CHARACTERIZATION OF STAPHYLOCOCCUS AUREUS ISOLATED FROM BURN WOUND; STRONG ANTIBACTERIAL ACTIVITY OF PHAGE COCKTAIL AGAINST VANCOMYCIN INTERMEDIATE-RESISTANT STAPHYLOCOCCUS AUREUS

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https://doi.org/10.55251/jmbfs.5366

ARTICLE INFO

Received 2. 10. 2021
Revised 22. 5. 2022
Accepted 6. 6. 2022
Published xx.xx.20xx

ABSTRACT

A universal problem is about spread of Staphylococcus aureus infections in burn patients. The present study aimed to learn about the molecular characteristics and the resistance pattern of S. aureus strains isolated from burn patients. In this cross-sectional study, we investigated 100 unique S. aureus isolated from burn patients by antimicrobial activity and biofilm formation and evaluated the effect of Complex Pyobacteriophage, a commercial bacteriophage cocktail, against the isolates mentioned above. Methicillin-resistant Staphylococcus aureus (MRSA) comprised 76%, and methicillin-susceptible Staphylococcus aureus (MSSA) comprised 24% of 100 S. aureus strains. The resistance rate among MRSA isolates was higher than compared of MSSA. Mupirocin resistance was found in 30% of isolates, with 28 (93.3%) and 2 (6.7%) strains of MRSA and MSSA, respectively, found. Vancomycin intermediate resistance in S. aureus (VISA) was 13% of MRSA strains. Two isolates were confirmed as vancomycin-resistant S. aureus (VRSA) strains and carried vanA. 31 and 62% of the total isolates showed inducible and constitutive resistance phenotypes. The rate of inducible and constitutive clindamycin resistance among MRSA strains was higher than MSSA strains. Biofilm production was detected in 66% of isolates. Strong, moderate, and weak producers accounted for 25%, 17%, and 24% of isolates. Phage analysis showed that 81% were susceptible to the phage cocktail, and only 19% were resistant to the phage cocktail. Our data indicated that VISA strains prevalence in the burn unit was mainly from S. aureus infections. Present work recommended that vancomycin treatment be closely monitored to prevent the spread of VISA and VRSA strains. Observations also highlighted the role of bacteriophage cocktails in eradicating S. aureus-related infections.

Keywords: Methicillin-Resistant Staphylococcus aureus, Vancomycin-Resistant Staphylococcus aureus, Biofilm, Bacteriophage, Wound infection

INTRODUCTION

Burning can cause disability and sometimes mortality in different ages in developed and developing countries (Robben, Ayalew, Chung, & Resnser, 2021; Savetamal, 2021). Damage to skin barrier function and weakening of immune responses in burned patients lead to increase susceptibility to the general systemic disorder, bacterial colonization, and different infections, which cause complicated the management of the disease in those hospitalized (Dou & Zhang, 2018). Patients with burn wound infections are at high risk for infections by various microorganisms, leading to death in more than 70% of burn patients (Dou & Zhang, 2018; Savetamal, 2021). Staphylococcus aureus remains increasingly common among infectious agents in burn patients (Robben et al., 2021; Yali et al., 2014). Mentioned bacterium causes a wide range of illnesses. Symptoms can range from small infections on the skin to life-threatening conditions like bacteremia, endocarditis, and osteomyelitis. Recent data has indicated a remarkable increase and a heavy burden of S. aureus burn infections worldwide (Dou & Zhang, 2018; Robben et al., 2021; Savetamal, 2021). Besides various virulence factors expression and emergence of drug-resistant strains, biofilms production is most critical abilities that makes S. aureus infection as remarkable problem in the patients (Tahaei et al., 2021). Some studies have revealed an increase in multidrug-resistant (MDR) S. aureus strains, with a limit in the chemotherapeutic agents availability and complicating disease management. Using mupirocin to treat skin and soft tissue infections (SSIs) and eliminate MRSA from patients, healthcare-workers, nurses and the control MRSA outbreaks is an excellent use of this topical antibiotic. The common use of mupirocin has consequence to increased resistance, documented in many countries worldwide. Vancomycin is a choice to treat severe MRSA infections. Globally, a major increase in VRSA prevalence strains over the last few decades has become a cause for concern, imposing high economic costs to governments and patients. Data worldwide indicate that macrolide-lincosamide-streptogramin group B (MLSB) antibiotics have been known as drugs choice to treat SSTIs caused by this pathogen. Clindamycin using can cause inducible and constitutive resistance, making it a hard pathogen to treat. Hence, reasonable use of antibiotics is essential.

