

Taxonomy of the *Picornaviridae*: Proposed New Species and Description of a 10th Genus

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Current Picornavirus Taxonomy

The 7th Report on virus taxonomy was published in 2000. However, since that report two major changes have been ratified - the creation of three new genera (*Kobuvirus*, *Erbovirus*, *Teschovirus*), each containing one species, and subsequently the creation of a second species (*Ljungan virus*) within the *Parechovirus* genus. The current situation is summarised in Table 1. One of the main criteria for defining genera and species is the sequence relationship between viruses, using amino acid sequence identities in the P1 and 2C+3CD regions. These regions are chosen as P1 defines the antigenic properties, the traditional way of defining the identity of viruses, while 2C+3CD is usually the most conserved and readily aligned region of the genome. Fig. 1 shows a comparison of the P1 capsid region for representatives of each of the current picornavirus species and two possible species within a new genus.

Table 1. Current picornavirus classification

Genus	Species	Abbrev.	No of serotypes	Serotypes
<i>Enterovirus</i>	<i>Poliovirus</i>	PV	3	PV-1, 2, 3
	<i>Human enterovirus A</i>	HEV-A	12	CV-A2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16; EV-71
	<i>Human enterovirus B</i>	HEV-B	37	CV-B1, 2, 3, 4, 5 (incl. SVDV); 6; CV-A9; E-1, 2, 3, 4, 5, 6, 7, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 24, 25, 26, 27, 29, 30, 31, 32, 33; EV-69, 73
	<i>Human enterovirus C</i>	HEV-C	11	CV-A1, 11, 13, 15, 17, 18, 19, 20, 21, 22, 24
	<i>Human enterovirus D</i>	HEV-D	2	EV-68, EV-70
<i>Rhinovirus</i>	<i>Human rhinovirus A</i>	HRV-A	74	See Table 2
	<i>Human rhinovirus B</i>	HRV-B	25	See Table 2
	<i>Equine rhinitis B virus</i>	ERBV	2	ERBV-1, ERBV-2
<i>Cardiovirus</i>	<i>Encephalomyocarditis virus</i>	EMCV	1	EMCV
	<i>Theilovirus</i>	THV	2-3	TMEV, VHEV, (REV)
<i>Aphthovirus</i>	<i>Foot-and-mouth disease virus</i>	FMDV	7	FMDV-O, A, C, Asia1, SAT1, SAT2, SAT3
	<i>Equine rhinitis A virus</i>	ERAV	1	ERAV
<i>Hepatovirus</i>	<i>Hepatitis A virus</i>	HAV	1	HAV
	"Avian encephalomyelitis-like viruses"	AELV	1	AELV
<i>Parechovirus</i>	<i>Human parechovirus</i>	HPeV	2	HPeV-1, HPeV-2
	<i>Ljungan virus</i>	LV	1	LV
<i>Erbovirus</i>	<i>Equine rhinitis B virus</i>	ERBV	2	ERBV-1, ERBV-2
	<i>Kobuvirus</i>	AIV	1	AIV
<i>Teschovirus</i>	<i>Porcine teschovirus</i>	PTV	11	PTV-1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11

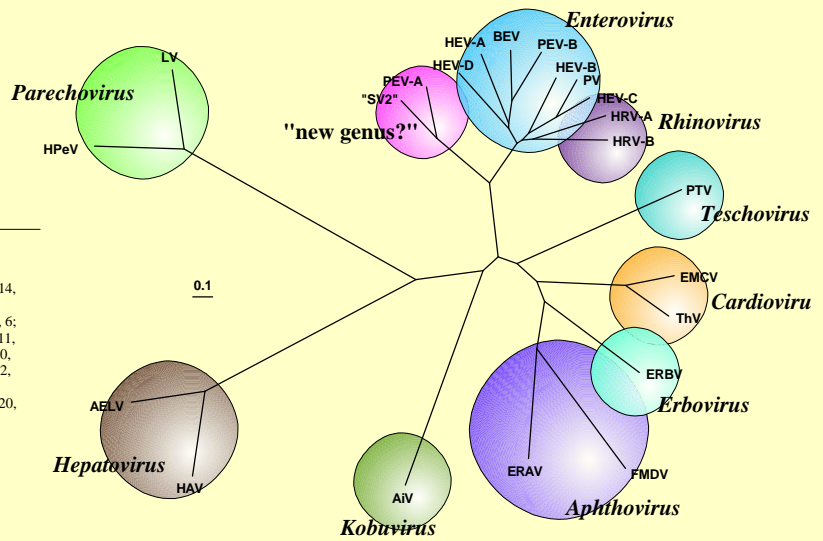


Fig. 1. Unrooted Neighbor-joining tree showing the relationships between the P1 capsid-coding regions of the 20 recognised species (in 9 genera), Ljungan virus (LV) and SV2. For a list of abbreviations see Table 1.

