

Template for Taxonomic Proposal to the ICTV Executive Committee To merge two existing Species

Code [†]	2005.261V.04	To remove from the existing genus in the family ^{°*}	<i>Enterovirus</i>
			<i>Picornaviridae</i>

the following species:

<p><i>Poliovirus</i> Human poliovirus 1 (PV-1) Human poliovirus 2 (PV-2) Human poliovirus 3 (PV-3)</p>

Code [†]	2005.262V.04	To assign the viruses above in the existing species:*	<i>Human enterovirus C</i>
		In the genus in the family ^{°*}	<i>Enterovirus</i>
			<i>Picornaviridae</i>

[†] 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	<i>Picornaviridae</i>
Genus	<i>Enterovirus</i>
Type Species	<i>Human enterovirus C</i>
Species	<i>Poliovirus</i>

New Taxonomic Order

Order	
Family	<i>Picornaviridae</i>
Genus	<i>Enterovirus</i>
Type Species	<i>Human enterovirus C</i>
Species	<i>Human enterovirus C</i>

ICTV-EC comments and response of the SG

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Argumentation to merge and rename the genus

It has been realised for many years that the sequences of members of the *Human enterovirus C* and *Poliovirus* species of the genus *Enterovirus* are very similar, particularly in the region encoding the non-structural proteins (Hughes et al., 1987; Hughes et al., 1989; Supanaranond et al., 1992). Recent complete nucleotide sequence analysis of representatives of all known serotypes contained within *Human enterovirus C* has definitively demonstrated this relationship (Brown et al., 2003; Newcombe et al., 2003). The species are not monophyletic in either of the regions used for *Picornaviridae* taxonomy, P1 and 2C+3CD (Figures 1 and 2), and in the 2C+3CD region amino acid identity is generally in excess of 90%. It has also been suggested in a number of studies that homologous recombination may take place between polioviruses and members of the *Human enterovirus C* species (e.g. Liu et al., 2003; Arita et al., 2005), which is one measure taken into account in the definition of picornavirus species. Although polioviruses have a distinct and specific receptor usage from other *Human enterovirus C* members, differences in receptor usage are also evident within the species *Human enterovirus B* and so this characteristic is currently not being considered equitably in *Enterovirus* taxonomy. These factors make the current division into two species untenable and the purpose of this proposal is to rationalize this situation by combining the *Human enterovirus C* and *Poliovirus* species, creating a single species.

Origin of the proposed new species name

Not applicable- the species name will remain unchanged. The species name, *Human enterovirus C*, is preferred over *Poliovirus*, the species containing viruses which were identified earlier and are better studied than those in the current species *Human enterovirus C*, as poliovirus implies a specific association with poliomyelitis, which is not applicable to the species as a whole.

References

- Arita, M., Zhu, S.L., Yoshida, H., Yoneyama, T., Miyamura, T., Shimizu, H. (2005). A Sabin 3-derived poliovirus recombinant contained a sequence homologous with indigenous human enterovirus species C in the viral polymerase coding region. *J. Virol.* 79: 12650-12657.
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- Hughes P.J., North C., Minor P.D., Stanway G. (1989). The complete nucleotide sequence of coxsackievirus A21. *J. Gen. Virol.* 70:2943-2952.
- Liu, H.M., Zheng, D.P., Zhang, L.B., Oberste, M.S., Kew, O.M., Pallansch, M.A. (2003). Serial recombination during circulation of type 1 wild-vaccine recombinant polioviruses in China. *J. Virol.* 77: 10994-11005.
- Supanaranond K., Takeda N., Yamazaki S. (1992). The complete nucleotide sequence of a variant of Coxsackievirus A24, an agent causing acute hemorrhagic conjunctivitis. *Virus Genes* 6:149-158.
- Brown B., Oberste M.S., Maher K., Pallansch M.A. (2003). Complete genomic sequencing shows that polioviruses and members of human enterovirus species C are closely related in the noncapsid coding region. *J. Virol.* 77:8973-8984.
- Newcombe N.G., Andersson P., Johansson E.S., Au G.G., Lindberg A.M., Barry R.D., Shafren D.R. (2003). Cellular receptor interactions of C-cluster human group A coxsackieviruses. *J. Gen. Virol.* 84:3041-3050.

