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# Genotype distribution of methicillin-susceptible *Staphylococcus aureus* clinical isolates in Iran: high multiresistant clonal complex 8

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## Abstract

**Objective:** Compared to methicillin-resistant *Staphylococcus aureus* (MRSA), there have been few studies focused on the molecular characterization of methicillin-susceptible *Staphylococcus aureus* (MSSA). In this cross-sectional study, 85 MSSA isolates were characterized by antimicrobial susceptibility testing, virulence genes analysis, accessory gene regulator (*agr*) typing, and *S. aureus* protein A locus (*spa*) typing.

**Results:** In present study, 9 different clonal complexes namely CC8-MSSA-t037 (22.4%), CC8-MSSA-t008 (11.8%), CC7-MSSA-t091 and CC30-MSSA-t021 (each 9.4%), CC8-MSSA-t037 (8.3%), CC398-MSSA-t034 (7.1%), CC22-MSSA-t005 (5.9%), CC5-MSSA-t002 and CC15-MSSA-t084 (each 4.7%), CC22-MSSA-t790 and CC59-MSSA-t437 (each 3.5%), CC22-MSSA-t1869, CC5-MSSA-t045, and CC45-MSSA-t015 (each 2.3%), CC30-MSSA-t318 and CC15-MSSA-t491 (each 1.2%) were found. *agr* types detected in tested strains were mainly type I (76.5%), II (12.9%), and III (10.6%). Of 85 MSSA examined isolates, 48 (56.5%) isolates were toxinogenic with 27 producing *pvl* (31.8%) and 21 *tst* (24.7%). The findings of the study show a high genetic diversity in MSSA strains warranting continued surveillance to provide critical insights into control and treatment of MSSA infections.

**Keywords:** *Staphylococcus aureus*, Methicillin-susceptible *S. aureus*, *agr* allotype, *spa*

## Introduction

*Staphylococcus aureus* is a common hospital- and community-acquired pathogen [1]. It is responsible for a multitude of human infections ranging from minor skin and soft tissue infections to serious and life-threatening conditions [2]. Although the epidemiology of *S. aureus* strain diversity appears to differ by geographic region, there has been a dramatic increase in the prevalence of *S. aureus* strains associated with human infections around the world and this appears to be especially true for methicillin-susceptible Staphylococcus aureus (MSSA) [3–5]. MSSA is a challenge for health-care settings and is becoming a public health concern [1, 6]. Compelling evidence suggests virulence genes may play an important role in serious MSSA infections, which are further exacerbated by the widespread circulation and emergence of drug-resistant strains [3]. Antimicrobial resistance is a barrier to successful control of *S. aureus* infections [7, 8]. Knowledge of genetic variability, clonal relatedness, and dissemination of staphylococcal infections may help to provide crucial insight for implementation of infection control programs, rational use of antibiotics, and better understand the evolution of these species [9, 10]. Although there is information about characteristics of MSSA strains in Iran, limited attention has been given

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to clonal diversity, and virulence gene prevalence among strains. To address these data limitations, the current study was performed to investigate the genetic background of MSSA strains isolated from patients.

## Main text

### Methods

#### *Bacterial isolates*

Eighty-five MSSA isolates were obtained from hospitalized patients at four hospitals affiliated to Shahid Beheshti University of Medical Sciences during an 9-month collection period from March 2019 to November 2019. This study protocol was approved by the Ethics Committee of the Shahid Beheshti University of Medical Sciences in Tehran, Iran (IR. SBMU. MSP.REC. 1398. 774). Furthermore, we confirmed *S. aureus* isolates phenotypically by using standard microbiological techniques. Polymerase chain reaction (PCR) assay targeting the *S. aureus*-specific *nuc* gene was applied to verify the isolates [11, 12]. The *S. aureus* isolates susceptible to cefoxitin disc (30 µg, Mast Co., UK) in a disc diffusion assay using established methods (CLSI 2018) and negative for the presence of *mecA* gene by PCR were considered as MSSA strains [12].

