Genetic diversity of common environmental Enterobacteriaceae bacilli in intensive care units of hospitals from central Iran

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Background: Environmental surfaces of intensive care units (ICUs) are suitable for the growth of Gram-negative bacteria. Normally, these strains that are circulating between the environment and patients can cause outbreaks of nosocomial infections among vulnerable patients. In this study, the genetic diversity of common Enterobacteriaceae bacilli family in the environment of the ICUs was evaluated.

Methods & Materials: During a 10-month period, samples were collected from environmental surfaces of ICU departments such as toilets, different surfaces, machinery, and injectable solutions from 5 hospitals located in Qom, central Iran. Swab samples were transferred on Blood Agar and sub-cultured on MacConkey medium, then suspected colonies were inoculated into the TSI media and differential diagnosis was done by using differential culture media and biochemical reactions for Enterobacteriaceae family. Results were confirmed by using API 20E kit. Genetic diversity was evaluated by using universal primers in ERIC-PCR method. The clonal relatedness of the strains were obtained using GelCompare II software.

Results: A total of 396 swab samples were collected and 1205 colonies were isolated including 194 colonies of Gram-negative bacilli. Totally, 22% of the isolates belonged to Enterobacteriaceae family including Klebsiella pneumoniae (7.21%) and Enterobacter cloacae (2.6%) as the most prevalent. Overall, 14 strains of K. pneumoniae were identified. Band patterns of 2 cluster each with 2 strains had 90% similarity (one clone): two strains were isolated from soap and pillow from hospitals I and III with one month interval, two other strains were isolated from dining table and sink from hospitals IV and V with 4 month interval. Overall, 5 strains of E. cloacae were identified from hospitals IV and V. Band patterns of these strains had less than 50% similarity and were considered as 5 distinct single types.

Conclusion: The results show the diversity of contaminating sources and presence of different circulating clones of E. cloacae. Isolation of similar clones of K. pneumonia from different hospitals is crucial in aspect of controlling the spread of same clone of nosocomial infections.

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