Annexes:

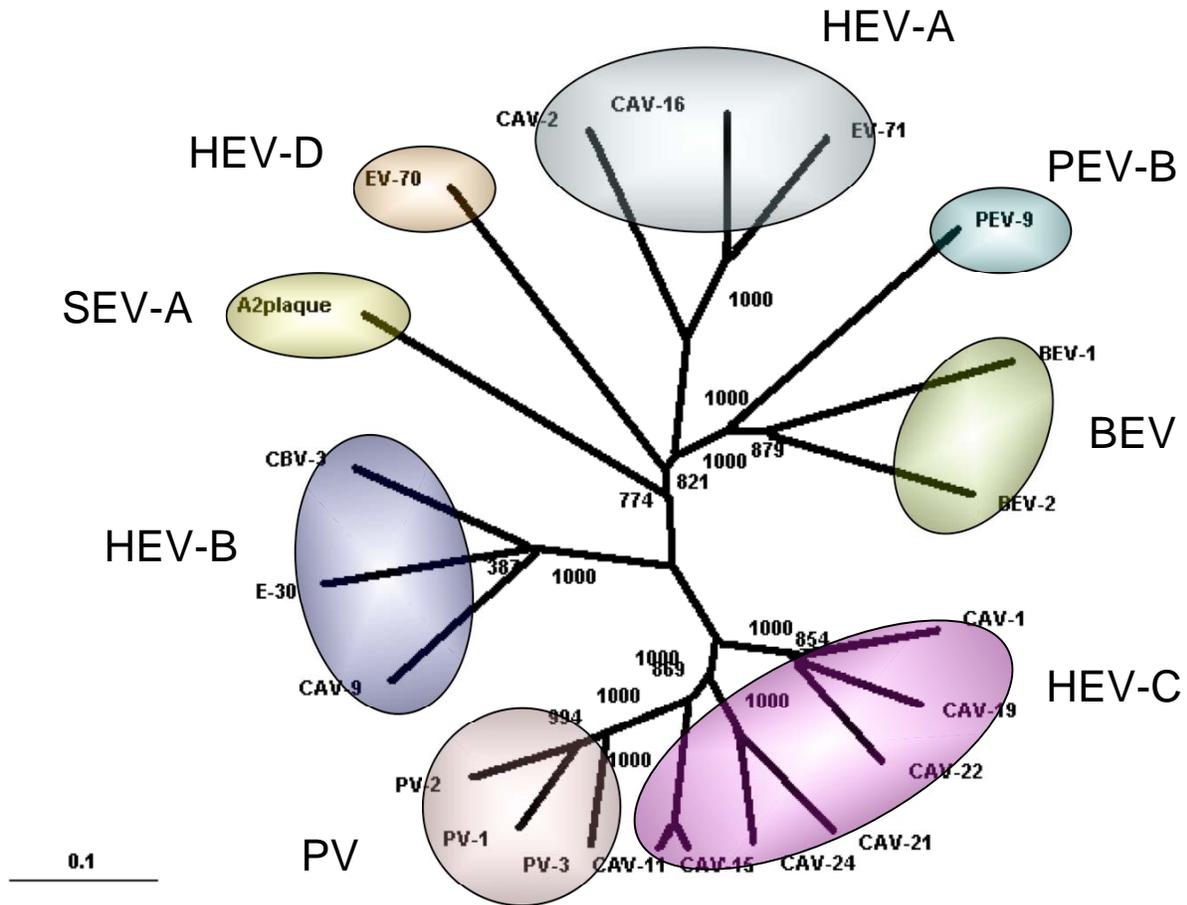


Figure 1. Unrooted tree, based on the P1 region, showing the genetic relationships between representatives of each of the Enterovirus species (indicated by coloured circles), together with several members of the existing *Poliovirus* and *Human enterovirus C* species. The tree was bootstrapped using Njplot and drawn using TreeView. Species abbreviations: HEV, *Human enterovirus*; PV, *Poliovirus*; BEV, *Bovine enterovirus*; PEV, *Porcine enterovirus*; SEV, *Simian enterovirus*.

