Prevalence and characteristics of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* nasal colonization among a community-based diabetes population in Foshan, China

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INTRODUCTION

*Staphylococcus aureus*, one of the most frequently occurring community- and hospital-associated pathogens, can cause infectious diseases including mild skin infection, endocarditis and even fulminant septicemia¹⁻³. *S. aureus* is a normal inhabitant of the nose, throat and oral cavity⁴⁻⁵. With the widespread use of antibiotics, methicillin-resistant *S. aureus* (MRSA) infections have become significant causes of morbidity and mortality both in the hospital and community settings⁶⁻⁸. Remarkably, investigations have reported that community-associated MRSA infections are increasing⁹⁻¹¹.

The prevalence of diabetes, especially type 2 diabetes mellitus, is increasing at a worrying rate in the world. In 2013, the numbers of diabetes patients in the world were 382 million, accounting for 9.3% of the total world population (6.7% in males, 11.1% in females)¹². In China, the number of diabetics has reached 110 million. In 2013, the number of diabetics aged 65 and over living in rural areas of China was 24.8 million, accounting for 17.55% of all diabetics in China¹³. These patients are more susceptible to infection and have a relatively high infection rate. The nasal carriage rate of MRSA in diabetes patients is 3.6% in the community settings, which is higher than that in non-diabetes patients (1.87%)¹⁴. The prevalence of diabetes, especially type 2 diabetes mellitus, is increasing at a worrying rate in the world. In 2013, the numbers of diabetes patients in the world were 382 million, accounting for 9.3% of the total world population (6.7% in males, 11.1% in females)¹². In China, the number of diabetics has reached 110 million. In 2013, the number of diabetics aged 65 and over living in rural areas of China was 24.8 million, accounting for 17.55% of all diabetics in China¹³. These patients are more susceptible to infection and have a relatively high infection rate. The nasal carriage rate of MRSA in diabetes patients is 3.6% in the community settings, which is higher than that in non-diabetes patients (1.87%)¹⁴.
382 million people had diabetes worldwide, and this number is expected to increase to 592 million by 2035\(^\text{12}\). Approximately 80% of diabetes patients are in low- and middle-income countries\(^\text{13}\). As a developing country, China has a large burden of diabetes; one in four people had the disease in 2013\(^\text{13}\). Furthermore, evidence suggests that diabetes can cause an increased colonization of \textit{S. aureus} and MRSA in both hospitals\(^\text{14-17}\) and community settings\(^\text{18,19}\). However, investigations regarding \textit{S. aureus} and MRSA nasal colonization among diabetes population are limited, and most of them are focused on the patients in hospitals\(^\text{17,20,21}\). Therefore, the aim of the present cross-sectional study was to determine the prevalence, influencing factors and molecular epidemiology of \textit{S. aureus} and MRSA nasal colonization among a community-based diabetes population in Foshan, Guangdong province, China.

**MATERIALS AND METHODS**

**Ethics Statement**

This study was approved by the ethics committee of Guangdong Pharmaceutical University, and it was carried out in accordance with the approved guidelines. All participants signed an informed consent form.

**Study Design and Population**

A cross-sectional study was carried out between April 2014 and May 2015 in 11 community settings (Ganjiao community, Xinxing community, Dachong community, Hecun community, Mashe community, Shachong community, Honggang community, Ganglian community, Shengli community, Zhoucun community and Jixi community) in Guangdong province, China. Those with clinically diagnosed diabetes were voluntarily included in the study. According to the diagnosis of diabetes by the World Health Organization and International Diabetes Federation, diabetes was diagnosed by fasting plasma glucose ≥7.00 mmol/L and/or 2 h postprandial plasma glucose ≥11.10 mmol/L. Additionally, diabetes participants were regarded as having well-controlled blood glucose when they had glycosylated hemoglobin <6.5%. Furthermore, we randomly selected the non-diabetes population from the same area, with the same sex and age ranges within 5 years as controls. We excluded participants who had used antibiotics within a week, had acute diseases, had significant wounds or had other private reasons for exclusion.

