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

Code†	**2007.093V**	To create a new genus in the family*	***Picornaviridae***
Code†	**2007.094V**	To name the new genus*	***Senecavirus***
Code†	**2007.095V**	To create the species and designate as the type species of the new genus*	***Seneca Valley virus***
Code†	**2007.096V**	To designate the following as species of the new genus*:	***Seneca Valley virus***
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

Nick Knowles (nick.knowles@bbsrc.ac.uk) representing the *Picornaviridae* Study Group.

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 ***Senecavirus***
Type Species ***Seneca Valley virus***
Species in the Genus ***Seneca Valley 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

Seneca Valley 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

Seneca Valley virus

List of Tentative Species in the created genus

None

Argumentation to create a new genus:

The complete genome sequence of Seneca Valley virus (SVV) has been determined (Knowles and Hallenbeck, 2005; Hales *et al*., 2007; DQ641257) and shown to be most closely related to the *Cardiovirus* genus in the $P1^{cap}$ (Fig. 1), 2C, $3C^{pro}$ and $3D^{pol}$ (Fig. 2) genome regions. However, in other genome areas, the 5' UTR (IRES), Leader, 2B and 3A, SVV is very different to all other picornaviruses (no detectable similarity on database searches). The SVV 2A is a short peptide with a predicted ribosome-skipping mechanism characterized by a NPG↓P motif similar to that found the aphthoviruses, erboviruses and teschoviruses and at the carboxy-terminus of the larger 2A of cardioviruses. The larger 2A of cardioviruses, lacking in SVV, inhibits cap-dependent mRNA translation (Aminev *et al*., 2003a) and cellular mRNA transcription (but not rRNA transcription; Aminev *et al*., 2003b). The SVV IRES is predicted to be related to that of hepatitis C virus (57% nt identity), porcine teschoviruses, avian encephalomyelitis virus, duck hepatitis virus 1 and members of a newly proposed picornavirus genus (which includes simian virus 2, porcine enterovirus 8 and duck picornavirus TW90A) (Hellen and de Breyne, 2007); this is very different to the cardiovirus type II IRES, which is similar to that of aphthoviruses (Jang *et al*., 1988). The cardiovirus leader polypeptide binds zinc, is phosphorylated during infection and plays a role in the regulation of viral genome translation (Dvorak et al., 2001), while the Leader of the aphthoviruses and erboviruses is a papain-like cysteine proteinase (Hinton *et al*., 2002). The SVV leader polypeptide lacks the catalytic residues necessary for proteolytic activity and does not contain either a zinc-finger motif [C-x-H-x(6)-C-x(2)C] in the leader amino-terminal region or a tyrosine phosphorylation motif [K-x(2)-E-x(2)-Y] approximately 14 residues downstream, possibly indicating a function distinct from that of both aphthoviruses and cardioviruses. SVV was first isolated as a cell culture contaminant, but has since been found in pigs throughout the United States (Knowles *et al*., 2006). There is no association with disease in pigs. In summary, although SVV is related to the cardioviruses in some genome regions, it is radically different in three proteins and the IRES. The Study Group feels that these differences are too large, following precedent, to permit SVV to be classified as a cardiovirus. It is necessary therefore to create a new genus.

Origin of the proposed genus name

Senecavirus is from the type species *Seneca Valley virus*.

References

Aminev, A.G., Amineva, S.P. and Palmenberg, A.C. (2003a). Encephalomyocarditis viral protein 2A localizes to nucleoli and inhibits cap-dependent mRNA translation. Virus Res. 95: 45-57.

Aminev, A.G., Amineva, S.P. and Palmenberg AC. (2003b). Encephalomyocarditis virus (EMCV) proteins 2A and 3BCD localize to nuclei and inhibit cellular mRNA transcription but not rRNA transcription. Virus Res. 95: 59-73.

Dvorak, C.M., Hall, D.J., Hill, M., Riddle, M., Pranter, A., Dillman, J., Deibel, M. and Palmenberg, A.C. (2001). Leader protein of encephalomyocarditis virus binds zinc, is phosphorylated during viral infection, and affects the efficiency of genome translation. Virology 290: 261-271.

Hales, L.M., Knowles, N.J., Xu, L., Hay, C., Police, S.R. and Hallenbeck, P.L. (2007). Complete genome sequence analysis of Seneca Valley virus-001, a novel oncolytic picornavirus. Manuscript submitted to Journal of General Virology.

Hellen, C.U.T. 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.

Hinton, T.M., Ross-Smith, N., Warner, S., Belsham, G.J. and Crabb, B.S. (2002). Conservation of L and 3C proteinase activities across distantly related aphthoviruses. J Gen Virol. 83: 3111-3121.

Jang, S.K., Krausslich, H.G., Nicklin, M.J., Duke, G.M., Palmenberg, A.C. and Wimmer, E. (1988). A segment of the 5' nontranslated region of encephalomyocarditis virus RNA directs internal entry of ribosomes during *in vitro* translation. J. Virol. 62: 2636–2643.

Knowles, N.J. and Hallenbeck, P.L. (2005). A new picornavirus is most closely related to cardioviruses. EUROPIC 2005: XIIIth Meeting of the European Study Group on the Molecular Biology of Picornaviruses, Lunteren, The Netherlands, 23-29th May 2005. Abstract A14.

