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

Code†	**2007.097V**	To create a new genus in the family*	***Picornaviridae***
Code†	**2007.098V**	To name the new genus*	***Tremovirus***
Code†	**2007.099V**	To create the species and designate as the type species of the new genus*	***Avian encephalomyelitis virus***
Code†	**2007.100V**	To designate the following as species of the new genus*:	***Avian encephalomyelitis virus*** (a species formerly named "avian encephalomyelitis-like viruses", a tentative member of the genus ***Hepatovirus***)
Code†		To designate the following as tentative species in the new genus*:	**None**

† 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	***Hepatovirus***
Type Species	***Hepatitis A virus***
Species in the Genus	***Hepatitis A virus***
Tentative Species in the Genus	**"Avian encephalomyelitis-like viruses"**
Unassigned Species in the family	

New Taxonomic Order

Order	
Family	***Picornaviridae***
Genus	***Tremovirus***
Type Species	***Avian encephalomyelitis virus***
Species in the Genus	***Avian encephalomyelitis virus***
Tentative Species in the Genus	
Unassigned Species in the family	

ICTV-EC comments and response of the SG

Argumentation to choose the type species in the genus

Avian encephalomyelitis virus is the only species in the genus.

Species demarcation criteria in the genus

Not applicable – genus comprised of a single species.

List of Species in the created genus

Avian encephalomyelitis virus

List of Tentative Species in the created genus

None

Argumentation to create a new genus:

One of the rationales for the re-classification of avian encephalomyelitis virus (AEV) follows from a need to have some "rules/guidelines" for inclusion of a new picornavirus in an existing genus (or creation of a new genus). The Study group has developed a preliminary list of simple rules for this purpose:

1) The Leader, 2A, 2B and 3A polypeptides would normally be expected to be homologous between members of a genus.
2) Members of a genus should normally share a structurally homologous internal ribosome entry site (IRES) (i.e. the same IRES type). This rule may not apply if rule 1 is true. [Note: Members of different genera may share the same IRES type.]
3) Members of a genus should normally share phylogenetically related P1, P2 and P3 genome regions, each sharing >40%, >40% and >50% amino acid identity, respectively.

Currently avian encephalomyelitis virus (AEV) is a tentative member of the genus *Hepatovirus* and only has a provisional species name, "Avian encephalomyelitis-like viruses". The Study Group feels that AEV has enough distinctive genome features to allow its classification in a novel genus:

i) AEV possesses a HCV-like IRES (Hellen and de Breyne, 2007) distinct from that of HAV. HAV has an IRES which is unique amongst the picornaviruses (Brown *et al*., 1994).
ii) AEV possesses a 2A distinct from HAV. The 2A protein of AEV is a member of the H-rev107 family of proteins involved in the control of cell proliferation (Hughes and Stanway, 2000). Similar 2A proteins are found in members of the genera *Parechovirus* and *Kobuvirus* (Hughes and Stanway, 2000) and a newly sequenced unassigned picornavirus, duck hepatitis virus (Kim *et al*., 2006; Tseng *et al*., 2007), but not in hepatitis A virus. The 2A of HEV is thought to inhibit cap-dependent gene expression by an unknown mechanism (Maltese *et al*., 2000).
iii) AEV has a 2B protein which is very different and possibly non-homologous to that of HAV.
iv) AEV and HAV have 3A polypeptides which share little primary sequence identity; however, both (in common with all picornaviruses) have a predicted transmembrane alpha-helix.
v) The percentage amino acid identities between AEV and HAV in the P1, P2 and P3 regions are 49.2, 28.0 and 37.3, respectively (Marvil *et al*., 1999). Only the P1 region exceeds the values in the new Study Group guidelines.

The complete genome sequences of three AEV strains have now been determined: Calnek (AJ225173; Marvil *et al*., 1999), L2Z-China (AY275539) and Van Roekel (AY517471); all are closely related and confirm the novel characteristics of the AEV genome.

The relationship of AEV to the other picornaviruses is shown in Fig. 1.

Origin of the proposed genus name

Tremovirus is from an alternative name given to avian encephalomyelitis virus, "epidemic tremor".

References

Brown, E.A., Zajac, A.J. and Lemon, S.M. (1994). In vitro characterization of an internal ribosomal entry site (IRES) present within the 5' nontranslated region of hepatitis A virus RNA: comparison with the IRES of encephalomyocarditis virus. J. Virol. 68: 1066-1074.

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.

Hughes, P.J. and Stanway, G. (2000). The 2A proteins of three diverse picornaviruses are related to each other and to the H-rev107 family of proteins involved in the control of cell proliferation. J. Gen. Virol. 81: 201-207.