**Data Collection and Processing**

After obtaining informed consent, a face-to-face questionnaire was administered to collect relevant information. Five trained interviewers used a structured questionnaire to collect demographic, behavioral and medical history information from participants. In addition, interviewers extracted relevant data from their patient medical records. During the interview, we inserted a sterile swab moistened with normal saline into each participant’s anterior nostrils to a depth of approximately 1.5 cm, and rotated the swab five times. For each specimen, we sampled both nostrils consecutively using the same swab. Each swab was placed into a sterile tube with 7.5% sodium chloride broth, and the tubes were transported to the laboratory immediately after sampling. After 24 h of incubation at 37°C, the swabs were transferred to mannitol salt agar plates for another 24 h of incubation. We then took all samples to be screened for \textit{S. aureus} by colony morphology, Gram staining, catalase test, deoxyribonuclease test and coagulase tests. All \textit{S. aureus} strains were tested to identify MRSA. Those \textit{S. aureus} strains that were positive for the \textit{mec}A gene\(^\text{22}\) and/or resistance to cefoxitin\(^\text{23}\) were identified as MRSA. And those \textit{S. aureus} strains that were negative for the \textit{mec}A gene\(^\text{22}\) and sensitive to cefoxitin\(^\text{23}\) were identified as methicillin-sensitive \textit{S. aureus}.

**Antibiotic Susceptibility Test**

All \textit{S. aureus} isolates were assessed for susceptibility to a panel of 11 antibiotics, including cefoxitin, clindamycin, penicillin, linezolid, gentamycin, teicoplanin, erythromycin, rifampicin, tobramycin, moxifloxacin, nitrofurantoin, linezolid and trimethoprim-sulfamethoxazol. The Kirby–Bauer disk diffusion method was used to test susceptibility to all antibiotics, and diameter interpretations were based on the protocol of the Clinical and Laboratory Standards Institute guidelines (2015)\(^\text{23}\). Strains were classified as multidrug resistant (MDR) if they were non-susceptible to ≥3 antibiotics with different mechanisms of action (note that these strains are already resistant to all beta-lactam antibiotics)\(^\text{24}\).

**Molecular Characterization**

We carried out polymerase chain reaction tests targeting the Panton–Valentine Leukocidin (PVL) toxin gene and the Staphylococcal cassette chromosome \textit{mec} (SCC\textit{mec}) type, using the previously described primers\(^\text{22,25}\). Multilocus sequence typing of the seven housekeeping genes was carried out using the previously described primers and protocols\(^\text{26}\). The sequence type was determined for each isolate by comparing the sequence obtained to known alleles at each locus in the multilocus sequence typing database (http://saureus.mlst.net), and clonal complexes (CCs) were determined using the eBURST algorithm (http://eburst.mlst.net)\(^\text{27}\).

**Statistical Analysis**

Means and standard errors were calculated for continuous variables, and frequencies (percentages) were calculated for categorical variables. Continuous variables were compared by the Student’s \(t\)-test. Categorical variables were compared by Pearson’s \(\chi^2\)-test or Fisher’s exact test when appropriate. The relationships between influencing factors and \textit{S. aureus} and MRSA nasal colonization were examined using multivariable logistic regression models. We carried out the multivariable logistic regression analysis of all variables with a \(P\)-value of <0.05, and then removed variables that were not significant at this level. All analyses were carried out using \textsc{Stata} version 13.1 (StataCorp LP, College Station, TX,
USA), and a two-sided \( P \)-value for statistical significance was defined as \( P < 0.05 \).

**RESULTS**

**Study Population**

A total of 956 participants were included in the study. Of those, 529 were the diabetes population and 427 were the non-diabetes population. There were 161 (30.43%) men and 368 (69.57%) women in the diabetes population, whereas there were 181 (42.39%) men and 246 (57.61%) women in the non-diabetes population. With regard to the average age, the diabetes population was aged 63.51–9.45 years (men 65.58 ± 9.84 years, women 66.14 ± 9.13 years), and the non-diabetes population was aged 64.39 ± 9.45 years (men 65.38 ± 9.85 years, women 63.51 ± 9.07 years). There was a statistically significant difference between the two populations with regard to age (\( t = 2.85, P = 0.002 \)), and this discrepancy was adjusted by applying the multivariable logistic regression model.

