

# Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Genus in an existing Family

Code <sup>†</sup>	<input type="text" value="2008.001V"/>	To create a new genus in the family*	<input type="text" value="Picornaviridae"/>
Code <sup>†</sup>	<input type="text" value="2008.002V"/>	To name the new genus*	<input type="text" value="Avihepatovirus"/>
Code <sup>†</sup>	<input type="text" value="2008.003V"/>	To create the species and designate as the type species of the new genus*	<input type="text" value="Duck hepatitis A virus"/>
Code <sup>†</sup>	<input type="text" value="2008.004V"/>	To assign the following species to the new genus*:	<input type="text" value="Duck hepatitis A virus"/>
Code <sup>†</sup>	<input type="text"/>	To designate the following as tentative species in the new genus*:	<input type="text" value="None"/>

<sup>†</sup> Assigned by ICTV officers

\* repeat these lines and the corresponding arguments for each genus created in the family

## Author(s) with email address(es) of the Taxonomic Proposal

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## Old Taxonomic Order

Order  
Family *Picornaviridae*  
Genus  
Type Species  
Species in the Genus  
Tentative Species in the Genus  
Unassigned Species in the family

## New Taxonomic Order

Order  
Family *Picornaviridae*  
Genus *Avihepatovirus*  
Type Species *Duck hepatitis A virus*  
Species in the Genus *Duck hepatitis A virus*  
Tentative Species in the Genus  
Unassigned Species in the family

## ICTV-EC comments and response of the SG

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### Argumentation to choose the type species in the genus

*Duck hepatitis A virus* is the only species in the genus.

The species name *Duck hepatitis A virus* is in line with some other existing picornavirus nomenclature, e.g. *Equine rhinitis A virus* (genus *Aphthovirus*) and *Equine rhinitis B virus* (genus *Erbovirus*). Within the family *Hepadnaviridae* the species (human) *Hepatitis B virus* is in the genus *Orthohepadnavirus* along with the species *Woolly monkey hepatitis B virus*, *Ground squirrel hepatitis virus* and *Woodchuck hepatitis virus* while the species *Duck hepatitis B virus* and *Heron hepatitis B virus* are both in the genus *Avihepadnavirus*. We feel that the name “duck hepatitis” should be maintained in the form of *Duck hepatitis A virus*. The discovery of DHV-1 (c.1949) pre-dates that of hepatitis B virus (c.1980).

### Species demarcation criteria in the genus

Not applicable – genus comprised of a single species.