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.

Maltese, E., Bucci, M., Macchia, S., Latorre, P., Pagnotti, P., Pierangeli, A. and Pérez Bercoff, R. (2000). Inhibition of cap-dependent gene expression induced by protein 2A of hepatitis A virus. J. Gen. Virol. 81: 1373-1381.

Marvil, P., Knowles, N.J., Mockett, A.P.A., Britton, P., Brown, T.D.K. and Cavanagh, D. (1999). Avian encephalomyelitis virus is a picornavirus and is most closely related to hepatitis A virus. J. Gen. Virol. 80: 653-662.

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:

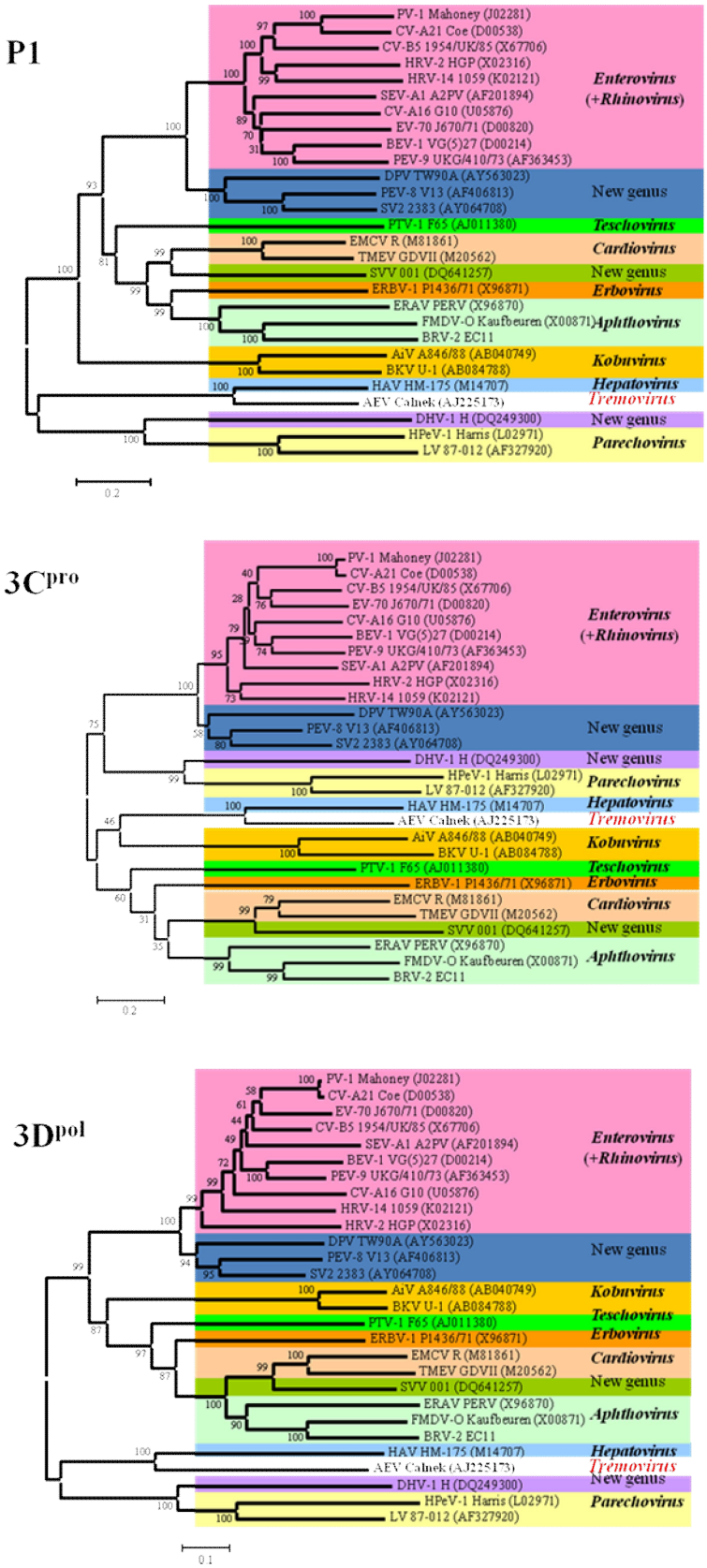

Fig. 1. Mid-pointed rooted Neighbor-joining trees showing the relationship of avian encephalomyelitis virus (AEV) to other picornaviruses in the P1 (capsid), 3C protease and 3D polymerase.