94%) isolates were resistant to at least one antibiotic, and only 34 isolates were fully susceptible. Resistance to penicillin, fusidic acid was observed in more than 65% of all staphylococcal isolates tested. 202 (33%) isolates were resistant to streptomycin, 190 (31%) to erythromycin, 161 (27%) to amoxicillin, 98 (16%) to tetracycline, 87 (14%) to mupirocin, 59 (10%) to gentamicin, 48 (8%) to cepafine, 36 (6%) oxacillin, and 21 (3%) chloramphenicol (Table 2).

mecA gene determination and SCCmec typing results
Sixty-eight (11%) mecA positive staphylococcal isolates were determined, however, no MRSA was determined in this study. S. sciuri had the highest mecA gene carriage (80%) among all 19 staphylococcal species, followed by S. cohnii (33%), S. haemolyticus (22%), and S. saprophyticus (20%). Other isolates demonstrated relatively lower carriage of mecA gene, including S. hominis (3%), S. capitis (8%), S. epidermidis (11%), S. warneri (11%), S. pasteuri (13%). No mecA gene was found in the remaining 10 species, including S. aureus, S. simiae, S. equorum, S. caprae, S. xylosus, S. auricularis, S. simulans, S. arlettae, S. pettenkoferi, and S. lugdunensis.

SCCmec types were fully determined in forty-six isolates. Twenty-two out of 68 isolates lacked either the mec gene complex or the ccr gene complex. Thirteen staphylococci (19%) carried SCCmec type V, followed by 8 isolates carrying SCCmec type I (2%), 5 isolates SCCmec type IV (7%), 4 isolates SCCmec type II (6%), 1 isolate SCCmec type III (2%), 1 isolate SCCmec type VI (2%), and 1 isolate SCCmec type VIII (2%). In addition, three isolates harboured a new SCCmec type 1A, which carried combination of class A mec complex and ccr type 1. Of the ten isolates that were non-typeable, three carried a combination of class A mec complex and ccrC, six carried a combination of class B mec and ccrC, and one carried class B mec and ccr type 3 (Table 3).

Multi-locus sequence typing of S. epidermidis
MLST was performed to determine the housekeeping genes of 13 oxacillin resistant and mecA positive S. epidermidis. MLST typing revealed that all S. epidermidis strains possess new MLST types. MLST types of S. epidermidis isolates with in house numbers of 279, 133, 134, 135, 126, 259, 124, 127, 234, 187, 308, 153 and 191 were respectively assigned as ST599, ST600, ST601, ST602, ST601, ST602, ST603, ST604, ST605, ST606, ST607 and ST608 (Table 4). Three S. epidermidis isolates shared the same sequence types (ST), including S. epidermidis 133, 134 and 135 that were isolated from different sites of a library (DSL) possessed ST600 whereas S. epidermidis 259, and S. epidermidis 124 that had ST602 sequence type were isolated from the human hands (HH) and different sites of hotels (DSH) respectively.

Discussion
Environmental staphylococcal species
Although antibiotic resistance is commonly linked to the clinic, recent studies from different ecological niches revealed multidrug resistant bacteria is widespread in the environment [11, 12, 17].

We have previously reported on high levels of antibiotic resistance in staphylococci isolated from different environmental/public settings [11, 12]. In this study we evaluated the dissemination of antibiotic resistant staphylococci recovered from a wide range of environmental settings, and characterised the carriage of the mecA gene and the diversity of SCCmec elements in these isolates.

Table 1 Predominant and common staphylococcal species recovered from the human hands and different environmental sites

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<th>Predominant species (%)</th>
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<td>S. epidermidis (36%)</td>
<td>S. hominis (23%)</td>
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</tbody>
</table>

BCF: baby care facilities, DSH: different sites of hotels, DSL: different sites of a library, DSR: different sites of restaurants, DSS: different sites of supermarkets; DST: different sites of transportation facilities, HB: handbags, HH: human hand
Six hundred and forty-three staphylococci isolates belonging to 19 species, including *S. epidermidis*, *S. hominis*, *S. haemolyticus*, *S. capitis*, *S. warneri*, *S. pasteuri*, *S. saprophyticus*, *S. cohnii*, *S. aureus*, *S. simiae*, *S. sciuri*, *S. pettenkoferi*, *S. lugdunensis*, *S. equorum*, *S. caprae*, *S. xylosus*, *S. auricularis*, *S. simulans*, and *S. arlettae*, were identified in this study. Interestingly, many of the staphylococci species recovered in our study have previously been associated with the community, preserved food, and wildlife [4, 10].

