This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

**Code(s) assigned:** 2008.084V (to be completed by ICTV officers)

**Short title:** New species in the genus Enterovirus (Picornaviridae)
(e.g. 6 new species in the genus Zetavirus; re-classification of the family Zetaviridae etc.)

**Modules attached** (please check all that apply):

1 [ ] 2 [ ] 3 [ ] 4 [ ] 5 [X]
6 [ ] 7 [ ]

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

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

**ICTV-EC or Study Group comments and response of the proposer:**
MODULE 5: NEW SPECIES

To create 1 new species assigned as follows:

<table>
<thead>
<tr>
<th>Code</th>
<th>2008.084V (assigned by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genus:</td>
<td>Enterovirus</td>
</tr>
<tr>
<td>Subfamily:</td>
<td></td>
</tr>
<tr>
<td>Family:</td>
<td>Picornaviridae</td>
</tr>
<tr>
<td>Order:</td>
<td>Picornavirales</td>
</tr>
</tbody>
</table>

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box).

Name(s) of proposed new species:

Human rhinovirus C

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Within-species criteria for the genus Enterovirus are:

- Share greater than 70 % aa identity in P1
- Share greater than 70 % aa 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 2.5 %
- Share a significant degree of compatibility in proteolytic processing, replication, encapsidation, and genetic recombination.

Additionally, the two existing human rhinovirus species share similar susceptibility of receptor attachment to inhibition by pocket-binding antiviral agents ("inhibitor group" A or B).

Viruses within the proposed “Human rhinovirus C” species:

Share less than 70 % aa identity in P1 with

- Human rhinovirus A (highest identity [in BLAST search] is 50% with HRV 89, 39, 16, and 2; 49 % with HRV 1B)
- Human rhinovirus B (47 % with HRV 14)
- Human enterovirus B (46 % E-16, SVDV(CV-B5); 45% E-4)
- Human enterovirus C (45 % with CV-A21, CV-A19)
- Human enterovirus D (43 % with EV-70)
- Human enterovirus A (42 % with CV-10, CV-8)

Share less than 70 % aa identity in the non-structural proteins 2C + 3CD with

- Human rhinovirus A (highest identity [in 'gap' comparison] is 55 % with HRV 39; 54 % with HRV 89)
- Human rhinovirus B (53 % with HRV 14)
- 50-53 % with HEVs or PVs

Viruses identified in humans; natural host range other than humans is not known.

Receptor interaction has not been characterized.
Argument to justify the creation of the new species:

Proteolytic processing sites appear compatible to other rhino- and enteroviruses (Annex Table 1)

Compared to other rhino- and enterovirus species, Human rhinovirus C viruses show a deletion of 2 aa at the C-terminus of VP4.

Phylogenetic analysis indicates the proposed “Human rhinovirus C” viruses belong to a genetic clade separate from the existing rhino- and enterovirus species (see Annex Figure 1).

References:


Annexes:
Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

Table 1. Proteolytic processing sites of the proposed “Human rhinovirus C” species viruses.

<table>
<thead>
<tr>
<th>Site</th>
<th>Sequence</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>VP4/VP2</td>
<td>ALM/SPS</td>
<td>similar to HRV-A</td>
</tr>
<tr>
<td>VP2/VP3</td>
<td>TRQ/GLP</td>
<td>similar to <em>Picornaviridae</em></td>
</tr>
<tr>
<td>VP3/VP1</td>
<td>IAQ/NPV</td>
<td>similar to HRV-A</td>
</tr>
<tr>
<td>VP1/2A</td>
<td>TNV/GPS or GPSDMF/VHT</td>
<td>both similar to HRV-A</td>
</tr>
<tr>
<td>2A/2B</td>
<td>EHQ/GVD</td>
<td>similar to HRV-A</td>
</tr>
<tr>
<td>2B/2C</td>
<td>SRQ/GDS</td>
<td>similar to HEV-C, PV</td>
</tr>
<tr>
<td>2C/3A</td>
<td>IFQ/GLG</td>
<td>no obvious similarity</td>
</tr>
<tr>
<td>3A/3B</td>
<td>IAQ/GPY</td>
<td>similar to HRV-A</td>
</tr>
<tr>
<td>3B/3C</td>
<td>VAQ/GPE</td>
<td>similar to HRV-A</td>
</tr>
<tr>
<td>3C/3D</td>
<td>TTQ/GEI</td>
<td>similar to HEV-D</td>
</tr>
</tbody>
</table>
Figure 1. Phylogenetic tree presented at EUROPIC 2008 by Jennifer Rathe (“Resolution of all known HRV-A and HRV-B complete genome sequences, and their relationship to a potential new species, HRV-C”).