#### *Evaluation of antimicrobial activities*

In present study, Kirby–Bauer disk diffusion method was applied to determine the antimicrobial susceptibility of isolates based on the clinical and laboratory standards institute (CLSI) criteria (CLSI 2018). The antimicrobial agents included penicillin, teicoplanin, gentamicin, kanamycin, amikacin, tobramycin, clindamycin, erythromycin, tetracycline, linezolid, rifampicin, mupirocin, ciprofloxacin, quinupristin–dalfopristin, and trimethoprim–sulfamethoxazole (Mast Co., UK). The minimal inhibitory concentrations (MIC) values of vancomycin was evaluated by broth microdilution method. Susceptibility test was quality controlled by using *S. aureus* ATCC 25923, ATCC 43300, and ATCC 29213 strains.

#### *DNA isolation and screening of the key virulence related genes*

Genomic DNA was isolated using the phenol–chloroform extraction method. All of the isolates were screened for virulence encoding genes namely: exfoliative toxin genes (*eta*, and *etb*), Panton-Valentine leukotoxin gene (*pvl*), and toxic shock syndrome toxin (*tsst-1*) by PCR assay [12–14]. The *S. aureus* ATCC49775 and toxin positive *S. aureus* strains obtained from our previous were used as reference strains [14]. The *S. aureus* strain ATCC 25923 were also used as negative control.

#### *Molecular typing methods*

Multiplex PCR was performed for *agr* type detection using primer set comprising a common forward primer (Pan) and reverse primers (*agr*1, *agr*2, *agr*3, and *agr*4) specific to each *agr* group [15]. *agr* types were identified by comparing the banding patterns of isolates to RN6390 (*agr* type I), RN6607 (*agr* type II), RN8465 (*agr* type III), RN4550 (*agr* type IV), and RN6911 (negative control), as reference strains. PCR amplification was used for *spa* typing as described previously [16]. In this method polymorphic X region of *spa* gene amplified by PCR with forward (5′-AGACGATCCTTCGGTGAG C-3′) and reverse (5′-GCTTTTGCAATGTCATTT ACTG-3′) primers. The purified PCR products were sequenced and then edited. The Ridom SpaServer database (http://www.spaserver.ridom.de) was applied to determine the *spa* type of each isolate. Each set of PCR reactions include a *spa*-type t008 isolate from our previous study as positive control sample (14), and a reaction mixture containing no template DNA as a control for possible false positive results.

### Results

The sources of isolates included: skin and soft tissue wounds (44.7%), purulent exudates from wounds or abscesses (17.7%), urine (14.1%), blood (11.8%), sputum (8.2%), and other body fluids (3.5%). Out of 85 MSSA isolates, 29 isolates were obtained from hospital H1 (34.1%), 25 isolates from hospital H2 (29.4%), 20 isolates from hospital H3 (23.5%), and 11 isolates from hospital H4 (13%). Among 85 MSSA isolates tested, the highest rate of resistance was detected for penicillin (74.1%), and gentamicin (54.1%). (Table 1). All isolates were susceptible to linezolid, teicoplanin, and vancomycin. Totally, 12 resistance patterns were identified. Multidrug resistance (MDR) represented 69.4% of the isolates examined in present research. Inducible and constitutive resistance to clindamycin were detected in 12 (14.1%), and 29 (34.1%) of the isolates tested. Of 85 MSSA examined isolates, 48 (56.5%) were toxinogenic with 27 producing *pvl* (31.8%) and 21 *tst* (24.7%).

*agr* typing discriminated the 85 MSSA isolates in 3 *agr* type namely I (76.5%), II (12.9%), and III (10.6%). *spa* results showed 16 types corresponding to nine clonal complexes (CCs), namely CC8 (42.3%), CC22 (11.8%), CC30 (10.6%), CC7 (9.4%), CC5 (7.1%), CC398 (7.1%), CC15 (5.9%), CC59 (3.5%), and CC45 (2.3%). *spa* type t037 was the most common *spa* type identified among 85 MSSA isolates, with a frequency of 22.3%, followed by t008 (11.8%), t021 and t091 (each 9.4%), t030 (8.2%), t034 (7%), t005 (5.9%), t084 and t002 (each 4.7%), t790 and t437 (each 3.5%), t1869, t045, and t015 (each 2.4%), t318

