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**Title:** Investigation of genetic diversity of Vibrio cholerae O1 strains isolated from patients in Iran using ERIC-PCR and MAMA-PCR genotyping methods  

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**Abstract:**  
Background and objectives: Vibrio cholerae O1 is the causative agent of cholera due to production of Cholera Toxin (CT). The toxin genes (A and B subunits) are encoded within the genome of CTX Φ phage, which exists in 2 biotypes of Classic and El Tor on the basis of its genome sequence. The objective of this study was to use MAMA-PCR and ERIC-PCR methods to determine the genetic diversity of V. cholerae population collected in a 5 year study (2004 to 2009) in Iran and to investigate the ctxB and consequently integrated phage biotype diversity.  

**Materials and Methods:** Enterobacteriaceae Repetitive Intergenic Consensus Sequences–PCR (ERIC-PCR) technique was done using primers which specifically were chosen to amplify within these regions. Mismatch Amplification Mutation PCR Assay MAMA-PCR was used to detect sequence polymorphism in ctxB region between the classical and El Tor biotypes.  

**Results:** ERIC-PCR with genomic DNA of 50 V. cholerae strains yielded identical DNA fingerprint pattern with 4 amplification bands ranging from 300 to 1100 bp. The results of MAMA-PCR showed that all 50 El Tor V. cholera strains cytosine nucleotide in position 203 which is indicative of classical ctxB sequence.  

**Conclusion:** Results of MAMA-PCR revealed that Iranian El Tor strains have been infected by classical CTXΦ which is an important finding in V. cholera El Tor biotype evolution. Genotyping analysis by ERIC-PCR showed a relatively homogenous population among the isolates. This homogeneity reveals clonal dissemination of strains in different years which is of great significance in epidemiological studies in Iran and Middle East.  

**Keywords:** Vibrio cholerae, ERIC-PCR, MAMA-PCR, ctxB.  

**Presentation:** Poster