

Template for Taxonomic Proposal to the ICTV Executive Committee

To merge two existing Genera

Code[†] To remove from the existing genus
in the family^{°*}

Rhinovirus

Picornaviridae

the following species:

Human rhinovirus A
Human rhinovirus B
And tentative species
Bovine rhinovirus 1 (BRV-1)
Bovine rhinovirus 2 (BRV-2)
Bovine rhinovirus 3 (BRV-3)

Code[†] To assign the species above in the existing genus:*

Enterovirus

in the family^{°*}

Picornaviridae

Code[†] To remove the existing genus:*

Rhinovirus

in the family^{°*}

Picornaviridae

[†] Assigned by ICTV officers

[°] leave blank if inappropriate

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

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Old Taxonomic Order

Order

Family

Picornaviridae

Genus

Enterovirus

Genus

Rhinovirus

Type Species

New Taxonomic Order

Order

Family

Picornaviridae

Genus

Enterovirus

Type Species

ICTV-EC comments and response of the SG

Argumentation to merge and rename the genus

Historically, the human pathogens enteroviruses and rhinoviruses have been classified into separate genera (*Enterovirus* and *Rhinovirus* respectively), largely on the basis of classical criteria such as pathogenicity and the acid stability of enteroviruses/ lability of rhinoviruses. Sequence analysis reveals that there are no significant differences in genome organisation or particle structure (Kitamura et al, 1981; Stanway et al, 1984; Laine et al., 2005). In both the standard regions used for picornavirus taxonomy (P1 and 2C+3CD) species representing these genera are much more closely related than those representing other distinct *Picornaviridae* genera (Figure 1). Also, in the P1 region, the genera are not monophyletic. Furthermore, it has recently been found that in sequence terms human rhinovirus 87 is in fact an acid labile member of the species *Human enterovirus D*, suggesting that acid stability/lability is not always a reliable classification criterion (Blomqvist et al., 2002; Savolainen et al., 2002). Thus, it is difficult to justify the current *Enterovirus/Rhinovirus* division and it is proposed to merge these genera, giving a single genus, *Enterovirus*.

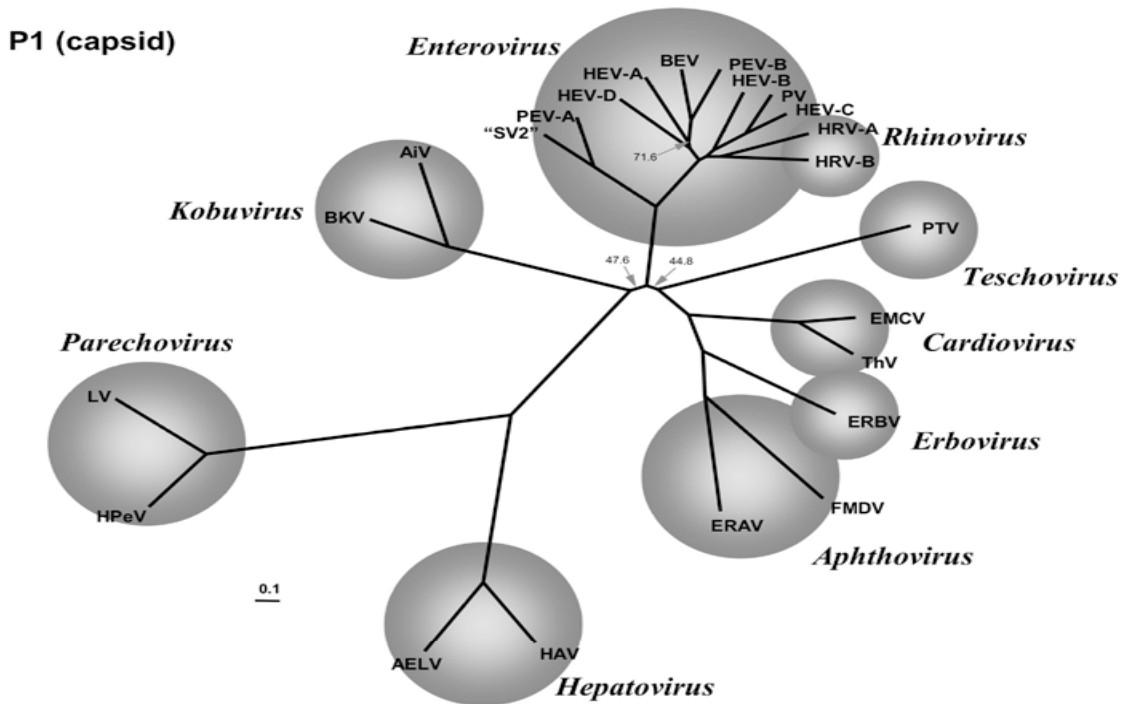
Origin of the proposed new genus name

The name *Enterovirus* is unchanged.

