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Prevalence, virulence genes, antimicrobial susceptibility, and genetic diversity of *Staphylococcus aureus* from young people from 18 to 25−year−old age in Ho Chi Minh City, Vietnam

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ABSTRACT

Objective: To investigate the prevalence, antimicrobial resistance and genetic diversity of *Staphylococcus (S.) aureus* among healthy young adults of 18 to 25 years in Ho Chi Minh City, Vietnam.

Methods: A cross-sectional, descriptive study was conducted between December 2023 and December 2024. Nasal swabs were processed for *S. aureus* isolation, antibiotic susceptibility testing, and PCR-based detection of *spa*, *pvl*, and *mecA* genes. Genetic similarity was assessed using the unweighted pair group method with arithmetic mean cluster analysis. Statistical significance was determined by *Chi*-square test.

Results: In this cross-sectional study of 428 students, the *S. aureus* carriage rate was 33.9%. Methicillin-resistant *S. aureus* (MRSA) prevalence was 54.5% (79/145). 10%-17% of MRSA isolates exhibited resistance to three to ten antibiotics, with two strains demonstrating resistance to 11 and 12 drugs, respectively. The *pvl* gene was detected in 5.8% of isolates. 55.17% *S. aureus* strains belonged to ten distinct *spa* types with 300-bp amplicons.

Conclusions: These findings provide valuable insights into *S. aureus* carriage patterns among youth in Ho Chi Minh City, informing public health strategies for prevention and treatment.

KEYWORDS: *Staphylococcus aureus*; Antibiotic resistance; *mecA*; *spa*; *pvl*

1. Introduction

Staphylococcus (S.) aureus is a widespread Gram-positive bacterium known for its ability to shift from a harmless commensal to a significant opportunistic pathogen, particularly as antibiotic resistance becomes more prevalent. Colonizing human skin and mucous membranes, *S. aureus* can cause a spectrum of diseases, from mild skin infections to severe conditions such as pneumonia, meningitis, and sepsis, especially in immunocompromised individual[1−4]. Both community and hospital environments are affected by *S. aureus* infections[1,5,6], but community-based data, particularly from Ho Chi Minh City, remain limited.

The emergence of methicillin-resistant *S. aureus* (MRSA) has

Summary

Question: What is the prevalence, antimicrobial resistance and genetic diversity of *Staphylococcus aureus* among healthy young adults in Ho Chi Minh City, Vietnam?

Findings: In this cross-sectional study of 428 students, the *Staphylococcus aureus* nasal carriage rate was 33.9% with MRSA accounting for 54.5% of isolates. Multidrug resistance was identified in 95.2% of isolates and 17.2% carried the *pvl* gene with phylogenetic analysis revealing substantial genetic heterogeneity across nine distinct clusters.

Meaning: The elevated prevalence of MRSA and multidrug-resistant strains in healthy youth underscores the urgent need for enhanced community surveillance and targeted antimicrobial stewardship programs in Vietnam.

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intensified the clinical challenges associated with *S. aureus*[7]. MRSA strains, first identified in 1960, acquired the *mecA* gene, which encodes the PBP2a protein, reducing the effectiveness of beta-lactam antibiotics such as methicillin, ampicillin, and penicillin[8-10]. More recently, vancomycin-resistant *S. aureus* (VRSA) has been reported due to gene transfer from *Enterococcus faecalis*, further complicating treatment option[11,12]. In Vietnam, despite regulations, the widespread practice of self-medicating with antibiotics contributes to the emergence of multidrug-resistant (MDR) *S. aureus* strains[13].

S. aureus pathogenicity is driven by various virulence factors, including enterotoxins, fibronectin-binding proteins, and Panton-Valentine leukocidin (PVL), which facilitate colonization, tissue invasion, and immune evasion[14-16]. PVL, in particular, is associated with severe skin and soft tissue infections, and its presence is a key marker in the molecular typing of MRSA isolates[14-17]. Understanding the prevalence of PVL-positive strains is essential for guiding effective treatment and prevention strategies.

