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

Code[†] **2007.103V**    To create a new genus in the family*    *Picornaviridae*

Code[†] **2007.104V**    To name the new genus*    *Sapelovirus*

Code[†] **2007.105V**    To designate the species    *Porcine sapelovirus*
as the type species of the new genus*

Code[†] **2007.106V**    To create the following species and assign to the new genus*:

> *Simian sapelovirus* (Simian virus 2 and related viruses)
> *Avian sapelovirus* (Duck picornavirus TW90A)

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** | |
| **Type Species** | |
| **Species in the Genus** | |
| **Tentative Species in the Genus** | |
| **Unassigned Species in the family** | |

## New Taxonomic Order

| | |
|---|---|
| **Order** | |
| **Family** | *Picornaviridae* |
| **Genus** | *Sapelovirus* |
| **Type Species** | *Porcine sapelovirus* |
| **Species in the Genus** | *Porcine sapelovirus* |
| | *Simian sapelovirus* |
| | *Avian sapelovirus* |
| **Tentative Species in the Genus** | none |
| **Unassigned Species in the family** | none |

## ICTV-EC comments and response of the SG

## Argumentation to choose the type species in the genus

*Porcine sapelovirus* (formerly *Porcine enterovirus A*) is a ubiquitous virus of pigs first recognized in the late 1950's. It is easily grown in cell culture and available for study anywhere in the world.

## Species demarcation criteria in the genus

The three sapelovirus species may be distinguished by i) different host species; and ii) sequence diversity. For example in the VP1 gene there is less than 50% amino acid identity between the species (Table 1; Fig. 1). The simian "sapeloviruses" (which probably belong to three [sero]types) have probably undergone some complicated recombination events as can be seen from a comparison of sequences in different genome regions (Figs. 1 and 2).

## List of Species in the created genus

*Porcine sapelovirus* (formerly *Porcine enterovirus A*; see accompanying proposal)
*Simian sapelovirus* (Simian virus 2 and related viruses)
*Avian sapelovirus* (Duck picornavirus TW90A)

## List of Tentative Species in the created genus

## Argumentation to create a new genus:

The complete genome sequences of three entero-like viruses have been determined, porcine enterovirus 8 (PEV-8) (currently classified with the enterovirus species *Porcine enterovirus A*), simian virus 2 (SV2) (an unassigned member of the genus *Enterovirus*) and an unclassified duck picornavirus (DPV) have been determined (Krumbholtz *et al*., 2002; Oberste *et al*., 2003; Tseng and Tsai, unpublished). These three viruses are related to each other (clustering together phylogenetically) (Figs. 3 and 4) and broadly resemble the enteroviruses. However, they are distinct for a number of reasons: i) they are all predicted to share a type IV (hepatitis C virus-like) internal ribosome entry site (IRES) (Hellen and de Breyne, 2007); ii) possess a Leader polypeptide; and iii) have very divergent 2A, 2B and 3A sequences such that cannot be directly compared with the same enterovirus proteins. Genetic distances from the enteroviruses in the $P1^{cap}$, 2C, $3C^{pro}$ and $3D^{pol}$ regions are large (31-37%; 35-45%, 39-52%, 52-58%, respectively).

## Origin of the proposed genus name

*Sapelovirus*, sigla from **S**imian, **A**vian and **P**orcine **E**ntero-**L**ike viruses.

## References

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.

Kaku, Y., Sarai, A. and Murakami, Y. (2001). Genetic reclassification of porcine enteroviruses. J. Gen. Virol. 82: 417-424.

Krumbholz, A., Dauber, M., Henke, A., Birch-Hirschfeld, E., Knowles, N.J., Stelzner, A. and Zell, R. (2002). Sequencing of porcine enterovirus groups II and III reveals unique features of both virus groups. J. Virol. 76: 5813-5821.

Oberste, M.S., Maher, K. and Mark A. Pallansch, M. (2003). Genomic evidence that simian virus 2 and six other simian picornaviruses represent a new genus in *Picornaviridae*. Virology 314: 283-293.

