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Isolation of a cDNA from the virus responsible for enterically transmitted non-A, non-B hepatitis

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Abstract

Major epidemic outbreaks of viral hepatitis in underdeveloped countries result from a type of non-A, non-B hepatitis distinct from the parenterally transmitted form. The viral agent responsible for this form of epidemic, or enterically transmitted non-A, non-B hepatitis (ET-NANBH), has been serially transmitted in cynomolgus macaques (cynos) and has resulted in typical elevation in liver enzymes and the detection of characteristic virus-like particles (VLPs) in both feces and bile. Infectious bile was used for the construction of recombinant complementary DNA libraries. One clone, ET1.1, was exogenous to uninfected human and cyno genomic liver DNA, as well as to genomic DNA from infected cyno liver. ET1.1 did however, hybridize to an approximately 7.6-kilobase RNA species present only in infected cyno liver. The translated nucleic acid sequence of a portion of ET1.1 had a consensus amino acid motif consistent with an RNA-directed RNA polymerase; this enzyme is present in all positive strand RNA viruses. Furthermore, ET1.1 specifically identified similar sequences in complementary DNA prepared from infected human fecal samples collected from five geographically distinct ET-NANBH outbreaks. Therefore, ET1.1 represents a portion of the genome of the principal viral agent, to be named hepatitis E virus, which is responsible for epidemic outbreaks of ET-NANBH.

References

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