Designing and Evaluation a Multiplex PCR for Rapid and Specific Detection of Shigella flexneri 2a Isolated from Patients with Acute Bacillary Dysentery

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Background & Objectives: Shigellosis or acute bacillary dysentery as major causes of infection is prevalent in Iranian children that suffer from diarrheal. *Shigella flexneri* serotype 2a is considered as a significant concern for public health in developing or developed countries, which due to the role of this pathogen in a shigellosis endemic and mortality. In current study, a multiplex PCR (mPCR) reaction, with purpose of rapid and specific detection of *Shigella flexneri* 2a separated from patient with shigellosis, was designed and evaluated.

Methods: A total of 27 isolated of *Shigella flexneri* were collected from children with acute bacillary dysentery or gastroenteritis (inflammation digestion system), who were admitted to Taleghani, Milad and Baqiyatollah hospitals during January up to July 2011. Using bioinformatics analysis with Shigella genome sequences, we designed the flex2a-F and flex2a-R primers, which exclusively amplify specific island (she) in Shigella genome. After extraction genomic DNA, in order to identify presence serotype 2a and to determine specifity and sensitivity, the mPCR as differential methods was done.

Results: By use of biochemical and serological tests, the presence of the shigella's species in the all of the hospital's samples was verified. The results of bioinformatics analysis demonstrated the region with length of 1697 bp in *Shigella flexneri* 2a, was exclusively specific. The results of mPCR confirmed 4serotype (19.04%) of hospital's samples was belong to shigella flexneri 2a. The specifiy of mPCR (100%) was determined. The reaction sensitivity detected 85 cfu (colony forming unit).

Conclusion: The she region on shigella genome, as particular region for identification present of serotype 2a in hospital's samples is specific. Furthermore, the mPCR methods as valuable tool in epidemiological studies is more suitable and reliable.

Keywords: Shigellosis; *Shigella flexneri* 2a; Multiplex PC; Bioinformatics