TRs analysis revealed *Staphylococcus epidermidis* transmission among patients and hospital

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Abstract

**Background.** As a great opportunistic pathogen, *Staphylococcus epidermidis* participates in a wide spectrum of infections by residing in the medical devices. Regardless of the clinical importance of *S. epidermidis*, there are a few data about typing of clinical and non-clinical isolates at the subspecies level in Iran. We used the technique of “Multiple-Locus Variable number tandem repeat Analysis” for genetic differentiation of 107 clinical and non-clinical *S. epidermidis* isolates.

**Methods.** Five appropriate Tandem Repeats were selected using bioinformatics programs and PCR-amplified using specific primers. Clustering of the “Multiple-Locus Variable number tandem repeat Analysis” profile was performed using BioNumerics. All isolates yielded a PCR product for all Variable Number Tandem Repeat loci.

**Results.** Approximately 28% of the isolates were Methicillin Resistant *S. epidermidis*. High level of genetic diversity between isolates was observed. Overly, the *S. epidermidis* isolates were discriminated into 43 various “Multiple-Locus Variable number tandem repeat Analysis” types. Twenty-seven isolates obtained from blood showed in 21 “Multiple-Locus Variable number tandem repeat Analysis” types, and 10 samples collected from the environment were distributed in three Multiple-Locus Variable number tandem repeat Analysis” types. There was a significant relationship between the Multiple-Locus Variable number tandem repeat Analysis types and isolated strains of blood and the environment indicating the successful colonization of environmental clones in the hospitalized patients in the surgical ward.

**Conclusions.** The Multiple-Locus Variable number tandem repeat Analysis technique showed information about the transmission of this bacterium among patients, staff and the hospital environment.

Introduction

*Staphylococcus epidermidis* is one of the most frequently identified bacteria in the medical setting, and it has emerged over one last two decades as a great opportunistic pathogen responsible for a huge range of nosocomial infections, particularly in patients with implanted medical devices (1-3). Nevertheless, the source of these infections is difficult to assess but possible using adjusted genotyping tools (4, 5).