Prevalence, risk factors, phenotypic and molecular characteristics for *Staphylococcus aureus* carriage in community-based drug users in Guangzhou, China

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**Abstract**

**Background:** *Staphylococcus aureus* (S. aureus), particularly methicillin-resistant *Staphylococcus aureus* (MRSA), remains the predominant cause of infections in drug users. This cross-sectional study aims to elucidate the prevalence, risk factors, phenotypic and molecular characteristics of *S. aureus* carriage among community-based drug users.

**Methods:** All eligible drug users, with both injection and non-injection route of drug administration, were asked to complete questionnaires and collect nasal swabs by trained personal during the period between May and December 2017 in Guangzhou, China. Swabs were processed for identification of *S. aureus*. Antimicrobial susceptibility test and polymerase chain reaction assays were used to detect phenotypic and molecular characteristics for identified isolates. Univariate and multivariate logistic regression analyses were used to assess risk factors for *S. aureus* carriage.

**Results:** Overall, 353 drug users were included in the study and the prevalence of *S. aureus* carriage was 15.01% (53/353). The prevalence of MRSA carriage was 6.80% (24/353). Cohabitation was a risk factor for *S. aureus* (adjusted OR = 8.80, 95% CI: 1.89–40.99). The proportion of multidrug resistance was 54.72% for *S. aureus* isolates and most of these isolates were resistant to penicillin, erythromycin and clindamycin. Seventeen MRSA isolates were multidrug resistant. The results of clonal complexes (CCs) and sequence types (STs) for *S. aureus* were diverse. The three predominant types for CCs were CC5 (64.15%, 34/53), CC59 (11.32%, 6/53), and CC7 (7.55%, 4/53); and for STs were ST188 (20.75%, 11/53), ST5 (11.32%, 6/53), and ST59 (11.32%, 6/53).

**Conclusion:** The prevalence of *S. aureus* nasal carriage was lower while the prevalence of MRSA carriage was moderate compared to previous studies. Phenotypic and molecular characteristics of *S. aureus* isolates, particularly MRSA isolates, revealed high proportions of antibiotic resistance, indicating the existence of cross-circulation, and implying high opportunity of virulence-related diseases. Decolonization and antibiotic stewardship might be implemented for drug users with MRSA carriage.

**Keywords:** *S. aureus*, MRSA, Risk factor, Antimicrobial susceptibility, Drug user, Molecular characteristics
Background
Staphylococcus aureus (S. aureus), particularly methicillin-resistant S. aureus (MRSA), continues to be a major pathogen in both hospital- and community-associated infections [1]. It has been reported that nasal carriers of S. aureus have an increased risk of being infected by this pathogen [2].

Based on the latest World Drug Report, an estimated 271 million people aged 15–64 used drugs, with both injection and non-injection route of drug administration and 35 million people were estimated to be suffering from drug use disorders in 2017 [3]. Obviously, illicit drug use is a global public health problem. In recent studies, the prevalence of S. aureus, particularly MRSA carriage, among drug users is higher compared to the general population [4, 5]. The phenotypic and molecular characteristics of S. aureus isolates in drug users were little reported. Most of these studies were conducted in developed countries, including the United States of America, Canada, and European countries. There is no similar work conducted among drug users in China.

According to the above facts, it is necessary to investigate the epidemiology of S. aureus carriage, particularly MRSA carriage, among drug users, in China. Therefore, in this study, we aimed to elucidate the prevalence, risk factors, phenotypic and molecular characteristics of S. aureus from the nasal cavity of community-based drug users in Guangzhou, China.

Methods
Ethics statement
The study was approved by the Ethics Committee of Guangdong Pharmaceutical University, and it was performed in accordance with the approved guidelines. Written informed consent were obtained from all participants.

Study design and participants
A cross-sectional study of S. aureus nasal carriage among all drug users, with both injection and non-injection route of drug administration, was conducted between May and December 2017 in three community health service centers, Guangzhou, China. Participants who had used drug in the previous 12 months were voluntarily recruited in the study. Drugs included opiates, heroin, methamphetamine (methamphetamine), morphine, marijuana, cocaine, and other addictive narcotic drugs and psychotropic substances. Those participants with psychiatric illness or acute diseases were excluded. A face-to-face questionnaire was used to collect relevant information, including demographics (age, sex), socioeconomic characteristics (employment status, living conditions, income levels, history of homelessness, and history of incarceration), behavior (history of sex and the number of sexual partners), health-related characteristics (human immunodeficiency virus (HIV) status, hepatitis, antibiotic use, skin infection, hospitalization, and history of needle exchange), and periods, and route of drug use. In this study, cohabitation refers to someone living together with another person without marriage.