Of the 529 diabetes participants, 46 (8.70%) were colonized with *S. aureus* and 22 (4.16%) were colonized with MRSA. Of the 427 non-diabetes participants, 25 (5.85%) were colonized with *S. aureus* and 12 (2.81%) were colonized with MRSA. There was no statistically significant difference between the two populations with regard to age (\( t = 2.85, P = 0.002 \)), and this discrepancy was adjusted by applying the multivariable logistic regression model.

**Influencing Factors of *S. aureus* and MRSA Nasal Colonization in the Diabetes Population**

We found that women (\( \chi^2 = 4.05, P = 0.044 \)) and well-controlled blood glucose (\( \chi^2 = 4.03, P = 0.045 \)) were associated with *S. aureus* nasal colonization among the diabetic population. Women (10.33%) were more likely than men (4.97%) to have *S. aureus* nasal colonization. Those with well-controlled blood glucose (10.61%) were more likely to have *S. aureus* nasal colonization than those without well-controlled blood glucose (5.53%). However, no influencing factor was associated with MRSA nasal colonization among the diabetic population in the present study. More details can be found in Table 1.

To account for potential confounding among the influencing factors, we further analyzed the relationship between the potential predictors with a logistic regression model. This model showed that when controlling for the effects of the other influencing factors, the relationships found in the univariable analyses did not change. The male diabetes population was less likely to have *S. aureus* nasal colonization (odds ratio 0.45, 95% confidence interval 0.20–0.99, \( P = 0.047 \)). Those with well-controlled blood glucose were more likely to have *S. aureus* nasal colonization (odds ratio 2.04, 95% confidence interval 1.01–4.13, \( P = 0.047 \)). More details can be found in Table 3.

**Antibiotic Resistance of *S. aureus* Nasal Colonization**

The highest proportion of antibiotic resistance in *S. aureus* nasal colonization among the diabetes population was to penicillin (89.13%), followed by erythromycin (73.91%), teicoplanin (65.22%), clindamycin (43.48%), tobramycin (26.09%), moxifloxacin (23.91%), cefoxitin (21.74%), gentamicin (19.57%), trimethoprim-sulfamethoxazol (13.04%), rifampicin (10.87%) and linezolid (2.17%). With regard to the non-diabetes population, the highest proportion of antibiotic resistance in *S. aureus* nasal colonization was to penicillin (96.00%), followed by clindamycin (60.00%), erythromycin (46.00%), teicoplanin (36.00%), tobramycin (32.00%), cefoxitin (24.00%), moxifloxacin (16.00%), gentamicin (12.00%), trimethoprim-sulfamethoxazol (12.00%) and linezolid (0.00%). Furthermore, the proportion of MDR *S. aureus* strains in the diabetes population (52.17%, 24/46) was higher than that in the non-diabetes population (28.00%, 7/25) (\( \chi^2 = 3.848, P = 0.050 \)).

The highest proportion of antibiotic resistance in MRSA nasal colonization among the diabetes population was to penicillin (95.45%), followed by erythromycin (81.82%), teicoplanin (59.09%), clindamycin (59.09%), cefoxitin (45.45%), moxifloxacin (33.33%), cefoxitin (33.33%), tobramycin (50.00%), trimethoprim-sulfamethoxazol (22.73%), rifampicin (13.64%) and linezolid (4.55%). With regard to the non-diabetes population, the highest proportion of antibiotic resistance in MRSA nasal colonization was to penicillin (100.00%), followed by erythromycin (75.00%), clindamycin (66.67%), cefoxitin (50.00%), teicoplanin (33.33%), moxifloxacin (33.33%), tobramycin (25.00%), trimethoprim-sulfamethoxazol (25.00%), rifampicin (16.67%), gentamicin (16.67%) and linezolid (0.00%).

