

***VanA* and *VanB* Positive Vancomycin-resistant *Staphylococcus aureus* Among Clinical Isolates in Shiraz, South of Iran**

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Abstract

Objective

The purpose of this study was to determine the prevalence of vancomycin-resistant *Staphylococcus aureus* isolated from clinical samples in Shiraz hospitals.

Methods

From March to December 2012, 100 *S. aureus* isolates (mainly from wound and blood) were collected from three hospitals in Shiraz, south of Iran. After identification of *Staphylococcus aureus* by biochemical, microbiological and molecular methods, antibiotic susceptibility testing was performed by Kirby-Bauer disc diffusion test for 13 different antibiotics. Vancomycin-resistant *Staphylococcus aureus* isolates were determined by vancomycin agar screening test and PCR for vancomycin resistant genes (*vanA* and *vanB*).

Results

The lowest and highest resistance was seen for quinupristin-dalfopristin (n=1) and ampicillin (n=95), respectively. Vancomycin agar screening test showed that 37 isolates can grow on these media. Further study by PCR also detected *vanA* and/or *vanB* genes in all of these strains. Also, 19 isolates showed either *vanA* or *vanB* but were susceptible according to vancomycin agar screening test. In total, *vanA* and *vanB* resistant genes were detected in 34% and 37% of clinical isolates, respectively.

Conclusion

The results showed that the frequency of vancomycin resistance genes (*vanA*, *vanB*) is very high in *Staphylococcus aureus* strains isolated from patients in south of Iran. Thus, urgent interventions are needed to keep the emergence and transmission of these isolates to a minimum.

Keywords: *Staphylococcus aureus*, Vancomycin Resistance, *vanA*, *vanB*, Iran