**Abstract:**

**Introduction:** A recently discovered DNA virus (SEN virus) has been assumed to be responsible for post transfusion hepatitis in humans. SEN virus is blood-borne, single-stranded, non-enveloped DNA virus. Phylogenetic analysis of the SEN virus has revealed the existence of 8 different genotypes (A-H). Two of its strains (D and H), appear to be associated with non-A-to-E hepatitis more frequently than the others. The prevalence of SEN virus in healthy individuals, including blood donors, differs markedly by geographic region. The aim of the present study was to investigate the frequency of SENV-D and SENV-H genotypes in hepatitis B and C infected individuals in Yazd province.

**Method:** Serum samples derived from 6 HIV/HCV co-infected, 50 HBV infected and 50 HCV infected individuals were examined for SENV-D and SENV-H viraemia by nested PCR. Fisher's Exact Test was used for statistical analyses.

**Results:** SENV-D was detected in 9 out of 50 (18%) HBV infected, in 5 out of 50 (10%) HCV infected. It was not detected in any of the HIV/HCV co-infected individuals. SENV-H was detected in 2 out of 6 (33.3%) HIV/HCV co-infected individuals, in 32 out of 50 (64%) HBV, and in 19 out of 50 (38%) HCV infected individuals.

**Conclusions:** Compare to SEN-D, the frequency of SEN-H was significantly (P< 0.001) higher in both HBV and HCV infected individuals. Although the number of HIV/HCV infected individuals tested were low, but the detection of only SEN-H in them confirms the higher frequency of the SEN-H genotype in the population studied.