Isolation and identification of S. aureus
After completing the questionnaire part of the study, trained personnel collected swabs from both anterior nares of the participants. The swabs were soaked in 7.5% sodium chloride broth at 4 °C during transportation, and then incubated at 37 ± 1 °C for 24 h for further experiments. The swabs were used to inoculate mannitol salt agar for 24–48 h incubation. Samples were identified as S. aureus isolates when they had specific colony morphology and were positive for gram staining, catalase reaction, hemolysis test, DNase test, coagulase tests, and 16S rRNA and nuc genes. Two colonies were picked from one mannitol plate. Those S. aureus isolates that were resistant to cefoxitin and/or positive for mecA gene were identified as MRSA isolates, all other S. aureus isolates were identified as methicillin-sensitive S. aureus (MSSA). More details were described in the previous work [6].

Phenotypic characterization
The antimicrobial susceptibility of all S. aureus isolates was determined by the disk diffusion method, following the guidelines of the Clinical and Laboratory Standards Institute of 2015. The following antibiotics were tested: clindamycin, erythromycin, penicillin, linezolid, gentamicin, teicoplanin, moxifloxacin, trimethoprim-sulfamethoxazole, rifampin, chloramphenicol, and tetracycline. The reference S. aureus strain ATCC 25923 and ATCC 29213 were used for quality and positive control. We classified the isolates as susceptible and resistant to each antibiotic. Those isolates resistant to ≥1 agent in ≥3 antimicrobial categories were identified as multidrug resistant (MDR) [7]. More details were described in previous work [6].

Molecular characterization
All S. aureus isolates were also tested for the carriage of tetracycline-resistant genes [tet(M), tet(K)] and erythromycin-resistant genes [erm(A), erm(C)]. All S. aureus isolates were further tested to confirm the presence of toxin genes including Panton-Valentine leukocidin genes (lukF-PV and lukS-PV), Toxic shock syndrome toxin-1 gene (tst), Exfoliative toxin A gene (eta), Exfoliative toxin B gene (etb) and Staphylococcal enterotoxins (SEs) (sea-see, seg-ser, seu) genes. Multilocus sequence typing (MLST) was performed to confirm clonal complexes (CCs) and sequence types (STs). Additionally, all MRSA isolates were tested for Staphylococcal cassette
Statistical analysis
The data were entered using Epidata 3.1 (EpiData Association, Odense Denmark) and exported to Stata 14.2 (College Station, Texas, USA) software for further analysis. We assessed the associations between S. aureus carriers and relevant characteristics by the following methods. Univariate analyses were conducted using the Pearson’s chi-squared test or the Fisher’s exact test when appropriate. Multivariate logistic regression models were used to determine risk factors associated with S. aureus carriage. Independent risk factors with a \( P < 0.1 \) in univariable logistic regression analysis were included in the multivariable models. Potential confounding covariates were adjusted in the models. A two-sided \( P \)-value of \( \leq 0.05 \) was defined as statistical significance.

Results
Prevalence of S. aureus carriage
A total of 353 drug users were eligible for inclusion in the study. The prevalence of S. aureus nasal carriage in drug users was 15.01% (53/353). The prevalence of MRSA carriage was 6.80% (24/353).

Risk factors of S. aureus carriage
Table 1 shows univariate analyses of S. aureus carriage among drug users. After adjusting for confounding covariates, current cohabitation was still a risk factor for S. aureus carriage (aOR = 8.80, 95% CI: 1.89–40.99) in drug users (Fig. 1).

Phenotypic characteristics
The antibiotic susceptibility testing results revealed that most S. aureus isolates were susceptible to linezolid, rifampin and gentamicin, but resistant to penicillin (92.45%), erythromycin (49.06%), clindamycin (45.28%) and tetracycline (32.08%) (Table 2). Eighteen S. aureus isolates were MDR. Notably, 38.89% of MDR S. aureus were resistant to erythromycin, clindamycin and chloramphenicol. For MRSA isolates, the proportion of MDR MRSA was 36.00% (9/24) (Fig. 2). The proportions of antibiotic resistance were higher in MRSA isolates than MSSA isolates (Table 2).