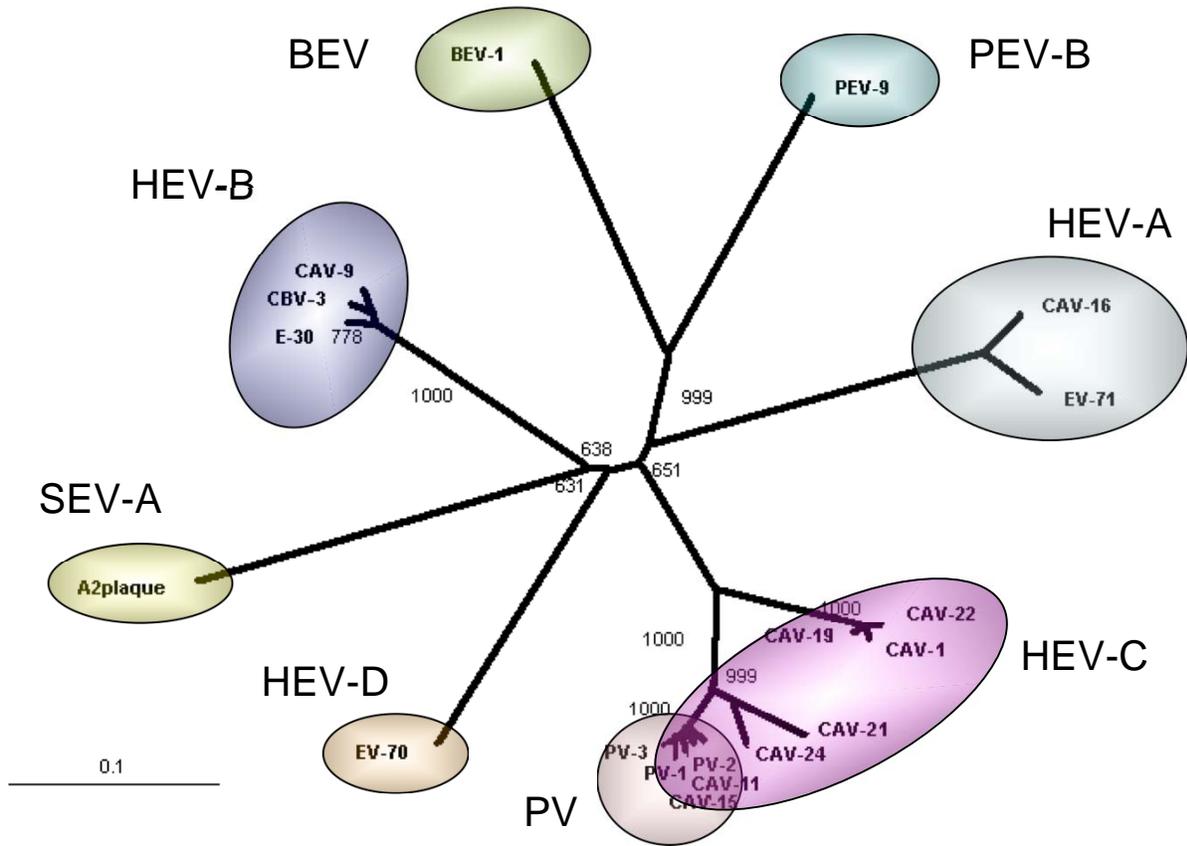


Figure 2. Unrooted tree, based on the 2C+3CD region, showing the genetic relationships between representatives of each of the Enterovirus species (indicated by coloured circles), together with several members of the existing *Poliovirus* and *Human enterovirus C* species. The tree was bootstrapped using Njplot and drawn using TreeView. Species abbreviations: HEV, *Human enterovirus*; PV, *Poliovirus*; BEV, *Bovine enterovirus*; PEV, *Porcine enterovirus*; SEV, *Simian enterovirus*.