There were statistically significant differences between the two populations in antibiotic resistance of *S. aureus* nasal colonization.

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**Table 1** Prevalence of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* nasal colonization

| Population | n | S. aureus | MRSA |
|------------|---|----------|------|
|            | n (%) | Adjusted† | \( \chi^2 \) | P-value | n (%) | Adjusted† | \( \chi^2 \) | P-value |
| Diabetes   | 529 | 46 (8.70%) | 8.09% | 2.77 | 0.096 | 22 (4.16%) | 3.70% | 1.25 | 0.263 |
| Non-diabetes | 427 | 25 (5.85%) | 5.70% | 2.69% | 12 (2.81%) | 2.69% | 2.69% | 0.263 |

†Prevalence after adjusted for sex and age. MRSA, methicillin-resistant *Staphylococcus aureus*; S. aureus, *Staphylococcus aureus*. 
| Influencing factors                  | n  | S. aureus | \( \chi^2 \) | P-value | MRSA | \( \chi^2 \) | P-value |
|-------------------------------------|----|-----------|--------------|---------|------|--------------|---------|
| **Demographic characteristics**    |    |           |              |         |      |              |         |
| Sex                                |    |           |              |         |      |              |         |
| Men                                | 161| 8 (4.97)  | 4.05         | 0.044   | 3 (1.86)| 3.06         | 0.080   |
| Women                              | 368| 38 (10.33)|              |         |      |              |         |
| Age (years)                        |    |           |              |         |      |              |         |
| ≤65                                | 267| 25 (9.36) | 0.30         | 0.582   | 12 (4.49)| 0.15         | 0.696   |
| >65                                | 262| 21 (8.02) |              |         |      |              |         |
| BMI                                |    |           |              |         |      |              |         |
| <18.5                              | 29 | 1 (3.45)  | 1.72         | 0.632   | 1 (3.45)| 3.38         | 0.337   |
| 18.5–24.9                          | 215| 17 (7.91) |              |         |      |              |         |
| 25–27.9                            | 210| 20 (9.52) |              |         |      |              |         |
| ≥28                                | 75 | 8 (10.67) |              |         |      |              |         |
| Monthly income (yuan)              |    |           |              |         |      |              |         |
| ≤2000                              | 469| 40 (8.53) | –            | 0.209   | 18 (3.84)| –            | 0.197   |
| 2000–2999                          | 43 | 6 (13.95) |              |         |      |              |         |
| ≥3000                              | 17 | 0 (0.00)  |              |         |      |              |         |
| Education                          |    |           |              |         |      |              |         |
| Illiterate                         | 91 | 11 (12.09)| 1.60         | 0.449   | 7 (7.69)|              |         |
| Primary school                     | 328| 26 (7.93) |              |         |      |              |         |
| Junior school and above            | 110| 9 (8.18)  |              |         |      |              |         |
| Medical history                    |    |           |              |         |      |              |         |
| Type of diabetes                   |    |           |              |         |      |              |         |
| 1                                  | 19 | 0 (0.00)  | –            | 0.396   | 0 (0.00)| –            | 1.000   |
| 2                                  | 507| 46 (9.07) |              |         |      |              |         |
| Duration of diabetes (years)       |    |           |              |         |      |              |         |
| <5                                 | 332| 32 (9.64) | 3.40         | 0.183   | 17 (5.12)| –            | 0.120   |
| 5–9                                | 113| 5 (4.42)  |              |         |      |              |         |
| ≥10                                | 84 | 9 (10.71) |              |         |      |              |         |
| Family history of diabetes         |    |           |              |         |      |              |         |
| Yes                                | 109| 12 (11.01)| 0.93         | 0.337   | 3 (2.75)| –            | 0.591   |
| No                                 | 420| 34 (8.1)  |              |         |      |              |         |
| Blood glucose monitoring            |    |           |              |         |      |              |         |
| Yes                                | 271| 26 (9.59) | 0.565        | 0.453   | 12 (4.43)| 0.10         | 0.751   |
| No                                 | 258| 20 (7.75) |              |         |      |              |         |
| Blood glucose controlling           |    |           |              |         |      |              |         |
| Yes                                | 513| 45 (8.77) | –            | 1.000   | 22 (4.29)| –            | 1.000   |
| No                                 | 16 | 1 (6.25)  |              |         |      |              |         |
| Well-controlled blood glucose       |    |           |              |         |      |              |         |
| Yes                                | 330| 35 (10.61)| 4.03         | 0.045   | 18 (5.45)| 3.70         | 0.055   |
| No                                 | 199| 11 (5.53) |              |         |      |              |         |
| Taking insulin now                 |    |           |              |         |      |              |         |
| Yes                                | 186| 16 (8.60) | 0.01         | 0.955   | 10 (5.38)| 1.07         | 0.302   |
| No                                 | 343| 30 (8.75) |              |         |      |              |         |
| Behavioral characteristics          |    |           |              |         |      |              |         |
| Smoking                            |    |           |              |         |      |              |         |
| Yes                                | 77 | 3 (3.90)  | 2.61         | 0.106   | 2 (2.60)| –            | 0.756   |
| No                                 | 452| 43 (9.51) |              |         |      |              |         |
| Taking alcohol drinks              |    |           |              |         |      |              |         |
| Yes                                | 26 | 0 (0.00)  | –            | 0.154   | 0 (0.00)| –            | 0.617   |
| No                                 | 503| 46 (9.15) |              |         |      |              |         |
colonization with regard to teicoplanin ($\chi^2 = 5.59, P = 0.018$) and erythromycin ($\chi^2 = 4.77, P = 0.029$). S. aureus strains were more likely to be resistant to teicoplanin and erythromycin in the diabetes population than those in the non-diabetes population. More details can be found in Table 4.