**Antibiotic resistance**

Antibiotic resistance of staphylococci associated with healthcare settings is well documented, however, little is known about the antibiotic resistance in staphylococci isolated from different ecological niches [4]. In this study, the majority of staphylococci were resistant to penicillin (65%) and fusidic acid (66%) (Fig. 1). Despite that 80% of hospital associated CoNS (across Europe) were reported to be resistant to oxacillin [18], only 6% of CoNS were resistant to oxacillin in this study. In addition, the levels of resistance to chloramphenicol (3%), cefepime (8%), gentamicin (10%), mupirocin (14%), tetracycline (16%), and erythromycin (31%) were lower compared to those reported in clinical settings [19–22]. In contrast, the rates of resistance to fusidic acid (66%), amoxicillin (27%) and streptomycin (33%) in environmental staphylococcal isolates were higher than those reported in clinical staphylococci isolates [21, 23, 24]. It is widely accepted that higher levels of antibiotic resistance in clinical isolates are due to consistent antibiotic exposure [25]. The environment may also contribute to the development of antibiotic resistance in microorganisms due to human/animal therapeutics, sewage, agriculture and industrial use of antibiotics [26]. Therefore, the wide dissemination of multidrug resistant CoNS in non-healthcare associated environments is a disturbing finding. In our study, 94% of staphylococcal isolates were phenotypically resistant to at least 1 antibiotic, 18% were resistant to five or more antibiotics and only 6% staphylococcal isolates were fully susceptible. The study also revealed that the number of isolates resistant to multiple antibiotics varied between the different isolation sites. The least number of multiple antibiotic resistant CoNS isolates were recovered from the public transport (58%), the highest was isolated from hotels (78%).

**Methicillin-resistant staphylococci**

Methicillin resistant staphylococci pose a major public health threat, and cause severe economic and health consequences [27]. Methicillin resistance is determined by the *mecA* gene, which encodes for penicillin binding protein 2a (PBP2a) that has a low affinity to β-lactam antibiotics [28]. Hussain et al. assessed the correlation between *mecA*
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</table>
gene and oxacillin susceptibility breakpoints (0.5 mg l⁻¹) of 493 clinical CoNS belonging to and classified into 4 categories [29]. The mecA gene positive staphylococci were categorized into groups I and II, and demonstrated that group I (S. haemolyticus (83.3%), S. epidermidis (61.9%), S. hominis (51.8%)) differs from group II (S. cohnii (28.5%), S. warneri (27.3%), S. saprophyticus (9.0%)) by their high levels of mecA-carriage [29]. Interestingly, S. hominis (38%), S. haemolyticus (22%), and S. epidermidis (7%) isolated in this study harboured significantly lower levels of the mecA gene. Moreover, in this study S. cohnii (33%) and S. saprophyticus (10%) showed higher mecA gene carriage than clinical isolates reported by Hussain, et al. [29], whereas the levels of mecA gene carriage in S. warneri (6%) were lower than in clinical isolates. No mecA gene was detected in staphylococcal species of groups III and IV, which included S. xylosus, S. lugdanensis, S. capitis, S. simulans, and S. schleiferi [29]. Similarly, in this study S. lugdanensis, S. xylosus and S. simulans were determined to be susceptible to oxacillin and lacked mecA gene. However, in contrast to the reports by Hussain, et al. [29] we found that mecA gene was present in 8% of S. capitis isolates.

Oxacillin susceptible mecA gene positive S. aureus (OS-MRSA) has been reported worldwide, and the risk of induced high levels of oxacillin resistance was determined in OS-MRSA [30, 31]. In this study, 68 (46%) staphylococcal isolates were confirmed by PCR to carry the mecA gene, however, they were phenotypically susceptible to oxacillin with the MICs (oxacillin) varying from 0.015 to 2 mg l⁻¹. This study demonstrates the prevalence of mecA positive but oxacillin susceptible CoNS (OS-CoNS) in the environment. Little is known about OS-CoNS isolates recovered from the environment and their epidemiological data are limited. Additional studies are necessary to further our understanding of the prevalence and molecular epidemiology of OS-CoNS in the environment.

