Molecular epidemiology of *Staphylococcus aureus* with ERIC-PCR method

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**Background and Objectives:** *S. aureus* is one of the most significant etiological agents responsible for healthcare-associated infections. The aim of this study was to show the genetic relationship in *S. aureus* isolates and their transmission pattern between hospitals.

**Materials and Methods:** 90 *S. aureus* strains, isolated from hospitalized patients in the intensive care unit and infectious wards of Besat and Toohid hospitals, Sanandaj. Antimicrobial susceptibilities were determined by the disc diffusion method, Methicillin resistance was done by agar screen test and the resistance inducible by the D-Test. By ERIC-PCR technique relationship of strains was determined based on the similarities between DNA fingerprints by using Jaccards coefficient in the SAHN program of the NTSYS-pc software.

**Results:** Fourteen different antimicrobial patterns were observed. 46.7% of the strains were susceptible to all antimicrobials tested. The ERIC–PCR profiles allowed typing of the 90 isolates into 75 ERIC-types which were grouped into eleven main clusters (C1–C11). The Fourth group with the largest number was formed 17 strains. Agreement between antibiotic patterns and rep-profiles was not observed for most isolates.

**Conclusion:** The results of our study also showed that most of Staphylococcus isolated produced different genomic fingerprint patterns, therefore, dissemination source of infection is different.

**Keywords:** *S. aureus*, ERIC–PCR, resistance