Young adults aged 18-25 years represent a critical reservoir for *S. aureus* transmission due to their high social mobility, frequent close contact, and tendency to be asymptomatic carriers[18,19]. The combination of these factors with irrational antimicrobial use creates a high-risk environment for the spread of antibiotic-resistant *S. aureus* strains.

This study aims to investigate the molecular epidemiology of *S. aureus* among the youth population in Ho Chi Minh City, Vietnam, focusing on the prevalence of key virulence and antibiotic resistance genes. The findings will provide important baseline data to inform antimicrobial stewardship and targeted infection control measures.

2. Methods

2.1. Study design

This study employed a cross-sectional, descriptive design utilizing a non-probability, convenience sampling strategy. The sample was drawn from available and consenting university students aged 18-25 years in Ho Chi Minh City. Data collection took place between December 2023 and December 2024. The required sample size was calculated using the formula below:

$$n=1.96^2\times \frac{0.33\times(1-0.33)}{0.05^2}=339.75$$

where n represents the sample size, p is the estimated prevalence of *S. aureus*. A 95% confidence level (z=1.96) was adopted. The estimated prevalence of p=0.33 was based on previous studies in the USA (30%) and Vietnam (35%)[19,20]. The calculation yielded n=339.75, necessitating a minimum sample size of 340 participants. Crucially, recruitment incorporated a sex quota to achieve an approximate 1:1 (male:female) ratio. This quota necessitated recruiting an additional number of participants (exceeding the calculated minimum of 340) to correct for any instantaneous sex imbalance observed during the convenience recruitment process.

2.2. Sampling criteria

S. aureus isolates were sampled from participants, who were healthy, voluntary students aged 18-25 years enrolled at university. Exclusion criteria included students from the Faculty of Medicine and Medical Practitioners, as well as individuals with a history of antibiotic use within two weeks prior to sampling.

2.3. Sampling and isolation of S. aureus

Nasal swabs were collected using sterile cotton swabs from the nasal vestibule (1-2 cm from the nasal openings). The swabs were rotated five times in each nostril and subsequently stored in 5 mL of 0.9% sterile saline solution within two hours of collection. Samples were vortexed and serially diluted to $1:10^{-3}$, $1:10^{-4}$, and $1:10^{-5}$. One hundred microliters (μL) of each dilution were plated onto Baird-Parker agar supplemented with 3.5% egg yolk tellurite emulsion. Plates were incubated at 37 ℃ for 48 hours under aerobic conditions. *S. aureus* colonies were identified based on their characteristic black appearance with clear zones of lecithinase activity (egg yolk precipitation). One representative colony from each positive sample was selected for catalase and coagulase testing, as well as Gram staining. Confirmed isolates were subcultured once or twice on fresh medium and then stored in Tryptone Soya broth (TSB) supplemented with 30% glycerol at -80 ℃ for further analysis.

2.4. Antibiogram test

Isolated *S. aureus* cultures were grown in Mueller-Hinton broth (MHB) to achieve an optical density (OD) of 0.5 McFarland standard (equivalent to 1.5×10^8 CFU/mL). The bacterial suspension was then diluted to match 0.5 McFarland turbidity standard, and 100 μL was spread evenly onto Mueller-Hinton agar (MHA) plates using a sterile swab.

Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method with commercially available antimicrobial disks containing the following agents: penicillin (10 units), ampicillin (10 μg), cefoxitin (30 μg), tetracycline (30 μg), doxycycline (30 μg), gentamicin (10 μg), chloramphenicol (30 μg), erythromycin (15 μg), clindamycin (10 μg), linezolid (30 μg),

ciprofloxacin (5 µg), levofloxacin (5 µg), ofloxacin (5 µg), rifampicin (5 µg), nitrofurantoin (300 µg), and sulfamethoxazole-trimethoprim (25 µg).

