

# Template for Taxonomic Proposal to the ICTV Executive Committee

## Creating Species in an existing genus

Code<sup>†</sup> **FT2003.058V.01** To designate the following viruses as species in the genus:

***Enterovirus***

belonging to the family<sup>°</sup> : ***Picornaviridae***

*Simian enterovirus A*

A2 plaque virus      AF201894

Simian virus 28      AF326757

Simian virus 4      AF326759

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

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

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### New Taxonomic Order

**Order**

**Family**

*Picornaviridae*

**Genus**

*Enterovirus*

**Type Species**

*Poliovirus*

**List of Species in the genus**

*Human enterovirus A through D*

*Bovine enterovirus*

*Poliovirus*

*Porcine enterovirus A*

*Porcine enterovirus B*

*Simian enterovirus A*

**List of Tentative Species in the Genus**

**List of Unassigned Species in the Family**

## Argumentation to justify the designation of new species in the genus

### Species demarcation criteria in the genus

Members of an enterovirus species:

- share greater than 70% amino acid identity in P1,
- share greater than 70% amino acid identity in the non-structural proteins 2C + 3CD,
- share a limited range of host cell receptors,
- share a limited natural host range,
- have a genome base composition (G + C) which varies by no more than 1%,
- share a significant degree of compatibility in proteolytic processing, replication,

### Argumentation to justify the designation of new species in the genus

The complete genome sequence of A-2 plaque virus has been published (Liu et al., 2000). This reveals that the virus, currently an unassigned enterovirus, is *Enterovirus*-like in terms of genome organisation and in the coding region is more closely related to members of this genus than to any other picornaviruses. However, it does not fall into any of the existing *Enterovirus* species as it shares less than 70% amino acid identity with any other species in both the P1 and 2C+3CD regions (members of an enterovirus species must share at least 70% identity). Phylogenetic trees of enteroviruses representing each species make clear its distinct nature and the need to create a new species (Fig.1). A-2 plaque virus was first isolated from the icteric-phase sera of a patient with viral hepatitis. However, it is isolated rarely from humans and recent analysis of enteroviruses isolated from simians has revealed viruses closely-related (>95% amino acid identity in VP1) to A-2 plaque virus, notably simian enterovirus 4 (SE4) and SE28 (Oberste et al., 2002). It is therefore proposed to name the new species *Simian enterovirus A* (SEV-A). The designation A is employed, as partial sequence analysis of other simian viruses suggests that further *Simian enterovirus* species will need to be created in the future.

