Genetic diversity of HCV among various high risk populations in Iran

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Objective: To determine the patterns of distribution of HCV genotypes among high risk population in north of Iran.

Methods: A cross-sectional study was conducted on 135 HCV RNApositive high risk individuals including thalassemia, hemophilia, patients under hemodialysis and intravenous drug addicts. HCV genotypes were determined based on amplification with type-specific primers methods.

Results: Among the 187 anti-HCV positive samples, only 135 (72.2%) gave HCV-RNA positvity. Over all, the most identified HCV type was genotype 3a (51.1%) followed by 1a (27.4%), 1b (8.2%). Sixteen (11.9%) out of 135 HCV RNA-positive participants have infected with more than one genotype or subtypes as follow; 1a/1b in 11 (8.2%), 2/3a in 3 (2.2%), and 1a/1b/3a in 2 (1.5%). Stratification of participants revealed that HCV subtype 3a was more prominent in thalassemia, hemophilia and HD patients but 1a and 1b were frequent in intravenous drug addicts.

Conclusions: This study is the first report on HCV genotypes among Iranian subjects with different exposure categories resided in Mazandaran, where genotype 3a was found to be the most frequent genotype in thalassemia, hemophilia, and hemodialysis patients but not in IDAs. Since the addiction age is decreasing in Iran and a lot of addicts are IDAs, it might change the subtype pattern of HCV in general population.

Keyword: HCV, thalassemia, hemophilia