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ORIGINAL ARTICLE

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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ABSTRACT

Aims/Introduction: Evidence suggests that diabetes might cause an increase in colonization of *Staphylococcus aureus* (*S. aureus*) and methicillin-resistant *S. aureus* (MRSA) in community settings. We carried out a cross-sectional study to determine the prevalence and influencing factors of *S. aureus* and MRSA nasal colonization among a community-based diabetes population, and to identify the characteristics of the isolated strains.

Materials and Methods: A total of 956 participants from 11 community settings were included in the study.

Results: Of the 529 diabetes participants, 46 were colonized with *S. aureus* and 22 were colonized with MRSA. Of the 427 non-diabetes participants, 25 were colonized with *S. aureus* and 12 were colonized with MRSA. Men (odds ratio 0.45, 95% confidence interval 0.20–0.99, $P = 0.047$) were less likely to have *S. aureus* nasal colonization, and those with well-controlled blood glucose (odds ratio 2.04, 95% confidence interval 1.01–4.13, $P = 0.047$) among the diabetes population were more likely to have *S. aureus* nasal colonization. The proportion of multidrug-resistant *S. aureus* strains in the diabetes population (52.17%) was higher than that in the non-diabetes population (28.00%; $\chi^2 = 3.848$, $P = 0.050$). The most common clonal complex type and Staphylococcal chromosome cassette *mec* type of MRSA in diabetes population was clonal complex 5 (40.91%) and type IV (27.27%), respectively. The proportion of Panton–Valentine leukocidin gene in MRSA strains was 17.65%. There was great sequence type diversity in MRSA strains.

Conclusions: The prevalence of MRSA in the community-based diabetes population was moderate, and the high proportions of multidrug-resistant *S. aureus* strains and diverse molecular characteristics in the diabetes population should be noticed.

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 septicemia[1–3]. *S. aureus* is a normal inhabitant of the nose, throat and oral cavity[4,5]. 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 settings[6–8]. Remarkably, investigations have reported that community-associated MRSA infections are increasing[9–11].

The prevalence of diabetes, especially type 2 diabetes mellitus, is increasing at a worrying rate in the world. In 2013,

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382 million people had diabetes worldwide, and this number is expected to increase to 592 million by 2035[12]. Approximately 80% of diabetes patients are in low- and middle-income countries[12]. As a developing country, China has a large burden of diabetes: one in four people had the disease in 2013[13]. Furthermore, evidence suggests that diabetes can cause an increased colonization of *S. aureus* and MRSA in both hospitals[14–17] and community settings[18,19]. However, investigations regarding *S. aureus* and MRSA nasal colonization among diabetes population are limited, and most of them are focused on the patients in hospitals[17,20,21]. Therefore, the aim of the present cross-sectional study was to determine the prevalence, influencing factors and molecular epidemiology of *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 Jinxi 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 *S. aureus* by colony morphology, Gram staining, catalase test, deoxyribonuclease test and coagulase tests. All *S. aureus* strains were tested to identify MRSA. Those *S. aureus* strains that were positive for the *mec*A gene[22] and/or resistance to cefoxitin[23] were identified as MRSA. And those *S. aureus* strains that were negative for the *mec*A gene[22] and sensitive to cefoxitin[23] were identified as methicillin-sensitive *S. aureus*.

Antibiotic Susceptibility Test

All *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)[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)[24].

Molecular Characterization

We carried out polymerase chain reaction tests targeting the Panton–Valentine Leukocidin (PVL) toxin gene and the Staphylococcal cassette chromosome *mec* (SCC*mec*) type, using the previously described primers[22,25]. Multilocus sequence typing of the seven housekeeping genes was carried out using the previously described primers and protocols[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)[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 χ^2-test or Fisher's exact test when appropriate. The relationships between influencing factors and *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 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 66.13 ± 9.34 years (men 66.12 ± 9.84 years, women 66.14 ± 9.13 years), and the non-diabetes population was aged 64.39 ± 9.45 years (men 65.58 ± 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 *S. aureus* and MRSA nasal colonization. After adjusted for sex and age, the prevalence of *S. aureus* and MRSA nasal colonization among the diabetes and non-diabetes population were 8.09%, 3.70%, and 5.70%, 2.69%, respectively. There was no statistically significant difference between the adjusted and unadjusted prevalence. More details can be found in Table 1.

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 2.

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%), gentamycin (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%), rifampicin (24.00%), moxifloxacin (16.00%), gentamycin (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 (36.36%), tobramycin (31.82%), gentamycin (27.27%), 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%), gentamycin (16.67%) and linezolid (0.00%).