Table 1 Univariate analysis of risk factor for S. aureus carriage among drug users in Guangzhou, China, 2017

| Characteristics                              | Non-S. aureus carriage (N = 300) | S. aureus carriage (N = 53) | P-value |
|----------------------------------------------|----------------------------------|-----------------------------|---------|
| Demographics-level                           |                                  |                             |         |
| Sex (Male)                                   | 262 (87.33)                      | 47 (88.68)                  | 0.784   |
| age (> 50)                                   | 169 (56.33)                      | 26 (49.06)                  | 0.326   |
| Social-level                                 |                                  |                             |         |
| Current employed (Yes)                       | 80 (26.67)                       | 14 (26.42)                  | 0.970   |
| Current cohabitation (Yes)                   | 3 (1.00)                         | 4 (7.55)                    | 0.011   |
| Low income (Yes)                             | 61 (20.33)                       | 17 (32.08)                  | 0.058   |
| History of homelessness in past 6 months (Yes) | 9 (3.00)                        | 3 (5.66)                    | 0.400   |
| History of incarceration (Yes)                | 240 (80.00)                      | 44 (83.02)                  | 0.609   |
| Behavior-level                               |                                  |                             |         |
| History of vaginal sex in past 1 month (Yes) | 97 (33.68)                       | 13 (26.53)                  | 0.324   |
| Number of sexual partners in past 1 year (> 1) | 28 (9.33)                        | 2 (3.77)                    | 0.283   |
| Health-level                                 |                                  |                             |         |
| Current HIV positive (Yes)                    | 22 (7.33)                        | 2 (3.77)                    | 0.553   |
| Current hepatitis (Yes)                      | 114 (38.00)                      | 24 (45.28)                  | 0.316   |
| Antibiotic use in past 6 months (Yes)        | 83 (27.67)                       | 16 (30.19)                  | 0.706   |
| History of hospitalization in past 1 year (Yes) | 32 (10.67)                     | 9 (16.98)                   | 0.186   |
| History of skin infection in past 6 months (Yes) | 130 (43.33)                     | 25 (47.17)                  | 0.604   |
| History of needle exchange in past 1 year (Yes) | 26 (8.67)                      | 4 (7.55)                    | 1.000   |
| Drug use-level                               |                                  |                             |         |
| Period of drug use (> 10 years)              | 18 (6.00)                        | 0 (0.00)                    | 0.087   |
| History of heroin snorting in past 3 months (Yes) | 188 (62.67)                     | 41 (77.36)                  | 0.039   |
| History of intravenous heroin in past 3 months (Yes) | 113 (37.67)                     | 14 (26.42)                  | 0.116   |
| History of using injection drugs in past 3 months (Yes) | 187 (62.33)                     | 39 (73.58)                  | 0.116   |

S. aureus Staphylococcus aureus; N Number of total participants; HIV Human immunodeficiency virus
In terms of macrolide-resistant genes, five (9.43%) S. aureus isolates were positive for the erm(C) and one (1.89%) was positive for the erm(A) gene. Only one S. aureus isolate was positive for both the erm(C) and erm(A) genes. For tetracycline-resistant genes, four (7.55%) S. aureus isolates were positive for the tet(K) and no isolate was positive for tet(M) gene. Additionally, only one S. aureus isolate was positive for erm(C), erm(A) and tet(K) genes. These gene-positive S. aureus isolates were all MRSA isolates.

Molecular characteristics

Overall, 8 CCs and 18 STs were detected from 53 S. aureus isolates (Fig. 2). Three of the most predominant CCs were CC5 (34), CC59 (6), and CC7 (4). Three of the most predominant STs were ST188 (11), ST5 (6), and ST59 (6). For 24 MRSA isolates, 7 CCs and 13 STs were detected. Two of the most predominant CCs were CC5 (13) and CC59 (6). Two of the most predominant STs were ST188 (6) and ST59 (6).

In terms of virulence genes (Table 2), 5.66% of S. aureus isolates were positive to lukF-PV and lukS-PV genes. Two MRSA isolates were positive to the tst gene. Notably, only one MRSA isolate was positive to the eta gene and one to the etb gene. For the SEs genes, the three most predominant genes were seg (49.06%), sei (34.96%) and sad (32.08%). All S. aureus isolates were negative to the sea and see genes.