### List of Species in the created genus

*Duck hepatitis A virus*

### List of Tentative Species in the created genus

None

## Argumentation to create a new genus:

The genome sequences of 15 duck hepatitis virus (DHV) type 1 isolates have recently been determined (Kim *et al.*, 2006; Tseng *et al.*, 2006; Ding and Zhang, 2007; Zhang *et al.*, unpublished; Zhang and Guo, unpublished; Luo *et al.*, unpublished; see [http://www.picornaviridae.com/unassigned/avian/dhv-1\\_seq.htm](http://www.picornaviridae.com/unassigned/avian/dhv-1_seq.htm)). The sequences are all closely related (e.g. 92.5-99.4% nucleotide identity in the VP1 gene). The relationship of DHV-1 to other picornaviruses is shown in Fig. 1. Comparative sequence analyses have shown that DHV-1 possesses a typical picornavirus genome organization apart from the putative possession of between one and three putative 2A genes. The putative 2A1 protein of DHV-1 is related to the 2A protein of aphthoviruses, cardioviruses, erboviruses and teschoviruses. This protein is involved in an unusual proteolytic activity at the conserved NPG↓P sequence motif at its own carboxy-terminus. However, this peptide sequence (20 residues long) may be the carboxy-terminus of VP1 and not be cleaved, as is probably the case with the putative 2A1 of Ljungan virus (genus *Parechovirus*) (Johansson *et al.*, 2003). The DHV-1 putative 2A2 protein (161 residues long) is not related to any known picornavirus protein, but has sequence similarities with the AIG1 protein of plants and gimap5 protein in mammals both of which share an NTP-binding motif (GxxGxGKS) with DHV-1. The putative 2A3 protein (124 residues long) of DHV-1 is related to the 2A proteins of avian encephalomyelitis virus, Aichi virus, bovine kobuvirus, human parechovirus (HPeV) and the 2A2 protein of Ljungan virus (LV) and contains an H-box/NC domain similar to the H-rev107 family of proteins. It is also possible that 2A2 and 2A3 are a single multi-domain protein. The percentage identity of the polyprotein amino acid sequence of DHV-1 to all other picornavirus is less than 30%. The percentage identity of the amino acid sequence at 3D region of DHV-1 with LV and HPeV-1 is only 38.6% and 36.6%, respectively, and less than 30% with all other picornaviruses. Like parechoviruses and kobuviruses, the DHV-1 capsid polypeptide VP0 does not appear to be proteolytically cleaved into VP4 and VP2. The DHV-1 internal ribosome entry site (IRES) has been shown to be related to that of a number of flavi- (e.g. hepatitis C virus) and picornaviruses (e.g. avian encephalomyelitis virus) (Hellen and de Breyne, 2007). Phylogenetic and evolutionary analysis reveals DHV-1 to form a new branch of the *Picornaviridae* and it has been proposed that DHV-1 should be assigned to a new picornavirus genus (Kim *et al.*, 2006; Tseng *et al.*, 2006). Additionally, two new DHV's have recently been described which are both serologically distinct from DHV-1, although they have not been compared with each other (Tseng and Tsai, 2007; Kim *et al.*, unpublished). Analysis of the complete genomes of both these viruses suggest that they would be classified in the same species as DHV-1 but as distinct (sero)types (Fig. 2). Note that recent nucleotide sequence data has shown that DHV-2 (already renamed duck astrovirus 1; Gough *et al.*, 1984, 1985) and DHV-3 (currently a candidate picornavirus; Haider and Calnek, 1979) are both astroviruses (N.J. Knowles, unpublished data).

## Origin of the proposed genus name

*Avihepatovirus* – from avian and liver (Greek hepato-, from hepar, hepat-, liver;)

## References

- Ding, C. and Zhang, D. (2007). Molecular analysis of duck hepatitis virus type 1. *Virology* 361: 9-17.
- Gough, R.E., Collins, M.S., Borland, E. and Keymer, L.F. (1984). Astrovirus-like particles associated with hepatitis in ducklings. *Vet Rec.* 114: 279.
- Gough, R.E., Borland, E.D., Keymer, I.F. and Stuart, J.C. (1985). An outbreak of duck hepatitis type II in commercial ducks. *Avian Pathol.* 14: 227-236.
- Haider, S.A, and Calnek, B.W. (1979). In vitro isolation, propagation, and characterization of duck hepatitis virus type III. *Avian Dis.* 23: 715-729.
- Hellen, C.U. and de Breyne, S. (2007). A distinct group of hepacivirus/pestivirus-like internal ribosomal entry sites in members of diverse picornavirus genera: evidence for modular exchange of functional noncoding RNA elements by recombination. *J. Virol.* 81: 5850-5863.
- Johansson, E.S., Niklasson, B., Tesh, R.B., Shafren, D.R., Travassos da Rosa, A.P. and Lindberg, A.M. (2003). Molecular characterization of M1146, an American isolate of Ljungan virus (LV) reveals the presence of a new LV genotype. *J. Gen. Virol.* 84: 837-844.
- Kim, M.C., Kwon, Y.K., Joh, S.J., Lindberg, A.M., Kwon, J.H., Kim, J.H. and Kim, S.J. (2006). Molecular analysis of duck hepatitis virus type 1 reveals a novel lineage close to the genus *Parechovirus* in the family *Picornaviridae*. *J. Gen. Virol.* 87: 3307-3316.
- Kim, M.C., Kwon, Y.K. and Joh, S.J. Recent Korean isolates of duck hepatitis virus reveal the presence of a new geno- and serotype comparing to duck hepatitis virus type 1. Unpublished.
- Tseng, C.-H. and Tsai, H.-J., (2007). Molecular characterization of a new serotype of duck hepatitis virus, *Virus Res.* 126: 19-31.
- Tseng, C.H., Knowles, N.J. and Tsai, H.J. (2007). Molecular analysis of duck hepatitis virus type 1 indicates that it should be assigned to a new genus. *Virus Res.* 123: 190-203. Epub 2006 Oct 25.

