RESEARCH ARTICLE

Molecular characteristics of antimicrobial resistance and virulence determinants of *Staphylococcus aureus* isolates derived from clinical infection and food

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Background: *Staphylococcus aureus* (*S. aureus*) is an important human etiologic agent. An investigation of the characteristics of common genotypes of *S. aureus* relating to pathogenicity and antibiotic resistance may provide a foundation to prevent infection.

Methods: This study collected 275 *S. aureus* isolates from Zhengzhou city in China, including 148 isolates from patient samples and 127 isolates from ready-to-eat food samples. Antimicrobial susceptibility testing was performed using the broth dilution method. Molecular characteristics of antimicrobial resistance, virulence, and genotypes were identified by polymerase chain reaction (PCR).

Results: In total, 34.18% (94/275) of *S. aureus* isolates were MRSA. Compared with food isolates, clinical isolates had significantly higher antibiotic resistance rates, carrying resistance genes such as *acc(6')*/*aph(2')*, *aph(3')*-III, *ermA*, and *ermB* and virulence genes such as *tetM*, *sea*, *seb*, *pvl*, and *etb*. MRSA-t030-*agr*I-SCCmecIII and MSSA-t002-*agr*II were the most common strain types among clinical strains, and MRSA-t002-*agr*II-SCCmecIII and MSSA-t002-*agr*II were the most common strain types among food strains. Additionally, some strains in the *agr* group were also *spa* type-specific, suggesting that there may be phenotypic consistency.

Conclusion: Clinical isolates contained higher numbers of resistance genes and demonstrated higher antibiotic resistance, while 2 source strains exhibited high toxicity. These results indicate that bacteria with different origins may have undergone different evolutionary processes. As resistance and virulence factors in food bacteria can be transmitted to humans, food handlers should strictly follow hygienic measures during food production to ensure the safety of human consumers.

KEYWORDS

antimicrobial resistance, genotypes, methicillin-resistant *S. aureus*, resistance genes, virulence genes

1 | INTRODUCTION

Staphylococcus aureus (*S. aureus*) is an important Gram-positive human etiologic agent that can cause a wide range of diseases, such

as pneumonia, toxic shock syndrome, and food poisoning.¹ *S. aureus* contamination is the third leading cause of food poisoning worldwide and is always related to nonstandard health measures. Based on β -lactam susceptibility, *S. aureus* is commonly divided into 2

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categories: methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA).² Since the emergence of resistant strains, especially MRSA, treatment of *S. aureus* infection is becoming more difficult, and this pathogen represents a serious threat to human health.³

The reasons underlying the difficulty in treating *S. aureus* infection in recent decades are partly attributable to the virulence factors produced by this pathogen. Various virulence determinants, including hemolysins, staphylococcal enterotoxins, toxic shock syndrome toxin-1 (TSST-1), and Panton-Valentine leukocidin (PVL), are associated with *S. aureus* infections.⁴ In general, different combinations of virulence genes may determine disparate infection outcomes.

At present, many molecular typing methods are used for the genotypic characterization of *S. aureus*. The main methods include pulsed-field gel electrophoresis (PFGE), multilocus sequence typing (MLST), staphylococcal protein A (*spa*) typing, and accessory gene regulator (*agr*) typing. PFGE has been acknowledged as the "gold standard" for molecular typing of *S. aureus* because of its excellent discriminatory power and ability to type most bacterial species.⁵ However, as it is difficult to compare results between laboratories and over time, PFGE is not appropriate for long-term and wide-ranging epidemiological studies.⁶ MLST and *spa*, both developed recently, are sequence-based typing methods. MLST depends on 7 housekeeping loci and nucleotide variations among them for typing.⁷ *Spa* typing relies on the features, order, and number of repeat sequences in the x region of *spa*.⁸ Furthermore, *spa* typing is easier and less costly than MLST and PFGE.⁶ *Agr* typing relies on detecting polymorphisms in the amino acid sequence of the *agr*-encoding auto-inducing peptide and its corresponding receptor and always encompasses 4 major groups (*agr*I-IV).⁹ It would be interesting to investigate different *spa* and *agr* types in *S. aureus* isolates with different origins. The aim of this study was to determine the prevalence of MRSA, antimicrobial resistance, and virulence-associated genes carried in bacterial strains and to compare the diversity of these factors in *S. aureus* obtained from different sources. Moreover, the molecular genetics underlying the relationships between isolates from clinical and food origins were analyzed using the *spa* and *agr* typing methods.