A total of four SCCmec types were detected from the 24 MRSA isolates, in which 12 isolates were type IVd, five were type IVa, one was type V, one was type II, and five were non-typeable (Fig. 2).

Discussion

To the best of our knowledge, this is a relatively comprehensive study which contributes to the understanding of the prevalence, risk factors, phenotypic and molecular characteristics for S. aureus nasal carriage among community-based drug users in China. The prevalence of S. aureus carriage in the study (15.01%) is lower than previously reported estimates which ranged from 19.79 to 45.05% [4, 8–11]. Participants of those previous studies were injection drug users. In this study, however, only 64.02% of participants had history of using injection drugs in the past 3 months. Additionally, we found that a majority of long-term drug users who took drugs by snorting had few vibrissae. This might also be a potential factor leading to a low prevalence of S. aureus carriage, further studies about the impact of snorting drugs on S. aureus carriage need to be conducted in the future. The prevalence of MRSA nasal carriage (6.80%) in the study is similar to the previous studies in other countries [4, 12–14], but higher than that in the general population in China [15]. Additionally, the proportion of MRSA in S. aureus isolates was higher than the observed studies [4, 14].

In this study, we found that current cohabitation might be a risk factor for S. aureus carriage in drug users, which is different from another study [4]. One of the possible reasons might be that most drug users cohabitated with other drug users. This could provide more opportunities for sharing drugs [11]. HIV infection has been reported to be a risk factor for S. aureus carriage [16], however, we did not find any significance in this study. This could be caused by the limited number of drug users with HIV infection. Therefore, further studies need to be carried out to identify the risk factors for S. aureus carriage in drug users.

The patterns of antibiotic resistance on S. aureus isolates are consistent with limited available studies [8, 17, 18], with high proportions of penicillin, erythromycin, clindamycin and tetracycline resistance. The proportions of antibiotic resistance were higher in MRSA isolates than MSSA isolates, which is also observed in other studies [8, 18]. Teicoplanin has been widely used as an anti-MRSA agent in infectious patients in the past decades [19, 20], which can partially explain the high proportion of
Table 2 Phenotypic and molecular characteristics of *S. aureus* isolates among drug users in Guangzhou, China, 2017

| Characteristics                        | S. aureus *(N = 53)* | MRSA *(N = 24)* | MSSA *(N = 29)* |
|----------------------------------------|----------------------|-----------------|-----------------|
| **Resistant phenotype (resistant)**    |                      |                 |                 |
| Clindamycin                            | 24 (45.28)           | 15 (62.50)      | 9 (31.03)       |
| Erythromycin                           | 26 (49.06)           | 15 (62.50)      | 11 (37.93)      |
| Penicillin                              | 49 (92.45)           | 23 (95.83)      | 26 (89.66)      |
| Linezolid                               | 1 (1.89)             | 1 (4.17)        | 0 (0.00)        |
| Gentamicin                              | 4 (7.55)             | 3 (12.50)       | 1 (3.45)        |
| Teicoplanin                             | 10 (18.87)           | 8 (33.33)       | 2 (6.90)        |
| Trimethoprim-sulfamethoxazole           | 7 (13.21)            | 4 (16.67)       | 3 (10.34)       |
| Moxifloxacin                            | 5 (9.43)             | 4 (16.67)       | 1 (3.45)        |
| Rifampin                                | 2 (3.77)             | 2 (8.33)        | 0 (0.00)        |
| Chloramphenicol                         | 11 (20.75)           | 7 (29.17)       | 4 (13.79)       |
| Tetracycline                            | 17 (32.08)           | 9 (37.50)       | 8 (27.59)       |
| **Resistant genotype (positive)**      |                      |                 |                 |
| *erm*(A)                                | 1 (1.89)             | 1 (4.17)        | 0 (0.00)        |
| *erm*(C)                                | 5 (9.43)             | 5 (20.83)       | 0 (0.00)        |
| *tet*(K)                                | 4 (7.55)             | 4 (16.67)       | 0 (0.00)        |
| *tet*(M)                                | 0 (0.00)             | 0 (0.00)        | 0 (0.00)        |
| **Virulence genes (positive)**         |                      |                 |                 |
| *luk-F-PV and luk-S-PV*                 | 3 (5.66)             | 3 (12.50)       | 0 (0.00)        |
| *tst*                                   | 2 (3.77)             | 2 (8.33)        | 0 (0.00)        |
| *eta*                                   | 1 (1.89)             | 1 (4.17)        | 0 (0.00)        |
| *etb*                                   | 1 (1.89)             | 1 (4.17)        | 0 (0.00)        |
| *sez*                                   | 0 (0.00)             | 0 (0.00)        | 0 (0.00)        |
| *seb*                                   | 1 (1.89)             | 0 (0.00)        | 1 (3.45)        |
| *sec*                                   | 3 (5.66)             | 1 (4.17)        | 2 (6.90)        |
| *sed*                                   | 17 (32.08)           | 11 (45.83)      | 6 (20.69)       |
| *sef*                                   | 0 (0.00)             | 0 (0.00)        | 0 (0.00)        |
| *seg*                                   | 26 (49.06)           | 13 (54.17)      | 13 (44.83)      |
| *seh*                                   | 3 (3.45)             | 3 (12.50)       | 0 (0.00)        |
| *sei*                                   | 18 (33.96)           | 9 (37.50)       | 9 (31.03)       |
| *sei*                                   | 6 (11.32)            | 3 (12.50)       | 3 (10.34)       |
| *sej*                                   | 11 (20.75)           | 8 (33.33)       | 3 (10.34)       |
| *sem*                                   | 4 (7.55)             | 2 (8.33)        | 2 (6.90)        |
| *sen*                                   | 16 (30.19)           | 6 (25.00)       | 10 (34.48)      |
| *sep*                                   | 12 (22.64)           | 4 (16.67)       | 8 (27.59)       |
| *seo*                                   | 13 (24.53)           | 4 (16.67)       | 9 (31.03)       |
| *seg*                                   | 4 (7.55)             | 1 (4.17)        | 3 (10.34)       |
| *ser*                                   | 5 (9.43)             | 2 (8.33)        | 3 (10.34)       |
| *seu*                                   | 12 (22.64)           | 7 (29.17)       | 5 (17.24)       |

