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**Prevalence of various Hepatitis C genotypes among chronic HCV patients in a private laboratory, Tehran, Iran**Solmaz Agha Amiri<sup>1</sup> and Najmeh Zarei<sup>2</sup><sup>1</sup>Danesh private laboratory, Tehran, Iran<sup>2</sup>Pasteur institute of Iran, Iran

**Background:** Hepatitis C (HCV) is a public health problem in many part of the world. Since HCV has different genotypes that showing different responses to treatment, determination of patient's HCV genotype is critical prior to the antiviral therapy. The aim of this study was to determine the prevalence of various HCV genotypes among patients who were referred to a private laboratory in Tehran.

**Material & Methods:** 100 patients with chronic Hepatitis was enrolled from 2012-2017. RNA was extracted using standard commercial kits from patient's serum. After cDNA synthesis, HCV RNA was detected using reverse transcriptase Nested-PCR (RT-Nested PCR) and then HCV genotypes were determined with restriction fragment length polymorphism (RFLP) assay.

**Results:** Out of 100 samples, 45 (45%) were positive for subtype 1a, and 41 (41%) were subtype 3a, followed by 11 (11%) genotype 1b, and genotypes 2a, 2b and 4 were 1 (1%) each. There are no mixed HCV genotypes found in the patients.

**Conclusion:** This study showed that the most frequent genotype among the patients in Tehran was 1a followed by 3a.

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