2 | MATERIALS AND METHODS

2.1 | Bacteria

In this study, we collected 275 *S. aureus* isolates from Zhengzhou city, Henan Province, China, from July 2013 to December 2015. Of the 275 isolates, 148 isolates were from patients at 2 hospitals in Zhengzhou city and included 85 isolates from secretions, 10 from transudation, 7 from cerebrospinal fluid, 20 from blood, 11 from phlegm, and 15 from urine. The remaining 127 isolates were from ready-to-eat food samples, comprising 55 isolates from fresh meat, 18 from meat products, 17 from fruits and vegetables, and 37 strains from cereal products. All bacterial strains were stored at -80°C before use.

2.2 | Antimicrobial susceptibility testing and DNA isolation

Antimicrobial susceptibility testing was performed using the broth dilution method according to the recommendations of the Clinical and Laboratory Standards Institute. Using the reference strain ATCC 29213 as a control, genomic DNA of *S. aureus* was extracted using a QIAamp DNA Mini Kit (Qiagen, Germany) according to the specifications for Gram-positive bacteria.

2.3 | Detection of resistance and virulence genes

A total of 9 resistance genes (*mecA*, *ermA*, *ermB*, *ermC*, *msrA*, *aac(6')*/*aph(2'')*, *aph(3')*-III, *ant(4',4'')*, and *tetM*) were detected by polymerase chain reaction (PCR) as described below.^{10,11} In addition, PCR was used to detect the presence of 9 virulence genes: *hla*, *hly*, *sea*, *seb*, *sec*, *pvl*, *eta*, *etb*, and *tsst*.^{12,13} *mecA* gene amplification was performed to identify MRSA isolates. SCC_{mec} typing of MRSA strains was analyzed by multiplex PCR as previously described.¹⁴

2.4 | *spa* and *agr* typing

The *spa* repeating region was amplified by PCR as described by Harmsen.¹⁵ *spa* types were determined using the *spa* server website (<http://spa.ridom.de/spaserver/>). *agr* allele types were determined through multiplex PCR as previously described.¹⁶

2.5 | Statistical analyses

The statistical methods used for analysis were the Chi-square test and Fisher's exact test. $P < .05$ was considered statistically significance. Statistical analyses of all data were performed using SPSS version 21.0 software.

3 | RESULTS

3.1 | Antibiotic resistance of *Staphylococcus aureus* isolates

Among the 275 *S. aureus* isolates, 34.18% (94/275) were MRSA; among these, 37.84% (56/148) were from patient samples and 29.92% (38/127) were from food samples. No significant difference ($P > .05$) was observed between the 2 sources (ie, clinical and food samples) of *S. aureus* isolates. However, there were different rates of resistance to various antibiotics among all isolates, including very high rates of resistance to penicillin, erythromycin, azithromycin, and clindamycin at 94.91%, 70.18%, 67.64%, and 64.00%, respectively. Resistance rates to tetracycline, trimethoprim/sulfamethoxazole, levofloxacin, gentamicin, moxifloxacin, and rifampin were 44.73%, 33.09%, 24.00%, 18.91%, 12.73%, and 7.27%, respectively. All strains were susceptible to vancomycin. Only 1 strain from a clinical source was resistant to linezolid. More details regarding antibiotic resistance are shown in Table 1. Moreover, resistance rates to erythromycin,

TABLE 1 Antibiotic resistance of *Staphylococcus aureus* isolates, n (%)