**Table 4** | Logistic regression analysis of influencing factors in Staphylococcus aureus nasal colonization among diabetic population

| Influencing factors          | OR    | P-value | 95% CI |
|-----------------------------|-------|---------|--------|
| Sex                         |       |         |        |
| Men                         | 0.45  | 0.047   | 0.20–0.99 |
| Women                       | 1.00  |         |        |
| Well-controlled blood glucose | 2.04  | 0.047   | 1.01–4.13 |
| No                          | 1.00  |         |        |

CI, confidence interval; OR, odds ratio.

**DISCUSSION**

The present study adds to the existing knowledge by giving insight into the genotypic and phenotypic characteristics of S. aureus and MRSA nasal colonization among the diabetes population in community settings. The prevalence of S. aureus (8.70%, 46/529) nasal colonization among the community-based diabetes population in this study was lower than those of a diabetic outpatient population in Turkey (41.78%, 127/304)\(^21\), long-term hemodialysis type 2 diabetes patients in Saudi Arabia (72.41%, 42/58)\(^28\), hospitalized diabetic patients in India (56.67%, 34/60)\(^19\), diabetes patients in Australia (39.09%, 258/660)\(^19\), and type 1 diabetes pediatric outpatients in Turkey (in 2005, 0.99%, 1/101; in 2013, 0.75%, 1/134)\(^29\).

The prevalence of MRSA (4.16%, 22/529) nasal colonization among the community-based diabetes population in this study was lower than those of type 2 diabetes patients in China (5.28%, 22/417)\(^18\), a diabetic outpatient population in Turkey (9.87%, 30/304)\(^21\) and long-term hemodialysis type 2 diabetes patients in Saudi Arabia (18.97%, 11/58)\(^28\), but was higher than those of hospitalized diabetic patients in China (0.50%, 1/200)\(^20\), diabetes patients in Australia (1.21%, 8/660)\(^19\) and type 1 diabetes pediatric outpatients in Turkey (in 2005, 0.99%, 1/101; in 2013, 0.75%, 1/134)\(^29\).

