

Picornavirus Taxonomy: Seventh ICTV Report, Species, and Other Issues

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Abstract. The Seventh Report of the International Committee for the Taxonomy of Viruses (ICTV), to be published next year, will contain a description of the Picornaviridae that, not surprisingly, will be more detailed than in our last report submitted in 1993, and will incorporate the revised assignments and new taxa that have since been agreed with the ICTV. There will also be a major change in the way the Seventh Report lists the members of each genus. To achieve this, the ICTV is promoting the concept of species as a broadly constituted class of viruses, distinguishable from other species by several independent diagnostic criteria. For example, the 7 serotypes of FMDV, each of which is currently listed as a separate species, would be lumped together as one species. This may seem like good sense for FMDV, but there are theoretical and practical objections to doing this with other rhinoviruses, which deterred the Study Group in 1994's from undertaking such fundamental revision of picornavirus taxonomy. We did, however, begin the task of grouping related serotypes into "clusters". These species are continuous in the contentions of the Study Group. However, following renewed requests to the Study Group from the ICTV, we have agreed a compromise, under which the Seventh Report will continue to list serotypes in full, with individual accession numbers and abbreviations, but they will now be grouped into these, subgeneric clusters, these clusters having the status of ICTV-approved "species". No existing serotype name will change, but superimposed above serotype will be the new taxonomic level of species, for which we have had to invent several names like *Human enterovirus A*, *Human enterovirus B*. In time, we hope the identities of these new species will become familiar and prove useful as a rational form of subgeneric classification. It is a common question concerning the Study Group (includid) whether avian encephalomyelitis virus should be assigned to its own genus, (ii) likewise equine rhinovirus type 2, and (iii) what is to do about the fact that the new, human picornavirus-like (HSPV) RNA viruses of insects that have recently been sequenced.

Names and assignments approved¹ since the last ICTV Report

Parechovirus:

The members of this new genus, human parechovirus types 1 and 2, were previously named echovirus 22 and 23, respectively. The new name is a contraction of *parechovirus*. They are highly divergent from all other branches of the Picornaviridae (Fig. 1, 2) and appear not to undergo the usual maturation cleavage in IAB (Fig 5).

Vilyuisk:

Vilyuisk human encephalomyelitis virus (VHEV), a close relative of Theiler's murine encephalomyelitis virus (TMEV), has been transferred to the genus *Cardiovirus*.

Equine rhinitis A virus (ERAV):

Equine rhinitis virus type 1 has been renamed to avoid confusion with human rhinoviruses, and assigned to the genus *Aphthovirus* on account of its many FMDV-like features (Fig 5). These include: axial labial sites of translation initiation, L-protease, and ultra-short 2A. The close alignment of the P1 sequences implies that the structure of the ERAV capsid is distinctly FMDV-like, and this further underlines the close relationship between the P1 sequences of ERAV and FMDV shown in Fig. 1.

Species, a new level of classification between serotype and genus:

Why? To conform with new ICTV guidelines, and to complete the within-genus system of classification previously embarked upon.

The species concept: We shall no longer refer to individual serotypes as "species". Instead, species will comprise groups of closely related strains whose members may differ from each other antigenically, but are otherwise substantially similar. These broader groupings are exactly the same as those that we previously called "clusters", but they are now to be given names which will be included in the Seventh Report.

Definition: A picornavirus species is a polythetic class of phylogenetically related strains which would normally be expected to share (i) a limited range of host and cellular receptors, (ii) a significant degree of compatibility in proteolytic processing, encapsidation and genetic recombination, and (iii) essentially identical genome maps.

Species list: We have prepared a draft list of species, with names and abbreviations, which has the blessing of the ICTV. Copies are available at this poster. [Note that species names, like genus and family names, are capitalised and italicised, as in e.g. "the species *Foot-and-mouth disease virus*"].

"Insect picornaviruses":

The picorna-like viruses of invertebrates are being moved from the Picornaviridae provisionally into a floating genus named "Cricket paralysis-like viruses".

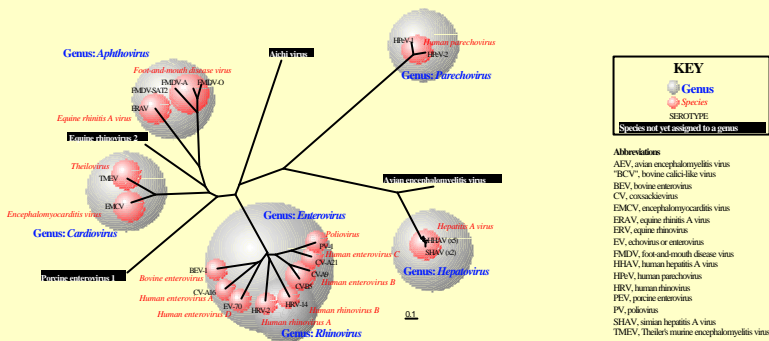


Fig. 1. Neighbor-joining tree of the P1 capsid region based on amino acid similarity matrices. Alignments and trees were produced using Clustal X and plotted using TreeView 1.5.2.