Infections by S. aureus are scandalously problematic to treat (Gordillo Altamirano & Barr, 2019). Recent data noted the critical role of phage therapy as a promising tool in controlling and treating bacterial infections (Azam & Tanji, 2019).

Unlike traditional therapy, phage therapy has some advantages (Duplessis & Biswas, 2020). They are self-propagating and self-limiting viruses that kill prokaryotes without harming humans (Dabrowska, 2019; Moore & Moore, 2021; Picoll et al., 2021; Topka-Bielecka et al., 2021).

However, the acquisition of knowledge on the prevalence, characterization, biofilm production, and phage therapy of S. aureus strains in Iran is limited. The objective of our study was to investigate antibiotic susceptibility and biofilm formation ability, including specific biofilm-responsible genes of S. aureus isolated from wound infections, and to study the effectiveness of phage therapy.

MATERIAL AND METHODS

Collection of samples and isolates

In the present research, 100 S. aureus strains from burn wounds were obtained from September 2018 to December 2019. Ethics Committee of the Shahid Beheshti University of Medical Sciences confirmed the study (IR.SBMU.MSP.REC.1398).
561) as well as consent was obtained from participants. Burned (high level) patients were sampled from wound area with sterile cotton swabs. Detection of S. aureus was done by standard bacteriological tests and coagulate production (Sigm, St. Louis, USA), catalase, and DNase (Merck, St. Louis, Germany). An PCR assay was used to confirm the mce gene presence in all isolates (Eftekhari et al., 2017). Confirmed isolates stored in trypticase soy broth (TSB, Merck, St. Louis, Germany), containing 30% glycerol, and stored at -70°C.

**Antimicrobial susceptibility testing**

Antibiogram was done by Kirby Baur method based on clinical and the laboratory standards institute (CLSI) instructions against tetracycline (TET 30µg), amikacin (AMK 30µg), clindamycin (CLI 2µg), penicillin (PEN 10 units), gentamicin (GEN 10 µg), erythromycin (ERY 15µg), and rifampicin (RIF 5µg) ( Mast Diagnostics Ltd, Meseyside, UK). To classify the strains as highly sensitive, intermediate, or highly resistant, they were incubated for 24 hours at 37°C and then measured and compared to the CLSI guidelines (CLSI 2021).

The screening of vancomycin (VAN) and mupirocin (MUP) resistance strains was performed by standard broth micro-dilution procedure in concurrence with CLSI guideline (CLSI 2021). Mupirocin had three different MIC breakpoints: susceptible (1 mg/L), low-level resistant (2-256 mg/L), and high-level resistant (>512 mg/L). The ability of these strains to grow in Mueller-Hinton agar (Merck, Germany) containing cefoxitin (30 g) disc and PCR amplification of the meca gene identified them as MRSA or MSSA (Eftekhari et al., 2017). S. aureus isolates with the zone of inhibition <21 mm around the cefoxitin disc were confirmed as MRSA strain. S. aureus ATCC 25923 was applied as positive control of antibiotic susceptibility testing.

**Inducible and constitutive screening**

D-test was used to determine isolates with inducible resistance phenotype (iMLSa). The screening of isolates with constitutive and inducible resistance phenotype (cMLSa and iMLSa) was performed under CLSI guideline (CLSI 2021). MS phenotype was defined for isolates with resistance to macrolide and streptogramin B.

**VISA and VRSA screening**

The MIC for vancomycin (VAN) was determined as previously described (Park, Lee, & Kim, 2019). The MIC titer obtained was compared to the MIC breakpoints according to CLSI 2021 recommendations, and the isolate was classified as resistant, intermediate or susceptible. According to the CLSI guideline, negative (ATCC 25923) and positive (Enterococcus faecalis ATCC 51299) strains were used.

