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Molecular Comparison of HEV Isolates from Sewage & Humans at Western India

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Abstract : Background: Hepatitis E virus (HEV) is a major cause of acute viral hepatitis in developing countries. It spreads feco orally mainly due to contamination of drinking water by sewage. There is limited data on the genotypic comparison of HEV isolates from sewage water and humans. The aim of this study was to identify genotype and conduct phylogenetic analysis of HEV isolates from sewage water and humans. Materials and Methods: 14 sewage water and 60 serum samples from acute sporadic hepatitis E cases (negative for hepatitis A, B, C) were tested for HEV-RNA by nested polymerase chain reaction (RTnPCR) using primers designed with in RdRp (RNA dependent RNA polymerase) region of open reading frame-1 (ORF-1). Sequencing was done by ABI prism 310. The sequences (343 nucleotides) were compared with each other and were aligned with previously reported HEV sequences obtained from GeneBank, using Clustal W software. A Phylogenetic tree was constructed by using PHYLIP version 3.67 software. Results: HEV-RNA was detected in 49/ 60 (81.67%) serum and 5/14 (35.71%) sewage samples. The sequences obtained from 17 serums and 2 sewage specimens belonged to genotype I with 85% similarity and clustering with previously reported human HEV sequences from India. HEV isolates from human and sewage in North West India are genetically closely related to each other. Conclusion: These finding suggest that sewage acts as reservoir of HEV. Therefore it is important that measures are taken for proper waste disposal and treatment of drinking water to prevent outbreaks and epidemics due to HEV.

Keywords : hepatitis E virus, nested polymerase chain reaction, open reading frame-1, nucleotidies
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