7.0 Conclusion
7.0 Conclusions/Observations

- Full-length genomes of HAV genotype IIIA strains from Indian subcontinent were sequenced for the first time.
- Nucleotide and amino acid sequence analyses of Indian strains and other genotype IIIA strains of HAV confirmed highly conserved nature of HAV genome from different geographic locations.
- Higher number of nonsynonymous changes observed in Indian strains suggested higher genomic variability within the strains from endemic region than that of low endemic region of hepatitis A.
- Phylogenetic analyses of all and nonsynonymous nucleotide positions of HAV strains representing most of the genotypes (except VI) indicated host (simian/human) specific evolution of HAV.
- Total number of nucleotide and amino acid substitutions was higher in GBS-IND strain as compared to any other IIIA strain.
- Unique and heterologous amino acid substitutions (n=4) identified in capsid region of GBS-IND strain were located in the B cell epitope region. Homology modeling approach applied to capsid proteins of HAV strains indicated a localized change in VP1 capsid protein of GBS-IND strain from positive and basic to negative and acidic suggesting a possibility of change in receptor binding specificity.
- Unique and heterologous amino acid substitutions (n=3) of GBS-IND strain were also detected within highly conserved amino acid stretches suggesting possible potential of viral genomic mutations to alter protein functions and clinical features of the disease.
- 5'NCR and VP4 regions were confirmed to be useful in diagnostic PCR due to overlapping PNI ranges and conserved nature.
- Phylogenetic analysis carried out by use of three different methods (NJ, ML and MP) identified VP3, 2A, 2C and 3D genomic regions comparable to VP1 region used as gold standard for clustering of the strains according to their genotypes and subgenotypes with high bootstrap support.
- Using Likelihood Mapping analysis, 2C region was second most suitable region for phylogenetic analysis, which has not been used for genotyping till date.