**Spot test assay**

The sensitivity of isolates to Complex Pyobacteriophages (Microgen, Russia) was explained by Kutter et al. with minor modifications (Kutter et al. 2009). Briefly, isolates were cultured overnight in TSB (Merck, St. Louis, Germany) at 37°C with gentle shaking. Then 50 µl of each isolate was added to 3-4 mL mollen top agar, LB medium with 0.4% agarose (Merck, Germany), mixed well, and poured on bottom agar (LM medium with 1.2% agarose). Subsequently, 5 µl of Complex Pyobacteriophage and SM buffer were spotted on the lawn of bacteria with proper morphology of the spot zone. The clear spots without turbidity are considered as “+”, substantial turbidity in spots or individual plaques as “++”, and no recognizable zone as “0” (Mahmoud, Ahmed, Abo-senna, Riad, & Abo-Shadi, 2020).

**Determination of biofilm production by microtiter plate (MIP) assay**

MIP assay performed based on Yousefi et al. protocol with no significant modification (Yousefi et al., 2016). The biofilm measured by ELISA reader absorbance (OD) at 490 nm. All tests were performed four times, and the results were then re-run triplicate to ensure duplicability. Stringent criteria were applied as positive and negative control strains. The degree of biofilm production (without biofilm, weak, moderate, and strong) was interpreted according to the study of Yousefi et al. (Yousefi et al., 2016).

**Deoxyribonucleic acid (DNA) extraction and screening for vanA and icaABCD genes**

DNA extraction done by Goudarzi et al. method. (Goudarzi et al., 2017). Strains were screened for vanA, and icaABCD genes by PCR assay (Chen et al., 2016; Park et al., 2019). Also, Enterococcus faecalis BM6217 was used for vanA genes as positive controls in each run of amplification. The entire isolates were investigated for the presence of icaA and icaD genes by multiplex PCR assay.

**Enterococcus faecalis**

BM6217 was used for vanA genes, as positive controls in each run of amplification. Agarose gel electrophoresis was applied to analyze PCR products at 90 V for 60 min. Amplified DNAs were observed with gel documentation, and their size was compared with 100bp DNA ladder (BioFact, Korea). Data analyzed by SPSS software (SPSS Inc no. 20).

**RESULTS**

Based on our results, 76% of isolates were MRSA and all harbored mecA gene (Figure 1).

![Figure 1](image1)

**Table 1** Distribution of resistance among MRSA and MSSA strains

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>S. aureus Resistance %</th>
<th>Total %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penicillin</td>
<td>71</td>
<td>14</td>
</tr>
<tr>
<td>Amikacin</td>
<td>72</td>
<td>16</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>52</td>
<td>6</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>73</td>
<td>22</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>55</td>
<td>6</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>53</td>
<td>9</td>
</tr>
<tr>
<td>Rifampin</td>
<td>33</td>
<td>7</td>
</tr>
<tr>
<td>Mupirocin</td>
<td>21</td>
<td>9</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>12</td>
<td>3</td>
</tr>
<tr>
<td>Total</td>
<td>76</td>
<td>24</td>
</tr>
</tbody>
</table>

The MIC test for vancomycin showed that 18 isolates (18%) inhibited by 0.5 µg/mL, 30 (30%) by 1 µg/mL, and 37 (37%) by 2µg/mL. VISA strains were detected in 13 (13%) isolates which 3 (23.1%) isolates were MRSA. Of 13 VISA strains, 8 strains were inhibited in MIC titer of 4 µg/mL of vancomycin and 5 strains in 8 µg/mL. Two isolates were resistant to vancomycin, of which one had MIC 32 µg/mL and another exhibited MIC titer of 128 µg/mL. Both VISA isolates harbored vanA gene (Figure 2).

![Figure 2](image2)
According to the MIC test, 30% of examined isolates were resistant to mupirocin (mup-R). Of these, 8 and 22 isolates displayed high (HLMUPR) and low-level (LLMUPR) resistance phenotypes. Of 100 isolates under study, 25 (25%) inhibited by 0.5 µg/mL of mupirocin, 10 isolates (10%) by 1 µg/mL, 13 isolates (13%) by 2 µg/mL, 22 isolates (22%) by 4 µg/mL, 15 isolates (15%) by 64 µg/mL, 7 isolates (7%) by 128 µg/mL, 5 isolates (5%) by 512 µg/mL and 3 isolates (3%) by more than 512µg/mL. Of the S. aureus strains that had mupirocin-resistant, 28 (93.3%) and 2 (6.7%) strains were MRSA and MSSA. Thoroughly, 90% of isolate were multidrug resistance (MDR). Of the total isolates, 62, 31, and 7 isolates showed cMLSb, IMLSB, and MS phenotypes accounting for 62%, 31%, and 7% respectively. As shown in Table 2, twelve patterns of resistance identified in AMK, CLI, ERY, GEN, PEN, TET, (28%), AMK, CLI, ERY, GEN, PEN, RIF, TET (20), and AMK, PEN, ERY, MUP (15%).