Antimicrobial disks were placed onto the inoculated MHA plates using sterile forceps, ensuring adequate spacing between disks. Plates were incubated at (35 ± 2) ℃ for 18-20 hours under aerobic conditions. Zone diameters were measured to the nearest millimeter, and results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) 2022 guidelines. *S. aureus* reference strains ATCC 29213 (methicillin-susceptible) and ATCC 33592 (methicillin-resistant) were used as quality control organisms.

2.5. Gene amplification

Target genes were amplified by PCR using specific primer sets (Table 1) designed based on the work of Stegger *et al.*[21]. The primers were synthesized by Integrated DNA Technologies (IDT, Singapore) and targeted the following genes: staphylococcal protein A (*spa*), methicillin resistance (*mecA*), and Panton-Valentine leukocidin (*pvl*). PCR amplification was performed under the following conditions: initial denaturation at 95 ℃ for 5 minutes, followed by 35 cycles of denaturation at 95 ℃ for 30 seconds, annealing at 55 ℃ for 30 seconds, and extension at 68 ℃ for 1 minute, with a final extension at 68 ℃ for 5 minutes. PCR products were analyzed by electrophoresis on 1.5% agarose gels prepared in a 1× TBE buffer. Electrophoresis was conducted at 120 V for 30 minutes, and DNA fragments were visualized under UV light using ethidium bromide staining. A 100-bp DNA ladder was used as a molecular weight marker to determine amplicon sizes.

Table 1. PCR primers used to amplify the gene in isolated *Staphylococcus aureus*.

Gene	Sequence	Product length (bp)	Annealing temperature (℃)
mecA	5'-TCCAGATTACAACTTCACCAGG-3' 5'-CCACTTCATATCTTGTAACG-3'	162	54
spa	5'-TAAAGACGATCCTTCGGTGAGC-3' 5'-CAGCAGTAGTGCCGTTTGCTT-3'	180-600	54
pvl	5'-GCTGGACAAAACTTCTTGGAATAT-3' 5'-GATAGGACACCAATAAATTCTGGATTG-3'	82	54

2.6. Assessment of genetic data

Molecular typing of *S. aureus* isolates was performed based on the presence or absence of target genes (*mecA*, *pvl*, and *spa*). A binary matrix was constructed where 1 indicated gene presence and 0 indicated gene absence. Genetic similarity among isolates was calculated using the Dice similarity coefficient, and a dendrogram was generated using the unweighted pair group method with arithmetic mean (UPGMA). Cluster analysis and dendrogram construction were performed using GelJ software according to the manufacturer's instructions.

2.7. Data analysis

Data was processed using Excel. Variate analysis was performed using *Chi*-square test, 95% confidence intervals (*CI*s) for required odds ratios (*OR*), and *P*-value <0.05 was considered statistically significant.

2.8. Ethical approval

This study received ethical approval from the Ethics in Biomedical Research (IRB-VN01002/IORG0008603/FWA00023448) with document number 30/HDDD-DHYD, signed date 2nd January 2024. All participants provided written informed consent after receiving detailed information about the study's objectives and procedures. Participant confidentiality was strictly maintained.

3. Results

3.1. S. aureus prevalence in the community

In our study, a total number of 428 students were invited and all agreed to take part in the study, resulting in 0% non-response rate. Table 2 shows that among 428 nasal swabs collected, 214 samples (50%) were obtained from male participants and 214 samples (50%) from female participants. In total, 145 samples (33.9%) tested positive for *S. aureus*, confirmed by phenotypic identification tests and *spa* gene amplification. *S. aureus* carriage prevalence was lower among males (65/214, 30.4%) compared to females (80/214, 37.4%). This difference, however, was not statistically significant based on *Chi*-square test (*P*=0.126).

3.2. MSSA and MRSA strains prevalence in the community

In our study, MRSA isolates were identified through *mecA* gene detection and cefoxitin resistance in disk diffusion testing, as cefoxitin serves as a reliable surrogate marker for *mecA*-mediated resistance. Table 2 shows that among *S. aureus*-positive samples, MSSA and MRSA prevalence were 45.5% (66/145) and 54.5% (79/145), respectively; however, *Chi*-square test showed no statistical significance (*P*=0.283).

