

Picornaviridae: the 9th ICTV Report and Beyond

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The family *Picornaviridae* currently consists of 29 species classified into 12 genera (*Enterovirus*, *Cardiovirus*, *Aphthovirus*, *Hepatovirus*, *Parechovirus*, *Erbovirus*, *Kobuvirus*, *Teschovirus*, *Sapelovirus*, *Senecavirus*, *Tremovirus* and *Avihepatovirus*) (1). Three new species proposals are under consideration by the International Committee on Taxonomy of Viruses (ICTV), "Enterovirus F" (bovine enterovirus group B), "Enterovirus J" (SV6, EV-103, EV-108, EV-112 & EV-115) and "Porcine kobuvirus" as well as a proposal to rename all enterovirus species names to remove host associations (e.g. Human enterovirus A to simply Enterovirus A). Additionally, four species/genus proposals are also being considered ("Aquamavirus A" / "Aquamavirus", "Cosavirus A" / "Cosavirus", "Turkey hepatitis virus" / "Megrivirus" and "Salivirus A" / "Salivirus"). However, the number of new picornaviruses being discovered is rapidly increasing with another ~20 viruses in urgent need of classification. Some of these present problems, particularly in genus assignment, and we may need to review criteria for defining genera and perhaps group genera into subfamilies, at least to allow the placement of new species in a subfamily. A recent publication describing a dicistronic virus in dogs (2), which phylogenetically falls among the picornaviruses, means we may have to re-examine the single ORF paradigm.

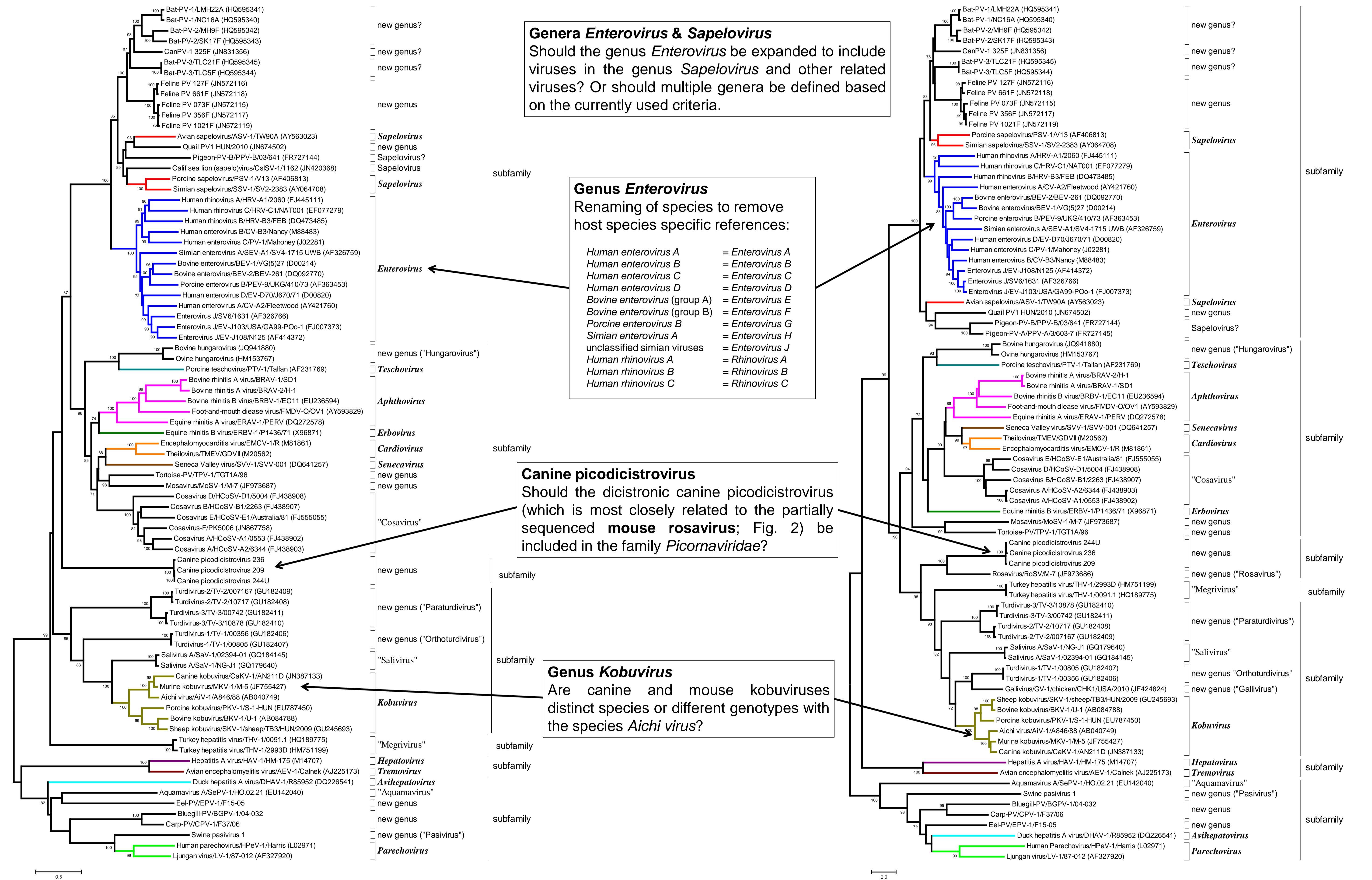


Figure 1. Midpoint-rooted Neighbor-joining tree (MEGA 5, JTT model) of the *Picornaviridae* based on a comparison of the P1 capsid. The 12 current genera are shown in italics. Potential new genera (as suggested in publications) are shown. Suggested subfamilies are also indicated.

Figure 2. Midpoint-rooted Neighbor-joining tree (MEGA 5, JTT model) of the *Picornaviridae* based on a comparison of the 3D^{pol}. The 12 current genera are shown in italics. Potential new genera (as suggested in publications) are shown. Suggested subfamilies are also indicated.

Phylogenetic trees

Different phylogenetic reconstructions (e.g. Neighbor-joining, Maximum Likelihood, Maximum Parsimony) are not always in agreement. This may be partly due to imperfect multiple sequence alignments; these need to be improved. Additionally some viruses have incongruous relationships in different genome regions due to the recombinant nature of some picornaviruses.

There are three major questions to address:

- 1) Should the *Picornaviridae* be divided into a number of subfamilies?
- 2) Should picornavirus genera have a broader, more inclusive definition?
- 3) Should canine picodicistrovirus be included in the *Picornaviridae*?

The latest classification and proposals may be viewed on the *Picornaviridae* Study Group website: <http://www.picornastudygroup.com> and on the ICTV website: <http://talk.ictvonline.org>.

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Your opinions are important to us:
If you have any views on the classification/taxonomy of the *Picornaviridae* please contact one of the Study Group members.