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The prevalence of *vanA* gene in clinical isolates of vancomycin-resistant *Staphylococcus aureus* in a hospital in Mazandaran, Iran

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ABSTRACT

Staphylococcus aureus is one of the most important causes of infections in hospitals. Although vancomycin is often prescribed for the treatment of methicillin-resistant *S. aureus* (MRSA), vancomycin-resistant *S. aureus* (VRSA) isolates remain a major problem in hospitals. In this study, we investigated the prevalence of vancomycin-resistant *S. aureus* isolates and also *vanA* gene in these clinical isolates in a hospital in Mazandaran Province, Iran. In this cross-sectional study, a total number of 60 *S. aureus* samples were identified from different clinical specimens after standard biochemical and microbiological tests. Disk agar diffusion test using Kirby-Bauer method was applied for antibiotics against *S. aureus* isolates. The presence of *vanA* gene was investigated in VRSA and intermediate resistance (VISA) isolates by PCR method using specific primers. Over 40% of isolates were resistant to commonly-used antibiotics, including gentamicin (46.67%), ceftazidime (45%) and carbenicillin (43.34%). Only few, however, were sensitive to gentamicin (33.33%) and ceftazidime (35%). Vancomycin was the most effective antibiotic against *S. aureus* isolates (56.66% sensitivity). Eleven isolates (18.34%) were resistant (VRSA) and 15 isolates (25%) were intermediate resistance (VISA) to vancomycin. Molecular analysis of *vanA* gene in 11 VRSA and 15 VISA showed that 8 VRSA (72.72%) and 6 VISA (40%) isolates were positive for *vanA* gene. The incidence of VRSA and VISA strains, as well as the frequency of *vanA* gene in these isolates are high and emerging in Mazandaran hospitals. There is a need to keep the emergence and spread of these strains to a minimum level.

Key words: Clinical isolates, Iran, *Staphylococcus aureus*, *vanA* gene, vancomycin-resistant.

INTRODUCTION

Staphylococcus aureus is one of the most important human pathogenic bacteria which causes various complications such as skin and tissues infections, surgical wound infections, bacteremia, endocarditis, and pneumonia (Hoban *et al.* 2003, Roberts & Chambers 2005). Although several antibiotics such as penicillin and methicillin were introduced during the last decades for the treatment of *S. aureus* infections, these isolates became rapidly resistant to these antibiotics (Wenzel *et al*. 1991). Methicillin-resistant *S. aureus* (MRSA) isolates can be also acquired during exposure to hospitals and causes serious healthcare-associated infections (Loomba *et al.* 2010). So that, MRSA isolates have become a significant threat to human health worldwide (McGuinness WA *et al*. 2017). In recent years, vancomycin has been introduced as an effective antibiotic for treatment of MRSA infections (Asadi 2016, Habibi *et al*. 2018). Unfortunately, *S. aureus* clinical isolates with complete (VRSA) and intermediate resistance (VISA) to vancomycin have emerged within the two past decades due to an increase in the use of this antibiotic for other infections in hospitalized patients (Ena *et al.* 1993, Hidayat *et al*. 2006). The first VISA was reported in 1997 from Japan (Hiramatsu *et al*. 1997), and then in USA, Europe, Australia and

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Asia countries (Howden BP *et al.* 2010). Thus, this is an important alarm for the medical community, as *S. aureus* causes life-threatening infections in hospitalized and non-hospitalized patients (SK 2001).

The exact mechanism of vancomycin resistance *S. aureus* clinical isolates is unclear. Recent studies have indicated that *vanA* operon, consisted of *vanA*, *vanH*, *vanX*, *vanS*, *vanR*, *vanY*, and *vanZ* genes, is likely a major factor required for vancomycin resistance phenotype and pathogenesis of these isolates (Hong *et al.* 2008). *vanA* gene is necessary for synthesizing the depsipeptide D-Ala-D-lactate peptidoglycan precursors which are critical for the pathogenesis of these isolates (Bugg *et al.* 1991). Incorporation of altered D-Ala-D- lactate into peptidoglycan yields a cell wall which is resistant to vancomycin (McGuinness *et al.* 2017).