*S. aureus* *Staphylococcus aureus*; MRSA *Methicillin-resistant S. aureus*; MSSA *Methicillin- sensitive S. aureus*
teicoplanin resistance in MRSA isolates. The most prevalent MDR pattern of *S. aureus* isolates could partially demonstrate the high use of antibiotics in community-based drug users and provide evidence that healthcare workers need to be more careful with selection of antibiotics for drug users. Therefore, the administration of antibiotics for drug users should be strengthened. The proportions of virulence genes were high in MRSA, suggesting the higher risks of MRSA isolates in causing virulence-related diseases, including *Staphylococcal* cassettes containing *mec* genes; MDR, Multidrug resistance; P, Penicillin; E, Erythromycin; DA, Clindamycin; TE, Tetracycline; C, Chloramphenicol; SXT, Trimethoprim-sulfamethoxazole; TEC, Teicoplanin; MXF, Moxifloxacin; CN, Gentamicin; RD, Rifampin; LZD, Linezolid.
scalded skin syndrome, toxic shock syndrome, Staphylococcal food poisoning, etc. [21–23]. The proportions of virulence genes for MRSA isolates were higher than the observed studies [6, 24–26]. The results implied that drug users with MRSA carriage harboring virulence associated genes, might have higher risks for relevant disease and should draw more attention.

We found high proportions of ST5 and ST59 in this study and these STs were also globally reported in communities [27]. We also found hospital- (ST188) [28, 29] and livestock- (ST398) [30, 31] associated STs in this study. The results of CCs and STs for S. aureus isolates could demonstrate the multiple transmissions among human beings, livestock and environment, which are similar to previous studies [6, 24]. According to the results of SCCmec types, we could know the source of MRSA isolates might be both communities and healthcare settings, which is similar to the observed studies [4, 9]. Additionally, we found some S. aureus isolates displayed identical molecular characteristics, suggesting the possibility of cross-transmission between the communities and healthcare settings and this might be a potential risk for other populations. Relevant decolonization methods could be taken for drug users with MRSA carriage, which would help prevent further MRSA circulation [32].

Our study contributes to the understanding of the prevalence, risk factors, phenotypic and molecular characteristics for S. aureus carriage, particularly MRSA carriage, among drug users in China. Despite the strengths of this study, there are several limitations. First, it was a cross-sectional study. Thus, we could not determine the persistence of S. aureus carriage. Secondly, we only collected nasal swabs instead of nasopharyngeal swabs, which may lead to underestimation of the prevalence of S. aureus carriage. Thirdly, we did not collect information whether male participants were those who have sex with men due to confidentiality. We will explore it in future research. Finally, the generality of this study is limited owing to the small number of drug users.

