

Abstract

Escherichia coli are the most common bacteria causing digestive and other extraintestinal infections in human and animals. Commensal *E. coli* isolates are phylogenetically distributed among geographically distinct human populations. The aim of this study was to determine the genetic diversity and phylogenetic background of commensal *E. coli* isolates collected from fecal samples of patients in Zabol, Iran using random amplified polymorphic DNA (RAPD) and triple-PCR respectively. A total 100 *E. coli* isolates were identified by conventional methods. Out of 100 *E. coli* isolates, 28%, 7%, 48% and 17% were fall in phylogenetic group A, B1, B2 and D respectively. The RAPD data showed a genetic similarity between 14 and 100%. In conclusion, phylogenetic group B2 and A predominated in fecal isolates, while the percentage of fecal isolates belonging to groups B1 and D was significantly lower than other.

Key words: *Escherichia coli*, fecal samples, genetic diversity, phylogeneticity



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Title

Genetic diversity and phylogenetic grouping of *Escherichia coli* isolates collected from fecal samples of patients attending hospitals in Zabol

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