Although the VRSA and VISA isolates are increasing, only few studies have reported the prevalence of these isolates is some parts of a country. Recent studies in different parts of Iran have demonstrated that this country may be a spot region for the emergence of these isolates (Aligholi *et al.* 2008, Askari *et al.* 2013). The current study aimed to determine the antimicrobial susceptibility patterns of *S. aureus* isolates from patients in Mazandaran hospitals in north of Iran with emphasis to the possible presence of vancomycin resistance and also *vanA* gene in these strains.

MATERIALS AND METHODS

Samples collection

In this cross-sectional study, a total number of 100 clinical samples were collected from laboratories of Imam Hospital (Behshahr City, Mazandaran Province) from January to August 2017. Bacterial strains were collected from different clinical specimens, including urine, sputum, wound swab and blood. Isolates were cultured in blood agar medium at 37 °C for 24 h. Standard biochemical and microbiological tests were performed for the identification of *S. aureus* isolates (TL 2003) (Table 1).

Table 1. The biochemical test results for *S. aureus* isolates.

Biochemical tests	Results
Gram staining	Gram positive, cocci- shaped
Coagulase test	+
Catalase test	+
DNase test	+
Bacitracin test	Susceptible
Novobiocin test	Susceptible

Antibiotic susceptibility test

Disk agar diffusion test using Kirby-Bauer method according to CLSI procedure was applied for the assessment of antibacterial effects of different antibiotics against *S. aureus* isolates (Bauer *et al.* 1996). The clinical *S. aureus* isolates (0.5 McFarland) were spread onto the surface of the Muller Hinton Agar (MHA) with a sterile swab. Gentamicin (10 µg), kanamycin (20 µg), cefotaxime (30 µg), amikacin (30 µg), piperacillin (100 µg), carbenicillin (100 µg), ceftazidime (30 µg), cefalotin (30 µg), and vancomycin (30 µg) disks were used as antibiotics. Vancomycin was purchased from the Sigma Aldrich Company (USA), while the other antibiotics were purchased from the PADTAN TEB Company (Tehran, Iran). The agar plates were incubated at 37 °C for 24 h and the diameter of the zone of inhibition for each microorganism was measured. All tests were performed as triplicate.

Detection of *vanA* gene by PCR

The *S. aureus* vancomycin resistance gene (*vanA*) was investigated in vancomycin- resistant and intermediate resistance isolates by PCR method using specific primers (Table 2). DNA was extracted with boiling method. Briefly, 100 µl of bacterial suspension in PBS were placed into a labeled micro-tube and boiled at 100 °C for 10 min. The micro-tube was then centrifuged at 10000 g for 5 min. Supernatants were collected and transferred into another sterile micro-tube. The quantity and quality of extracted DNA were evaluated with Nanodrop (Thermo 2000) and agarose gel electrophoresis methods, respectively. The supernatants containing the DNA were stored at -20 °C further analyses.

PCR amplification was carried out in a 25 µL reaction mixture with each primer (contained 13 µL Master Mix; 1.2 µL each primer; 2.6 µL DNA sample; and 7 µL dH_2O) as the following steps: an initial denaturation step at 95°C for 60 sec; followed by 30 cycles denaturation at 95°C for 30 sec, annealing at 56 °C for 30 sec and extension at 72 °C for 60 sec and a final extension at 72 °C for 5 min (Bamigboye *et al.* 2018). The PCR products were

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electrophoresed in a 1% agarose gel for 20 min at 100 V. The gels were then stained with ethidium bromide and visualized using UV trans-illuminator.

Table 2. Primers used for *vanA* amplification.