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

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

Population	*n*	*S. aureus*				MRSA			
		n (%)	Adjusted†	χ^2	*P*-value	*n* (%)	Adjusted†	χ^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%			12 (2.81%)	2.69%		

†Prevalence after adjusted for sex and age. MRSA, methicillin-resistant *Staphylococcus aureus*; *S. aureus*, *Staphylococcus aureus*.

Table 2 | Influencing factors of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* nasal colonization among the diabetic population

Influencing factors	*n*	*S. aureus*			MRSA		
		n (%)	χ^2	*P*-value	*n* (%)	χ^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)			19 (5.16)		
Age (years)							
≤65	267	25 (9.36)	0.30	0.582	12 (4.49)	0.15	0.696
>65	262	21 (8.02)			10 (3.82)		
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)			11 (5.12)		
25–27.9	210	20 (9.52)			5 (2.38)		
≥28	75	8 (10.67)			5 (6.67)		
Monthly income (yuan)							
<2000	469	40 (8.53)	–	0.209	18 (3.84)	–	0.197
2000–2999	43	6 (13.95)			4 (9.30)		
≥3000	17	0 (0.00)			0 (0.00)		
Education							
Illiterate	91	11 (12.09)	1.60	0.449	7 (7.69)		
Primary school	328	26 (7.93)			11 (3.35)	–	0.197
Junior school and above	110	9 (8.18)			4 (3.64)		
Medical history							
Type of diabetes							
1	19	0 (0.00)	–	0.396	0 (0.00)	–	1.000
2	507	46 (9.07)			22 (4.34)		
Duration of diabetes (years)							
<5	332	32 (9.64)	3.40	0.183	17 (5.12)	–	0.120
5–9	113	5 (4.42)			1 (0.88)		
≥10	84	9 (10.71)			4 (4.76)		
Family history of diabetes							
Yes	109	12 (11.01)	0.93	0.337	3 (2.75)	–	0.591
No	420	34 (8.1)			19 (4.52)		
Blood glucose monitoring							
Yes	271	26 (9.59)	0.565	0.453	12 (4.43)	0.10	0.751
No	258	20 (7.75)			10 (3.88)		
Blood glucose controlling							
Yes	513	45 (8.77)	–	1.000	22 (4.29)	–	1.000
No	16	1 (6.25)			0 (0.00)		
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)			4 (2.01)		
Taking insulin now							
Yes	186	16 (8.60)	0.01	0.955	10 (5.38)	1.07	0.302
No	343	30 (8.75)			12 (3.50)		
Behavioral characteristics							
Smoking							
Yes	77	3 (3.90)	2.61	0.106	2 (2.60)	–	0.756
No	452	43 (9.51)			20 (4.42)		
Taking alcohol drinks							
Yes	26	0 (0.00)	–	0.154	0 (0.00)	–	0.617
No	503	46 (9.15)			22 (4.37)		

Table 2 (*Continued*)

Influencing factors	*n*	*S. aureus*			MRSA		
		n (%)	χ^2	*P*-value	*n* (%)	χ^2	*P*-value
Taking physical activity							
Yes	386	34 (8.81)	0.02	0.880	19 (4.92)	2.09	0.149
No	143	12 (8.39)			3 (2.10)		
Antibiotic use past year							
Yes	121	8 (6.61)	0.86	0.355	5 (4.13)	0.00	0.987
No	408	38 (9.31)			17 (4.17)		
Hospitalization past year							
Yes	244	23 (9.43)	0.41	0.523	11 (4.51)	0.11	0.742
No	280	22 (7.86)			11 (3.93)		

–, Calculated with Fisher's exact test; BMI, body mass index (weight [kg] / height [m]^2); MRSA, methicillin-resistant *Staphylococcus aureus*; *S. aureus*, *Staphylococcus aureus*.

Table 3 | 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			
Yes	2.04	0.047	1.01–4.13
No	1.00		

CI, confidence interval; OR, odds ratio.

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.

Genotypic and Phenotypic Characteristics of MRSA Nasal Colonization

The most common CC type of MRSA in the 22 members of the diabetes population was CC5 (9), followed by CC398 (5), CC59 (4), CC45 (2), CC30 (1) and CC182 (1). The most common CC type of MRSA in the 12 members of the non-diabetes population was CC5 (5), followed by CC59 (3), CC7 (1), CC30 (1) and CC88 (1).

We identified 19 unique STs from 34 MRSA strains. MRSA strains from the diabetes population showed great ST diversity. ST59 was common among the two populations. ST398 was common among the diabetes population, but absent from the non-diabetes population. Among the 34 MRSA strains, the predominant ST was ST398 for the diabetes population and ST544 for the non-diabetes population.