From the aforementioned statistics, we know that the prevalence of S. aureus nasal colonization was lower in this community-based diabetes population than in the hospital-based...
diabetes population. The proportion of MRSA nasal colonization in *S. aureus* strains (47.83%, 22/46) among the diabetes population in the present study was higher than the nationally average proportion of MRSA in *S. aureus* strains in 2013 (45.20%) and 2014 (44.60%) in China, which can be partially explained by the high prevalence of MRSA nasal colonization in the present community-based diabetes population. However, there was no statistical difference in the prevalence of *S. aureus* and MRSA nasal colonization between the two populations, which was consistent with several studies.

The multivariable logistic regression model showed that women and well-controlled blood glucose were associated with a higher prevalence of *S. aureus* nasal colonization among the diabetes population, which was different to some other studies. Most of the existing studies reported that sex was irrelevant to the prevalence of *S. aureus* nasal colonization among diabetes populations, which was contrary to the present study. The possible reasons were that the majority of included diabetes patients in the present study were women, and the women were older than the men. Furthermore, there were studies that showed that women with older age had weaker immune systems and were more likely to be infected with many infectious diseases, which might be the reason for this result. With regard to the relationship between well-controlled blood glucose and the prevalence of *S. aureus* nasal colonization among the diabetes population, it varied in different countries and regions. It was reported as a protective factor, a risk factor, or an irrelevant factor. This might have resulted from the different races, sample size, therapies and other elements, so it requires further investigation.

We found that *S. aureus* strains of both the diabetes population and non-diabetes population in the present study were highly resistant to erythromycin and penicillin, which was similar to several other studies. This might be as a result of the extensive use of these antibiotics in medical institutions. We also found that 54.93% of *S. aureus* strains were resistant to teicoplanin, which was higher than several studies. The reason for the high rate of teicoplanin resistance might partly be due to the standard of antibiotic resistance, which included both intermediate and resistant strains in the present study, which caused the high rate of teicoplanin resistance. Furthermore, the proportion of MDR *S. aureus* strains in the diabetes population (52.17%) was higher than that in the non-diabetes population (28.00%), which should be noticed by healthcare workers to reasonably utilize antibiotics.

There were studies that reported that the PVL toxin gene was related to skin soft tissue infection and necrotizing pneumonia. Of 34 MRSA strains, six (17.65%) were positive for the PVL toxin gene for the high rate of teicoplanin resistance might partly be due to the standard of antibiotic resistance, which included both intermediate and resistant strains in the present study, which caused the high rate of teicoplanin resistance. Furthermore, the proportion of MDR *S. aureus* strains in the diabetes population (52.17%) was higher than that in the non-diabetes population (28.00%), which should be noticed by healthcare workers to reasonably utilize antibiotics.

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There were several limitations to the present study. First, we did not follow up the outcomes of *S. aureus* and MRSA nasal colonization in the community settings.
colonization among the diabetes population because of limited financial support. Second, we did not investigate the environmental factors, which might be potential influencing factors of *S. aureus* and MRSA nasal colonization, because of limited human resources. Finally, we did not use an MIC method because of limited financial support, and we will further consider it in future research.

There was no statistical difference of *S. aureus* and MRSA nasal colonization between the community-based diabetes population and non-diabetes population. Women and those with well-controlled blood glucose in the community-based diabetes population were more likely to have *S. aureus* and MRSA nasal colonization. The majority of antibiotic resistance proportions in MRSA strains were higher than those in the methicillin-sensitive *S. aureus* strains. The proportions of MDR *S. aureus* and MRSA strains were higher in the diabetes population than in the non-diabetes population. The proportion of the PVL toxin gene in MRSA strains was moderate. MRSA strains in the present study were mainly from community settings, but there were some strains from hospital settings. There was great ST diversity in MRSA strains among the community-based diabetes population, and this was closely related to internationally epidemiological strains.

Therefore, the present results suggest a need for surveillance of MDR *S. aureus* and MRSA in community-based diabetes populations. More research is still required to establish the exact transmission routes and explore measures for preventing the spread of the bacterium in community settings.