Primer	Sequences	Product size
Forward	5'-CTGGAGAGACTAAGCCCTCC-3'	425 bp
Reverse	5'-ATTACTGACGCTGATTGTGC-3'	

Statistical analysis

Descriptive statistics was applied for the analysis of frequencies among patients group. Data were analyzed using SPSS software (IBM, version 19).

RESULTS

In this study, *S. aureus* was isolated from 4 different clinical samples of 100 patients with different infective conditions. After standard biochemical and microbiological tests analysis, 60 clinical samples were positive for *S. aureus* (Table 1). The antibiotic susceptibility of isolated *S. aureus* assessed by the disk agar diffusion method is shown in Table 4. More than 40% of isolates were resistant to commonly used antibiotics, including gentamicin (46.67%), ceftazidime (45%) and carbenicillin (43.34%). Only few, however, were sensitive to gentamicin (33.33%) and ceftazidime (35%). Approximately, 50% of isolates were sensitive to vancomycin, kanamycin, and piperacillin. Vancomycin was the most effective antibiotics against *S. aureus* isolate (with 56.66% sensitivity). Totally, 11 isolates (18.34%) were resistant to vancomycin (VRSA) and 15 isolates (25%) were intermediate resistance (VISA) (Table 3). Fig. 1 shows the molecular analysis of *vanA* gene. Agarose gel electrophoresis revealed a major band with 425 bp in positive isolates with *vanA* gene. Molecular analysis of *vanA* gene in 11 VRSA and 15 VISA showed that 8 VRSA (72.72%) and 6 VISA (40%) were positive for *vanA* gene (Fig. 1).

Table 3. Antimicrobial resistance rates of *S. aureus* isolates.

Antibiotics	Sensitive (S)	Intermediate resistance (I)	Resistant (R)
Gentamicin	20 (33.33%)	12 (20%)	28 (46.67%)
Kanamycin	30 (50%)	18 (30%)	12 (20%)
Cefotaxime	26 (43.34%)	14 (23.23%)	20 (33.33%)
Amikacin	24 (40%)	20 (33.33%)	16 (26.67%)
Piperacillin	32 (53.34%)	13 (21.66%)	15 (25%)
Carbenicillin	24 (40%)	10 (16.66%)	26 (43.34%)
Ceftazidime	21 (35%)	12 (20%)	27 (45%)
Cefalotin	28 (46.67%)	14 (23.33%)	18 (30%)
Vancomycin	34 (56.66%)	15 (25%)	11 (18.34%)