### List of created Species in the genus

*Simian enterovirus A*

A2 plaque virus AF201894

Simian virus 28 AF326757

Simian virus 4 AF326759

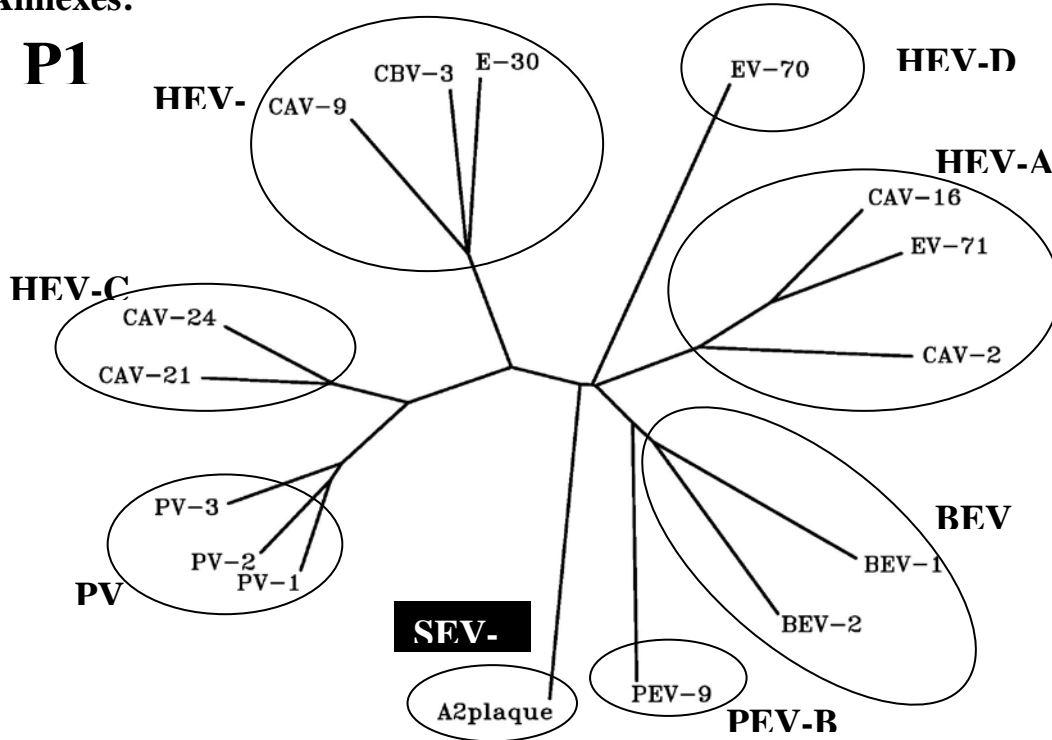
### References

Liu Z, Donahue RE, Young NS, Brown KE (2000) Sequencing and characterization of A-2 plaque virus: A new member of the picornaviridae family. *Virology* 272:168-176.

Oberste MS, Maher K, Pallansch MA (2002) Molecular phylogeny and proposed classification of the simian picornaviruses. *Journal of Virology* 76:1244-1251.

Annexes:

**P1**



**2C3C**

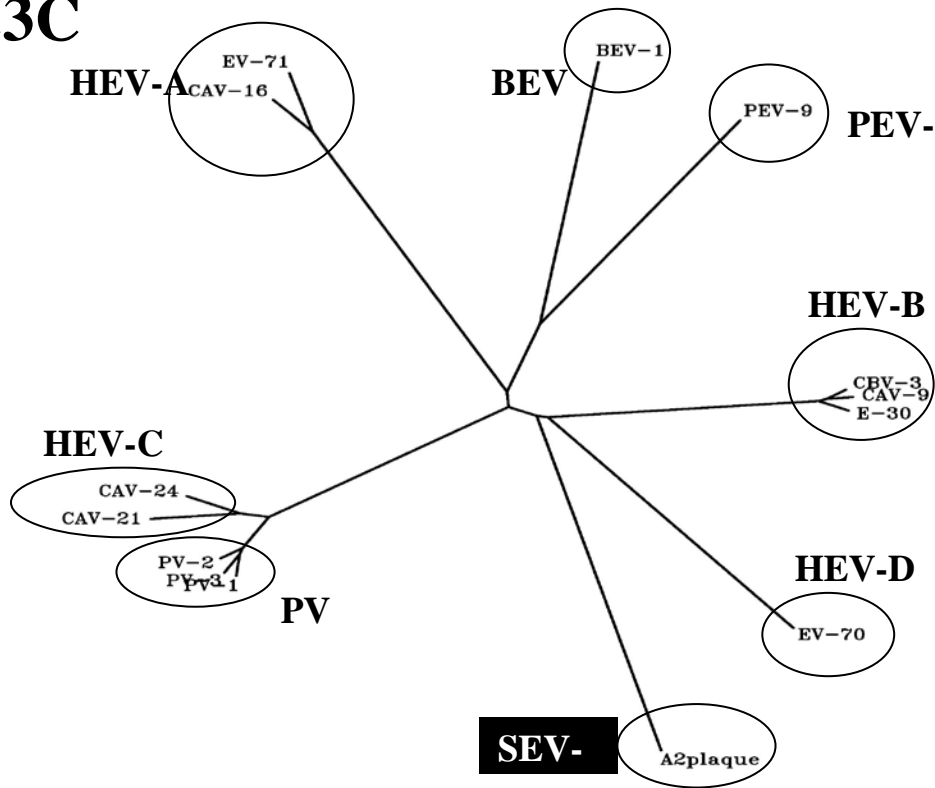


Fig.1 Phylogenetic trees showing the relationship between selected members of each enterovirus species and the proposed species *Simian enterovirus* (SEV-A; exemplified by A-2 plaque virus), using P1 or 2C+3CD amino acid identities. Members of each species are enclosed within ellipses and the species are labelled with the standard abbreviation.