## Annexes:

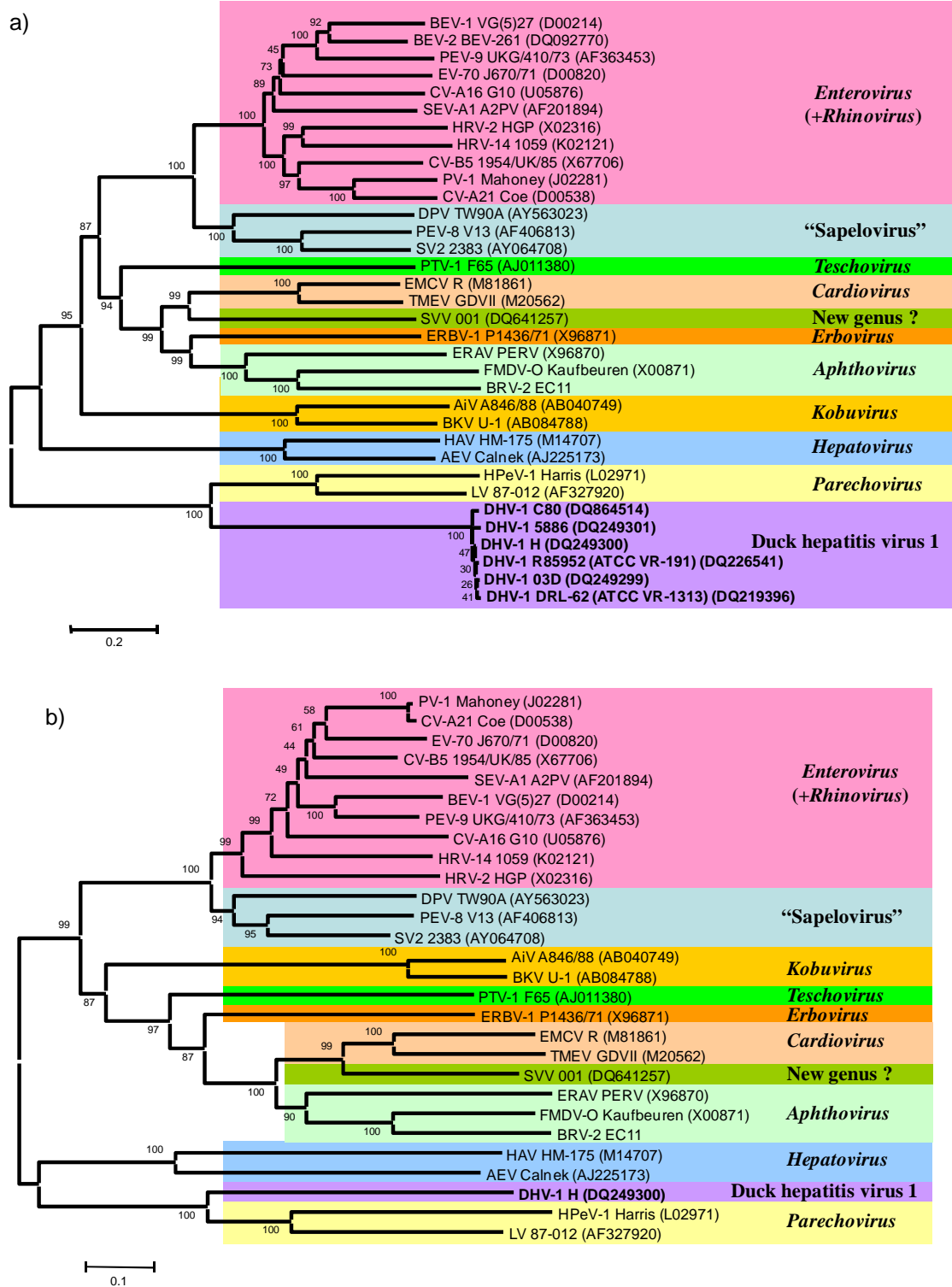


Fig. 1. Mid-point-rooted Neighbor-joining trees showing the relationships between duck hepatitis virus 1 and other picornaviruses. a) P1 capsid; b) 3D<sup>pol</sup>.