3.3. Prevalence of S. aureus strains with pvl genes in the community

Table 2 shows that 25 isolates (5.8% of total 428 samples) tested positive for the *pvl* gene, representing 17.2% of all 145 *S. aureus*-positive isolates. The *pvl* gene prevalence differed between strain types: 3 of 66 MSSA isolates (4.5%) and 22 of 79 MRSA isolates

(27.8%) harboured the *pvl* gene. *Chi*-square test showed PVL carriage is significantly associated with the MRSA strain compared to the MSSA strain (P=0.000 2) and OR=8.09, implying MRSA having 8.09-fold greater odds of being PVL-positive than MSSA.

Table 2. *Staphylococcus (S.) aureus* prevalence in the study per sex and types.

Variable	Male	Female	Total
Total nasal swabs (n=428)	214 (50.0)	214 (50.0)	428 (100.0)
S. aureus (n=145)	65 (44.8)	80 (55.2)	145 (33.9)
MSSA (n=66)	30 (45.5)	36 (54.5)	66 (15.4)
MRSA (n=79)	35 (44.3)	44 (55.7)	79 (18.5)
S. aureus carrying *pvl* (n=25)	17 (68.0)	8 (10.0)	25 (5.8)
MSSA carrying *pvl*	3 (4.5)	0 (0.0)	3 (4.5)
MRSA carrying *pvl*	14 (17.7)	8 (10.0)	22 (27.8)

Data were expressed as n (%); MSSA: methicillin sensitive *S. aureus*; MRSA: methicillin resistant *S. aureus*.

3.4. Antibiotic resistance among S. aureus

Antimicrobial susceptibility patterns of *S. aureus* isolates, including both MRSA and MSSA strains, were determined using disk diffusion testing with multiple antimicrobial agents (Table 3).

All MRSA isolates demonstrated complete resistance to penicillin and ampicillin, whereas resistance among MSSA isolates was 87.9% for penicillin and 77.3% for ampicillin. In comparison, resistance to antibiotics that inhibit protein synthesis was generally lower. Among the tetracyclines, 26.6% of MRSA strains and 18.2% of MSSA strains were fully resistant to tetracycline, with intermediate resistance observed in 0% and 4.5% of isolates, respectively. Doxycycline resistance was rare, with complete resistance in 6.3% of MRSA and none of the MSSA strains, and intermediate resistance in 1.3% of MRSA and 6.1% of MSSA isolates.

For other protein synthesis inhibitors, MRSA strains consistently exhibited higher resistance rates than MSSA: gentamicin (54.4% *vs*. 19.7%), erythromycin (59.5% *vs*. 22.7%), clindamycin (54.4% *vs*. 21.2%), and linezolid (8.9% *vs*. 6.1%). Resistance to chloramphenicol was similar in both groups (26.6% for MRSA and 27.2% for MSSA). Intermediate resistance for these agents remained below 10.0% for both strain types, except for erythromycin in MSSA (16.7%).

Regarding antibiotics targeting nucleic acid synthesis, MRSA strains showed moderate resistance to fluoroquinolones: ciprofloxacin (35.4%), levofloxacin (27.8%), and ofloxacin (44.3%). MSSA isolates had substantially lower resistance rates to these agents: ciprofloxacin and levofloxacin (10.6% each) and ofloxacin (9.1%). Intermediate resistance to quinolon remained below 15.0% for all tested agents. Both MRSA and MSSA isolates were universally susceptible to rifampicin. No resistance to nitrofurantoin was detected in any *S. aureus* isolate. For sulfonamides, complete resistance was observed in 11.4% of MRSA and 3.0% of MSSA strains, with intermediate resistance present in 2.5% of MRSA isolates.