Table 2 The resistant pattern in 100 S. aureus strains isolated from patients with burn wound

<table>
<thead>
<tr>
<th>MDR</th>
<th>Resistance pattern</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nine</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP, VAN</td>
<td>5</td>
</tr>
<tr>
<td>Seven</td>
<td>PEN, GEN, TET, AMK, ERY, RIF, CLI</td>
<td>20</td>
</tr>
<tr>
<td>Six</td>
<td>PEN, GEN, AMK, TET, ERY, CLI</td>
<td>28</td>
</tr>
<tr>
<td>Five</td>
<td>PEN, AMK, RIF, MUP, VAN</td>
<td>4</td>
</tr>
<tr>
<td>Four</td>
<td>PEN, AMK, ERY, MUP</td>
<td>15</td>
</tr>
<tr>
<td>Three</td>
<td>TET, ERY, CLI, VAN</td>
<td>2</td>
</tr>
<tr>
<td>One</td>
<td>ERY</td>
<td>8</td>
</tr>
<tr>
<td>without</td>
<td>-</td>
<td>2</td>
</tr>
</tbody>
</table>

S. aureus biofilm production was found in 66% of the 100 strains studied. There were 25 (25%) strong, 17 (17%) moderate, and 24 (24%) weak producers of biofilm among the isolates analyzed in the study. Our results showed that icaA was present in 94 strains (94%) and icaD in 95 (95%) strains. Four isolates were negative for both icaA and icaD genes and confirmed as non-biofilm producer isolates. One isolate was negative only for icaD and 2 isolates were negative only for icaA (Figure 3).

Table 3 Characterization of VISA and VRSA strains isolated from burn wounds

<table>
<thead>
<tr>
<th>Strain number</th>
<th>Biofilm</th>
<th>Resistance</th>
<th>Mupirocin resistance</th>
<th>MLSb phenotype</th>
<th>Cocktail spot test</th>
<th>mecA</th>
<th>vanA/MIC(µg/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR1-VRSA</td>
<td>Strong producer</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP</td>
<td>High level</td>
<td>Constitutive</td>
<td>+</td>
<td>+</td>
<td>+/32</td>
</tr>
<tr>
<td>IR2-VRSA</td>
<td>Strong producer</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP</td>
<td>High level</td>
<td>Constitutive</td>
<td>++</td>
<td>+</td>
<td>+/128</td>
</tr>
<tr>
<td>IR1-VISA</td>
<td>Weak producer</td>
<td>PEN, AMK, TET, ERY, VAN</td>
<td>Low level</td>
<td>Inducible</td>
<td>++</td>
<td>+</td>
<td>-/4</td>
</tr>
<tr>
<td>IR2-VISA</td>
<td>Weak producer</td>
<td>TET, ERY, CLI, VAN</td>
<td>Low level</td>
<td>Constitutive</td>
<td>++</td>
<td>-</td>
<td>-/4</td>
</tr>
<tr>
<td>IR3-VISA</td>
<td>Moderate producer</td>
<td>PEN, AMK, RIF, MUP, VAN</td>
<td>High level</td>
<td>-</td>
<td>++</td>
<td>-</td>
<td>-/4</td>
</tr>
<tr>
<td>IR4-VISA</td>
<td>Strong producer</td>
<td>PEN, AMK, RIF, MUP, VAN</td>
<td>High level</td>
<td>-</td>
<td>++</td>
<td>+</td>
<td>-/8</td>
</tr>
<tr>
<td>IR5-VISA</td>
<td>Strong producer</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP</td>
<td>High level</td>
<td>Constitutive</td>
<td>++</td>
<td>+</td>
<td>-/8</td>
</tr>
<tr>
<td>IR6-VISA</td>
<td>Strong producer</td>
<td>PEN, AMK, RIF, MUP, VAN</td>
<td>High level</td>
<td>-</td>
<td>++</td>
<td>+</td>
<td>-/8</td>
</tr>
<tr>
<td>IR7-VISA</td>
<td>Weak producer</td>
<td>PEN, AMK, TET, ERY, VAN</td>
<td>Low level</td>
<td>Inducible</td>
<td>++</td>
<td>-</td>
<td>-/4</td>
</tr>
<tr>
<td>IR8-VISA</td>
<td>Strong producer</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP</td>
<td>High level</td>
<td>Constitutive</td>
<td>++</td>
<td>+</td>
<td>-/8</td>
</tr>
<tr>
<td>IR9-VISA</td>
<td>Moderate producer</td>
<td>TET, ERY, CLI, VAN</td>
<td>Low level</td>
<td>Constitutive</td>
<td>++</td>
<td>-</td>
<td>-/4</td>
</tr>
<tr>
<td>IR10-VISA</td>
<td>Weak producer</td>
<td>PEN, AMK, TET, ERY, VAN</td>
<td>Low level</td>
<td>Inducible</td>
<td>++</td>
<td>+</td>
<td>-/4</td>
</tr>
<tr>
<td>IR11-VISA</td>
<td>Moderate producer</td>
<td>AMK, ERY, VAN</td>
<td>Low level</td>
<td>Inducible</td>
<td>++</td>
<td>-</td>
<td>-/4</td>
</tr>
<tr>
<td>IR12-VISA</td>
<td>Weak producer</td>
<td>PEN, AMK, TET, ERY, VAN</td>
<td>Low level</td>
<td>Inducible</td>
<td>++</td>
<td>+</td>
<td>-/4</td>
</tr>
<tr>
<td>IR13-VISA</td>
<td>Strong producer</td>
<td>PEN, GEN, AMK, TET, ERY, CLI, RIF, MUP</td>
<td>High level</td>
<td>Constitutive</td>
<td>+</td>
<td>+</td>
<td>-/8</td>
</tr>
</tbody>
</table>

