

Taxonomy of Picornaviridae: Current Situation and Possible Future Changes



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Current Picornaviridae taxonomy

Following the recent publication of the 8th ICTV Report on Taxonomy of Viruses (1) and subsequent minor changes, *Picornaviridae* currently consists of 23 species in 9 genera: *Enterovirus*, *Rhinovirus*, *Cardiovirus*, *Aphthovirus*, *Hepatovirus*, *Parechovirus*, *Erbovirus*, *Kobuvirus* and *Teschovirus* (Table 1). The genome organisation associated with each genus is shown in Figure 1.

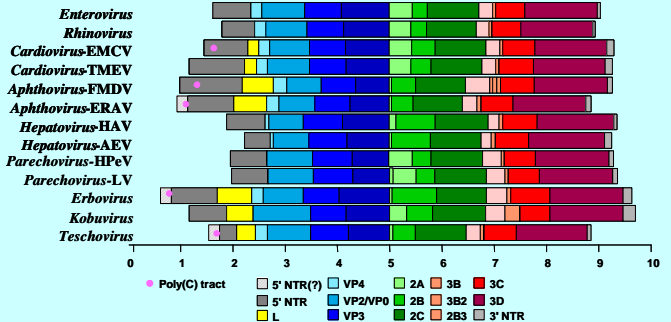


Figure 1. Genome organisation of members of the Picornaviridae family, showing the relative size of protein-encoding and untranslated regions.

Table 1. Classification of the family *Picornaviridae*. The table shows the 9 genera and 23 species (with standard abbreviations), together with virus serotypes included in these.

Genus	Species	Serotypes
<i>Aphthovirus</i>	<i>Foot-and-mouth disease virus</i> (FMDV)	Foot-and-mouth disease virus A, C, O, Asia 1, SAT1, SAT2, SAT3
	<i>Equine rhinitis A virus</i> (ERAV)	Equine rhinitis A virus
<i>Cardiovirus</i>	<i>Encephalomyocarditis virus</i> (EMCV)	Encephalomyocarditis virus,
	<i>Theilovirus</i> (ThV)	Theiler's murine encephalomyelitis virus, Vilyuisk human encephalomyelitis virus, Rat encephalomyelitis virus
<i>Enterovirus</i>	<i>Poliovirus</i> (PV)	Poliovirus 1-3
	<i>Human enterovirus A</i> (HEV-A)	Coxsackievirus A2-10, 12,14,16 & Enterovirus 71,76
	<i>Human enterovirus B</i> (HEV-B)	Coxsackievirus B1-6, Coxsackievirus A9, Enterovirus 69, 73, 74, 75, 77, 78, Echovirus 1-7, 9,11-21,24-27,29-33
	<i>Human enterovirus C</i> (HEV-C)	Coxsackievirus A1,11,13,15,17-22,24
	<i>Human enterovirus D</i> (HEV-D)	Enterovirus 68,70
	<i>Simian enterovirus A</i> (SEV-A)	Simian enterovirus A1
	<i>Bovine enterovirus</i> (BEV)	Bovine enteroviruses 1,2
	<i>Porcine enterovirus A</i> (PEV-A)	Porcine enteroviruses 8
	<i>Porcine enterovirus B</i> (PEV-B)	Porcine enteroviruses 9,10
<i>Erbovirus</i>	<i>Equine rhinitis B virus</i> (ERBV)	Equine rhinitis B virus 1 and 2
<i>Hepatovirus</i>	<i>Hepatitis A virus</i> (HAV)	Hepatitis A virus
	<i>Avian encephalomyelitis-like viruses</i> (AEV)	Avian encephalomyelitis virus
<i>Kobuvirus</i>	<i>Aichi-virus</i> (AiV)	Aichi-virus
	<i>Bovine kobuvirus</i> (BKV)	Bovine kobuvirus
<i>Parechovirus</i>	<i>Human parechovirus</i> (HPeV)	Human parechovirus 1, 2, 3
	<i>Ljungan virus</i> (LV)	Ljungan virus
<i>Rhinovirus</i>	<i>Human rhinovirus A</i> (HRV-A)	Human rhinovirus 1,2,7-13,15,16,18-25,28-34,36,38-41,43-47, 49-68,71-78,80-81,85,88-90,94-96,98,100
	<i>Human rhinovirus B</i> (HRV-B)	Human rhinovirus 3-6,14,17,26,27,35,37,42,48,52,69,70,72,79,83, 84,86,91,92,93,97,99
<i>Teschovirus</i>	<i>Porcine teschovirus</i> (PTV)	Porcine teschovirus 1-11

Issues to be resolved

New picornaviruses, particularly new enteroviruses, are being identified frequently. Although isolates usually fall into one of the existing species, in some cases their taxonomic position is more complex. In addition, as more nucleotide sequences become available, inconsistencies in the existing taxonomy have become evident. The main current issues are:

- Porcine enterovirus 8 is currently a member of the *Porcine enterovirus A* species of *Enterovirus*. However, together with related simian viruses and a virus recently isolated from ducks, it is relatively diverse from other enteroviruses in nucleotide sequence identity terms (Figure 2). These viruses also have a number of features which distinguish them from typical enteroviruses, such as the presence of a leader protein and unusual 5'UTR, and their taxonomic status is currently being evaluated.
- It has long been known that enteroviruses and rhinoviruses are very closely related in sequence and functional terms and this may point to them being amalgamated in one genus. The name *Enterhinovirus* has been suggested for this combined genus.
- Another change being considered is merging the *Poliovirus* species with the *Human enterovirus C* (HEV-C) species, as extensive sequence analysis shows that members of these species cluster closely together.
- Similarities between picornaviruses and several other positive sense RNA viruses could justify the establishment of higher taxonomic groupings, such as an Order of picornavirus-like viruses.

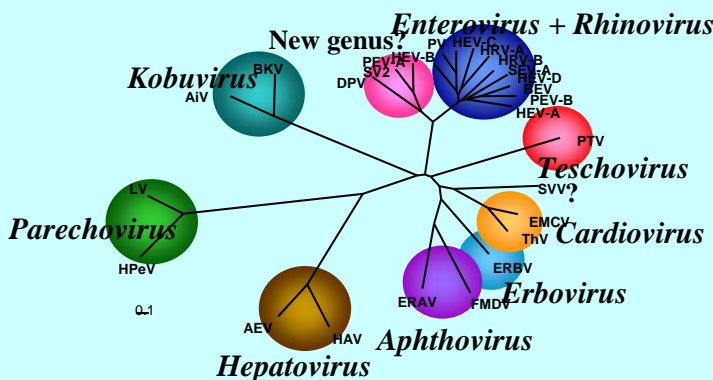


Figure 2. Genetic relationships (unrooted Neighbor-joining tree of the P1 region derived using Clustal X) among the existing *Picornaviridae* genera (marked with coloured circles) and species listed in Table 1. Potentially new species and/or genera are also included.

Reference

1. Stanway, G., Brown, F., Christian, P., Hovi, T., Hyypiä, T., King, A.M.Q., Knowles, N.J., Lemon, S.M., Minor, P.D., Pallansch, M.A., Palmenberg, A.C. and Skern, T. (2004). Picornaviridae. In: "Virus Taxonomy, VIIIth Report of the ICTV" (C.M. Fauquet, M.A. Mayo, J. Maniloff, U. Desselberger, and L.A. Ball, eds), 757-778. Elsevier/Academic Press, London.