Tseng, C.H. and Tsai, H.J. Sequence analysis of a duck picornavirus isolate indicates that it together with porcine enterovirus type 8 and simian picornavirus type 2 should be assigned a new picornavirus genus. Unpublished.

# Annexes:

Table 1. Percentage amino acid sequence identities between the VP1 sequences of simian and porcine sapeloviruses.

| | SV2 | SV16 | SV45 | SV18 | SV44 | SV42 | SV49 | PEV-8 Po-5116 | PEV-8 16-S-X | PEV-8 26-T-XII | PEV-8 Sek 1562/98 | PEV-8 V13 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SV2 | 100* | 72 | 72 | 70 | 68 | 69 | 53 | 45 | 43 | 45 | 45 | 44 |
| SV16 | 72 | 100 | 92 | 84 | 83 | 86 | 51 | 48 | 46 | 47 | 48 | 47 |
| SV45 | 72 | 92 | 100 | 84 | 83 | 87 | 52 | 46 | 45 | 46 | 46 | 45 |
| SV18 | 70 | 84 | 84 | 100 | 96 | 86 | 49 | 47 | 46 | 47 | 47 | 45 |
| SV44 | 68 | 83 | 83 | 96 | 100 | 85 | 50 | 47 | 47 | 48 | 48 | 46 |
| SV42 | 69 | 86 | 87 | 86 | 85 | 100 | 51 | 45 | 45 | 46 | 46 | 46 |
| SV49 | 53 | 51 | 52 | 49 | 50 | 51 | 100 | 46 | 47 | 46 | 46 | 48 |
| PEV-8 Po-5116 | 45 | 48 | 46 | 47 | 47 | 45 | 46 | 100 | 82 | 79 | 95 | 82 |
| PEV-8 16-S-X | 43 | 46 | 45 | 46 | 47 | 45 | 47 | 82 | 100 | 86 | 83 | 92 |
| PEV-8 26-T-XII | 45 | 47 | 46 | 47 | 48 | 46 | 46 | 79 | 86 | 100 | 81 | 88 |
| PEV-8 Sek 1562/98 | 45 | 48 | 46 | 47 | 48 | 46 | 46 | 95 | 83 | 81 | 100 | 82 |
| PEV-8 V13 | 44 | 47 | 45 | 45 | 46 | 46 | 48 | 82 | 92 | 88 | 82 | 100 |