**Conclusion**

In summary, the prevalence of S. aureus nasal carriage was lower, while the prevalence of MRSA nasal carriage was moderate among community-based drug users but higher than that of general population in China. Co-habitation is a risk factor for S. aureus carriage. Phenotypic and molecular characteristics of MRSA isolates reveal serious antibiotic resistance, indicate the cross-circulation of MRSA isolates between communities and healthcare settings, and imply high opportunity of virulence-related diseases. Decolonization and antibiotic stewardship might be implemented for drug users with MRSA carriage, especially for those with risk factors.

**Abbreviations**
aOR: Adjusted odds ratio; CI: Confidence interval; CN: Gentamicin; DA: Clindamycin; E: Erythromycin; HIV: Human immunodeficiency virus; LZD: Linezolid; MDR: Multidrug resistance; MLST: Multilocus sequence typing; MRSA: Methicillin-resistant S. aureus; MSSA: Methicillin-sensitive S. aureus; MXF: Moxifloxacin; P: Penicillin; RD: Rifampin; S: Staphylococcus aureus; SCCmec: Staphylococcal cassette chromosome mec; SE: Staphylococcal enterotoxin; ST: Sequence type; SXT: Trimethoprim-sulfamethoxazole; TE: Tetracycline; TEC: Teicoplanin

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**Authors’ contributions**

WY and JL performed the experiments, participated in data analysis and contributed to manuscript writing. JZ collected information, performed the experiments, and analyzed the results. ZY and ZH designed the study and critically reviewed the manuscript. All authors revised the manuscript and approved the final form.

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**Availability of data and materials**

The data supporting the conclusions of this manuscript will be made available by the corresponding authors to any qualified researcher.

**Ethics approval and consent to participate**

The study was approved by the Ethics Committee of Guangdong Pharmaceutical University, and it was performed in accordance with the approved guidelines. Written informed consent were obtained from all participants.

**Consent for publication**

Not applicable.

**Competing interests**

The authors declare that they have no competing interests.

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**References**

1. Paterson GK, Harrison EM, Holmes MA. The emergence of mecC methicillin-resistant Staphylococcus aureus. Trends Microbiol. 2014;22(2):42–7.
2. Wertheim HF, Melles DC, Vos MC, van Leeuwen W, van Belkum A, Verbrugh HA, Nouwen JL. The role of nasal carriage in Staphylococcus aureus infections. Lancet Infect Dis. 2005;5:751–62.
3. World drug report 2019. https://wdr.unodc.org/wdr2019/prelaunch/pre-launchpresentation_WDR_2019.pdf.
4. Leung NS, Padgett P, Robinson DA, Brown EL. Prevalence and behavioural risk factors of Staphylococcus aureus nasal colonization in community-based injection drug users. Epidemiol Infect. 2015;143:2480–9.
5. El-Sharif A, Ashour HA. Community-acquired methicillin-resistant Staphylococcus aureus (CA-MRSA) colonization and infection in intravenous and inhalational opiate drug abusers. Exp Biol Med (Maywood). 2008;233:874–80.
6. Lin J, Liang J, Zhang T, Bai C, Ye J, Yao Z. Dose-response associations of methicillin-resistant Staphylococcus aureus between school environmental
7. Magnorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18:268–81.

8. Al-Rawahi GN, Schreager AG, Porter SD, Roscoe DL, Gustafson R, Bryce EA. Meticillin-resistant Staphylococcus aureus nasal carriage among injection drug users: six years later. J Clin Microbiol. 2008;46:6477–9.

9. Gwizdala RA, Miller M, Bhat M, Vavagiakis P, Henny C, Neaigus A, Shi Q, Lowy FD. Staphylococcus aureus colonization and infection among injection drug users: identification of hidden networks. Am J Public Health. 2011;101:1268–76.

10. Bassetti S, Wolfsberg L, Jaussi B, Frei R, Kunze MF, Battenay M, Widmer AF. Carriage of Staphylococcus aureus among injection drug users: lower prevalence in an injection heroin maintenance program than in an oral methadone program. Infect Control Hosp Epidemiol. 2004;25:133–7.

