



## Prevalence of Hepatitis C Virus Genotypes in Mashhad, Northeast Iran

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(Received 23 Feb 2012; accepted 11 Aug 2012)

### Abstract

**Background:** Hepatitis C is a disease with significant global impact. The distribution of hepatitis C virus (HCV) genotypes in Mashhad (the Northeast and the biggest city after the capital of Iran) is unknown. The purpose of this study was to determine the prevalence of HCV genotypes among HCV seropositive patients, and to study the relationship between types, virologic and demographic features of patients in Mashhad.

**Methods:** Three hundred and eighty-two clinical specimens obtained from HCV-infected patients referred to Ghaem Hospital in Mashhad during a period of 2009 to 2010 were selected. HCV genotype was determined by Nested PCR amplification of HCV core gene using genotype specific primers.

**Results:** Totally, 299 patients were male (79.9%). The most common HCV genotype was genotype 3a, with 150 (40%) of subjects. Genotype 1a was the other frequent genotype, with 147(39.2%) subjects. Frequency of genotypes for 1b, 5 and 2 was 41(10.9%), 13(3.4%) and 9(2.4%), respectively. Mix genotype including 1a+1b in 4 (1.04%), 1a+3a in 3 (0.8%) was found in 7 patients. Four percent out of these samples had an undetermined genotype. Among the hemophilia patient, there were 13(48.1%) genotypes as 1a, 3(11.1%) 1b and 10(37%) 3a, respectively.

**Conclusion:** The dominant HCV genotype among patients living in Mashhad was 3a. This study gives added evidence of the predominant HCV genotypes in Iran.

**Keywords:** HCV, Genotyping, Nested PCR, Iran

### Introduction

Hepatitis C infection is known as a serious health problem. It is one of the main causes of chronic viral hepatitis, and also cirrhosis and hepatocellular carcinoma in the world (1). The worldwide prevalence of hepatitis C virus (HCV) infection is estimated as 2% to 3% of the global population with approximately 200 million infected people (2). Prevention of HCV depends on an evaluation of global HCV infection distribution, assessment of

its risk factors, and determination of accelerating factors in disease progression. Several host factors such as male sex, older age at infection, long disease duration, and various viral factors such as genotype and peripheral viral load have been described to effect on disease progression. However, due to the lack of a vaccine or some form of post-exposure prophylaxis, an accurate epidemiological