**Table 1 Resistant pattern and distribution of samples in 85 MSSA strains isolated from clinical sources**

| Number of antibiotic classes | Antibiotic resistance pattern, no (%) | Number of isolates (%) | Samples (no, %) |
|---|---|---|---|
| 7 | PEN, GEN, KAN, AMK, ERY, CLI, TET | 15 | W (5, 33.4), P (6, 40), S (2, 13.3), B (2, 13.3) |
| | PEN, KAN, CLI, ERY, CIP, SYN, MUP | 6 | W (6, 100) |
| 6 | PEN, GEN, AMK, CLI, ERY, CIP | 8 | W (2, 25), P (6, 75) |
| 5 | AMK, ERY, TET, CIP, RIF | 10 | W (4, 40), P (2, 20), B (2, 20), S (2, 20) |
| | PEN, GEN, TOB, SXT, SYN | 3 | U (3, 100) |
| | PEN, KAN, ERY, TET, MUP | 2 | W (2, 100) |
| 4 | PEN, GEN, TOB, TET | 9 | W (4, 44.5), S (2, 22.2), B (3, 33.3) |
| | PEN, GEN, CLI, SYN | 1 | B (1, 100) |
| 3 | PEN, AMK, RIF | 5 | W (5, 100) |
| 2 | PEN, GEN | 10 | W (4, 40), B (2, 20), P (1, 10), BF (3, 30) |
| | CIP, SXT | 9 | U (9, 100) |
| 1 | PEN | 4 | W (4, 100) |
| Without resistance | – | 3 | W (2, 66.7), S (1, 33.3) |

*PEN* penicillin, *ERY* erythromycin, *TET* tetracycline, *CLI* clindamycin, *GEN* gentamicin, *SXT* trimethoprim–sulfamethoxazole, *CIP* ciprofloxacin, *SYN* quinupristin–dalfopristin, *TOB* tobramycin, *AMK* amikacin, *RIF* rifampicin, *KAN* kanamycin, *MUP* mupirocin, *W* wound, *P* pus, *U* urine, *B* blood, *S* sputum, *BF* other body fluids

**Table 2 Molecular characterization of MSSA strains isolated from patients**

| Clonal complex (CC) | *spa* types (no; %) | *agr* type | Virulence genes (no; %) | Hospitals (no; %) | Total N (%) |
|---|---|---|---|---|---|
| CC8 | t037 (19; 73.1), t030 (7; 26.9) | I | *tst* (15; 57.7) | H1 (8; 30.8), H2 (6; 23.1), H3 (10; 38.5), H4 (2; 7.6) | 26 (30.5) |
| | t008 (10; 100) | I | *pvl* (10; 100) | H1 (4; 40), H2 (2; 20), H3 (4; 40) | 10 (11.8) |
| CC22 | t005 (5; 50), t790 (3; 30), t1869 (2; 20) | I | *pvl* (5; 50), *tst* (3; 30) | H1 (4; 40), H2 (6; 60) | 10 (11.8) |
| CC30 | t021 (8; 88.9), t318 (1; 11.1) | III | *pvl* (8; 88.9) | H1 (3; 33.3), H2 (3; 33.3), H3 (2; 22.3), H4 (1; 11.1) | 9 (10.6) |
| CC7 | t091 (8; 100) | I | – | H1 (4; 50), H2 (4; 50) | 8 (9.4) |
| CC5 | t002 (4; 66.7), t045 (2; 33.3) | II | – | H1 (1; 16.7), H2 (2; 33.3), H3 (1; 16.7), H4 (2; 33.3) | 6 (7.1) |
| CC398 | t034 (6; 100) | I | – | H1 (5; 83.3), H3 (1; 16.7) | 6 (7.1) |
| CC15 | t084 (4; 80), t491 (1; 20) | II | *pvl* (4; 80) | H4 (5; 100) | 5 (5.9) |
| CC59 | t437 (3; 100) | I | *tst* (3; 100) | H2 (2; 66.7), H4 (1; 33.3) | 3 (3.5) |
| CC45 | t015 (2; 100) | I | – | H3 (2; 100) | 2 (2.3) |

and t491 (each 1.2%) (Table 2). All the mupirocin resistant strains belonged to CC8-MSSA type.

Inducible clindamycin resistance was observed in CC8-MSSA-t037 (n = 5), CC30-MSSA-t021 (n = 4) CC8-MSSA-t008 (n = 3) isolates; while constitutive resistance phenotype was observed in CC8-MSSA-t037 (n = 8), CC8-MSSA-t030 (n = 3), CC-MSSA-t034 (n = 4), CC-MSSA-t091 (n = 5), CC-MSSA-t045 (n = 4), CC-MSSA-t005 (n = 4), and CC-MSSA-t790 (n = 1) isolates. Detailed results of the genotype distribution are presented in Table 2.