SCCmec elements
SCCmec is a mobile genetic element with two essential components: the mec gene complex, and the cassette chromosome recombinase (ccr) gene complex [32]. The combination of the mec gene complex and ccr gene complex confers different SCCmec types [32]. SCCmec type I, II, III are reported to be associated with MRSA recovered from healthcare settings, whereas SCCmec type IV and V are mainly associated with the community [32]. Moreover, it has been shown that the size of SCCmec types IV and V are smaller than SCCmec types I, II and III, thus conferring

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**Table 3** Molecular characterisation and antibiotic resistance of mecA gene positive staphylococci (Continued)

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<th>MUP</th>
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<th>T</th>
<th>C</th>
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Note: * S. epidermidis isolates with similar MLST types

R: resistant, S sensitive. I intermediate

BCF baby care facility, DSH different sites of hotels, DSL different sites of a library, DSR different sites of restaurants, DSS different sites of supermarkets, DST different sites of transportation facilities, HH handbags, HH human hands

A amoxicillin (10 μg), CEF cefepime (30 μg), C chloramphenicol (30 μg), E erythromycin (5 μg), FC fusidic acid (10 μg), GM gentamicin (10 μg), MUP mupirocin (20 μg), OX oxacillin (1 μg), PG penicillin G (1 unit), S streptomycin (10 μg), T tetracycline (10 μg)

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**Table 4** MLST types of 13 oxacillin resistant and mecA positive S. epidermidis

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HH human hands, DSL different sites of a library, DSH different sites of hotels, DSS different sites of supermarkets
MLST Multi-locus sequence typing
increased mobility by their smaller size and contributing the spread of these smaller SCCmec elements [33]. In this study, SCCmec type I, II or III were found in 19% (n = 13) of meca-positive CoNS, whereas 27% (n = 18) of CoNS were determined to harbour SCCmec type IV or V. SCCmec type VI and VIII were previously identified in Portugal (2006) and Canada (2009) in hospital associated MRSA (HA-MRSA) [33, 34]. In this study, we identified one of each type, however, we did not detect SCCmec types IX.

Becker et al., have previously summarized the community and livestock associated staphylococcal species and their SCCmec types, which included S. capitis (I, IA, II, III, IV, IVa, V, non-typeable: NT), S. cohnii (NT), S. epidermidis (I, Ila, IIb, III, III (variant), IV, IVa, IVb, IVc, IVd, IVe, IVg, V, VI, NT), S. haemolyticus (I, II, II.1, III, III (variant), IV, V, NT), S. hominis (I, III, IV, NT), S. pasteuri (IVc), S. saprophyticus (III, NT), S. sciuri (I, III, IIIA, V, VII, NT) and S. warneri (IV, IV.1, IVb, IVe) [4]. In this study, species associated SCCmec types differed and included the following: S. capitis (I, NT), S. haemolyticus (I, II, V, NT) and S. hominis (I, V, NT), S. cohnii (I, V, NT), S. pasteuri (NT), S. saprophyticus (IV, NT), S. sciuri (II, VIII), S. warneri (I, V, NT). S. epidermidis possessed SCCmec types similar to those reported previously [4].

Thirteen unclassified SCCmec types were determined in this study, including three carrying class A meca complex and ccrC, six had a combination of class B meca and ccrC, one carried class B meca and ccr3, and three had a combination of class A meca complex and ccr type I. The 1A was previously defined as a new SCCmec type 1A by others [35]. Pseudo (ψ)-SCCmec harbours the meca complex but lacks ccr, while, SCCmec12263 is reported to carry the ccr complex but lacks meca complex [36, 37]. In this study, 21 isolates (29%) were categorized as (ψ)-SCCmec and SCCmec12263 since they lacked either meca complex or ccr complexes. ψ SCC element is characterized by lacking genes for ccr and meca [4]. One of S. saprophyticus isolates in this study was found to possess the ψ SCC element (Table 5).

