



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

<b>Code assigned:</b>	<b>2011.018a,bV</b>	(to be completed by ICTV officers)
<b>Short title:</b> In the genus <i>Enterovirus</i> , family <i>Picornaviridae</i> , create 2 new species, named <i>Enterovirus F</i> and <i>Enterovirus G</i> , respectively, and rename 10 existing species. (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input checked="" type="checkbox"/> 9 <input checked="" type="checkbox"/>	

**Author(s) with e-mail address(es) of the proposer:**

Nick Knowles ([nick.knowles@iah.ac.uk](mailto:nick.knowles@iah.ac.uk)) on behalf of the *Picornaviridae* Study Group.

**List the ICTV study group(s) that have seen this proposal:**

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

*Picornaviridae* Study Group

**ICTV-EC or Study Group comments and response of the proposer:**

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Date first submitted to ICTV:

22/08/2011

Date of this revision (if different to above):

01/07/2012

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MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	<b>2011.018bV</b>	(assigned by ICTV officers)
<b>To create two new species within:</b>		
Genus:	<b><i>Enterovirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:	n/a	
Family:	<b><i>Picornaviridae</i></b>	
Order:	<b><i>Picornavirales</i></b>	
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<i>Enterovirus F</i>		DQ092770, DQ092795, DQ092794
<i>Enterovirus J</i>		AF326766, FJ007373, AF414372, AF414373

<p><b>Reasons to justify the creation and assignment of the new species:</b></p> <ul style="list-style-type: none"> <li>• Explain how the proposed species differ(s) from all existing species.                     <ul style="list-style-type: none"> <li>○ If species demarcation criteria (see module 3) have previously been defined for the genus, <b>explain how the new species meet these criteria.</b></li> <li>○ If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.</li> </ul> </li> <li>• Further material in support of this proposal may be presented in the Appendix, Module 9</li> </ul>
<p><i>Enterovirus F</i></p> <p>Frequency distribution of pairwise amino acid identity scores of the four capsid proteins (1A–1D) and the 3D polymerase have demonstrated that bovine enteroviruses can be divided into two species (Fig. 1.; Zell et al., 2006). It is proposed that bovine enteroviruses belonging to BEV group 2 be placed in a new genus, <i>Enterovirus F</i>, while members of BEV group 1 are placed in a species named <i>Enterovirus E</i> (renamed from the species <i>Bovine enterovirus</i>).</p> <p><i>Enterovirus J</i></p> <p>Five unassigned enterovirus types (SV6, EV-103, EV-108, EV-112 and EV-115) which have been isolated from African and Asian monkeys, <i>Cercocebus atys</i> (sooty mangabey), <i>Macaca mulatta</i> (rhesus macaque), <i>Macaca nemestrina</i> (southern pig-tailed macaque), <i>Papio cynocephalus</i> (yellow baboon) group together phylogenetically and are proposed to form a novel enterovirus species (Fig. 2). Complete genome sequences are available for SV6, EV-103, EV-108 and they cluster together in the P1, P2 and P3 genome regions (Oberste et al., 2008).</p>

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	<b>2011.018bV</b>	(assigned by ICTV officers)
<b>Title of proposal: Rename enterovirus species names</b>		

**Text of proposal:**

Enteroviruses have traditionally been named after the host species from which they were first isolated. It has become clear that, although in many cases the major host is probably correctly identified, enteroviruses may be isolated from many hosts (Table 1). Most of the human enterovirus species contain serotypes isolated from non-human primates which have not been isolated from humans.

Rename *Human enterovirus A* as *Enterovirus A*

Rename *Human enterovirus B* as *Enterovirus B*

Rename *Human enterovirus C* as *Enterovirus C*

Rename *Human enterovirus D* as *Enterovirus D*

Rename *Bovine enterovirus* as *Enterovirus E* (only currently designated type 1 viruses to be included)

Rename *Porcine enterovirus B* as *Enterovirus G*

Rename *Simian enterovirus A* as *Enterovirus H*

Rename *Human rhinovirus A* as *Rhinovirus A*

Rename *Human rhinovirus B* as *Rhinovirus B*

Rename *Human rhinovirus C* as *Rhinovirus C*

The (sero)type designations for the human (and simian) entero- and rhinoviruses would remain as they are now, but the bovine and porcine ones would probably change, e.g. BEV-1 would become EV-E1 (plus other new types), BEV-2 would be EV-F1 (plus other new types); PEV-9 and PEV-10 would become EV-G1 and EV-G2 (plus other new types).