3.5. Multiple antibiotic resistance in S. aureus

Figure 1 illustrates the distribution of MDR among *S. aureus* isolates. Among MSSA strains, the highest proportion demonstrated resistance to two antimicrobial classes (33%), followed by resistance to three (21%), four (13%), and five (10%) classes. Resistance to six and nine antibiotic classes was observed in 6% and 2% of MSSA isolates, respectively. All MRSA isolates exhibited resistance to cefoxitin, ampicillin and penicillin, indicating resistance to at least two to three antimicrobial classes. The proportion of MRSA strains resistant to three to ten antibiotic classes ranged from 10% to 17%, while 2% of MRSA isolates showed resistance to eleven and twelve classes. Notably, all MRSA isolates met the definition of MDR, being resistant to three or more antimicrobial classes.

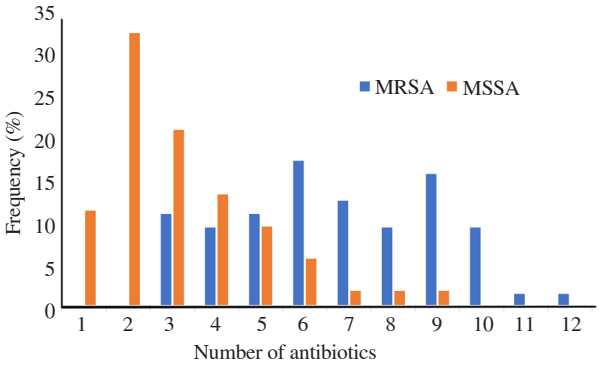

Figure 1. Multiple antibiotic resistance (both resistance and intermediate resistance) frequence in isolated *Staphylococcus aureus*.

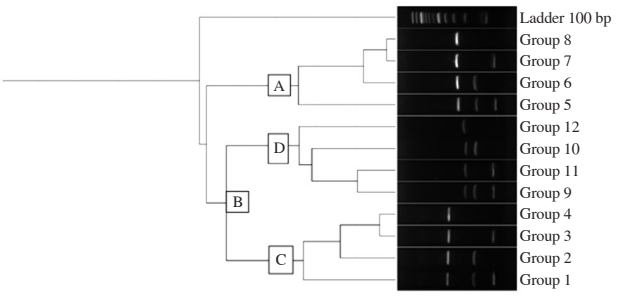

Figure 2. Phylogenetic relationship between the *Staphylococcus aureus* isolated in the study. See Table 4 for genotypes of each group.

3.6. Phylogenetic relationship between S. aureus strains in the community

Cluster analysis based on the presence or absence of *mecA*, *pvl*, and *spa* genes, as well as *spa* amplicon size variation, revealed substantial genetic diversity among the *S. aureus* isolates[21]. The dendrogram constructed using UPGMA grouped the isolates into nine main clusters, distinguished by combinations of *mecA* and *pvl* gene carriage and *spa* gene amplicon sizes (200 bp, 300 bp, and 400 bp) (Table 4 and Figure 2).

Table 3. Prevalence of full and intermediate resistance against each of the tested antibiotics by the isolated MRSA and MSSA strains (CLSI) [*n* (%)].

