

Phylogenetic analysis and antibiotic pattern determination of isolated *Escherichia coli* from water and Shoreline of Genaveh province

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Abstract

Escherichia coli belong to a group of bacteria called coliform which is member of Entrobacteriaceae family. For many years, the bacterium are using as fecal indicator for public health. *Escherichia coli* are as an important organism which could disseminate antibiotic resistance in water shoreline. Accordingly, the present study tried to isolate the bacterium from Genaveh shoreline and sediments. Then phylogenetically categorized based on Clermont technique and evaluate their antibiotics pattern. For this purpose, 60 samples (30 water and 30 sediment) were collected from water and sediments between April to August 2016. Then the samples were evaluated by MPN technique and for confirmation they were cultivated on MacConkey and Eosin methylene blue agar. After that they were identified using Gram stain, Catalase and oxidase tests. The phylogenetical analysis of *E.coli* was done using set of primers: ChuA, yjaA, TSPE 4.C2 and antibiotic pattern were assessed using antibiogram test. Out of 60 collected samples, 6 samples were identified as *E.coli*, 5 from water and 1 from sediments. Based on antibiogram test all of the isolates with 100% were sensitive to Gentamicin, Ceftriaxone and Cefotaxime. The most common phylogenic group was belonging to groups A, B2 and D. Based on elucidated results it could be concluded that the best antibiotic on the isolates were Gentamicin, Ceftriaxone and Cefotaxime. Therefore, suggesting for remedy of gastrointestinal infections caused by *Escherichia coli* the selected antibiotics could be use along with other techniques in this geographical area.

Keywords: *Escherichia coli*, Antibiotic pattern, Triplex PCR, Genaveh shoreline.