Antibiotic	Patients			No. of patients (n = 148)	Food			No. of food (n = 127)	p ^c	Total (n = 275)
	MRSA (n = 56)	MSSA (n = 92)	p ^a		MRSA (n = 38)	MSSA (n = 89)	p ^b			
Penicillin	55 (98.21)	90 (97.83)	1.000	145 (97.97)	36 (94.74)	80 (89.89)	.586	116 (91.34)	.013	261 (94.91)
Erythromycin	52 (92.86)	66 (71.74)	.002	118 (79.73)	25 (65.79)	50 (56.18)	.313	75 (59.06)	.000	193 (70.18)
Azithromycin	52 (92.86)	68 (73.91)	.004	120 (81.08)	16 (42.11)	50 (56.18)	.146	66 (51.97)	.000	186 (67.64)
Clindamycin	45 (80.36)	61 (66.30)	.066	106 (71.62)	25 (65.79)	45 (50.56)	.114	70 (55.12)	.004	176 (64.00)
Trimethoprim/sulfamethoxazole	22 (39.29)	30 (32.61)	.409	52 (35.14)	10 (26.32)	29 (32.58)	.483	39 (30.71)	.437	91 (33.09)
Linezolid	1 (1.79)	0	.378	1 (0.68)	0	0	-	0	.538	1 (0.36)
Vancomycin	0	0	-	0	0	0	-	0	-	0
Rifampin	19 (33.93)	1 (1.09)	.000	20 (13.51)	0	0	-	0	.000	20 (7.27)
Moxifloxacin	24 (42.86)	11 (11.96)	.000	35 (23.65)	0	0	-	0	.000	35 (12.73)
Levofloxacin	33 (58.93)	29 (31.52)	.001	62 (41.89)	0	4 (4.49)	1.000	4 (3.15)	.000	66 (24.00)
Gentamicin	26 (46.43)	18 (19.57)	.001	44 (29.73)	5 (13.16)	3 (3.37)	.093	8 (6.30)	.000	52 (18.91)
Tetracycline	39 (69.64)	30 (32.61)	.000	69 (46.62)	17 (44.74)	37 (41.57)	.741	54 (42.52)	.495	123 (44.73)

^aThe prevalence of antibiotic resistance among MRSA and MSSA isolates of clinical origin was compared.^bThe prevalence of antibiotic resistance among MRSA and MSSA isolates of food origin was compared.^cThe prevalence of antibiotic resistance among clinical isolates and food isolates was compared.

azithromycin, rifampin, moxifloxacin, levofloxacin, gentamicin, and tetracycline in clinical MRSA isolates were significantly higher than those in clinical MSSA isolates ($P < .05$). No significant difference in antibiotic resistance rates was observed between MRSA and MSSA isolates from food strains ($P > .05$). Overall, the prevalence of resistance to penicillin, erythromycin, azithromycin, clindamycin, rifampin, moxifloxacin, gentamicin, and levofloxacin among clinical strains was higher than that among food strains ($P < .05$). Rates of resistance to trimethoprim/sulfamethoxazole, linezolid, vancomycin, and tetracycline showed no differences between the 2 sources ($P > .05$).

3.2 | Distribution of resistance genes in *Staphylococcus aureus* isolates

The most frequent resistance gene among the 275 *S. aureus* isolates was *ant(4',4'')*, with 73.45% (202/275) of isolates being positive, followed by *acc(6')/aph(2'')* (70.55%), *ermC* (64.36%), *aph(3')-III* (48.36%), *ermB* (37.45%), *ermA* (29.09%), *msrA* (21.82%), and *tetM* (18.91%). More information about the distribution of resistance genes is provided in Table 2. The *ermA*, *msrA*, and *tetM* carriage rates were significantly higher for MRSA than MSSA among clinical isolates ($P < .05$). There was no significant difference in resistance genes between MRSA and MSSA among food isolates ($P > .05$). Furthermore, no isolates of food origin were positive for *ermA* and *tetM*. In general, the *acc(6')/aph(2'')*, *aph(3')-III*, *ermA*, *ermB*, and *tetM* carriage rates among isolates of clinical origin were higher than among those of food origin ($P < .05$). Conversely, the frequency of *ant(4',4'')* in food isolates was higher than that among clinical isolates ($P < .05$).

3.3 | Prevalence of virulence genes in *Staphylococcus aureus* isolates

Of the 275 isolates, the percentage of *hla* was highest (97.09%), followed by *sea* (69.82%), *hlyB* (66.91%), *seb* (57.45%), *pvl* (52.36%), *eta* (45.82%), *sec* (38.91%), *tsst* (37.82%), and *etb* (34.55%). Most virulence genes demonstrated no difference in frequency between MRSA and MSSA isolates of clinical origin ($P > .05$), with the exception of the *sec* gene, which had a higher percentage in MSSA than in MRSA isolates ($P < .05$). Interestingly, only the *etb* percentage was higher in MRSA strains than in MSSA strains among food isolates ($P < .05$). The *sea*, *seb*, *pvl*, and *etb* carriage rates among isolates of clinical origin were significantly higher than those among isolates of food origin ($P < .05$). In contrast, the *hla* and *hlyB* carriage rates were higher among food isolates than among clinical isolates ($P < .05$). Moreover, all food strains were positive for *hla*. The prevalence of virulence genes in *S. aureus* isolates is shown in Table 3.