Mechanism	Antibiotic family	Antibiotic	Resistant		Intermediate	
			MRSA (*n*=79)	MSSA (*n*=66)	MRSA (*n*=79)	MSSA (*n*=66)
Suppression of cell wall synthesis	Penicillin	Penicillin (10 UI)	79 (100.0)	58 (87.9)	0 (0.0)	0 (0.0)
		Ampicillin (10 µg)	79 (100.0)	51 (77.3)	0 (0.0)	0 (0.0)
	Cephalosporin 2nd generation	Cefoxitin (30 µg)	79 (100.0)	0 (0.0)	NA	NA
Suppression of protein synthesis	Tetracyclines	Tetracycline (30 µg)	21 (26.6)	12 (18.2)	0 (0.0)	3 (4.5)
		Doxycycline (30 µg)	5 (6.3)	0 (0.0)	1 (1.3)	4 (6.1)
	Aminoglycoside	Gentamicin (10 µg)	43 (54.4)	13 (19.7)	0 (0.0)	1 (1.5)
	Chloramphenicol	Chloramphenicol (30 µg)	21 (26.6)	18 (27.2)	4 (5.1)	0 (0.0)
	Macrolides	Erythromycin (15 µg)	47 (59.5)	15 (22.7)	6 (7.6)	11 (16.7)
	Lacosamide	Clindamycin (10 µg)	43 (54.4)	14 (21.2)	1 (1.3)	5 (7.6)
	Oxazolidinones	Linezolid (30 µg)	7 (8.9)	4 (6.1)	NA	NA
Suppression of nucleic acid synthesis	Quinolone	Ciprofloxacin (5 µg)	28 (35.4)	7 (10.6)	4 (5.1)	7 (10.6)
		Levofloxacin (5 µg)	22 (27.8)	7 (10.6)	5 (6.3)	6 (9.1)
		Ofloxacin (5 µg)	35 (44.3)	6 (9.1)	2 (2.5)	0 (0.0)
		Nitrofurantoin (300 µg)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
		Rifampicin (5 µg)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Suppression of vitamin synthesis	Sulfonamide	Sulfamethoxazole (25 µg)	9 (11.4)	2 (3.0)	2 (2.5)	0 (0.0)

MSSA: methicillin sensitive *Staphylococcus aureus*; MRSA: methicillin resistant *Staphylococcus aureus*. NA: not available.

Table 4. Genotypes and phylogenetic groups of the isolated *Staphylococcus aureus*.

Group	Genotype	Sample amount (*n*=145)	Percentage (%)
Group 1	*spa* 400 bp, *mecA*, *pvl*	2	1.38
Group 2	*spa* 400 bp, *mecA*	10	6.90
Group 3	*spa* 400 bp, *pvl*	1	0.69
Group 4	*spa* 400 bp	12	8.28
Group 5	*spa* 300 bp, *mecA*, *pvl*	11	7.59
Group 6	*spa* 300 bp, *mecA*	37	25.52
Group 7	*spa* 300 bp, *pvl*	4	2.76
Group 8	*spa* 300 bp	28	19.31
Group 9	*spa* 200 bp, *mecA*, *pvl*	5	3.45
Group 10	*spa* 200 bp, *mecA*	14	9.66
Group 11	*spa* 200 bp, *pvl*	2	1.38
Group 12	*spa* 200 bp	19	13.10

Branch A, characterized by the 300 bp *spa* variant, comprised most isolates (55.17%), including the reference strain MSSA ATCC 29213. Within this branch, group 6 (*mecA* and *spa* 300 bp) 25.52% and group 8 (*spa* 300 bp only) 19.31% each accounted for the most of all isolates. Smaller proportions were observed for group 5 (*mecA*, *pvl*, and *spa* 300 bp; 7.59%) and group 7 (*pvl* and *spa* 300 bp; 2.76%).

Branch C, containing the 400 bp *spa* variant, was the least common (17.24%). This branch included group 2 (*mecA* and *spa* 400 bp; 6.90%), group 1 (*mecA*, *pvl* and *spa* 400 bp; 1.38%), group 4 (*spa* 400 bp only; 8.28%), and group 3 (*pvl* and *spa* 400 bp; 0.69%).

Branch D, defined by the 200 bp *spa* variant, represented 25.52% of isolates. Group 12 (*spa* 200 bp only) made up 13.10%, while group 10 (*mecA* and *spa* 200 bp), group 9 (*mecA*, *pvl*, and *spa* 200 bp), and group 11 (*pvl* and *spa* 200 bp) accounted for 9.66%, 3.45%, and 1.38% of isolates, respectively.

These findings indicate that while a predominant lineage with the 300 bp *spa* variant circulates in the community, there is considerable genetic heterogeneity among *S. aureus* isolates, reflecting the coexistence of multiple molecular types within the population.