**Table 5** Genotypic and phenotypic characteristics of methicillin-resistant *Staphylococcus aureus* nasal colonization

| Population | CC | MLST | SCC | mec | PVL | MDR | Antibiotic resistance patterns |
|------------|----|------|-----|-----|-----|-----|-------------------------------|
| Diabetes (n = 22) | CC5 | ST544 | IV | – | + | PEN-GEN-TEC-TOB |
| | CC5 | ST1 | NT | – | + | PEN-TEC-ERY-SXT-TOB-MXF-CLI |
| | CC5 | ST1 | II | – | + | FOX-PEN-GEN-ERY-TOB-MXF-CLI |
| | CC5 | ST6 | NT | + | – | – |
| | CC5 | ST6 | I | – | – | PEN-TEC-CLI |
| | CC5 | ST5 | V | – | + | PEN-GEN-ERY-SXT-CLI |
| | CC5 | ST72 | IV | – | + | FOX-PEN-ERY |
| | CC5 | ST9 | IV | – | + | FOX-PEN-GEN-ERY-SXT-TOB-CLI |
| | CC5 | ST188 | NT | – | – | PEN-TEC |
| | CC30 | ST30 | IV | – | – | PEN-TEC-ERY |
| | CC45 | ST45 | IV | – | + | FOX-PEN-TEC-ERY-CLI |
| | CC45 | ST3154 | NT | – | – | FOX-PEN-TEC-ERY |
| | CC59 | ST338 | III | + | + | FOX-PEN-TEC-ERY-MXF-CLI |
| | CC59 | ST338 | III | + | + | FOX-PEN-ERY-SXT-CLI |
| | CC59 | ST59 | IV | – | + | LZX-FOX-PEN-ERY-MXF-CLI |
| | CC59 | ST59 | V | – | + | FOX-PEN-TEC-ERY-MXF-CLI |
| | CC182 | ST944 | II | – | – | PEN-ERY-CLI |
| | CC398 | ST398 | IV | – | + | PEN-GEN-ERY-SXT-TOB-MXF-CLI |
| | CC398 | ST2504 | V | – | + | PEN-GEN-ERY-SXT-TOB-MXF-CLI |
| | CC398 | ST1937 | II | – | + | FOX-PEN-TEC-ERY-MXF-CLI |
| | CC398 | ST398 | III | – | + | PEN-TEC-ERY-CLI |
| | CC398 | ST398 | NT | – | + | PEN-TEC-ERY-TOB |
| Non-diabetes (n = 12) | CC5 | ST9 | IV | – | + | FOX-PEN-GEN-TEC-ERY-SXT-TOB-MXF-RIF-CLI |
| | CC5 | ST544 | IV | – | – | PEN |
| | CC5 | ST544 | IV | + | – | PEN-TEC |
| | CC5 | ST72 | II | – | + | PEN-TEC-ERY-MXF-CLI |
| | CC5 | ST5 | V | – | + | FOX-PEN-ERY-MXF-CLI |
| | CC7 | ST7 | IV | – | + | PEN-GEN-ERY-SXT-TOB-CLI |
| | CC30 | ST30 | IV | – | – | PEN-ERY-MXF |
| | CC59 | ST59 | IV | – | – | FOX-PEN-ERY-CLI |
| | CC59 | ST59 | IV | – | – | FOX-PEN-ERY-CLI |
| | CC59 | ST338 | III | + | – | FOX-PEN-ERY-CLI |
| | CC88 | ST88 | NT | + | + | FOX-PEN-ERY-SXT-TOB-RIF-CLI |
| | CC2483 | ST2483 | III | – | – | PEN-TEC |

+, Positive; –, negative; CC, clonal complex; CLI, clindamycin; ERY, erythromycin; FOX, cefoxitin; GEN, gentamycin; LZX, linezolid; MDR, multidrug resistant; MLST, multilocus sequence typing; MXF, moxifloxacin; NT, non-typeable; PEN, penicillin; PVL, Panton–Valentine leukocidin; RIF, rifampicin; SCC, staphylococcal chromosome cassette; ST, sequence type; SXT, trimethoprim-sulfamethoxazol; TEC, teicoplanin; TOB, tobramycin.
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DISCLOSURE
The authors declare no conflict of interest.

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