3.4 | Molecular characteristics of *Staphylococcus aureus* genotypes

A total of 63 *spa* types were found among the 275 *S. aureus* isolates. The most prominent *spa* type was t030, which accounted for 15.64% (43/275) of isolates, followed by t002 (10.55%), t189 (8.36%), t091

TABLE 2 Distribution of resistance genes, n (%)

Gene	Patients		No. of patients (n = 148)	Food			p ^b	No. of food (n = 127)	p ^c	Total (n = 275)
	MRSA (n = 56)	MSSA (n = 92)		MRSA (n = 38)	MSSA (n = 89)					
<i>acc(6')/aph(2'')</i>	47 (83.93)	82 (89.13)	.359	129 (87.16)	20 (52.63)	45 (50.56)	.831	65 (51.18)	.000	194 (70.55)
<i>aph(3')-III</i>	34 (60.71)	64 (69.57)	.270	98 (66.22)	11 (28.95)	24 (26.97)	.819	35 (27.56)	.000	133 (48.36)
<i>ant(4',4'')</i>	40 (71.43)	61 (66.30)	.516	101 (68.24)	30 (78.95)	71 (79.78)	.916	101 (79.53)	.035	202 (73.45)
<i>ermA</i>	38 (67.86)	42 (45.65)	.009	80 (54.05)	0	0	-	0	.000	80 (29.09)
<i>ermB</i>	27 (48.21)	40 (43.48)	.575	67 (45.27)	14 (36.84)	22 (24.72)	.165	36 (28.35)	.004	103 (37.45)
<i>ermC</i>	37 (66.07)	52 (56.52)	.250	89 (60.14)	28 (73.68)	60 (67.42)	.483	88 (69.29)	.114	177 (64.36)
<i>msrA</i>	18 (32.14)	14 (15.22)	.015	32 (21.62)	11 (28.95)	17 (19.10)	.220	28 (22.05)	.932	60 (21.82)
<i>tetM</i>	30 (53.57)	22 (23.91)	.000	52 (35.14)	0	0	-	0	.000	52 (18.91)

^aThe prevalence of resistance genes among MRSA and MSSA isolates of clinical origin was compared.
^bThe prevalence of resistance genes among MRSA and MSSA isolates of food origin was compared.
^cThe prevalence of resistance genes among clinical isolates and food isolates was compared.

TABLE 3 The prevalence of virulence genes in *Staphylococcus aureus* isolates, n (%)

Gene	Patients		No. of patients (n = 148)	Food			p ^b	No. of food (n = 127)	p ^c	Total (n = 275)
	MRSA (n = 56)	MSSA (n = 92)		MRSA (n = 38)	MSSA (n = 89)					
<i>sea</i>	54 (96.43)	81 (88.04)	0.148	135 (91.22)	18 (47.37)	39 (43.82)	0.713	57 (44.88)	0.000	192 (69.82)
<i>seb</i>	47 (83.93)	74 (80.43)	0.594	121 (81.76)	12 (31.58)	25 (28.09)	0.692	37 (29.13)	0.000	158 (57.45)
<i>sec</i>	16 (28.57)	46 (50.00)	0.010	62 (41.89)	14 (36.84)	31 (34.83)	0.828	45 (35.43)	0.273	107 (38.91)
<i>pvl</i>	39 (69.64)	59 (64.13)	0.492	98 (66.22)	17 (44.74)	29 (32.58)	0.192	46 (36.22)	0.000	144 (52.36)
<i>hla</i>	52 (92.86)	88 (95.65)	0.723	140 (94.59)	38 (100)	89 (100)	-	127 (100)	0.008	267 (97.09)
<i>hly</i>	33 (58.93)	54 (58.70)	0.978	87 (58.78)	32 (84.21)	65 (73.03)	0.175	97 (76.38)	0.002	184 (66.91)
<i>eta</i>	20 (35.71)	45 (48.91)	0.117	65 (43.92)	16 (42.11)	45 (50.56)	0.382	61 (48.03)	0.495	126 (45.82)
<i>etb</i>	29 (51.79)	47 (51.09)	0.934	76 (51.35)	10 (26.32)	9 (10.11)	0.019	19 (14.96)	0.000	95 (34.55)
<i>tsst</i>	27 (48.21)	35 (38.04)	0.224	62 (41.89)	16 (42.11)	26 (29.21)	0.157	42 (33.07)	0.133	104 (37.82)

^aThe prevalence of virulence genes among MRSA and MSSA isolates of clinical origin was compared.
^bThe prevalence of virulence genes among MRSA and MSSA isolates of food origin was compared.
^cThe prevalence of virulence genes among clinical isolates and food isolates was compared.