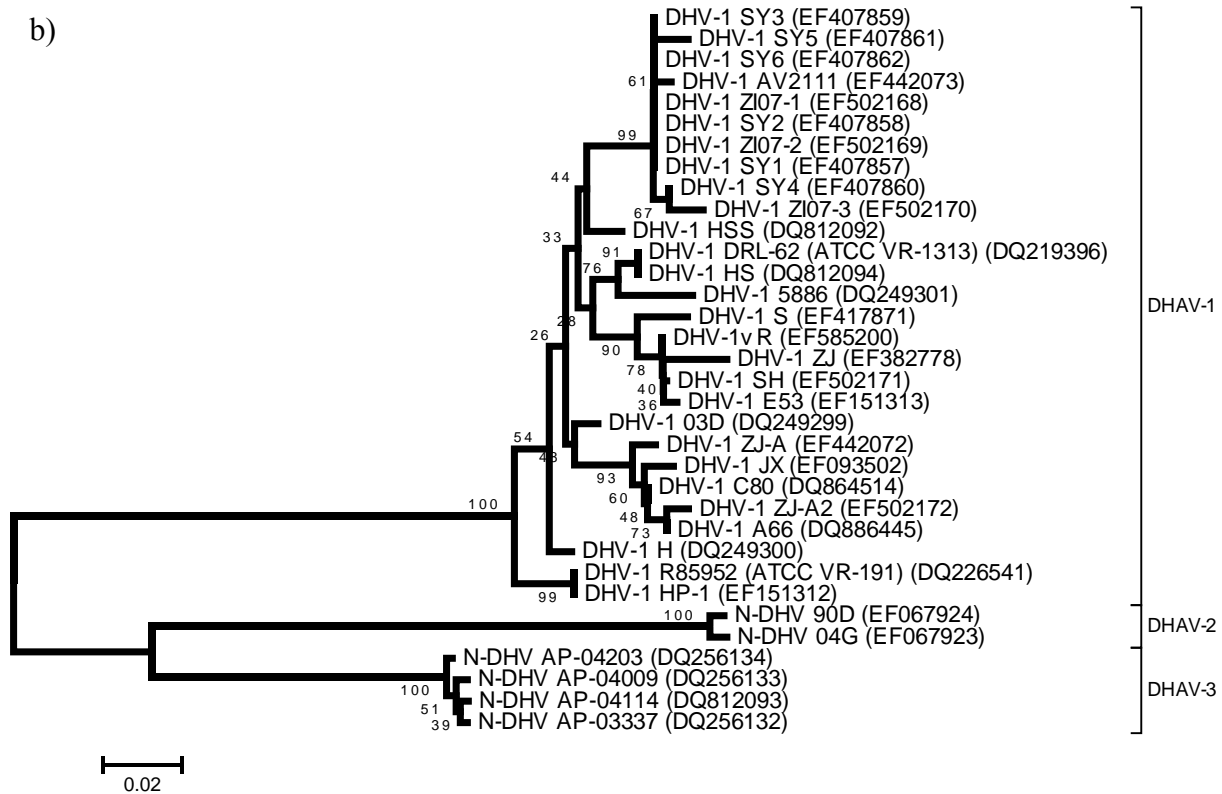
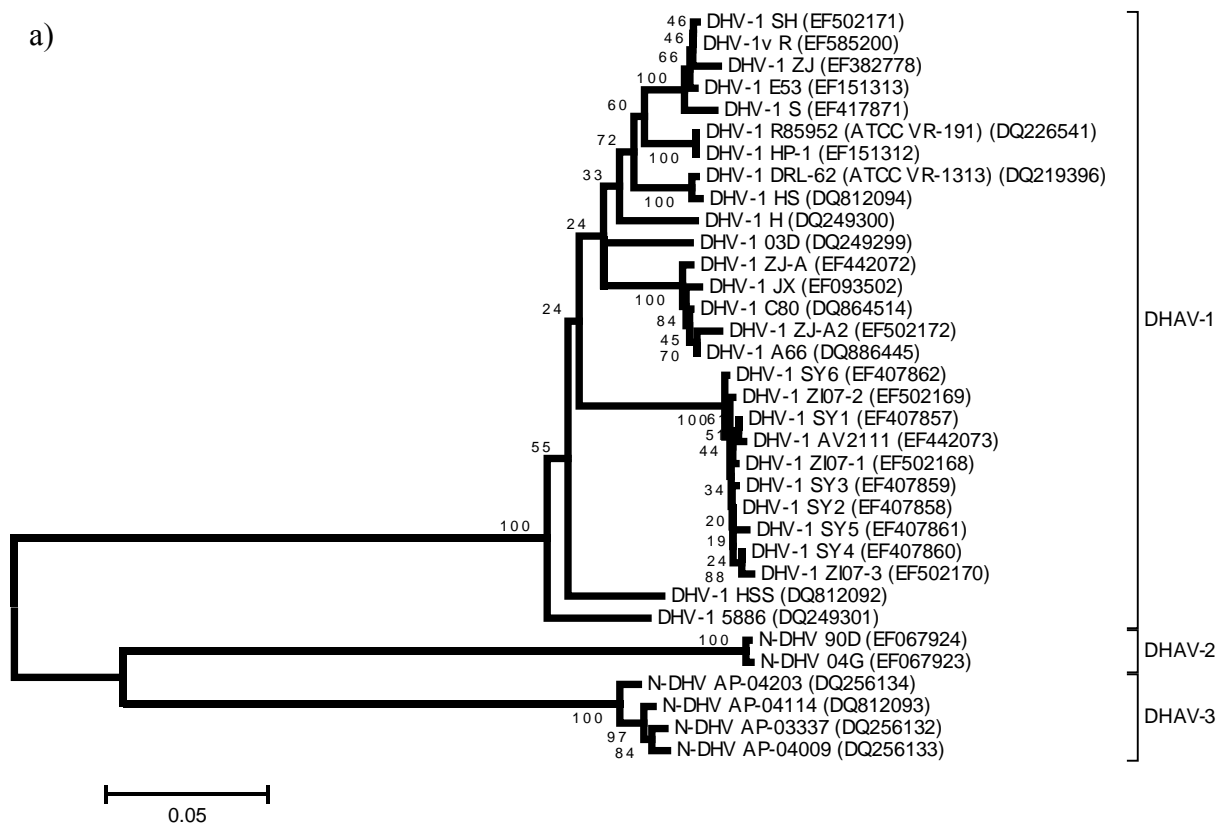


Fig. 2. Mid-point-rooted Neighbor-joining trees showing the relationships between three genotypes (serotypes?) of duck hepatitis virus proposed to form a single species, *Duck hepatitis A virus*, in a new genus *Avihepatovirus*. a) VP1 nucleotide sequences; b) VP1 amino acid sequences. DHAV, duck hepatitis A virus.