The most common SCC*mec* type of MRSA strains in the diabetes population was type IV (27.27%), followed by non-typeable (22.73%), type V (18.18%), type II (13.64%), type III (13.64%) and type I (4.54%). The most common SCC*mec* type of MRSA strains in the non-diabetes population was type IV (58.34%), followed by type III (16.67%), non-typeable (8.33%), type V (8.33%), type II (8.33%) and type I (0.00%).

The proportion of the virulence gene PVL of the MRSA strains in the diabetes population (13.64%, 3/22) was lower than that in the non-diabetes population (25.00%, 3/12).

The patterns of MDR in the diabetes population and non-diabetes population were different. More details can be found in Table 5.

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)[17], diabetes patients in Australia (39.09%, 258/660)[19], hospitalized diabetic patients (20.50%, 41/200) in China[20] and type 2 diabetes outpatients in China (10.31%, 43/417)[21].

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

Table 4 | Antibiotic resistance of *Staphylococcus aureus* nasal colonization

Antibiotic	Diabetic population		Non-diabetic population		*P*-value*	*P*-value**
	MRSA (*n* = 22)	MSSA (*n* = 24)	MRSA (*n* = 12)	MSSA (*n* = 13)		
Cefoxitin	10 (45.45)	0 (0.00)	6 (50.00)	0 (0.00)	0.828	0.800
Linezolid	1 (4.55)	0 (0.00)	0 (0.00)	0 (0.00)	1.000***	1.000***
Penicillin	21 (95.45)	20 (83.33)	12 (100.00)	12 (92.31)	0.320	0.453
Gentamycin	6 (27.27)	3 (12.50)	2 (16.67)	1 (7.69)	0.417	0.486
Teicoplanin	13 (59.09)	17 (70.83)	4 (33.33)	5 (38.46)	0.018	0.151
Erythromycin	18 (81.82)	16 (66.67)	9 (75.00)	3 (23.08)	0.029	0.638
Trimethoprim-sulfamethoxazol	5 (22.73)	1 (4.17)	3 (25.00)	0 (0.00)	0.900	0.881
Tobramycin	7 (31.82)	5 (20.83)	3 (25.00)	5 (38.46)	0.597	0.677
Moxifloxacin	8 (36.36)	3 (12.50)	4 (33.33)	0 (0.00)	0.435	0.860
Rifampicin	3 (13.64)	2 (8.33)	2 (16.67)	4 (30.77)	0.144	0.812
Clindamycin	13 (59.09)	7 (29.17)	8 (66.67)	7 (53.85)	0.184	0.664

Data presented as *n* (%). **P*-value was calculated the antibiotic resistance proportions of *Staphylococcus aureus* between the two populations. ***P*-value was calculated the antibiotic resistance proportions of methicillin-resistant *Staphylococcus aureus* (MRSA) between the two populations. ****P*-value was calculated with Fisher's exact test. MSSA, methicillin-sensitive *Staphylococcus aureus*.

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%)[30] and 2014 (44.60%)[31] 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[19,32].

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[19,21,32–34], 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[35,36] 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[21], a risk factor[33,37] or an irrelevant factor[19,32]. 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[20,38,39]. 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[40]. 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[41–43]. Of 34 MRSA strains, six (17.65%) were positive to it. However, there was no statistical difference between the two populations. The most common SCC*mec* type in the two populations was type IV, which was consistent with the source of the two populations. ST59 was common among MRSA strains from the two populations, which was consistent with a study that ST59 was mainly in community settings from the Asian area[44]. ST398, which was mainly from swine in North America and Europe[45,46], but found in humans in China[47,48], was common among the diabetes population, which might be associated with poor immune function in the diabetes population. The CC types among the two community-based populations were diverse. CC5, the most common CC type of MRSA strains in the two community-based populations, was reported to be the main CC type among MRSA infection in hospital settings[49,50], which might indicate that there were hospital-associated MRSA in these 11 community settings.

There were several limitations to the present study. First, we did not follow up the outcomes of *S. aureus* and MRSA nasal

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	–	+	LZD-FOX-PEN-ERY-MXF-CLI
	CC59	ST59	V	–	+	FOX-PEN-TEC-ERY-MXF-CLI
	CC182	ST944	II	–	–	PEN-ERY-CLI
	CC398	ST398	V	–	+	PEN-GEN-ERY-SXT-TOB-MXF-CLI
	CC398	ST2504	V	–	+	PEN-GEN-TEC-ERY-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; LZD, 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.

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.

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DISCLOSURE

The authors declare no conflict of interest.

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