Knowles, N.J., Hales, L.M., Jones, B.H., Landgraf, J.G., House, J.A., Skele, K.L., Burroughs, K.D. and Hallenbeck, P.L. (2006). Epidemiology of Seneca Valley virus: identification and characterization of isolates from pigs in the United States. Northern Lights EUROPIC 2006: XIVth Meeting of the European Study Group on the Molecular Biology of Picornaviruses, Saariselkä, Inari, Finland, 26th November-1st December 2006. Abstract G2.

Annexes:

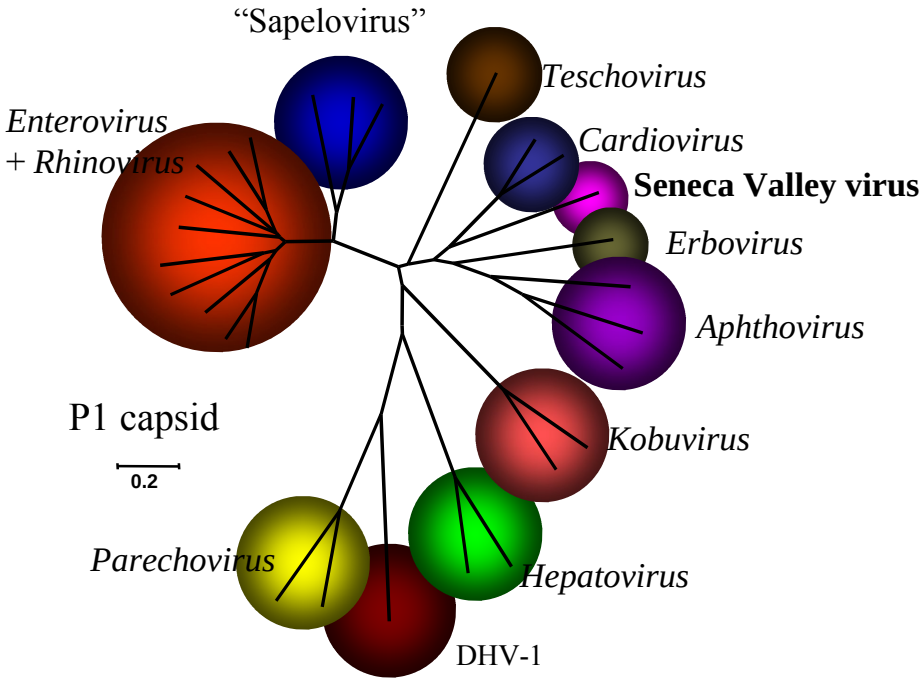

Fig. 1. Unrooted Neighbor-joining tree showing the relationships between picornaviruses in the P1 capsid region. All genus branches are supported by 99-100% bootstrap values based on 1000 pseudo-replicates.

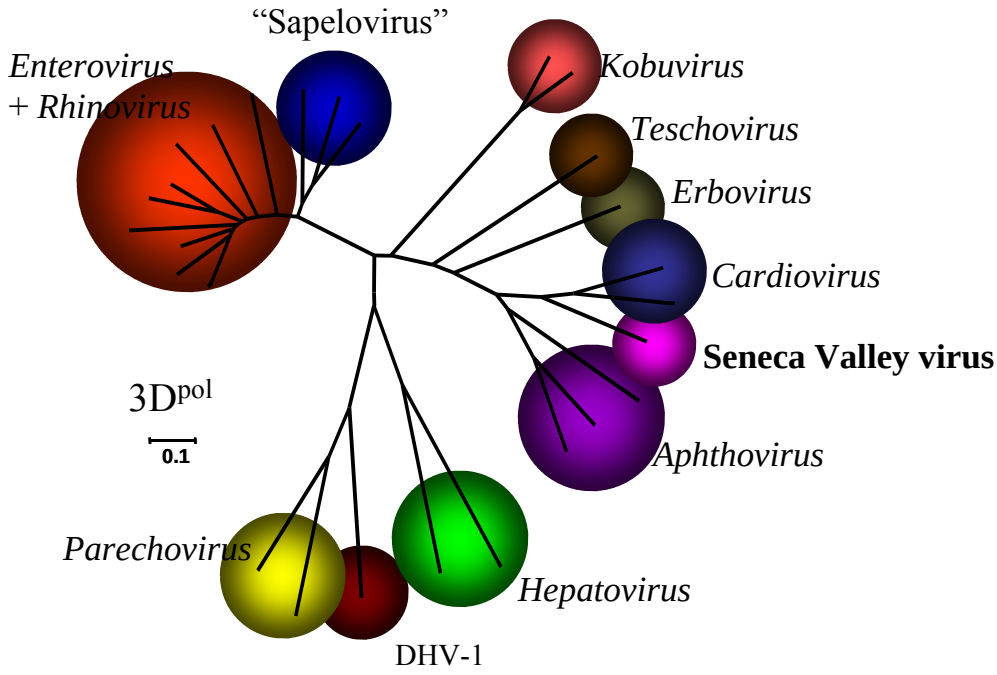

Fig. 2. Unrooted Neighbor-joining tree showing the relationships between picornaviruses in the 3D polymerase region. All genus branches are supported by 99-100% bootstrap values based on 1000 pseudo-replicates.