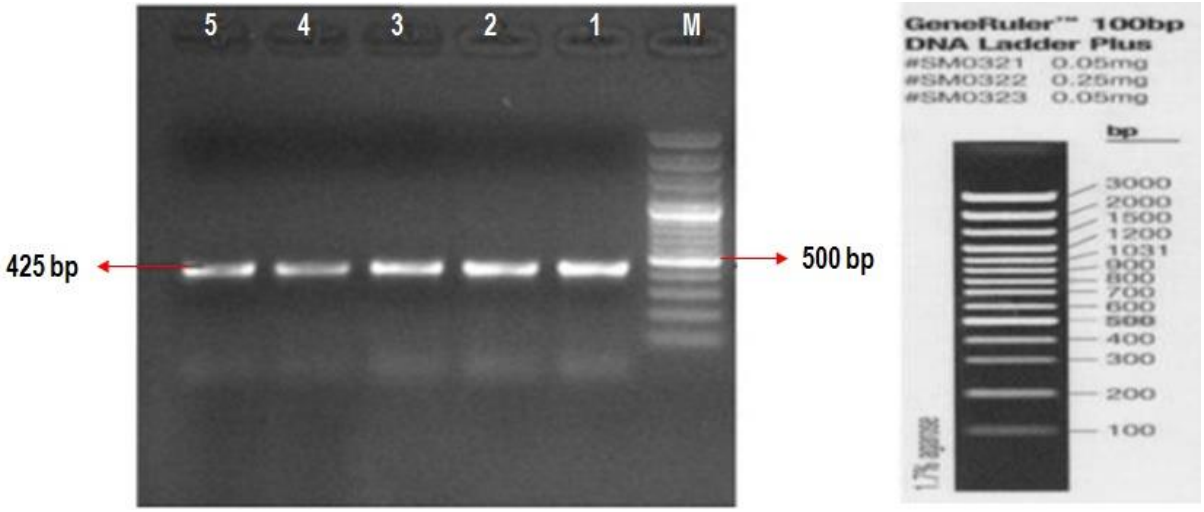

Fig. 1. Agarose gel electrophoresis of PCR-amplified vancomycin resistance gene (*vanA*). Lanes: M, 100-bp ladder; 1-5: *S. aureus* isolates showing 425 bp *vanA* amplicon.

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DISCUSSION

Staphylococcus aureus has become a major cause of infections, morbidity and mortality in hospitals because of its rapidly acquired resistance to various antibiotics such as penicillin, methicillin and vancomycin (Friães *et al.* 2015). So that, information about the incidence of vancomycin-resistance *S. aureus* in a hospital or society and its treatment have been of great concern for public health.

This has made the study of VRSA and VISA as a significant topic for clinical research. However, a few studies have investigated the prevalence and clinical infections caused by *S. aureus* throughout the world (Thati *et al.* 2011). In the present study, we investigated the prevalence of *vanA* gene in clinical isolates of vancomycin-resistant *S. aureus* in Mazandaran Province, Iran. We detected VRSA in 11 (18.34%) and VISA in 15 (25%) out of 60 *S. aureus* clinical isolates. Further molecular analysis by PCR has revealed the presence of *vanA* gene in 8 VRSA (72.72%) and 6 (40%) VISA isolates.

There are a few studies with different reports of VRSA and VISA prevalence throughout the world. For example, Bamigboye *et al*. (2018) detected VRSA in 1 (1.4%) out of 73 *S. aureus*-clinical isolates in a hospital in Nigeria. This isolate did not contain *vanA* and *vanB* genes. There is also another study from Nigeria worked on the prevalence's of VRSA and VISA clinical isolates, reporting that 25 (51.0%) out of 49 clinical isolates were susceptible to vancomycin (MIC $\leq$ 2 µg ml^{-1}), while 18 (36.7%) isolates were VISA and 6 (12.2%) were VRSA (Taiwo *et al*. 2011). A recent study has reported the first case of infection with vancomycin-resistant *S. aureus* in Europe, in a Portuguese hospital (Melo-Cristino *et al*. 2013). There is also another study in Brazil reporting that a 35-year-old male had with blood culture positive for methicillin-resistant VRSA (Makhdoumi 2018).

In contrast to these reports, we found higher prevalence of VRSA and VISA clinical isolates harboring *vanA* gene in our hospital. In another study in Iran, Saadat *et al*. (2014) found that the prevalence of VRSA clinical isolates was 37%. Interestingly, vanA and vanB genes were found approximately in all vancomycin-resistant strains. Further molecular analysis exhibited that *vanA* and *vanB* genes were detected in 34% and 37% of all clinical isolates, respectively. Firouzi *et al*., (2016) studied the prevalence of VISA strains of *S. aureus* in 447 healthcare staff and inpatients in Iran, finding that 31.31% of the isolates were resistant to methicillin (MRSA), while 16.1% were VISA. In another study, Hadadi *et al*. (2011) evaluated the prevalence of methicillin- and vancomycin-resistant *S. aureus* among hospitalized patients in Sina Hospital in Tehran, Iran. MRSA was detected in 50% of isolates, while VISA in one isolate (1.17%) out of 85 clinical ones. These data indicate the higher incidence of vancomycin-resistance strains in clinical specimens in Iran compared to the other countries. More importantly, these findings implicate that VRSA and VISA isolates are increasingly emerging in several parts of the world, especially in Iran. Therefore, there remains a public health threat from these increasing *S. aureus* isolates which can no longer be ignored (Bamigboye *et al*. 2018).