## Discussion

Infection with MSSA as the most common pathogen in hospitalized patients is becoming increasingly problematic globally and requires special attention [3]. As presented in Table 2, our results indicated 9 different clonal complexes and 16 *spa* types among MSSA isolates. We detected CC8 in 42.3% of isolates. Although multiresistant CC8 was previously reported as one of the main international CCs of MRSA, the predominance of the CC8-MSSA clone has previously been reported in Europe [17] and Africa [18, 19]. We showed that all the mupirocin resistant strains belonged to CC8-MSSA clone. In this connection, similar findings have been reported from Kuwait [20], Ireland [21], and Nigeria [22]. We confirmed the presence of CC22 as the second dominant MSSA genotypes (11.8%). This clone is widely spread both as MSSA and MRSA in Kuwait, China, Ireland, the United Arab Emirates, Japan, Korea, and Australia [3, 20,

21]. As mentioned, the frequency of CC30 was found to be 10.6%. The presence of ST30-MSSA, known as the Southwest Pacific clone, has been noted in Australia, the UK, Germany, Lebanon, Abu Dhabi, and Kuwait [21, 23].

We noted a relatively low prevalence of CC7 (9.4%), CC5 (7.1%), CC398 (7.1%), CC15 (5.9%), CC59 (3.5%), and CC45 (2.3%) in our study. A study conducted in China during the 4-year period indicated that CC22-t309 (26.0%), CC188-t189 (5.1%), CC796-t796 (4.8%), CC121-t435 (4.8%), and CC398-t571 (3.6%) were the most dominant clones among MSSA isolates [3]. Ahigh diversity of MSSA isolates was reported by Uzunovic et al. from Bosnia and Herzegovina [24]. They demonstrated that MSSA clones were associated with 14 CCs with the majority of CC42, CC22, CC5, and CC30. A 2015 study in Korea showed that the most prevalent MSSA clones were CC72 (29.3%), followed by CC188 (21.9%), CC121 (19.5%) and CC30 (9.6%) [25]. A recent study by Shore et al. (2014) in Ireland also showed that CC22, CC30, and CC121 were found in MSSA isolates [26].

Present results demonstrated that out of the 85 tested MSSA, 27 isolates (31.8%) carried *pvl* encoding gene. Prevalence PVL positive MSSA strains has varied among studies from different geographic regions including China (34.4%) [3], Lebanon (12%) [23], Ireland (17%) [26], Colombia (32.3%) [4], England (60%) [27], Africa (57%) [22], Russia (55%) [6]. In a recent study conducted during a 9-year period in Ireland, Shore et al. indicated a decreasing trend of PVL among MSSA strains (20% to 2.5%) [26]. However, there are reports that indicate greater potential of MSSA strains to secrete toxins, such as PVL implying the important role PVL-MSSA strains generally play as reservoirs for highly virulent PVL-positive MRSA clones [16, 19]. In agreement with other studies [3, 18, 26, 28], high genetic diversity of PVL-positive MSSA isolates belonging to CC8 (11.8%), CC30 (9.4%), CC/22 (5.9%), and CC/15 (4.7%) clones were observed in our study. This finding supports previous result from UK in which CC22, CC88, CC30, and CC1 were detected as major sequence types among PVL-positive MSSA isolates [27]. Shore et al's study on 39 PVL-positive MSSA isolates in Ireland depicted that CC30 was the dominant clone (38.5%), followed by CC22 (25.6%), CC121 (18%), CC1 (10.3%), and CC88 (7.7%) clones [26]. Another study from Greece reported that PVL-positive MSSA belonged to ST14, ST97 and ST101 [11].