11. Quagliarello B, Cespedes C, Miller M, Toro A, Vavagiakis P, Klein RS, Lowy FD. Differences in Staphylococcus aureus nasal carriage and molecular characteristics among community residents and healthcare workers at Sun Yat-Sen University, Guangzhou, Southern China. BMC Infect Dis. 2015;15:303.

12. Chen B, Dai X, He B, Pan K, Li H, Liu X, Bao Y, Yao Y, Huang S. Staphylococcus aureus colonization in a community sample of HIV-infected and HIV-uninfected drug users. Eur J Clin Microbiol Infect Dis. 2003;22:659–63.

13. Fleisch F, Zbinden R, Vanoli C, Ruef C. Epidemic spread of a single clone of methicillin-resistant Staphylococcus aureus among injection drug users in Zurich, Switzerland. Clin Infect Dis. 2001;32:581–6.

14. Dahman D, Jalalvand F, Blome MA, Hakansson A, Janson H, Quick S, Nilsson AC. High Perineal and overall frequency of Staphylococcus aureus in people who inject drugs, compared to non-injectors. Curr Microbiol. 2017;74:159–67.

15. Chen B, Dai X, He B, Pan K, Li H, Liu X, Bao Y, Yao Y, Wu X, Yao Y, Huang S. Coagulase-negative staphylococci infection among drug users in Shanghai, China. J Antimicrob Chemother. 2017;72:1006–13.

16. Lee CH, Tsai CY, Li CC, Chien CC, Liu JW. Teicoplanin therapy for MRSA neonatal skin syndrome in a very low birth weight premature infant. Z Geburtshilfe Neonatol. 2016;220:35–9.

17. Fleisch F, Oechslin EC, Gujer AR, Reinhart WH. Transregional spread of a single clone of methicillin-resistant Staphylococcus aureus between groups of drug users in Switzerland. Infect. 2005;33:273–7.

18. Lloyd-Smith E, Hull MW, Tyndall MW, Zhang R, Wood E, Montanier JS, Kerr T, Romney MG. Community-associated methicillin-resistant Staphylococcus aureus is prevalent in wounds of community-based injection drug users. Epidemiol Infect. 2010;138:713–20.

19. Chen B, Dai X, He B, Pan K, Li H, Liu X, Bao Y, Yao Y, Wu X, Yao Y, Huang S. Staphylococcus aureus nasal carriage in neonates: the role of maternal carriage and phenotypic and molecular characteristics. Infect. Dis. 2018;11:555–65.

20. Wu D, Li X, Yang Y, Zheng Y, Wang C, Deng L, Liu L, Li C, Shang Y, Zhao C, et al. Superantigen gene profiles and presence of exfoliative toxin genes in community-acquired meticillin-resistant Staphylococcus aureus isolated from Chinese children. J Med Microbiol. 2011;60:345–55.

21. Medavilla JR, Chen L, Mathema B, Krestelith BN. Global epidemiology of community-associated methicillin resistant Staphylococcus aureus (CA-MRSA). Curr Opin Microbiol. 2012;15:588–95.

22. Yu F, Li T, Huang X, Xie J, Xie Y, Tu J, Qin Z, Parsons C, Wang J, Hu L, Wang L. Virulence gene profiling and molecular characterization of hospital-acquired Staphylococcus aureus isolates associated with bloodstream infection. Diagn Microbiol Infect Dis. 2012;74:363–8.

23. Soge O, No D, Michael KE, Dankoff J, Lane J, Vogel K, Smedley J, Roberts MC. Transmission of MDRI MRSA between primates, their environment and personnel at a United States primate Centre. J Antimicrob Chemotherapy. 2016;71:2798–803.

24. Cony C, Köck R, Witte W. Livestock associated MRSA (LA-MRSA) and its relevance for humans in Germany. Int J Med Microbiol. 2013;303:331–7.

25. García-Garells C, Antoine J, Larij J, Catry B, Skov R, Denis O. Livestock veterinarians at high risk of acquiring meticillin-resistant Staphylococcus aureus ST398. Epidemiol Infect. 2011;140:383–9.

26. Huang SS, Singh R, McKinnell JA, Park S, Gombocê A, Eells SJ, Gillen DL, Kim D, Rashid S, Macias-Gil R, et al. Decolonization to reduce Postdischarge infection risk among MRSA carriers. N Engl J Med. 2019;380:358–60.