DISCUSSION

In the present research, we reported several main findings. A high VISA rate among S. aureus isolated from burn patients was primarily found. Second, a high prevalence of MDR rate emphasized improper prescription of antibiotics in infected with related to burn patients. Third, biofilm formability was observed in two-thirds of the isolates. Fourthly, the phage cocktail exhibited an effective inhibitory effect on S. aureus strains isolated from patients who burned; meanwhile, all VISA and VRSA isolates were susceptible to the phage cocktail. Data relating to antimicrobial activity revealed that 76% of S. aureus isolates were resistant to methicillin and MRSA confirmed strains. Different frequency of MRSA strains in burn patients (between 69% to 80%) was reported in researches.
performed from Iran (Abbasi-Montazeri et al., 2013; Emaneini et al., 2018; Sehbanasgh, Saderi, & Owlia, 2014). Recently published data by Dadashi et al. reported a 43% prevalence of MRSA clinical isolates, which was lower than the study (Dadashi et al., 2018). However, various frequencies of MRSA, including 45%, 93%, 47%, 53.4%, and 11.8%, were reported in the study published by Dadashi et al. (2020). Dadashi et al. reported a 43% prevalence of MRSA (Dadashi et al., 2022). From the survey, one- thirds of strains were mupirocin-resistant (30%), which was close to the reported rate in the USA (31.3%) and India (25.5%) (Antonov et al., 2015). However, lower rates reported from France (2.1%) and China (17.6%) (Desroches et al., 2013; Liu et al., 2017). Shittu et al. presented a relatively low prevalence (14%) of mupR MRSA strains (Shittu et al., 2020).

In the current study, 8% of examined isolates were confirmed as HLMUPR S. aureus. Our results were in parallel by Dadashi et al. who indicated an 8.1% prevalence of HLMUPR MRSA with a high prevalence in Asia comparing Europe and the USA (12.1% vs. 8% and 5.9%) (Dadashi, Hajikhani, Darban-Sarokhalil, Vali-Kheli, & Goudarzi, 2020). Different data were reported from Iran (25.5%) in Africa (0.5-38%), India (26.1%), USA (26.9%), and Africa (23.5%) (Dadashi et al., 2020; Shittu et al., 2018).