In our strain collection, 24.7% of isolates were *tst* positive. This reported rate was different from the earlier studies in Africa (7%) [19], China (4%) [29] and Turkey (14.2%) [30]. Contrary to earlier studies [11, 31] which indicated CC30 MSSA as a prevalent lineage, our MSSA isolates harboring *tst* gene were associated with CC8-MSSA-t037 (11.8%), CC8-MSSA-t0307 (5.9%), CC22-MSSA-t790 (3.5%), and CC59-MSSA-t437 (3.5%) clones. A multicenter study from china reported that 4.0% of MSSA isolates carried *tst* gene which belonged to CC5 clone [29]. A recent study from Greece, displayed that *tst*-positive MSSA was distributed into four STs and the majority of them belonged to CC30 clone [11]. A recent systematic review and meta-analysis study in Iran reported a relatively high prevalence of the *tst* encoding gene among *S. aureus* clinical isolates (21.3%) [32]. In a study conducted by Motamedifar et al. (2015), the carriage rates of *tst* were significantly higher in MSSA isolates in comparison to MRSA isolates (18.1% vs. 11.6%) [33]. Overall, distribution of *tst*-positive MSSA clones seems geographically different and CC8 may represent a newly emerging clone in Iran.

According to the evidence, the *agr* genotypes are strictly associated with the clonal lineages [34, 35]. In the current study, the *agr* type I, as the most predominant type (76.4%), was associated with CC8, CC22, CC7, CC45, CC398, and CC59 isolates. In line with our results, Croes et al. demonstrated that CC7, CC8, CC22, CC25 and CC45 clonal lineages harbored *agr* I [7]. A study conducted by Zhao et al. in China demonstrated a high prevalence of *agr* type I (68.8%), followed by *agr* III (18.7%), and *agr* IV (12.5%) among MSSA isolates [9].

## Limitations

Our research had some limitations. Firstly, present work lacks detailed clinical information about the patients, Secondly, our samples were not collected consecutively. Thirdly, whole genome sequencing technique was not applied in the present work due to some of technical limitations.

### Abbreviations

PVL: Panton-Valentine leukotoxin; TST: Toxic shock syndrome toxin; MDR: Multidrug resistance; *spa*: Surface protein A; MLST: Multi-locus sequence typing; *agr*: Accessory gene regulator; PCR: Polymerase chain reaction; MRSA: Methicillin-resistant *S. aureus*; MSSA: Methicillin-sensitive *S. aureus*.

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### Authors' contributions

MG and HG designed the study. MD, MG, and ZT performed the laboratory investigations. MG, HG drafted the manuscript. MG, MD critically reviewed the manuscript and approved the final version of the manuscript. All authors read and approved the final manuscript.

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**Availability of data and materials**
The datasets generated and analyzed during this study were included in the main document of this manuscript.

**Ethics approval and consent to participate**
The entire procedures were approved by the Ethics Committee of the Shahid Beheshti University of Medical Sciences in Tehran, Iran (IR.SBMU.MSP.REC.1397.1374). A written informed consent was obtained from participants.

