A comparative study on clinical Methicillin resistant *Staphylococcus aureus* isolates with different susceptibilities to Vancomycin

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Introduction

- **The marked increase in antibiotic use for treating S. aureus infections has driven a rise in frequency of drug-resistant staphylococcal strains.**
- **Methicillin-resistant S. aureus (MRSA) is at present the most commonly identified antibiotic-resistant pathogen in many parts of the world. The main cause of methicillin resistance in S. aureus is acquiring mecA gene that located in a mobile genomic element known as the staphylococcal cassette chromosome (SCC).**
- **Overuse of vancomycin for treatment of MRSA infections has led to emergence of vancomycin-intermediate and vancomycin-resistant MRSA.The resistance of VRSA strains has resulted from the probable conjugal transfer of the *vanA* operon from a vancomycin-resistant *E. faecalis* and these strains is characterized by inducible, high-level resistance to vancomycin and teicoplanin.**
- **The success of resistant strains of S. aureus (MRSA and VRSA) is attributed to a multitude of virulence factors that are responsible of host colonization, tissue invasion and dissemination.**
- **Expression of virulence determinants is under control of the accessory gene regulators (*agr*) where it upregulate a wide variety of virulence determinants and downregulate expression of surface binding proteins**

Aim

The prevalence of different vancomycin resistance categories among MRSA isolates collected from Mansoura hospitals to detect different virulence factors harbored by these isolatesand to gain further insight into the genetic relations between VRSA, VISA and VSSA.

Methods

- **Collection, isolation and identification of *S. aureus* isolates collected from various clinical sources.**
- **Phenotypic detection of methicillin resistance by cefoxitin and oxacillin disc diffusion method and vancomycin resistance by broth microdilution method of *S.aureus* isolates.**
- **Genotypic analysis including:**

a) Preparation of total DNA content (Zhang *et al.*, 2004).

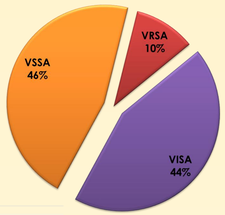
b) Polymerase chain reaction (PCR) for the detection of resistance genes (*mecA* and *vanA*).

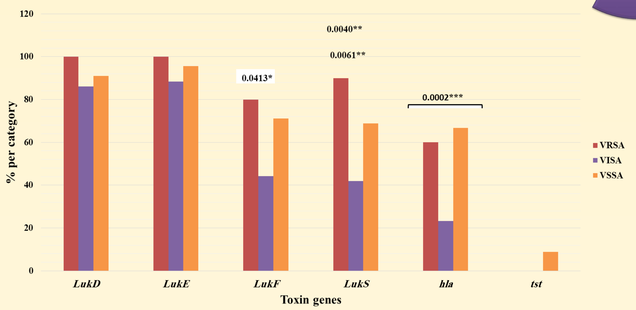
c) Polymerase chain reaction (PCR) for the detection of ten virulence factors encoding genes (*LukD, LukE, LukF, LukS, hla, tst, icaA, icaD, geh and cna*).

d) Multiplex PCR for typing of accessory gene regulator (*agr*) locus (I, II, III and IV).

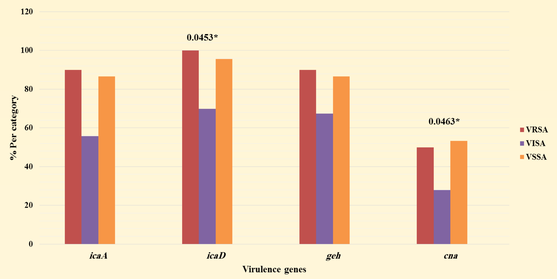
Results

vancomycin susceptibility of MRSA isolates by broth microdilution method

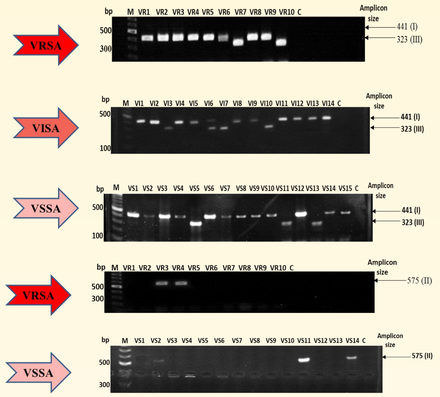


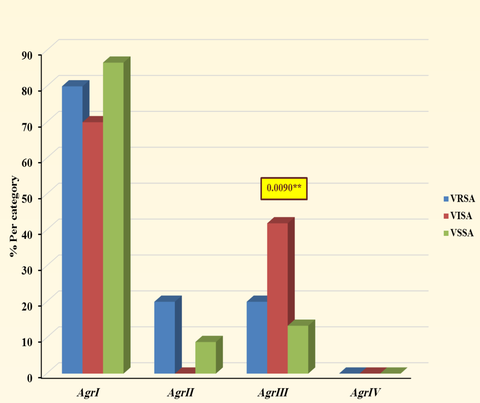


Correlation between VRSA, VISA and VSSA isolates according to the prevalence of toxin genes

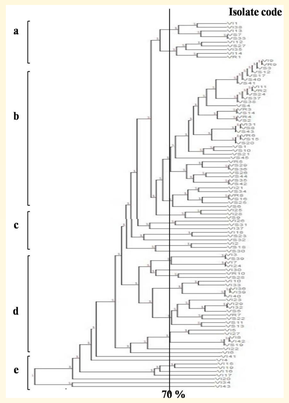


Correlation between VRSA, VISA and VSSA isolates according to the prevalence of virulence genes





Prevalence of *agr* types among VRSA, VISA and VSSA isolates



Dendrogram of virulence factor profiles and *agr* typing of VRSA, VISA and VSSA isolates

Conclusion

- **The present study reveals high level of VISA/VRSA in Mansoura city and indicates increased extent of antibiotic resistance in the study area. The major cause of this situation may be unawareness and misuse of broad-spectrum antibiotics. Therefore, a strict regulation on indiscriminate antibiotic use might be an effective approach in the control of such infection.**
- **The emergence of Linezolid resistance in VRSA isolates represents an extreme challenge as the available therapeutic options for VRSA are limited and the development of novel molecules to control VRSA infection is not easily accomplished.**
- **Virulence and toxin genes are more prevalent in VRSA, followed by VSSA then VISA isolated from Mansoura hospitals.**
- **VRSA and VSSA isolates exhibited high genetic relatedness as investigated by dendogram analysis while VISA isolates were genetically more diverse.**
- **The high variability in the distribution of toxin and virulence factors genes among different vancomycin resistance categories create a compelling arguments to reconsider the suitability of assessing virulence potential among these isolates to control VRSA infection.**

References

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