**MLST of S. epidermidis**

Whilst many studies have reported on the changing epidemiology of S. aureus, epidemiological data of other staphylococcal species are limited [38, 39]. In this study, 10 new MLST types were determined in 13 S. epidermidis isolates. Interestingly, although isolates recovered from human hands (S. epidermidis 259/ SCCmec V) and hotels (S. epidermidis 124/ SCCmec IV) harbour ed different SCCmec types, they shared the same MLST type ST602. In addition, three S. epidermidis isolates recovered from libraries (S. epidermidis 133, S. epidermidis 134, S. epidermidis 135) shared the same MLST type ST600 (Table 4). However, despite sharing the same MLST type S. epidermidis 133, S. epidermidis 134 and S. epidermidis 135 harbored SCCmec type 3B, I, IV respectively. Others reported that S. epidermidis ST2 was associated with type II, III, IV and non-typeable SCCmec, and S. epidermidis ST22 harboured SCCmec type III, IV and V [40].

**Conclusions**

Systematic analysis of staphylococci isolated from non-healthcare environments provided insights into the diversity and antibiotic susceptibility patterns of these
isolates. Multi-drug resistance was commonly seen in each staphylococcal species. The prevalence of multiple antibiotic resistant staphylococci in this study provides evidence that antibiotics in the natural environments can contribute to the selection of antibiotic resistance in microorganisms. The finding of various SCC\emph{mec} types in non-healthcare associated environments emphasizes the complexity of SCC\emph{mec} elements. In addition to this, we also report on new MLST types that were assigned for all \emph{S. epidermidis} isolates. This highlights the genetic variability of these isolates. In conclusion, the non-healthcare environments may act as a reservoir of multidrug resistant staphylococci, and current infection control measures are ineffective in limiting the spread of these bacteria.

**Additional file**

**Additional file 1:** Table S1. Isolates collected from different environmental sites and human hands (PDF 46 kb)

### Table 5 The diversity of SCC\emph{mec} types of \emph{mecA} gene positive staphylococci

| ID | Sites     | Species      | PG  | MUP | CEF | GM  | FC  | S   | A   | E   | T   | C   | \emph{mecA} | \emph{mec} | \emph{ccr} | SCC\emph{mec} | MIC/OX (mg l\(^{-1}\)) |
|----|-----------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----------|----------|----------|----------------|-------------------|
| 75 | HH        | \emph{S. capitis} | R   | S   | S   | R   | R   | S   | S   | S   | S   | +   | Class A | NT       | Pseudo (\(\psi\))-SCC\emph{mec} | 0.5   |
| 81 | HH        | \emph{S. capitis} | R   | S   | R   | R   | R   | R   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.5   |
| 70 | HH        | \emph{S. capitis} | R   | S   | S   | S   | S   | R   | S   | S   | R   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.25  |
| 83 | HH        | \emph{S. capitis} | S   | R   | S   | R   | S   | S   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.12  |
| 24 | DSH       | \emph{S. capitis} | S   | S   | S   | S   | S   | R   | S   | S   | S   | +   | NT       | 1        | SCC\emph{mec}12263 | 0.12  |
| 108 | HH | \emph{S. cohnii} | S   | S   | I   | S   | R   | S   | R   | R   | S   | +   | Class A | NT | Pseudo (\(\psi\))-SCC\emph{mec} | 1     |
| 308 | HH | \emph{S. epidermidis} | R   | R   | S   | R   | S   | R   | R   | S   | S   | +   | Class B | NT | Pseudo (\(\psi\))-SCC\emph{mec} | 2     |
| 234 | HB | \emph{S. epidermidis} | R   | S   | S   | S   | R   | S   | R   | S   | R   | +   | Class A | NT | Pseudo (\(\psi\))-SCC\emph{mec} | 1     |
| 249 | DSH | \emph{S. epidermidis} | R   | S   | S   | S   | R   | S   | S   | R   | S   | +   | NT       | 2        | SCC\emph{mec}12263 | 0.12  |
| 125 | DSH | \emph{S. epidermidis} | S   | S   | I   | S   | R   | S   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.06  |
| 185 | DSS | \emph{S. epidermidis} | R   | S   | S   | S   | S   | S   | S   | S   | S   | +   | Class C | NT       | Pseudo (\(\psi\))-SCC\emph{mec} | 0.06  |
| 498 | DSS | \emph{S. hominis} | R   | S   | S   | R   | S   | S   | R   | S   | S   | +   | Class A | NT | Pseudo (\(\psi\))-SCC\emph{mec} | 0.5   |
| 426 | DSH | \emph{S. hominis} | R   | S   | I   | S   | R   | R   | R   | R   | S   | +   | Class A | NT | Pseudo (\(\psi\))-SCC\emph{mec} | 0.25  |
| 412 | DSH | \emph{S. hominis} | R   | S   | S   | S   | R   | R   | R   | S   | S   | +   | NT       | 1        | SCC\emph{mec}12263 | 0.06  |
| 391 | BCF | \emph{S. hominis} | R   | S   | S   | S   | S   | S   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.03  |
| 593 | HH | \emph{S. pasteuri} | R   | S   | S   | R   | R   | R   | R   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.5   |
| 597 | HH | \emph{S. pasteuri} | R   | I   | S   | R   | S   | S   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.5   |
| 616 | BCF | \emph{S. saprophyticus} | R   | R   | S   | S   | S   | R   | R   | R   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 256   |
| 612 | BCF | \emph{S. saprophyticus} | R   | R   | S   | S   | R   | S   | S   | R   | S   | +   | NT       | \(\psi\) SCC | 1     |
| 659 | DSH | \emph{S. warneri} | R   | S   | R   | S   | R   | S   | R   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.5   |
| 648 | BCF | \emph{S. warneri} | R   | S   | R   | R   | S   | R   | S   | S   | S   | +   | NT       | 5        | SCC\emph{mec}12263 | 0.06  |
| 645 | BCF | \emph{S. warneri} | R   | S   | S   | S   | S   | S   | S   | s   | S   | +   | NT       | 4        | SCC\emph{mec}12263 | 0.015 |