(6.55%), t437 (6.18%), t701 (5.82%), and t127 (5.45%). The main *spa* types among clinical isolates were t030 (29.05%, 43/148), t437 (8.78%, 13/148), t189 (6.08%, 9/148), and t002 (5.41%, 8/148), while the main *spa* types among food isolates were t002 (16.54%, 21/127), t189 (11.02%, 14/127), t091 (11.02%, 14/127), and t127 (11.02%, 14/127). The newly identified *spa* types t15478, t15920, t15922, t15923, t16751, and t16752 were all present in MSSA strains; t15478 was present in clinical strains, while t15920, t15922, t15923, t16751, and t16752 were present in food strains. The molecular characteristics of *spa* types are shown in Table S1. Among the 56 MRSA strains of clinical origin, 52 strains had 3 SCCmec types (types II, III, and IVa). Of these, SCCmec type III was the most common, detected in 69.64% (39/56) of clinical MRSA isolates, followed by SCCmec type IVa in 19.64% (11/56) and SCCmec type II in 3.57% (2/56) of clinical MRSA isolates. No SCCmec type was established for the remaining 4 MRSA clinical strains. Of the 38 MRSA strains of food origin, 27 had 2 SCCmec types; SCCmec type III accounted for 60.53% (23/38) and SCCmec type IVa for 10.53% (4/38). The remaining 11 MRSA food strains had no SCCmec type. For *agr* typing, the proportions of the 4 groups among the 2 sources of *S. aureus* isolates were different. In clinical isolates, *agr* groups I, III, II, and IV were present in 64.19%, 12.84%, 11.49%, and 4.05% of isolates, respectively, while the *agr* proportions in food isolates for groups I, II, III, and IV were 56.69%, 22.05%, 17.32%, and 3.94%, respectively. However, there were 11 clinical isolates that were negative for any of the 4 *agr* groups. Among the strains of clinical origin, MRSA-t030-*agr*I-SCCmecIII (19/56) and MRSA-t437-*agr*I-SCCmecIVa (7/56) were the most common types among MRSA isolates, while MSSA-t002-*agr*II (8/92) and MSSA-t189-*agr*I (7/92) were the most common among MSSA isolates. Among strains of food origin, the most common were MRSA-t002-*agr*II-SCCmecIII (6/38), MRSA-t701-*agr*I-SCCmecIII (3/38), and MRSA-t437-*agr*I-SCCmecIVa (3/38) for MRSA and MSSA-t002-*agr*II (15/89), MSSA-t189-*agr*I (12/89), and MSSA-t127-*agr*III (12/89) for MSSA.

4 | DISCUSSION

Staphylococcus aureus is one of the most common pathogenic bacteria in the clinic and in the community, and the presence or absence of resistance and virulence genes is closely related to the pathogenicity of *S. aureus* infection. Analysis of the features of antibiotic resistance and detecting the distribution of resistance and virulence genes in *S. aureus* isolates from different sources will guide rational drug use among clinicians and prevent the dissemination of infection.

In the present study, 34.18% of all *S. aureus* isolates (275) were MRSA. The MRSA rate was ~37.84% among clinical isolates, which was consistent with the prevalence of MRSA in China.¹⁷ All 148 clinical isolates demonstrated differing degrees of resistance to antibiotics with the exception of vancomycin, and resistance to penicillin reached 97.97%. This revealed that antibiotic resistance was widely distributed among clinical strains, and the drug resistance of clinical bacteria remains serious. Compared with MSSA, resistance rates