The molecular mechanisms underlying for the pathogenesis and resistant pattern of VRSA to different antibiotics are not well-understood. It seems that *vanA* and vanB genes play an important role in the pathogenesis of VRSA strains. In the present study, 72.72% of VRSA and 40% of VISA isolates contained *vanA* gene suggesting the critical role of this gene in the pathogenesis of this strain.

CONCLUSION

In conclusion, our results exhibited that the prevalence of vancomycin- and intermediate-resistant *S. aureus* strains isolated from patients in Mazandaran hospitals is high and emerging. More importantly, the frequency of *vanA* gene in these isolates, particularly in VRSA isolates, was very high which may be a reason for its pathogenesis and multiple-antibiotic resistance. Therefore, there is a need to keep the emergence and spread of these strains to a minimum level through an appropriate antibiotic prescribing and also initiating infection control measures.

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بررسی میزان شیوع ژن *vanA* *استافیلوکوکوس اورئوس* جدا شده مقاوم به ونکومایسین از نمونه‌های کلینیکی در یک بیمارستان در مازندران، ایران

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چکیده

استافیلوکوکوس اورئوس از جمله عوامل مهم ایجاد عفونت در بیمارستان‌هاست. اگرچه ونکومایسین اغلب در درمان استافیلوکوک‌های مقاوم به متی سیلین (MRSA) استفاده می‌شود، اما سویه‌های مقاوم به ونکومایسین (VRSA) همچنان به عنوان یک مشکل اساسی در بیمارستان‌ها محسوب می‌شوند. در این مطالعه شیوع *استافیلوکوکوس اورئوس* مقاوم به ونکومایسین و همچنین ژن *vanA* در سویه‌های جدا شده از نمونه‌های بالینی در یک بیمارستان در مازندران بررسی شده است. در این مطالعه توصیفی- مقطعی تعداد ۶۰ سویه *استافیلوکوکوس اورئوس* با استفاده از آزمایش‌های بیوشیمیایی و میکروب شناسی در نمونه‌های مختلف بالینی شناسایی شدند. روش انتشار از دیسک و *Kirby-Baure* برای بررسی مقاومت سویه‌ها به آنتی‌بیوتیک انجام شد. وجود ژن *vanA* در باکتری‌های *استافیلوکوکوس اورئوس* مقاوم و نیمه حساس به ونکومایسین با روش PCR و با استفاده از پرایمرهای اختصاصی بررسی شد. بیش از ۴۰٪ از ایزوله‌ها نسبت به آنتی بیوتیک‌های رایج، شامل جنتامایسین (۴۶/۶۷ ٪)، سفتازیدیم (۴۵ ٪) و کاربنی سیلین (۴۳/۳۴ ٪) مقاوم بودند. هر چند تنها تعداد کمی نسبت به جنتامایسین (۳۳,۳۳٪) و سفتازیدیم (۳۵٪) حساس بودند. ونکومایسین موثرترین آنتی‌بیوتیک علیه سویه‌های استافیلوکوکوس اورئوس (با ۵۶/۶۶ ٪ حساسیت) بود. تعداد ۱۱ سویه (۱۸,۳۴٪) و ۱۵ سویه (۲۵٪) به‌ترتیب نسبت به ونکومایسین مقاوم (VRSA) و نیمه حساس (VISA) بودند. بررسی مولکولی ژن *vanA* در ۱۱ سویه VRSA و ۱۵ سویه VISA نشان داد که ۸ (۷۲/۷۲٪) سویه VISA و ۶ سویه VRSA (۴۰٪) دارای ژن *vanA* بودند. شیوع سویه‌های VRSA و VISA، همچنین فراوانی ژن *vanA* در این سویه‌ها در بیمارستان‌های مازندران بالا و در حال افزایش است. بنابراین، به حداقل رساندن انتشار این سویه‌ها ضروری است.

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