References

- Blomqvist S., Savolainen C., Raman L., Roivainen M., Hovi T. (2002). Human rhinovirus 87 and enterovirus 68 represent a unique serotype with rhinovirus and enterovirus features. *J. Clin. Microbiol.* 40:4218-4223.
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- Laine P., Savolainen C., Blomqvist S., Hovi T. (2005). Phylogenetic analysis of human rhinovirus capsid protein VP1 and 2A protease coding sequences confirms shared genus-like relationships with human enteroviruses. *J. Gen. Virol.* 86:697-706.
- Savolainen C., Blomqvist S., Mulders M.N., Hovi T. (2002). Genetic clustering of all 102 human rhinovirus prototype strains: serotype 87 is close to human enterovirus 70. *J. Gen. Virol.* 83:333-340.
- Stanway G., Hughes P.J., Mountford R.C., Minor P.D., Almond J.W. (1984). The complete nucleotide sequence of a common cold virus: human rhinovirus 14. *Nucleic Acids Res.* 12:7859-7875.

Annexes:



Proteins 2C + 3CD

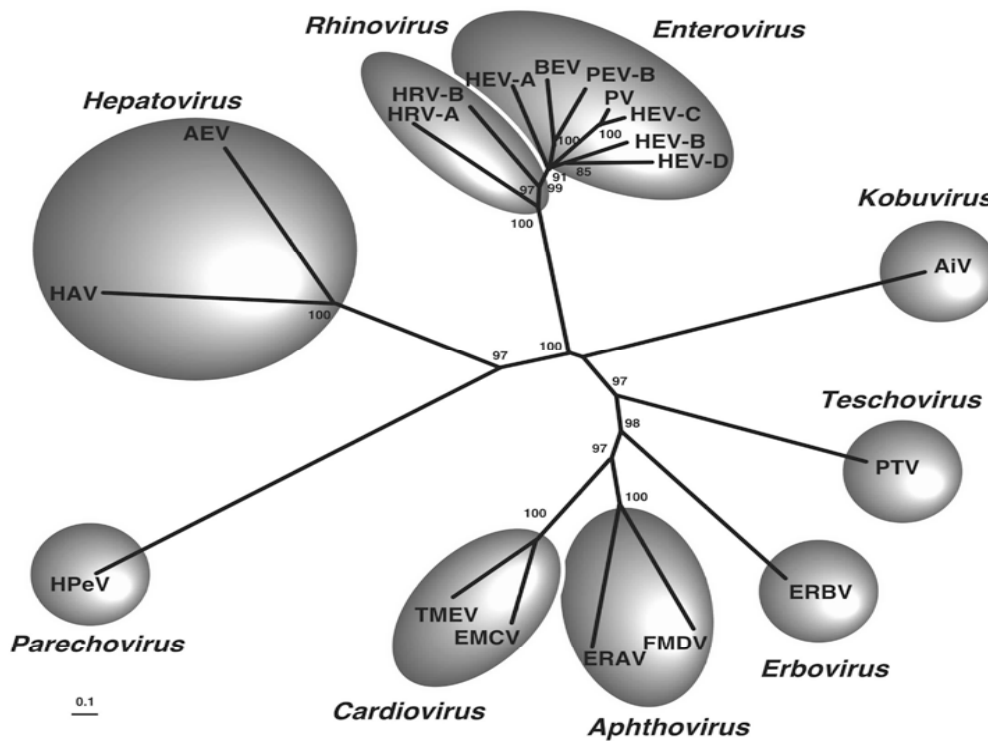


Figure 1: Phylogenetic trees showing the relationships between the species and genera of the family *Picornaviridae*. (a) Protein P1 and (b) Protein 2C+3CD. The Neighbor-joining trees were produced and bootstrapped (1000 replicates) using CLUSTALX and an amino acid weight matrix (BLOSUM). The trees were drawn using TreeView v1.5.2. Only bootstrap values of >90% are indicated. Figure taken from the 8th Report.