**Consent for publication**
Not applicable.

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

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**References**

1. Tong SY, Davis JS, Eichenberger E, Holland TL, Fowler VG. *Staphylococcus aureus* infections: epidemiology, pathophysiology, clinical manifestations, and management. Clin Microbiol Rev. 2015;28(3):603–61.
2. Chuang Y-Y, Huang Y-C. Molecular epidemiology of community-associated meticillin-resistant *Staphylococcus aureus* in Asia. Lancet Infect Dis. 2013;13(8):698–708.
3. Yuan W, Liu J, Zhan Y, Wang L, Jiang Y, Zhang Y, et al. Molecular typing revealed the emergence of pvl-positive sequence type 22 methicillin-susceptible *Staphylococcus aureus* in Urumqi, Northwestern China. Infect Drug Resist. 2019;12:1719.
4. Salazar-Ospina L, Jiménez JN. High frequency of methicillin-susceptible and methicillin-resistant Staphylococcus aureus in children under 1 year old with skin and soft tissue infections. Jornal de Pediatria (Versão em Português). 2018;94(4):380–9.
5. Chen F-J, Siu L-KK, Lin J-C, Wang C-H, Lu P-L. Molecular typing and characterization of nasal carriage and community-onset infection methicillin-susceptible *Staphylococcus aureus* isolates in two Taiwan medical centers. BMC Infect Dis. 2012;12(1):343.
6. Baranovich T, Zaraket H, Shabana I, Nevzorova V, Turcutyuicov V, Suzuki H. Molecular characterization and susceptibility of methicillin-resistant and methicillin-susceptible *Staphylococcus aureus* isolates from hospitals and the community in Vladivostok, Russia. Clin Microbiol Infect. 2010;16(6):575–82.
7. Croes S, Deurenberg RH, Boumans M-LL, Beisser PS, Neef C, Stobberingh EE. *Staphylococcus aureus* biofilm formation at the physiologic glucose concentration depends on the *S. aureus* lineage. BMC Microbiol. 2009;9(1):229.
8. Atshan SS, Shamsudin MN, Lung T, Than L, Sekawi Z, Ghaznavi-Rad E, et al. Comparative characterisation of genotypically different clones of MRSA in the production of biofilms. Biomed Res Int. 2012;2012:1–7.
9. Zhao H, Hu F, Jin S, Xu X, Zou Y, Ding B, et al. Typing of Panton-Valentine leukocidin-encoding phages and lukSF-PV gene sequence variation in *Staphylococcus aureus* from China. Front Microbiol. 2016;7:1200.
10. Li S, Sun S, Yang C, Chen H, Yin Y, Li H, et al. The changing pattern of population structure of *Staphylococcus aureus* from bacteremia in China from 2013 to 2016: ST239-030-MRSA replaced by ST59-t437. Front Microbiol. 2018;9:332.
11. Papadimitriou-Olivgeris M, Drougka E, Fligou F, Dodou V, Kolonitsiou F, Filos KS, et al. Spread of Tst-Positive *Staphylococcus aureus* strains belonging to ST30 clone among patients and healthcare workers in two intensive care units. Toxins. 2017;9(9):270.
12. Yousefi M, Pourmand MR, Fallah F, Hashemi A, Mashhadi R, Nazari-Alam A. Characterization of *Staphylococcus aureus* biofilm formation in urinary tract infection. Iran J Public Health. 2016;45(4):485.
13. Avila-Novoa M-G, Iñíguez-Moreno M, Solís-Velázquez O-A, González-Gómez J-P, Guerrero-Medina P-J, Gutiérrez-Lomelí M. Biofilm formation by *Staphylococcus aureus* isolated from food contact surfaces in the dairy industry of Jalisco. Mexico. J Food Qual. 2018;2018:1–8.
14. Rashidi Nezhad R, Meybodi SM, Rezaee R, Goudarzi M, Fazeli M. Molecular characterization and resistance profile of methicillin resistant *Staphylococcus aureus* Strains isolated from hospitalized patients in Intensive Care Unit, Tehran-Iran. Jundishapur J Microbiol. 2017;10(3):e41666. https://doi.org/10.5812/jjm.41666.
15. Zhang Y, Xu D, Shi L, Cai R, Li C, Yan H. Association between agr type, virulence factors, biofilm formation and antibiotic resistance of *Staphylococcus aureus* isolates from pork production. Front Microbiol. 2018;9:1876.
16. Ilczyszyn WM, Sabat AJ, Akkerboom V, Szkarlat A, Klepacka J, Sowa-Sierant I, Wasik B, Kosecka-Strojek M, Buda A, Miedzobrodzki J, Friedrich AW. Clonal structure and characterization of *Staphylococcus aureus* strains from invasive infections in paediatric patients from South Poland: association between age, spa types, clonal complexes, and genetic markers. PLoS ONE. 2016;11(3):1–25.
17. Grundmann H, Schouls LM, Aanensen DM, Pluister GN, Tami A, Chlebowicz M, et al. The dynamic changes of dominant clones of *Staphylococcus aureus* causing bloodstream infections in the European region: results of a second structured survey. Euro Surveill. 2014;19:20987.
18. Shittu AO, Oyedara O, Okon K, Raji A, Peters G, von Müller L, Schaumburg F, Herrmann M, Ruffing U. An assessment on DNA microarray and sequence-based methods for the characterization of methicillin-susceptible *Staphylococcus aureus* from Nigeria. Front Microbiol. 2015;6:1160.
19. Breurec S, Fall C, Pouillot R, Boisier P, Brisse S, Diene-Sarr F, et al. Epidemiology of methicillin-susceptible *Staphylococcus aureus* lineages in five major African towns: high prevalence of Panton-Valentine leukocidin genes. Clin Microbiol Infect. 2011;17(4):633–9.
20. Boswihi SS, Udo EE, Al-Sweih N. Shifts in the clonal distribution of methicillin-resistant *Staphylococcus aureus* in Kuwait hospitals: 1992–2010. PLoS ONE. 2016;11(9):1–21
21. Monecke S, Coombs G, Shore AC, Coleman DC, Akpaka P, Borg M, et al. A field guide to pandemic, epidemic and sporadic clones of methicillin-resistant *Staphylococcus aureus*. PLoS ONE. 2011;6(4):1–24.
22. O'Malley S, Emele F, Nwaokorie F, Idika N, Umeizudike A, Emeka-Nwabunnia I, et al. Molecular typing of antibiotic-resistant *Staphylococcus aureus* in Nigeria. J Infect Public Health. 2015;8(2):187–93.
23. Harastani HH, Araj GF, Tokajian ST. Molecular characteristics of *Staphylococcus aureus* isolated from a major hospital in Lebanon. Int J Infect Dis. 2014;19:33–8.
24. Uzunović S, Ibrahimagić A, Kamberović F, Rijnders MI, Stobberingh EE. Molecular characterization of methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* in Food handlers in Bosnia and Herzegovina. Open Infect Dis J. 2013;7(1):15–20.
25. Park SH, Kim KJ, Kim BK, Hwang SM. Molecular characterization of community-associated methicillin-resistant and methicillin-susceptible *Staphylococcus aureus* isolates from children with skin infections in Busan, Korea. J Bacteriol Virol. 2015;45(2):104–11.
26. Shore AC, Tecklenborg SC, Brennan GI, Ehricht R, Monecke S, Coleman DC. Panton-Valentine leukocidin-positive *Staphylococcus aureus* in Ireland from 2002 to 2011: 21 clones, frequent importation of clones, temporal shifts of predominant methicillin-resistant *S. aureus* clones, and increasing multiresistance. J Clin Microbiol. 2014;52(3):859–70.
27. Otokunefor K, Sloan T, Kearns AM, James R. Molecular characterization and Panton-Valentine leucocidin typing of community-acquired methicillin-sensitive *Staphylococcus aureus* clinical isolates. J Clin Microbiol. 2012;50(9):3069–72.
28. Yang Y, Hu Z, Shang W, Hu Q, Zhu J, Yang J, et al. Molecular and phenotypic characterization revealed high prevalence of multidrug-resistant methicillin-susceptible *Staphylococcus aureus* in Chongqing, Southwestern China. Microb Drug Resist. 2017;23(2):241–6.
29. Zhao H, Xu S, Chunyan H, Xu X, Hu F, Shu W, et al. Molecular typing and variations in amount of tst gene expression of TSST-1-producing clinical *Staphylococcus aureus* isolates. Front Microbiol. 2019;10:1388.

