

Housekeeping Genes Sequence Diversity Analysis of Outbreak-related Versus Sporadic Environmental *Vibrio Cholerae* Isolates in Iran

Abolfazl Dashtbani Roozbehani*¹; Bita Bakhshi²; Mohammad Reza Pourshafie¹;

1-Pasteur Institute of Iran, Tehran, Iran

2-Tarbiat Modares University, Jalal-Al-Ahmad Avenue, Tehran, Iran

dashtbani@gmail.com

Background & Objectives: *Vibrio cholerae*, the cause of cholera, is still a health concern in many developing countries. Emergence of new strains is a challenge for combating against cholera. Among molecular techniques, comparative sequence analysis of housekeeping genes accounts for an accurate and reliable typing Methods. The aim of this study was to determine genetic relatedness among Iranian clinical and environmental *V. cholerae* isolates by comparative sequence analysis of four housekeeping genes.

Methods: A collection of 24 *V. cholerae* isolates obtained from both cholera patients and surface waters were studied. Each of the four housekeeping genes (*recA*, *dnaE*, *hlyA* and *asd*) was amplified by PCR, followed by sequencing. Sequence data were analyzed and were subjected to construction of gene dendrograms using MEGA4 software.

Results: The cluster analysis of gene dendrograms differentiated our strains into 11, 10, 7 and 7 sequence types based on *recA*, *dnaE*, *asd* and *hlyA* genes, respectively. The *recA* gene showed higher discriminatory power. Clinical isolates were grouped in a same cluster, whereas environmental isolates showed diverse sequence types except for one which was grouped with clinical strains. Combination of analysis results showed that two environmental strains had high genetic similarity with clinical isolates. No relationship between serogroup and housekeeping gene sequences were found.

Conclusion: Our analysis could be used for determination of genetic relationship among *V. cholerae* isolates for efficient monitoring of *V. cholerae* in surface waters and fecal samples. Such data give insights for cholera surveillance programs.

Keywords: *Vibrio Cholerae*; Housekeeping Genes; Diversity