This proposal was presented both on a poster and orally at the seventeenth meeting of the European Study Group on the Molecular Biology of Picornaviruses (EUROPIC 2012), in Saint Raphaël, France, 3-7 June 2012. Approximately 250 picornavirologists were present and were specifically asked if there were any objections to this proposal. None were forthcoming.

The proposal was also posted on the following websites following EC43:

<http://www.picornaviridae.com/enterovirus/enterovirus.htm>

[http://www.picornastudygroup.com/proposals/2011/psg\\_proposals\\_2011.htm](http://www.picornastudygroup.com/proposals/2011/psg_proposals_2011.htm)

No objections have been received.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Knowles, N.J. (2005). Genetic relationships between bovine enteroviruses in VP1 and 3D<sup>pol</sup>. EUROPIC 2005: XIIIth Meeting of the European Study Group on the Molecular Biology of Picornaviruses, Lunteren, The Netherlands, 23-29th May 2005. Abstract A19.

Nix, W.A., Jiang, B., Maher, K., Strobert, E. and Oberste M.S. (2008). Identification of enteroviruses in naturally infected captive primates. *J. Clin. Microbiol.* 46: 2874-2878.

Oberste, M.S., Maher, K. and Pallansch, M.A. (2002). Molecular phylogeny and proposed classification of the simian picornaviruses. *J. Virol.* 76: 1244-1251.

Oberste, M.S., Maher, K. and Pallansch, M.A. (2007). Complete genome sequences for nine simian enteroviruses. *J. Gen. Virol.* 88: 3360-3372.

Oberste, M.S., Jiang, X., Maher, K., Nix, W.A. and Jiang B. (2008). The complete genome sequences for three simian enteroviruses isolated from captive primates. *Arch. Virol.* 153: 2117-2122.

Zell, R., Krumbholz, A., Dauber, M., Hoey, E., Wutzler, P. (2006). Molecular-based reclassification of the bovine enteroviruses. *J. Gen. Virol.* 87: 375-385.

**Annex:**

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Diverse host range of enteroviruses.

Present species name	Proposed species name*	Known hosts†
<i>Human enterovirus A</i>	<i>Enterovirus A</i>	<i>Cercocebus atys</i> (sooty mangabey) <b><i>Homo sapiens</i> (man)</b> <i>Macaca fascicularis</i> (cynomolgus monkey) <i>Macaca mulatta</i> (rhesus macaque) <i>Macaca nemestrina</i> (southern pig-tailed macaque) <i>Papio cynocephalus</i> (yellow baboon)
<i>Human enterovirus B</i>	<i>Enterovirus B</i>	<i>Canis lupus familiaris</i> (dog) <i>Cercopithecus aethiops</i> (vervet monkey) <b><i>Homo sapiens</i> (man)</b> <i>Pan troglodytes</i> (common chimpanzee) <i>Pongo pygmaeus</i> (Orangutan) <i>Rhinopithecus roxellana</i> (Sichuan snub-nosed monkey) <i>Sus scrofa domesticus</i> (pig)
<i>Human enterovirus C</i>	<i>Enterovirus C</i>	<i>Canis lupus familiaris</i> (dog) <b><i>Homo sapiens</i> (man)</b>
<i>Human enterovirus D</i>	<i>Enterovirus D</i>	<b><i>Homo sapiens</i> (man)</b>