4. Discussion

4.1. S. aureus, MRSA and MSSA prevalence in the community

The nasal carriage prevalence of *S. aureus* in this study was 33.9% (145/428), which is identical to the age-adjusted prevalence previously reported in northern Vietnam (29.8%, 303/1016; adjusted for age: 33.8%)[20]. Among *S. aureus* positive individuals, MRSA accounted for 54.5% (79/145), corresponding to 18.5% of the total study population. This MRSA prevalence is more than double that observed in the earlier Vietnamese community based study, where MRSA comprised 26.4% (80/303) of *S. aureus* carriers[20].

When compared regionally, the MRSA prevalence in this study (54.5%) is lower than that reported in Taiwan China (66.7%, 20/30)[1], but higher than in Myanmar (47.5%, 1 331/2 801)[22], the Philippines (41.5%, 34/82 among patients with skin infection; 45.76%, 108/236 in general patients)[23], Macau China (36.3%, 183/504)[24], Malaysia (14.9%)[25], Thailand (17%, 147/890)[26], and Indonesia (3.1%, 8/257)[27]. Notably, the Philippines also reported a much lower MRSA prevalence of 5% among patients without skin infection[23]. These differences may reflect variations in study design, population characteristics, healthcare infrastructure, antimicrobial stewardship, and the potential impact of the COVID-19 pandemic on transmission dynamics[28]. The elevated MRSA prevalence identified in this community-based cohort highlights the critical need for strengthened surveillance and the implementation of

targeted infection control strategies to address the growing burden of antimicrobial resistant *S. aureus* in the community.

4.2. Prevalence of S. aureus strains with pvl genes in the community

In this study, the *pvl* gene was detected in 17.2% (25/145) of *S. aureus* isolates obtained from nasal carriage in young adults. Among MRSA strains, the prevalence of *pvl* was 27.8% (22/79), which was significantly higher than in MSSA strains (4.5%, 3/66). The odds ratio for *pvl* carriage in MRSA compared to MSSA was 8.1, indicating that MRSA isolates were over eight times more likely to harbor the *pvl* gene. The *pvl* prevalence in MRSA in Vietnam (27.8%) is lower than that reported in the Philippines (37.9%)[23], but higher than in Taiwan China (15.0%)[1], and Indonesia (0.0%)[27]. For all *S. aureus* isolates, Vietnam's *pvl* prevalence (17.2%) is intermediate, with Indonesia reporting a higher rate (21.8%) and Taiwan China a lower rate (10.0%)[1].

4.3. Antibiotic resistance among S. aureus

Our findings reveal high resistance rates of *S. aureus* to penicillin 94.5% [(79+58)/145], and erythromycin 54.5% [(47+15+6+11)/145], consistent with previous reports in Vietnam[20] and neighboring co untries[1,9,15,17,22,25-27,29-33]. Methicillin resistance was confirmed at 54.5% (79/145) among isolates, reflecting the significant MRSA burden in the community. Resistance to clindamycin [43.4%, (43+14+1+5)/145] and ciprofloxacin [31.7%, (28+7+4+7)/145] was also notable, limiting the options for empirical therapy. Importantly, all isolates remained susceptible to linezolid, supporting their continued use as last-resort treatments.

The MDR phenotype was observed in 95.2% (138/145) of isolates while only 4.8% (7/145) isolates resisted to one antibiotic, emphasizing the widespread antimicrobial pressure in this population and the risk of therapeutic failure[16]. These resistance patterns likely reflect both self-medication practices and insufficient antimicrobial stewardship, which contribute to the emergence and spread of resistant strains. Continuous monitoring and rational antibiotic use are critical to controlling resistance and guiding effective treatment strategies.