New Information on Picornaviruses

Simian and porcine viruses

Recently, a large amount of sequence data has been generated from simian and porcine viruses and this sheds light on their current classification as simian and porcine enteroviruses (Oberste et al., 2002; Krumboltz et al., 2002). The information suggests that it will be necessary to create new species within the enterovirus genus and an additional genus (see panel to left), containing both simian and porcine members, is indicated (Oberste et al., 2002; Krumboltz et al., 2002). See Figs. 1 and 2 and Table 3.

Human rhinoviruses

The generation of sequence information from all human rhinoviruses (Savolainen et al., 2002) allows each serotype to be assigned to one of the two existing species, *Human rhinovirus A* and *Human rhinovirus B*. Although not formally the remit of the Picornavirus Study Group, as this decision is below the species level, we would suggest that the rhinovirus serotypes are assigned as in Table 2. One complication is that one serotype, HRV-87, does not fall into either species, but appears to be a member of the *Human enterovirus D* species, despite fulfilling the rhinovirus-specific criterion of acid lability (Andeweg et al., 1999; Savolainen et al., 2002).

Equine rhinovirus 3

The genome sequence of the unassigned equine rhinovirus 3 (ERhV-3) has recently been determined (Huang et al., 2001) enabling its placement within the *Erbovirus* genus as a second serotype within the species *Equine rhinitis B virus*. Thus, ERBV has been renamed ERBV-1 and ERhV-3 has been renamed ERBV-2.

Table 2. Assignment of human rhinoviruses to species

Human rhinovirus	Species
Human rhinovirus A	1, 2, 7, 8, 9, 10, 11, 12, 13, 15, 16, 18, 19, 20, 21, 22, 23, 24, 25, 28, 29, 30, 31, 32, 33, 34, 36, 38, 39, 40, 41, 43, 44, 45, 46, 47, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 71, 73, 74, 75, 76, 77, 78, 80, 81, 82, 85, 88, 89, 90, 94, 95, 96, 98, 100
Human rhinovirus B	3, 4, 5, 6, 14, 17, 26, 27, 35, 37, 42, 48, 52, 69, 70, 72, 79, 83, 84, 86, 91, 92, 93, 97, 99

Human rhinovirus 87, based on 5' UTR and VP4/2 sequences, is an enterovirus and is almost identical to human enterovirus 68 (species *Human enterovirus D*) (Andeweg et al., 1999; Savolainen et al., 2002).

References

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A Possible Tenth Genus

Two members of a possible new genus, closely related to the *Enterovirus* and *Rhinovirus* genera, have recently been sequenced. They are porcine enterovirus 8 (Krumboltz et al., 2002) and SV2 (Oberste et al., 2002; Oberste et al., unpublished data). The VP1 coding regions of a number of other simian viruses have been sequenced and shown to be related to SV2 (Oberste et al., 2002). These VP1 relationships are shown in Table 3 and Fig. 2.

Although these viruses are closely related to the enteroviruses, they have some very distinctive features which, along with their phylogenetic distinctness, may warrant their classification in a new genus:

- a leader polypeptide precedes the capsid region;
- the 2A, 2B and 3A polypeptides are very different from the enteroviruses. These proteins (including L) also differ considerably between PEV-8 and SV2.

A proposal to create this tenth genus will be considered by the Study Group in relation to the ongoing debate about whether the rhino/enteroviruses should continue to be split into separate genera (see Fig. 1).

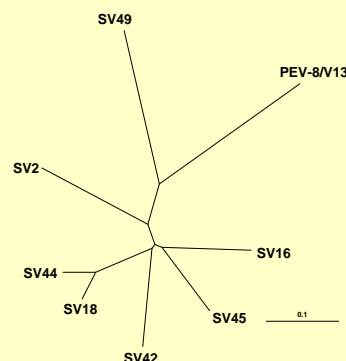


Fig. 2. Unrooted Neighbor-joining tree based on a comparison of complete VP1 nucleotide sequences.

Table 3. Relationships between the VP1-coding regions of members of a possible new genus.

	SV16	SV45	SV18	SV44	SV42	SV2	SV49	PEV-8
SV16	0.0*							
SV45	23.0	0.0						
SV18	25.9	24.9	0.0					
SV44	27.6	25.5	8.4	0.0				
SV42	27.3	24.7	25.8	25.5	0.0			
SV2	31.8	30.6	32.5	34.4	33.1	0.0		
SV49	42.1	41.6	41.3	41.5	44.5	42.3	0.0	
PEV-8	45.4	45.3	43.6	43.0	44.7	45.9	44.4	0.0

* percentage nucleotide difference

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