		<i>Pan troglodytes</i> (common chimpanzee)
<i>Bovine enterovirus</i> (current type 1)	<i>Enterovirus E</i>	<i>Aepyceros melampus</i> (impala) <b><i>Bos taurus</i></b> (cow) <i>Bubalus bubalis</i> (water buffalo) <i>Canis lupus familiaris</i> (dog) <i>Capra aegagrus hircus</i> (goat) <i>Cervus nippon</i> (Sika deer) <i>Equus ferus caballus</i> (horse) (serology only) <i>Homo sapiens</i> (man) (serology only) <i>Ovis aries</i> (sheep) <i>Syncerus caffer</i> (African buffalo) <i>Tursiops truncatus</i> (bottle-nosed dolphin)
<i>Bovine enterovirus</i> (current type 2)	<i>Enterovirus F</i>	<b><i>Bos taurus</i></b> (cow) <i>Branta canadensis</i> (Canada goose) <i>Equus ferus caballus</i> (horse) <i>Odocoileus virginianus</i> (white-tailed deer) <i>Ovis aries</i> (sheep) <i>Trichosurus vulpecula</i> (common brushtail possum)
<i>Porcine enterovirus B</i>	<i>Enterovirus G</i>	<i>Homo sapiens</i> (man) <i>Macaca mulatta</i> (rhesus macaque) <i>Ovis aries</i> (sheep) <b><i>Sus scrofa domestica</i></b> (pig)
<i>Simian enterovirus A</i>	<i>Enterovirus H</i>	<i>Cercopithecus aethiops</i> (vervet monkey) <i>Homo sapiens</i> (man) <i>Macaca mulatta</i> (rhesus macaque)
Unassigned simian enteroviruses (SV6, EV-103, EV-108, EV-112, EV-115)	<i>Enterovirus J</i>	<i>Cercocebus atys</i> (sooty mangabey) <i>Macaca mulatta</i> (rhesus macaque) <i>Macaca nemestrina</i> (southern pig-tailed macaque) <i>Papio cynocephalus</i> (yellow baboon)
<i>Human rhinovirus A</i>	<i>Rhinovirus A</i>	<b><i>Homo sapiens</i></b> (man)
<i>Human rhinovirus B</i>	<i>Rhinovirus B</i>	<b><i>Homo sapiens</i></b> (man)
<i>Human rhinovirus C</i>	<i>Rhinovirus C</i>	<b><i>Homo sapiens</i></b> (man)

\*, the letter "I" has been skipped as it may be confused with the number one.

†, virus isolation or RT-PCR amplification (except where stated). The principle host, where known, is shown in bold type.