to erythromycin, azithromycin, rifampin, moxifloxacin, levofloxacin, gentamicin, and tetracycline in MRSA were higher, and similarly, the *ermA*, *msrA*, and *tetM* carriage rates among MRSA were also higher than the carriage rates among MSSA. *S. aureus* possesses 2 main methods to obtain antibiotic resistance: The first is mutations to bacterial chromosomal genes, and the second is the acquisition of resistance genes from other organisms via plasmids or mobile genetic elements (MGEs).^{18,19} The molecular basis of resistance among MRSA isolates is the MGE designated staphylococcal cassette chromosome *mec* (SSCmec),²⁰ which contains the *mecA* gene encoding resistance to β -lactam antibiotics via an altered penicillin-binding protein (PBP2a).²¹ In addition, MRSA strains obtain a variety of resistance genes that undergo transfer under the pressure of antibiotic selection, leading to high resistance and multidrug resistance rates in MRSA isolates. Notably, 1 MRSA strain was resistant to linezolid. This number seems low, as there have been some outbreaks of healthcare infections associated with linezolid resistance, such as a linezolid-resistant MRSA outbreak in a Spanish ICU caused by the extensive use of this antibiotic.²² Therefore, it is important to use new antibiotics appropriately despite the fact that they treat pathogens effectively. The presence of virulence genes in the 148 clinical strains was high, ranging from 41.89% to 94.59%; in particular, the carriage rate for *pvl* (66.22%) was much higher than that described in an earlier report (10.7%).²³ Moreover, our study found that only the *sec* rate was higher in MSSA isolates than in MRSA isolates. This finding was in agreement with a previous study. However, the same previous study also detected higher frequencies of *pvl* and *tsst* genes in MSSA strains and higher frequencies of *sea* and *eta* genes in MRSA strains among clinical isolates,²⁴ unlike our results, which showed no differences in the *sea*, *seb*, *hla*, *hly*, *pvl*, *eta*, *etb*, and *tsst* rates between MRSA and MSSA strains of clinical origin. The reasons underlying these differences may be related to the different strain origins.

Staphylococcus aureus is a major food-borne pathogen. Symptoms of *S. aureus* infection include nausea, vomiting, abdominal cramping, and sometimes diarrhea.²⁵ In this study, 127 isolates were collected from food samples. Of these, 38 (29.92%) isolates were MRSA; this rate did not differ from that among clinical strains, indicating that MRSA contamination in food has become a serious problem. Interestingly, among the 127 food isolates, there were no differences in antibiotic resistance rates between MRSA and MSSA strains, unlike clinical isolates. Similarly, there were no differences in resistance gene rates between MRSA and MSSA strains, probably because exposure to agricultural and environmental sources of antibiotics initiated the development of resistance in these strains. MRSA strains did not show higher rates of resistance than MSSA strains among isolates of food origin, unlike clinical isolates, probably because hospitals utilize many antibiotics to maintain selective pressure. According to antimicrobial susceptibility testing, the penicillin resistance rate reached 91.34%, making it the least effective drug. Second to penicillin was erythromycin, demonstrating a resistance rate of 59.06%. This result differed from a report indicating that resistance to trimethoprim/sulfamethoxazole was most common in bacteria isolated from goat milk.²⁶ The present

study did not identify food-derived isolates resistant to linezolid, vancomycin, rifampin, and moxifloxacin, but 94.49% of food isolates were resistant to at least 1 antibiotic. Furthermore, a higher rate (51.97%) of multidrug resistance (resistance to 3 or more antimicrobial categories) was identified in ready-to-eat food samples compared with a rate of 3.8% in Malaysia.²⁷ The 127 food isolates were also screened for virulence genes to determine their pathogenic risk. All food strains were positive for *hla*, in accordance with a study conducted in Asturias, which found that all strains isolated from cow milk harbored the *hla* virulence gene.²⁸ Moreover, it was reported that *hla* was related to an outbreak of staphylococcal food poisoning.²⁹ Another important factor underlying staphylococcal food poisoning is the presence of enterotoxins, although the percentage of staphylococcal enterotoxin genes in isolates of food origin varies in different studies. Different levels of enterotoxin genes indicate different pathogenic potential. This current study showed that *sea* was present in 44.88% of food isolates, *sec* in 35.43%, and *seb* in 29.13%; these percentages were higher than those identified in chicken products from Egypt,³⁰ indicating that the genes may significantly contribute to staphylococcal food poisoning. The transmission of bacterial virulence factors to humans through the food chain as well as the higher multidrug resistance rates in those strains represents large risks for human infection. When resistance gene carriage rates were compared between MRSA and MSSA strains of food origin, only the *etb* rate was higher in MRSA strains; other genes demonstrated no differences. Combined with the results obtained for clinical isolates, our study suggested that the difference in virulence gene carriage rates between MRSA and MSSA strains might be insignificant.

