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** ☒	**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**

Code	***2008.084V***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Enterovirus***
Subfamily:	
Family:	***Picornaviridae***
Order:	***Picornavirales***

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:

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Kistler, A., Avila, P.C., Rouskin, S., Wang, D., Ward, T,, Yagi. S,, Schnurr, D., Ganem, D., DeRisi, J.L. and Boushey, H.A. (2007). Pan-viral screening of respiratory tract infections in adults with and without asthma reveals unexpected human coronavirus and human rhinovirus diversity. *J. Infect. Dis.* 196: 817-825. Epub 2007 Aug 6.

Lamson, D., Renwick, N., Kapoor, V., Liu, Z., Palacios, G., Ju, J., Dean, A., St George, K., Briese, T. and Ian Lipkin, W. (2006). MassTag polymerase-chain-reaction detection of respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like illness in New York State during 2004-2005. *J. Infect. Dis.* 194: 1398-1402.

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Lee, W.-M., Kiesner, C., Pappas, T., Lee, I., Grindle, K., Jartti, T., Jakiela, B., Lemanske, R.F. Jr., Shult, P.A. and Gern, J.E. (2007). A Diverse group of previously unrecognized human rhinoviruses are common causes of respiratory illnesses in infants. *PLoS ONE* 2(10): e966. doi:10.1371/journal.pone.0000966.

McErlean, P., Shackelton, L.A., Lambert, S.B., Nissen, M.D., Sloots, T.P. and Mackay, I.M. (2007). Characterisation of a newly identified human rhinovirus, HRV-QPM, discovered in infants with bronchiolitis. *J. Clin. Virol.* 39: 67-75 .

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.

Site	Sequence	Comments
VP4/VP2	ALM/SPS	similar to HRV-A
VP2/VP3	TRQ/GLP	similar to *Picornaviridae*
VP3/VP1	IAQ/NPV	similar to HRV-A
VP1/2A	TNV/GPS or GPSDMF/VHT	both similar to HRV-A
2A/2B	EHQ/GVD	similar to HRV-A
2B/2C	SRQ/GDS	similar to HEV-C, PV
2C/3A	IFQ/GLG	no obvious similarity
3A/3B	IAQ/GPY	similar to HRV-A
3B/3C	VAQ/GPE	similar to HRV-A
3C/3D	TTQ/GEI	similar to HEV-D

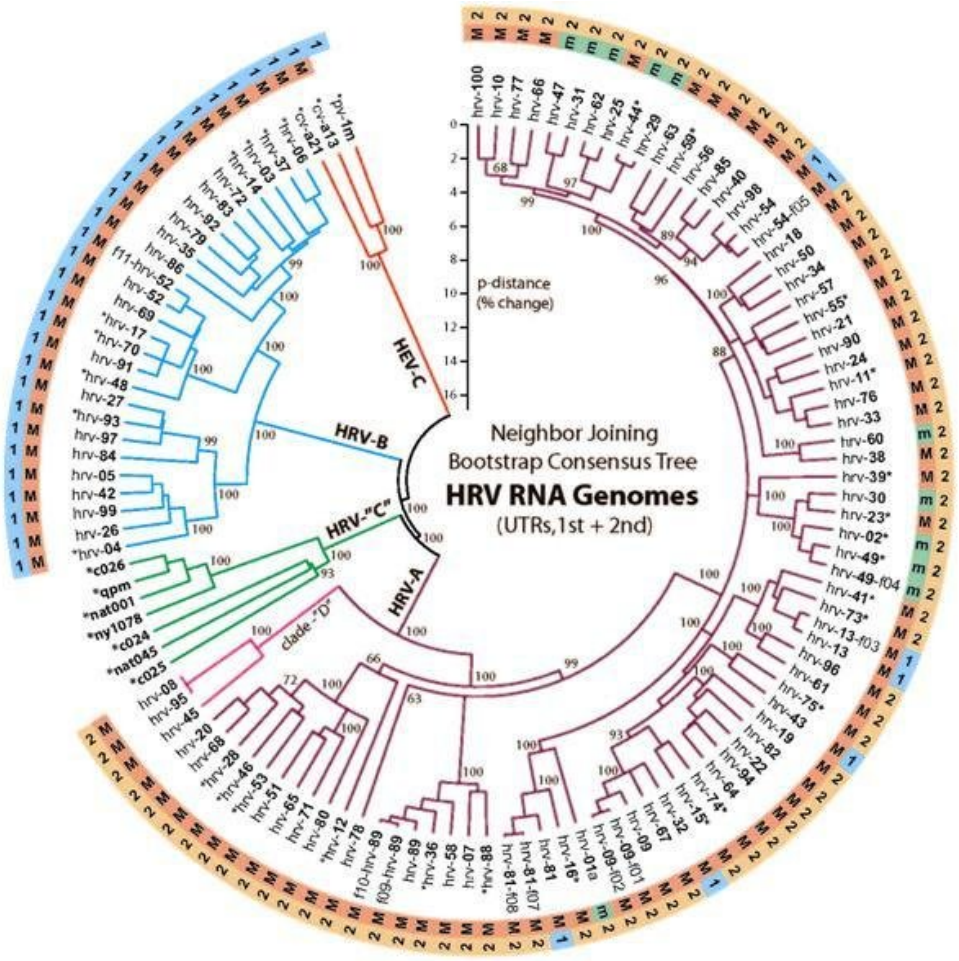

Figure 1. Phylogenetic tree presented at EUROPIC 2008 by Jennifer Rathe ("Resolution of all known HRV-A and HRV-B complete genome sequences, and their relationship to a potential new species, HRV-C").