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

<table>
<thead>
<tr>
<th>Code assigned:</th>
<th><strong>2011.018a,bV</strong></th>
<th>(to be completed by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Short title:</td>
<td>In the genus <em>Enterovirus</em>, family <em>Picornaviridae</em>, create 2 new species, named <em>Enterovirus F</em> and <em>Enterovirus G</em>, respectively, and rename 10 existing species. (e.g. 6 new species in the genus <em>Zetavirus</em>)</td>
<td></td>
</tr>
<tr>
<td>Modules attached</td>
<td>1 2 3 4 5 6 7 8 9</td>
<td>(modules 1 and 9 are required)</td>
</tr>
</tbody>
</table>

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

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

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

<table>
<thead>
<tr>
<th>A list of study groups and contacts is provided at <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Picornaviridae Study Group</td>
</tr>
</tbody>
</table>

**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
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.

<table>
<thead>
<tr>
<th>Code</th>
<th>2011.018bV (assigned by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>To create two new species within:</strong></td>
<td>Fill in all that apply.</td>
</tr>
<tr>
<td>Genus:</td>
<td>Enterovirus</td>
</tr>
<tr>
<td>Subfamily:</td>
<td>n/a</td>
</tr>
<tr>
<td>Family:</td>
<td>Picornaviridae</td>
</tr>
<tr>
<td>Order:</td>
<td>Picornavirales</td>
</tr>
<tr>
<td>And name the new species:</td>
<td>GenBank sequence accession number(s) of reference isolate:</td>
</tr>
<tr>
<td>Enterovirus F</td>
<td>DQ092770, DQ092795, DQ092794</td>
</tr>
<tr>
<td>Enterovirus J</td>
<td>AF326766, FJ007373, AF414372, AF414373</td>
</tr>
</tbody>
</table>

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - 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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

**Enterovirus F**

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, Enterovirus F, while members of BEV group 1 are placed in a species named Enterovirus E (renamed from the species Bovine enterovirus).

**Enterovirus J**

Five unassigned enterovirus types (SV6, EV-103, EV-108, EV-112 and EV-115) which have been isolated from African and Asian monkeys, Cercopithecus asytis (sooty mangabey), Macaca mulatta (rhesus macaque), Macaca nemestrina (southern pig-tailed macaque), Papio cynocephalus (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).
non-standard proposal

<table>
<thead>
<tr>
<th>Code</th>
<th><strong>2011.018bV</strong> (assigned by ICTV officers)</th>
</tr>
</thead>
</table>

**Title of proposal: Rename enterovirus species names**

**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.picornaviridae.com/enterovirus/enterovirus.htm)

No objections have been received.
MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:


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.

<table>
<thead>
<tr>
<th>Present species name</th>
<th>Proposed species name*</th>
<th>Known hosts†</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Human enterovirus A</strong></td>
<td>Enterovirus A</td>
<td>Cercocebus atys (sooty mangabey)</td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Homo sapiens</em> (man)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Macaca fascicularis (cynomolgus monkey)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Macaca mulatta (rhesus macaque)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Macaca nemestrina (southern pig-tailed macaque)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Papio cynocephalus (yellow baboon)</td>
</tr>
<tr>
<td><strong>Human enterovirus B</strong></td>
<td>Enterovirus B</td>
<td>Canis lupus familiaris (dog)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cercopithecus aethiops (vervet monkey)</td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Homo sapiens</em> (man)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pan troglodytes (common chimpanzee)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pongo pygmaeus (orangutan)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rhinopithecus roxellana (Sichuan snub-nosed monkey)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sus scrofa domesticus (pig)</td>
</tr>
<tr>
<td><strong>Human enterovirus C</strong></td>
<td>Enterovirus C</td>
<td>Canis lupus familiaris (dog)</td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Homo sapiens</em> (man)</td>
</tr>
<tr>
<td><strong>Human enterovirus D</strong></td>
<td>Enterovirus D</td>
<td><em>Homo sapiens</em> (man)</td>
</tr>
<tr>
<td><strong>Bovine enterovirus</strong> (current type 1)</td>
<td><strong>Enterovirus E</strong></td>
<td><strong>Pan troglodytes</strong> (common chimpanzee)</td>
</tr>
<tr>
<td>--------------------------------------</td>
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<td>--------------------------------------</td>
</tr>
<tr>
<td></td>
<td>Aepyceros melampus (impala)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Bos taurus (cow)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Bubalus bubalis (water buffalo)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Canis lupus familiaris (dog)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Capra aegagrus hircus (goat)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cervus nippon (Sika deer)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Equus ferus caballus (horse) (serology only)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Homo sapiens (man) (serology only)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Ovis aries (sheep)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Syncerus caffer (African buffalo)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Tursiops truncates (bottle-nosed dolphin)</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Bovine enterovirus</strong> (current type 2)</th>
<th><strong>Enterovirus F</strong></th>
<th><strong>Bos taurus</strong> (cow)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Branta canadensis (Canada goose)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Equus ferus caballus (horse)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Odocoileus virginianus (white-tailed deer)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Ovis aries (sheep)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Trichosurus vulpecula (common brushtail possum)</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Porcine enterovirus B</strong></th>
<th><strong>Enterovirus G</strong></th>
<th><strong>Homo sapiens</strong> (man)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Macaca mulatta (rhesus macaque)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Ovis aries (sheep)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sus scrofa domestica (pig)</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Simian enterovirus A</strong></th>
<th><strong>Enterovirus H</strong></th>
<th><strong>Cercopithecus aethiops</strong> (vervet monkey)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Homo sapiens (man)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Macaca mulatta (rhesus macaque)</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Unassigned simian enteroviruses</strong> (SV6, EV-103, EV-108, EV-112, EV-115)</th>
<th><strong>Enterovirus I</strong></th>
<th><strong>Cercopithecus atys</strong> (sooty mangabeys)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Homo sapiens (man)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Macaca mulatta (rhesus macaque)</td>
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<td></td>
<td>Papio cynocephalus (yellow baboon)</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Human rhinovirus A</strong></th>
<th><strong>Rhinovirus A</strong></th>
<th><strong>Homo sapiens</strong> (man)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Human rhinovirus B</strong></th>
<th><strong>Rhinovirus B</strong></th>
<th><strong>Homo sapiens</strong> (man)</th>
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</table>

<table>
<thead>
<tr>
<th><strong>Human rhinovirus C</strong></th>
<th><strong>Rhinovirus C</strong></th>
<th><strong>Homo sapiens</strong> (man)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*, 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.