

Taxonomic Proposals from the ICTV “HEV-like viruses” Study Group

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Sandra Chang

2002.V099.02: To create a new family to accommodate the “HEV-like virus” genus

2002.V100.02: To name this new family *Hepeviridae*

2002.V101.02: To rename the genus “HEV-like viruses” *Hepevirus* 

2002.V102.02: To assign the *Hepevirus* genus as type genus in the family

Proposal 1: It is proposed to create a new family and assign the name *Hepeviridae*

The background of this proposal is as follows.

The previous *Caliciviridae* Study Group removed hepatitis E virus from the family *Caliciviridae*. A provisional "HEV-like Viruses" name was given to the new family.

The SG informally recommended two names *Hearviridae* or *Hepeliviridae* to the ICTV in March 2002. The EC did not support either name. *Hearviridae* is difficult to pronounce and the EC does not favor using the words 'virus-like' in any name so *Hepeliviridae* is not a good name. The EC suggested the SG consider *Hepeviridae*.

Purpose: Virions are 27-34nm, nonenveloped icosahedrons. Virion buoyant density is 1.35g/cm³ in CsCl and 1.29g/cm³ in glycerol potassium tartrate gradients. The genome is a positive sense ssRNA of approximately 7.2 kb, with a 5'cap and a 3'-poly(A) tail and three open reading frames. Phylogenetic analyses comparing hepatitis E virus (HEV) with the *Picornaviridae*, *Caliciviridae*, and *Togaviridae* suggest that, based on non-structural genes, HEV is outside of the calciviruses. HEV shows highest, but limited, amino acid similarity in its replicative enzymes with Rubella virus and alphaviruses, and with plant furoviruses and members of the family *Togaviridae*.

Summary: A new family *Hepeviridae* would be recognized.

Derivation of name: The family name was chosen to denote relationship with a disease (hepatitis E).

References:

Berke, T and Matson, DO (2000). Reclassification of the *Caliciviridae* into distinct genera and exclusion of hepatitis E virus from the family on the basis of comparative phylogenetic analysis. *Archives of Virology* 145:1421-1436.

Proposal 2: To assign the name *Hepevirus* to the genus previously named “HEV-like viruses”

Purpose: Currently there is only a single group of closely related viruses which would belong to the *Hepeviridae*.

Derivation of name: The genus name was chosen to denote relationship with a disease (hepatitis E).

References:

Balayan, MS, Andjaparidze, AG, Savinskaya, SS, Ketiladze, ES, Braginsky, DM, Savinov, AP and Poleschuk, VF (1983). Evidence for a virus in non-A, non-B hepatitis transmitted via the fecal-oral route. *Intervirology* 20:23-31.

Proposal 3: To assign hepatitis E virus as the type species of the Hepevirus genus.

Purpose: Hepatitis E virus is associated in humans with outbreaks and sporadic cases of enterically transmitted acute hepatitis.

Derivation: The name hepatitis E virus was chosen to denote the disease (hepatitis) and the group (E) of viruses that cause this disease in contrast to the A, B, C and D groups of viruses which cause other types of hepatitis and are not genetically related to HEV.

References:

Tam, AW, Smith, MM, Guerra, ME, Huang, CC, Bradley, DW, Fry, KE, and Reyes, GR(1991). Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome. *Virology* 185,120-131.

Summary:

The family Hepeviridae would be described as follows:

Family: Hepeviridae

Genus: Hepevirus

Type species: Hepatitis E virus

Species: Hepatitis E virus

Thus far all strains isolated from humans and swine appear to be serologically and genetically closely related and therefore would comprise one species. Recently, a virus has been isolated from chickens and shown to cause hepatitis in these birds. The sequence of this virus has been determined for the 4kb 3' terminal end: compared to other hepatitis E virus isolates, it shares only 47-61% amino acid and 48-60% nucleotide identity in various regions. There is not enough information available at this time to determine if it should be in a separate genus. There are also data indicating that there is a virus which infects rodents and has some serological cross-reactivity with human strains of hepatitis E virus but there is not enough information to determine how closely related it is to either the human or the avian virus. Thus, it may be necessary eventually to create one or more additional genera, but it would be premature to do it at this time.

References:

Meng, X, Halbur, PG, Shapiro S, Govindarajan, S, Bruna, JD, Mushahwar, IK, Purcell, RH, Emerson, SU (1998). Genetic and experimental evidence for cross-species infection by swine hepatitis E virus. *J Virol* 72:9714-9721.

Haqshenas, G, Shivaprasad, HL, Woolcock, PR, Read, DH and Meng, XJ (2001). Genetic identification and characterization of a novel virus related to human hepatitis E virus from chickens with hepatitis-splenomegaly syndrome in the United States. *J Gen Virology* 82:2449-2462.