30. Demir C, Aslantaş Ö, Duran N, Ocak S, Özer B. Investigation of toxin genes in *Staphylococcus aureus* strains isolated in Mustafa Kemal University Hospital. Turk J Med Sci. 2011;41(2):343–52.
31. Sharma H, Smith D, Turner CE, Game L, Pichon B, Hope R, et al. Clinical and molecular epidemiology of staphylococcal toxic shock syndrome in the United Kingdom. Emerg Infect Dis. 2018;24(2):258.
32. Shahini Shams-Abadi M, Halaji M, Hoseini-Alfatemi SM, Gholipour A, Mojtahedi A, Sedigh Ebrahim-Saraie H. Epidemiology of toxic shock-syndrome toxin-1 harboring *Staphylococcus aureus* obtained from clinical samples in Iran: a systematic review and meta-analysis. Ann Ig. 2018;30(5):391–400.
33. Motamedifar M, Ebrahim-Saraie HS, Alfatemi SM, Zalipour M, Kaveh M, Khoshkharam-Roodmajani H. Frequency of the toxic shock syndrome toxin-1 gene in methicillin-susceptible and-resistant *Staphylococcus aureus* isolates from teaching hospitals in Shiraz, Iran. Rev Soc Bras Med Trop. 2015;48:90–3.
34. Monecke S, Slickers P, Ehricht R. Assignment of *Staphylococcus aureus* isolates to clonal complexes based on microarray analysis and pattern recognition. FEMS Immunol Med Microbiol. 2008;53(2):237–51.
35. Lindsay JA, Moore CE, Day NP, Peacock SJ, Witney AA, Stabler RA, Husain SE, Butcher PD, Hinds J. Microarrays reveal that each of the ten dominant lineages of *Staphylococcus aureus* has a unique combination of surface-associated and regulatory genes. J Bacteriol. 2006;188(2):669–76.


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