Although some reports of vancomycin resistance have emerged,³¹ the 275 strains examined in this study were all sensitive to vancomycin, suggesting that vancomycin remains an effective drug for the treatment of serious *S. aureus* infections in our region. When we tested resistance to twelve types of antibiotics, clinical strains had higher resistance rates to penicillin, erythromycin, azithromycin, clindamycin, rifampin, moxifloxacin, gentamicin, and levofloxacin than food strains. This revealed that clinical isolates demonstrated higher levels of drug resistance compared with food isolates. The acquisition of antibiotic resistance in clinical *S. aureus* isolates may be attributable to the inappropriate use of antibiotics in hospitals. In addition, drug resistance can spread by plasmid transfer between strains and cross-contamination in hospitals, resulting in higher resistance among clinical strains. Accordingly, we found that the carriage rates of the resistance genes *acc(6')/aph(2')*, *aph(3')-III*, *ermA*, *ermB*, and *tetM* were higher among clinical isolates than among isolates of food origin; only the rate of *ant(4',4'')* was higher in food isolates. This inconsistency between resistance phenotypes and genes may be associated with the differential replication and expression of resistance-related plasmids in bacteria, as well as other mechanisms of drug resistance. Moreover, we found that clinical strains carried more resistance genes (≥ 5) compared with food strains (Table S2). Consistent with this, the genomes of clinical strains contained more virulence genes (≥ 5) (Table S3), and

virulence gene rates were not low among either source of isolates; almost every strain contained at least 2 virulence genes, indicating that strains from both clinical and food sources had high virulence potential. These results also suggested that food contaminated with *S. aureus* has higher pathogenic potential, with implications for human health. Thus, food safety issues should be taken seriously. During processes associated with food production and sales, food handlers should endeavor to follow hygienic measures to ensure the safety of human consumers.

Among the 275 *S. aureus* isolates, a total of 63 *spa* types were identified. Clinical isolates contained 37 *spa* types, and food strains included 38 *spa* types. The most prevalent *spa* type was t030, although it was only found in clinical strains. This finding was in agreement with a previous survey showing that t030 is one of the most common *spa* types in Chinese hospitals.³² t030 demonstrates high resistance to antibiotics that are commonly used in clinical settings, which may be the reason for its widespread distribution in hospitals, and our results indicate that some *spa* types may only appear in strains with specific origins. The most common *spa* type among food strains was t002, followed by t127, t189, and t901. It was previously reported that t127 is associated with serious human infections in the United States and Germany,³³ indicating food safety measures must be strengthened to minimize the infection rate. t189 is frequently identified in food isolates; for example, 1 study showed that the most prevalent *spa* type in raw and processed food commodities in Shanghai was t189.³⁴ In our study, t189 was present in 6.08% of clinical strains and ranked third in prevalence. This result indicates the important correlation between food-originating *S. aureus* and popular *spa* types in clinical isolates. A previous study showed that different *spa* types may contain different numbers of virulence genes,³⁵ but the present study did not corroborate those findings. Of the 275 *S. aureus* strains obtained from 2 sources, MRSA SCCmec type III was the most common. It was previously reported that the most common MRSA type in Asian regions other than Japan and South Korea, which primarily carry the SCCmecII genotype, is SCCmec type III.³⁶ In MRSA strains of clinical origin, the most common type was MRSA-t030-*agrI*-SCCmecIII, which was consistent with the results of a previous study in central-southern China.¹⁰ We also found that some strains belonging to the same *spa* type were present in the same *agr* group. For example, strains carrying *spa* type t127 were all present in *agr* group III. In addition, t189, t091, and t078 strains all belonged to *agr* group I. These results imply that some *spa* types may belong to 1 specific *agr* group, and there are relationships between different genotypes.

In conclusion, clinical isolates contained more resistance genes and demonstrated higher rates of antibiotic resistance than food strains, although all strains from both sources exhibited high virulence. These results indicate that bacteria of different origins may undergo different evolutionary processes. *S. aureus* can infect humans through food contamination, so it is necessary to follow strict hygienic measures during food production processes. To

date, many researchers have reported on *S. aureus* isolates with different origins worldwide, but studies comparing the characteristics of clinical strains and food strains are scarce. Our results provide information with implications for human health and food safety.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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