Agenda for Europic '98

1. Agree any amendments to the proposed species list before it is submitted for publication in the Seventh Report.

2. Propose taxonomic assignments, and where necessary genus names, for:

- Equine rhinovirus type 2
- Avian encephalomyelitis virus
- Aichi virus
- Porcine enterovirus type 1*
- Porcine enterovirus type 8
- Ljungjan River virus*

Figs. 1 - 4 illustrate the genetic relationships involving these, recently sequenced, picornaviruses.

Help!

Please give your taxonomy Study Group feedback about what we have done and your suggestions for the future. Our names are at the head of this poster.

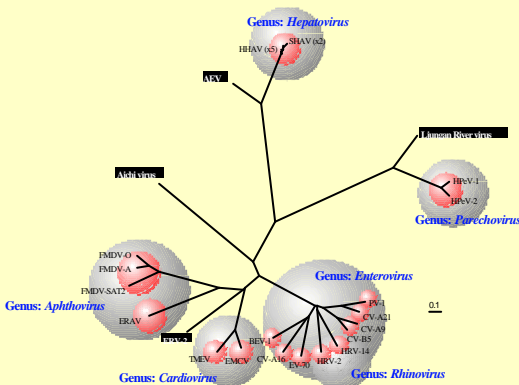


Fig. 3. Neighbor-joining tree of the 1ABC capsid region based on amino acid similarity matrices illustrating the relationship of Ljungjan River virus to the genus *Parechovirus*.

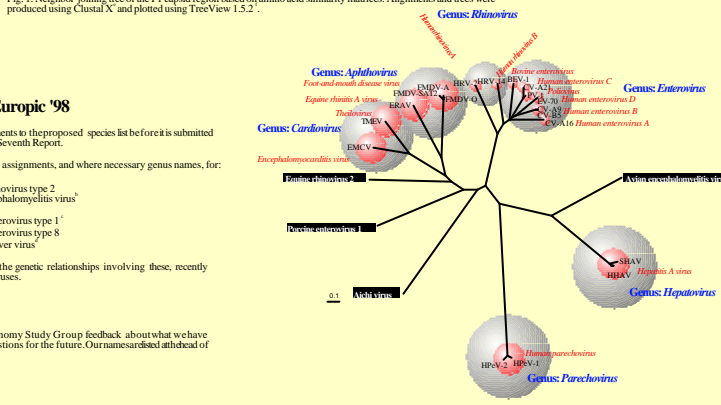


Fig. 2. Neighbor-joining tree of the combined 2C and 3CD regions based on amino acid similarity matrices.

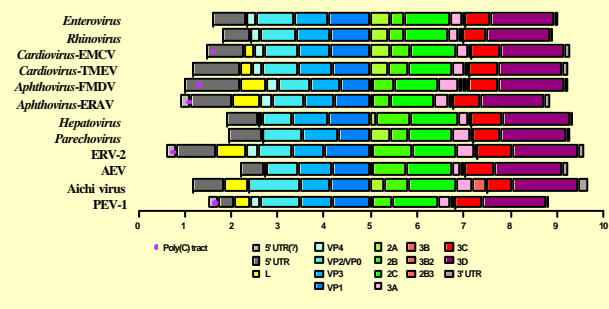


Fig. 5. Schematic diagram showing the genome layout and size of picornavirus genes. The sequences (and lengths) of the shaded 5' UTRs have not yet been determined.

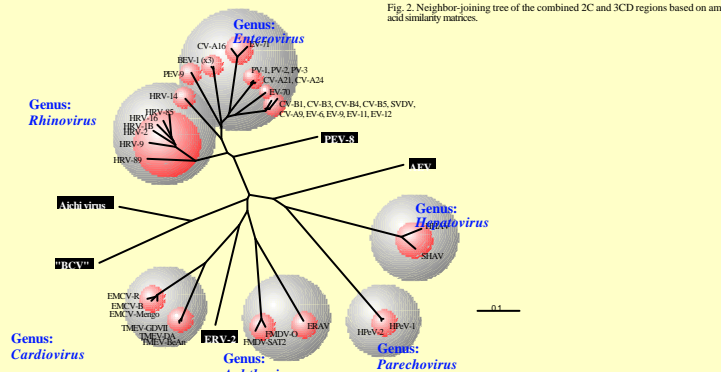


Fig. 4. Neighbor-joining tree of the partial 3D polymerase region based on amino acid similarity matrices illustrating (i) the relationship of porcine enterovirus type 8 (J. H. Peng, F. Lin and N.J. Knowles, unpublished data) to the enterovirus and rhinovirus genera and (ii) the relationship of a sequence obtained from a supposed bovine enteric calicivirus (I.N. Clarke, personal communication, 1997) to the newly described Aichi virus.

References

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- b) Poster V70 by Philip Marvil *et al* at this meeting.
- c) Poster V71 by Michelle Doherty *et al* at this meeting.
- d) Poster V72 by Johansson *et al* at this meeting.
- e) Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F. and Higgins, D.G. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acid Research* **25**: 4876-4882.
- f) Page, R.D.M. (1996). TREEVIEW: An application to display phylogenetic trees on personal computers. *Computer Applications in the Biosciences* **12**: 357-358.

Refer also to our ICTV Picornaviridae Study Group web page at:

<http://www.iah.bbsrc.ac.uk/virus/Picornaviridae/picornastudygroup/psg.htm>

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