How Design Primers for Iranian Genotype 1a of HCV for Full Genome Analysis

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Background & Objectives: Hepatitis caused by hepatitis C virus (HCV) has become a major emerging infectious disease problem, with an estimated 170 million people infected worldwide. Hepatitis C virus isolates have been classified into six main genotypes and a variable number of subtypes within each genotype. Analyses of the genetic relationship among genotypes and subtypes are more reliable when complete genome sequences .The high degree of sequence heterogeneity found in Hepatitis C virus (HCV) isolates, makes robust nucleic acid-based assays difficult to generate. Polymerase chain reaction based techniques, require efficient and specific primers. Generation of robust primers capable of recognizing a wide range of isolates is a difficult task. At The goal of this study was to design and making primer to amplify large PCR fragments from the genome of hepatitis C virus (HCV) isolates 1a using Iranian clinical samples.

Methods: In this study, we performed RNA extraction, ONE STEP RT- nested PCR and PCR products were detected by agarose gel. We employed in our assay the primers that cover all of genome of HCV.

Results: We have a success rate of over 95% in RT-PCR amplification. This Strategy was effective for amplifying all amplicons for genotype 1a.

Conclusion: These primers can useful for molecular, epidemiological and clinical studies of hepatitis C where samples are limited but complete virus sequence are required.

Keywords: Primer Design; HCV, Iran