Genotyping of Clinical Isolates of Coagulase-Negative Staphylococci Species by PCR-Sequencing of Tuf Gene

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Background & Objectives: Over the last two decades CONs have emerged as opportunistic pathogens, especially among immunocompromised hosts and patients with implanted biomatherials. The increasing incidence of these micro-organisms in hospital- acquired infections, necessitates the need for an accurate identification of staphylococcus isolates at the species level. Since tuf gene is known as the most accurate for specifying CONs, we aimed to identify species of 50 consecutive clinical CONs isolates by phenotypic characteristics and tuf gene sequencing.

Methods: A total of 50 CONs was isolated from various clinical specimens of hospitalized patients in Shahid Mohammadi hospital, Bandar-Abbass. Phenotyping was carried out by differential - biochemical tests. Genotyping was performed by sequencing of tuf gene, followed by blast and construction of phylogenetic tree.

Results: The clinical isolates consisted of 25(50%) *S. epidermidis*, 22(44%) *S. saprophyticus* and 3(6%) *S. hemolyticus*. *S. epidermidis* and *S. saprophyticus* strains were mostly isolated from blood and urine cultures, respectively. Vancomycin was found to be the most effective antibiotic followed by cefalexin and ofloxacin. Blast searches and phylogenetic tree inferred from the neighbor-joining methods of 8 isolates revealed that 5 isolates had a tuf sequence 100 % identical to tuf gene of *S. epidermidis* strain SeMCV45, and the tuf gene of 3 isolates was 99% similar to that of *S. haemolyticus* strain ShlMCV14.

Conclusion: CONS are involved in a wide range of nosocomial infections. PCR and sequencing of the tuf gene is a reliable and valuable approach for the genotyping and identification of CONS species in epidemiological studies.

Keywords: Coagulase Negative Staphylococci; Tuf Gene; Clinical Samples