4.4. Multiple antibiotic resistance in S. aureus

The MDR, defined as resistance to three or more antibiotic classes, was prevalent among *S. aureus* isolates in this study. All MRSA strains exhibited inherent resistance penicillin and ampicillin with beta lactams, with many showing resistance to multiple other classes. Specifically, MRSA isolates demonstrated resistance to 3 to 12 antibiotic classes, with 10%-17% resistant to 3-10 classes, and a small proportion (2%) resistant to 11 or 12 classes. In contrast, most MSSA strains were resistant to 2 or 3 antibiotic classes, though some showed resistance to as many as 9 classes. These findings reflect the extensive antimicrobial pressure and highlight the clinical challenge posed by MDR MRSA in the community.

Regional studies corroborate these patterns, showing widespread MDR in MRSA isolates across Southeast Asia[29]. The emergence of strains resistant to numerous antibiotic classes, including those critical for treatment, raises concerns about therapeutic options. This underscores the urgent need for robust antimicrobial stewardship and continuous surveillance to monitor resistance trends and guide treatment strategies effectively.

4.5. Phylogenetic relationship between S. aureus strains in the community

Phylogenetic analysis based on the presence or absence of *mecA*, *pvl*, and *spa* genes, as well as *spa* amplicon size variation, revealed considerable genetic diversity among community *S. aureus* isolates. The isolates were grouped into nine major clusters, with the majority (55.17%) belonging to Branch A, characterized by a 300 bp *spa* gene variant, which included both MRSA and MSSA strains. Notably, groups within Branch A, such as those harboring only *mecA*, both *mecA* and *pvl*, or neither resistance nor virulence genes, suggest the co-circulation of multiple successful lineages in this population.

Branches C and D, representing 400 bp and 200 bp *spa* variants respectively, comprised smaller proportions of isolates, further highlighting the genetic heterogeneity of *S. aureus* in this setting. The detection of diverse molecular profiles indicates ongoing transmission and evolution within the community. However, definitive conclusions on evolutionary relationships and transmission pathways will require more comprehensive genomic analyses, such as whole genome sequencing and comparative genomics. These findings underscore the importance of continued molecular surveillance to better understand the dynamics of *S. aureus* in the community and to inform effective infection control strategies[33].

Our study has several limitations. The age-restricted (18-25 years), single university design and convenience sampling limit generalizability and introduce selection bias. Exclusion of medical students and recent antibiotic users may also affect prevalence estimates. The cross-sectional design precludes causal inference and assessment of temporal trends. Laboratory methods using conventional PCR and *spa* typing provide limited genetic resolution compared to whole genome sequencing, restricting analysis of strain diversity and transmission dynamics.

In conclusion, our study provides comprehensive data on *S. aureus* molecular profiles and antimicrobial resistance patterns

among youth and student populations in Ho Chi Minh City, contributing valuable insights into the regional epidemiology and resistance landscape of this important pathogen. The observed *S. aureus* carriage rate of 33.9% aligns with previous community-based studies, with notably higher prevalence among females than males. However, the community MRSA prevalence of 18.5% and *pvl*-positive *S. aureus* prevalence of 17.2% represent significant increases compared to earlier Vietnamese studies, raising substantial public health concerns. Our analysis revealed concerning patterns of multidrug resistance, with many MRSA isolates exhibiting resistance to 3-10 antimicrobial classes, while most MSSA isolates showed resistance to two classes, and several *S. aureus* strains demonstrated resistance to more than eight antimicrobial classes. These findings underscore the critical importance of implementing comprehensive infection control measures to prevent *S. aureus* transmission within community settings and the urgent need for antimicrobial stewardship programs to mitigate the emergence and spread of multidrug-resistant strains, particularly MRSA, reflecting broader challenges documented in Vietnamese healthcare settings where antimicrobial resistance has become a major contemporary public health threat.

Conflict of interest statement

The authors declare that there are no conflicts of interest.

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Authors' contributions

P.H.N., A.N.T.T. performed the data collection, data management. P.H.N, L.L.T., T.N.T.X., H.V.Q. performed data and statistical analysis. P.H.N, L.L.T. and H.V.Q. finalized the data and result writing. H.V.Q. provided overall supervision and finalized the final version of the manuscript for submission.

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