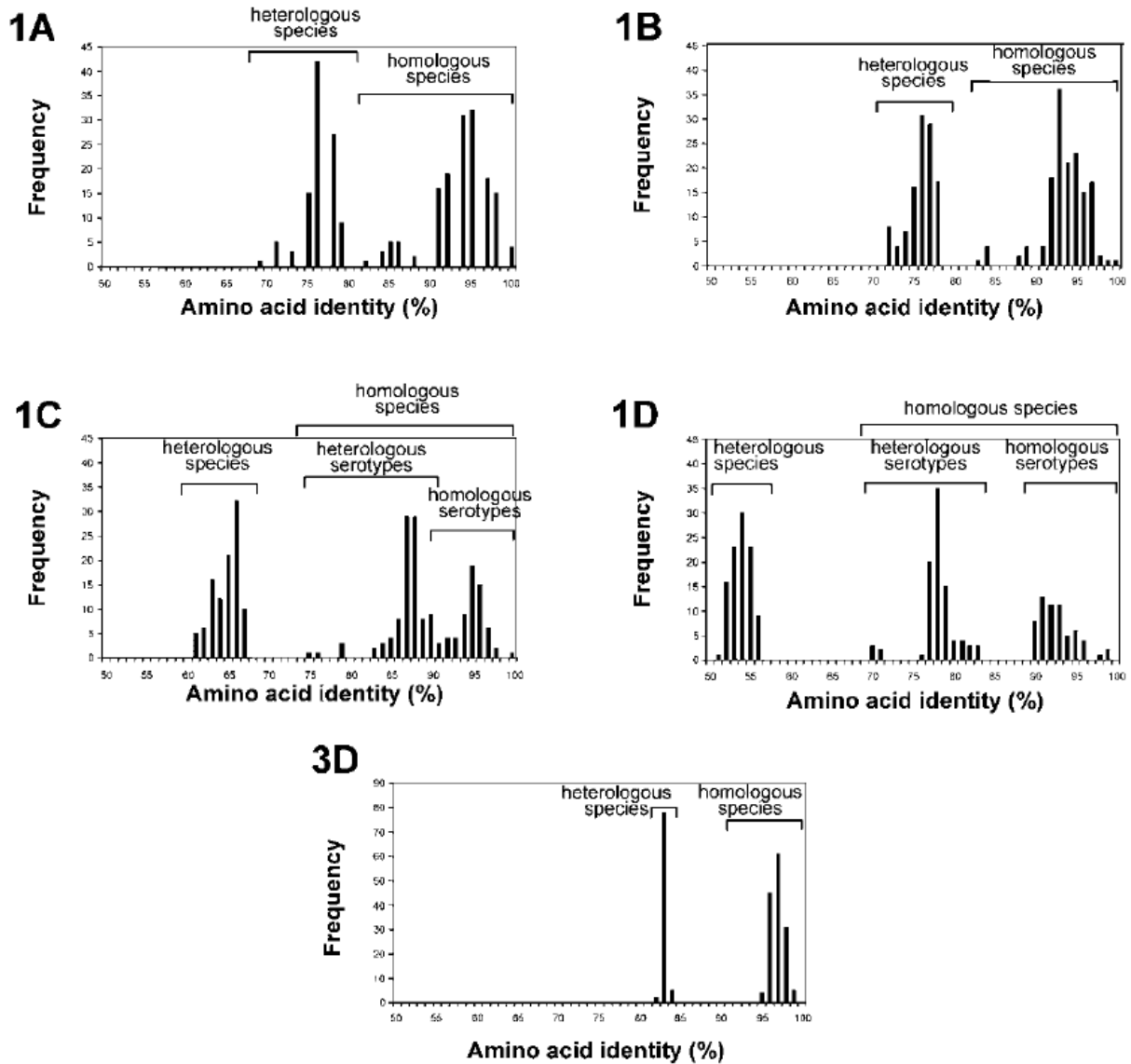


Fig. 1. Frequency distribution of pairwise amino acid identity scores of the four capsid proteins (1A–1D) and the 3D polymerase. Amino acid sequences of 22 BEV strains and field isolates were compared with each other in order to calculate amino acid identities. The discontinuous frequency distribution of the plotted amino acid identities indicates the existence of heterologous geno-/serotypes and species. From Zell et al., 2006.

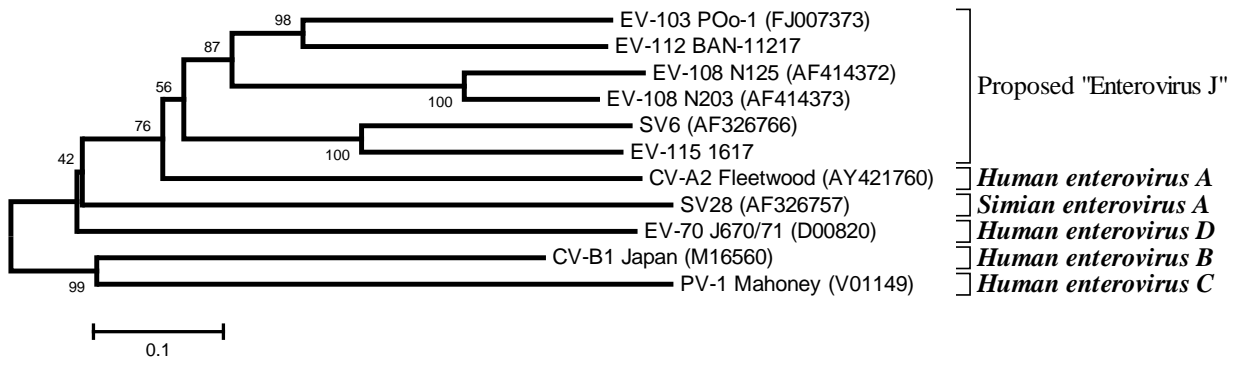


Fig. 2. Neighbor-Joining tree (Nucleotide: Kimura 2-parameter; 1000 bootstrap replicates; MEGA 5) showing the relationships between the human and simian enteroviruses in the VP1-coding region.