* green background indicates an 80% cutoff.
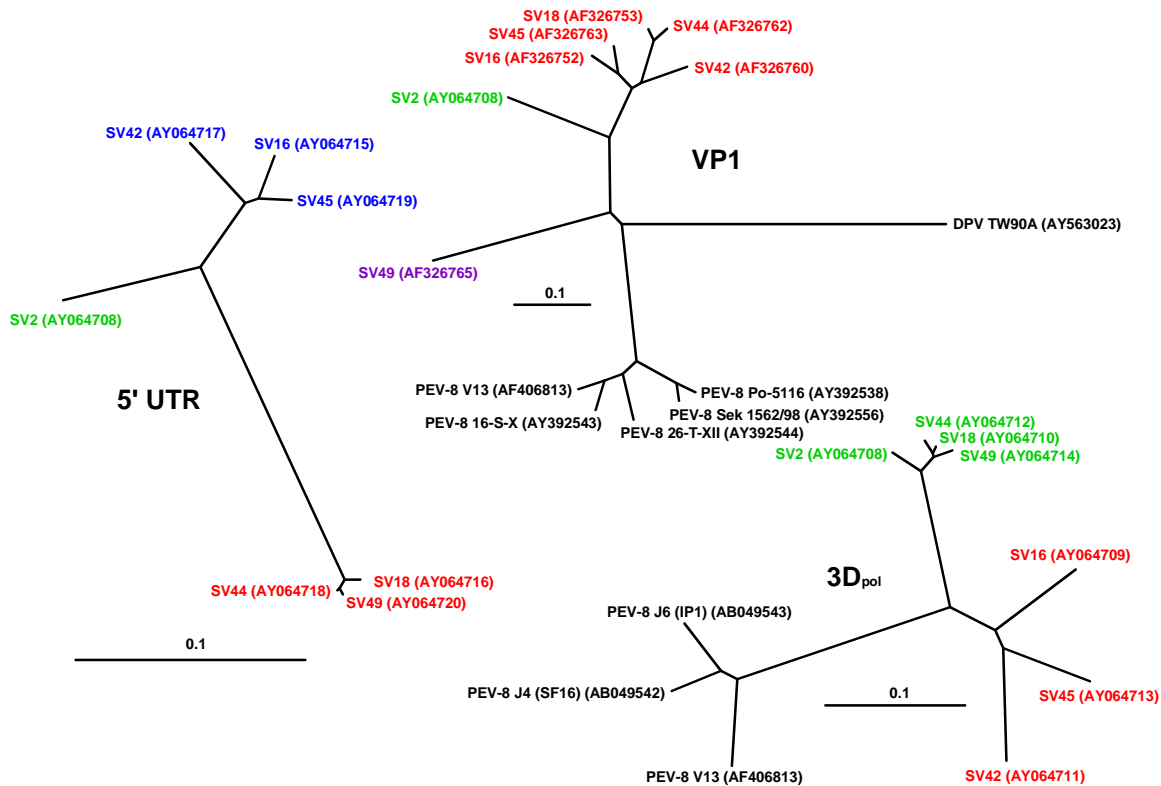


Fig. 1. Unrooted Neighbor-joining trees showing the relationships between simian sapeloviruses in the 5' UTR, VP1 (aa) and 3D$^{pol}$ (aa) regions. Porcine enterovirus 8 sequences are shown on the VP1 and 3D trees and additionally duck picornavirus TW90A is shown on the VP1 tree.
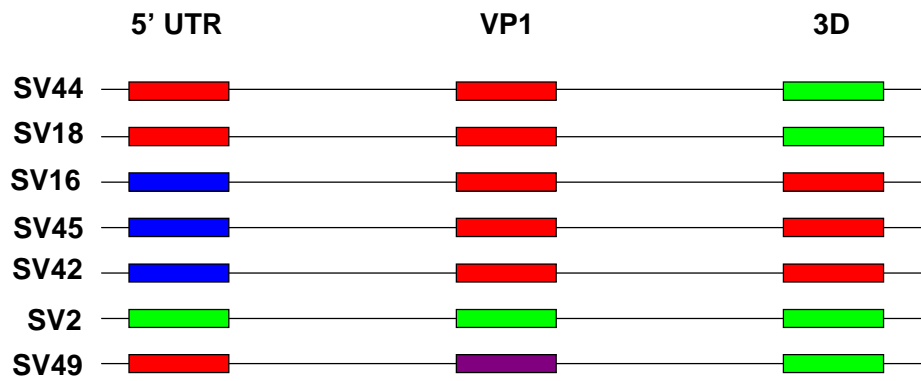
Fig. 2. Relationships between different genome regions of simian "sapeloviruses". Colours indicate related sequences (see Fig. 1).
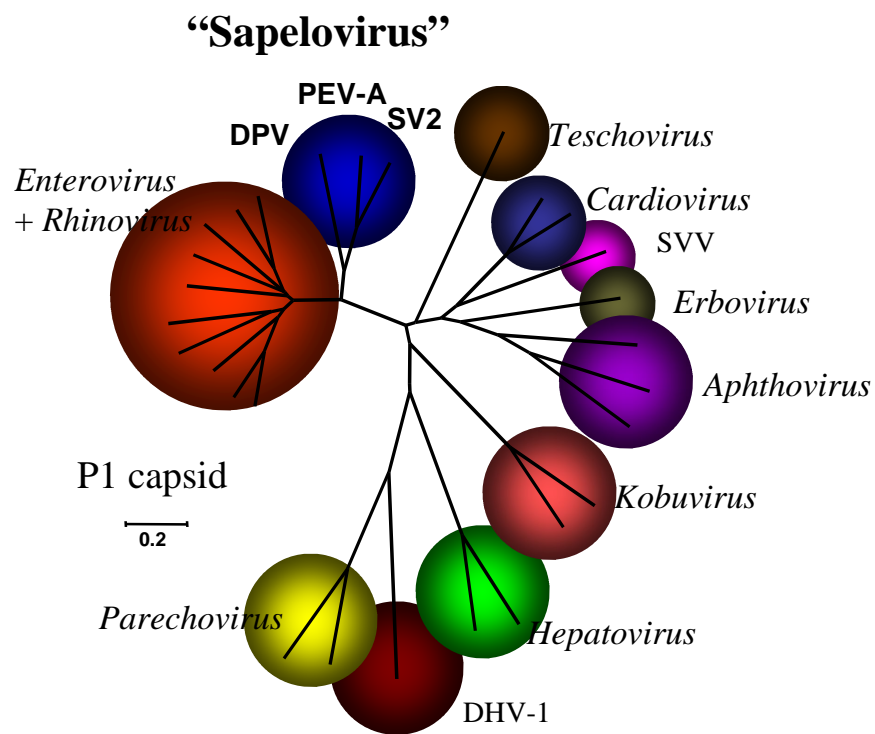