\(R\) resistant, \(S\) sensitive, \(I\) intermediate

**BCF:** baby care facility, **DSH:** different sites of hotels, **DSL:** different sites of a library, **DSR:** different sites of restaurants, **DSS:** different sites of supermarkets; **DST:** different sites of transportation facilities; \(HB\): handbags, \(HH\): human hands

\(A\) amoxicillin (10 \(\mu\)g), \(CEF\): cefepime (30 \(\mu\)g), \(CHL\): chloramphenicol (30 \(\mu\)g), \(E\): erythromycin (5 \(\mu\)g), \(FC\): fusidic acid (10 \(\mu\)g), \(GM\): gentamicin (10 \(\mu\)g), \(MUP\): mupirocin (20 \(\mu\)g), \(OX\): oxacillin (1 \(\mu\)g), \(PG\): penicillin G (1 unit), \(ST\): streptomycin (10 \(\mu\)g), \(T\): tetracycline (10 \(\mu\)g)

**Abbreviations**

AM: Amoxicillin; BCF: Baby care facility; CEP: Cefepime; CHL: Chloramphenicol; CoNS: Coagulase-negative staphylococci; DSH: Different sites of hotels; DSL: Different sites of a library; DSR: Different sites of restaurants; DSS: Different sites of supermarkets; DST: Different sites of transportation facilities; ERY: Erythromycin; FC: Fusidic acid; GEN: Gentamicin; HBO: Handbags; HH: Human hands; MALDI-TOF-MS: Matrix-assisted laser desorption ionization time flight mass-spectroscopy; MIC: Minimum Inhibitory Concentrations; MLST: Multi-locus sequence typing; MR-CoNS: Methicillin resistant coagulase negative staphylococci; MRSA: Methicillin resistant \emph{Staphylococcus aureus}; MUP: Mupirocin; OX: Oxacillin; PEN: Penicillin; SCC\emph{mec}: Staphylococcal cassette chromosome \emph{mec}; ST: Sequence types; STR: Streptomycin; TET: Tetracycline

**Funding**

This work was part of Zhen Xu’s PhD study funded by China Scholarship Council.

**Availability of data and materials**

All data generated or analysed during this study are included in this published article and its supplementary information files.

**Authors’ contributions**

ZX: samples collection, laboratory work, data analysis, manuscript preparation. HS: study design, critically reviewing the paper. RM: Data analysis, critically reviewing the paper. JC: data analysis, critically reviewing the paper. YL: data analysis,
critically reviewing the paper. RRC: conception and design of the study. HW: conception and design of the study; data analysis; writing and critically reviewing the paper. All authors read and approved the final manuscript.

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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Received: 19 April 2018 Accepted: 6 June 2018
Published online: 13 June 2018

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