

# Infection rates and phylogenetic analysis Of hepatitis G virus (HGV)/GB virus C (GBV-C) among Qatari blood donors

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## **Abstract**

**Background:** A new emerging nonpathogenic single stranded human RNA virus known as GBV-C/HGV was discovered in 1995. Both GBV-C virus and HCV have similar genome, but they replicate in different cell types. The incidence of GBV-C infection has been studied worldwide, however, to our knowledge; no previous studies were conducted in Qatar, thus the objectives of this study are: (i) to determine the rate of GBV-C infection in Qatar among healthy blood donors and liver-diseased patient and (ii) to determine the most predominant GBV-C genotype in Qatar. **Methods:** 755 blood plasma samples from blood bank (593) and virology section (162) at HMC were collected. RNA was extracted, reversed transcribed, and then subjected for GBV-C detection by nested PCR using primers targeting a 205 bp of the 5' hypervariable untranslated region (5'-UTR) of the GBV-C/HGV. For genotyping, the 5'-UTR PCR product were T/A cloned into pDrive plasmid. The plasmids were transformed into DH5™, and then plasmids were purified and digested by EcoRI to detect the positive clones. Plasmid were then purified and sequenced. Phylogenetic analysis was conducted by analyzing the 5'-UTR sequence from randomly picked positive clones. The resulted sequences were assembled and analyzed using CLC and MEGA5 software. **Results:** we found that HGV infection rate among healthy blood donors was 13.5 %, while in liver-diseased patient was 8.6 %. Moreover, there was no significant difference in the GBV-C infection rate among Qatari (13.3%) and Non-Qatari (14.4%) healthy donors. Sequence analysis of 25 5'-UTR PCR amplicons yielded the European genotype (genotype 2) as the most predominant in Qatar. **Conclusion:** Our results indicate that there is no correlation between GVC- infection rate and other liver-infecting viruses such as HB&CV. Not surprising, genotype 2 was also reported to be dominant in countries surrounding Qatar such as UAE and Kuwait. Finally, we think our results should benefit epidemiologists in the region and may have an impact on the blood screening policy in blood banks.