Fig. 3. Unrooted Neighbor-joining tree showing the relationships between picornaviruses in the P1 capsid region. All genus branches are supported by 99-100% bootstrap values based on 1000 pseudo-replicates.
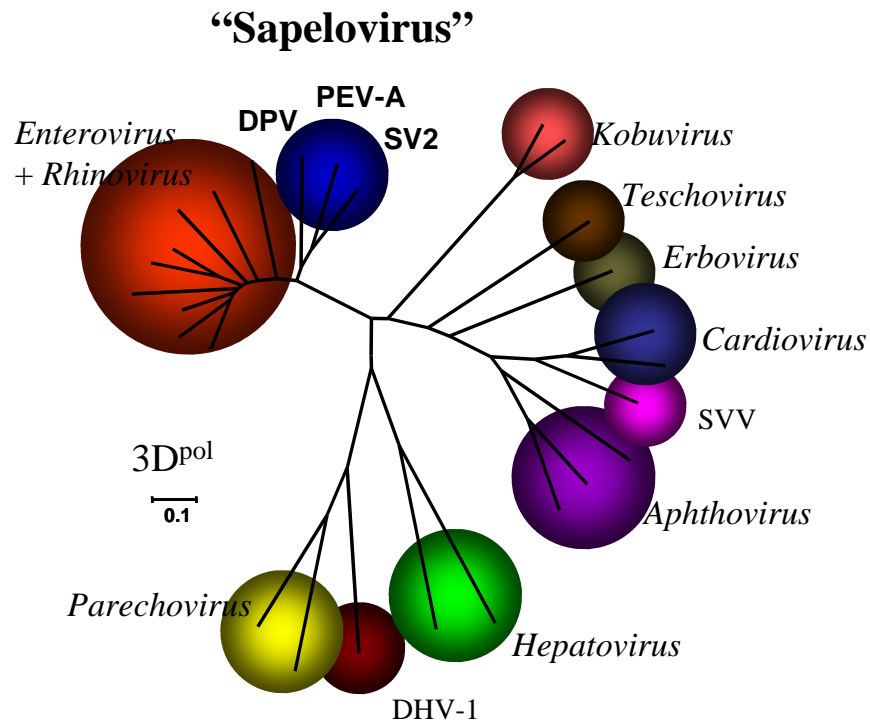
Fig. 4. Unrooted Neighbor-joining tree showing the relationships between picornaviruses in the 3D polymerase region. All genus branches are supported by 99-100% bootstrap values based on 1000 pseudo-replicates.