According to our research, irrational use, different prescription policies, drug availability, low cost, and the spread of dominant types are all potential causes of the high resistance rate in Asian countries. Earlier findings have demonstrated an increased use of drugs such as clindamycin and Vancomycin in Iran (Shittu et al., 2020). Our study showed S. aureus isolates were resistant to vancomycin at an intermediate level. Previous research conducted by Shittu et al. and colleagues revealed a clindamycin rate of VRSAs and VISA in different regions. They found that 1.3% and 1.7% of isolates were VRSAs and VISA, respectively, and also demonstrated a remarkable increase in VRSAs and VISA after 2010 compared to before 2010. Shittu et al. found that the prevalence rate of VISA in Asia, especially in Iran and India (67%), was higher than in other countries (Shariati et al., 2020). These discrepancies could be excessive use, irrational policies in the consumption, drug availability, low public hygiene standards, and dissemination of specific clones in these regions.

Our analysis revealed the prevalence of IMLSB phenotype in 31% of isolates. The inducible resistance reported in the present work is lower than studies conducted in Jordan (76.7%) (Jarajreh, Aqel, Alzoubi, & Al Zereini, 2017) and higher rate reported from Brazil (7.9%) (Bottega et al., 2014) and Nepal (21%) (Adhihari, Shrestha, Bajracharya, Karki, Dhakal, Shrestha, et al., 2017). The prevalence of S. aureus producing biofilm was high in the current study (66%). The magnitude of biofilm producers in the present study is consistent with the study findings reported from China (66%) (Wang et al., 2010) and Iran (62.9%) (Yousefi et al., 2016). As referenced in study of Hosseini et al., biofilm-formation prevalence exceeds 80% in MRSA strains. As well, we also evaluated 22.5%, 45.3%, and 52.9% of MRSA could produce weak, moderate and strong biofilms (Hosseini et al., 2020). Past research has been indicated that some S. aureus isolates need polysaccharide intercellular adhesin (PIA) for producing of biofilm and its regulation is controlled by the icaADBC operon. In this study, 94% and 95% of the isolates were found to have icaC and icaD, which is in agreement with the findings of Azmi et al. (Azmi, Qrei, & Abdeen, 2019), which is in agreement with the findings of Azmi et al. (Azmi, Qrei, & Abdeen, 2019) and supports those of Sharma and coworkers (Sharma et al., 2017) who reported that icaAD was found abundantly among biofilm-producing isolates. However, these findings suggest an indirect role for ica in biofilm formation. Our study investigated the in-vitro effectiveness of phage cocktail against S. aureus isolated from burn patients. Our findings indicated that the phage cocktail had an indirect effect on 84.6% of isolates, suggesting the role of its potent inhibitory against MRD S. aureus.

This agreed with Chhibber et al. from India that showed Phage Cocktail could be an effective treatment against MRSA strains related to SSTIs (Chhibber et al., 2017). In another study, Tahil et al. investigated the effect of Phage Cocktail against the prevalence of VRSAS and clinical isolates and indicated that planktonic colony growth was reduced significantly in the presence of Phage Cocktail (Tahil et al., 2021). In a 2020 study, Kifelew et al. assessed the efficacy of Myoviridae phages cocktail on three S. aureus in treatment wound of diabetic mouse caused by MDR S. aureus infections compared with vancomycin. They indicated that S. aureus was eradicated from the wounds of phage-treated compared to saline-treated mice, while the bacterium was detected in all the vancomycin-treated mice (Kifelew et al., 2020). The obtained results justified in-vitro effectiveness of phage cocktail against S. aureus isolated from burn patients; it has certain limitations. Pulsed-field gel electrophoresis and next-generation sequencing were not performed. The number of tested strains for characterization of VRSAs and VISA strains was small, which may only display regional data and not reflect the perfect epidemiological picture of the variability of these isolates.

CONCLUSION

We showed evidence to effectiveness of Phage Cocktail against S. aureus strains isolated from burn patients. VRSA and VISA strains in our country indicate that studying phages as topical antimicrobials against these isolates more in-depth can help us minimize the spread of the isolates.

ACKNOWLEDGMENTS

This study supported by Research Department of the School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran (Grant No. 17819). The funding agency has no role in the project's design, work execution, analysis, interpretation of the data, and manuscript writing and submission.

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