This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2013.001a-aaaV***	(to be completed by ICTV officers)

Short title: Rationalization and extension of the taxonomy of the family Parvoviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)					
	1 ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☒	**9** ☒	

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Parvoviridae

ICTV-EC or Study Group comments and response of the proposer:

EC comments: Add table showing how current species relate to the new ones. Explain scales on phylogenetic trees.
Proposer response: Table added on page 8. Note on scales added to page 59. Index on page 2 amended to correspond to new pagination.

Date first submitted to ICTV:	28th May 2013
Date of this revision (if different to above):	19 July 2013

Index

Summary

CURRENT TAXONOMY

Family *Parvoviridae*

PROPOSED TAXONOMY

Name changes in bold blue type

New genera in red bype

Vertebrate hosts

Subfamily *Parvovirinae*

Genus	# species	# viruses or strains
Amdovirus	1	1
Bocavirus	2	6
Dependovirus	12	13
Erythrovirus	4	9
Parvovirus	12	18

3 new genera

5 names expanded

Species identity levels decreased and new species introduced

Binomial species names used

Subfamily *Parvovirinae*

Genus	# species	# viruses or strains
*Amdo**parvo**virus*	2	2
Aveparvovirus	1	2
*Boca**parvo**virus*	12	22
Copiparvovirus	2	2
*Dependo**parvo**virus*	7	23
*Erythro**parvo**virus*	6	12
***Proto**parvovirus*	5	25
Tetraparvovirus	6	10

Arthropod hosts

Subfamily *Densovirinae*

Genus	# species	# viruses or strains
Brevidensovirus	2	2
Densovirus	2	2
Iteravirus	1	1
Pefudensovirus	1	1

2 new genera for shrimp viruses

2 names expanded

Pefudensovirus removed and viruses transferred into *Ambidensovirus*

Species identity levels decreased and new species introduced

Binomial species names used

Subfamily *Densovirinae*

Genus	# species	# viruses or strains
***Ambi**densovirus*	6	11
Brevidensovirus	2	8
Hepandensovirus	1	7
*Itera**denso**virus*	5	6
Penstyldensovirus	1	4

The classification of the family *Parvoviridae* was last modified in 1994, prior to publication of the 8th ICTV Report, and is now significantly dated. To address this issue, the Study Group has carried out a root and branch re-evaluation of the taxonomic structure and nomenclature of the family. This prompted a reassessment of the criteria by which viruses are assigned to taxa, and was followed by radical modifications at the level of genus and species. However, the family remains divided into two subfamilies: *Parvovirinae*, which is defined predominantly by the ability of constituent viruses to infect vertebrate hosts, and *Densovirinae*, which includes viruses that infect arthropods, most notably insects but now extended to include decapod shrimp.

The proposals introduce new taxa into both subfamilies, resolve one misclassified species, and inject clarity by employing the following systematic measures (see Module 9 for details).

1. Specifying the level of sequence similarity required for viruses to belong to the same genus, and decreasing the current level of sequence similarity required for viruses to belong to the same species. The former will define typical genus demarcation levels for the field, while the latter will facilitate recognition of major phylogenetic branches within the genera and will help eliminate the current apparent near-identity between species and the eponymous viruses they represent.

2. For species, establishing systematic binomial names that do not recapitulate virus names.

3. For genera, expanding the current names to indicate subfamily affiliation and reduce ambiguity resulting from vernacular use of different taxon levels ("parvovirus" can be used currently to represent a member of the family *Parvoviridae*, the subfamily *Parvovirinae* or the genus *Parvovirus*, and "densovirus" to represent a member of the subfamily *Densovirinae* or the genus *Densovirus*).

In accordance with these measures, the proposals involve renaming most current genera, with the exceptions of the genera *Brevidensovirus* (which will remain unchanged) and *Pefudensovirus* (which will be removed), and creating additional genera. Viruses in the genus *Pefudensovirus* share multiple genomic characteristics with those in the genus *Densovirus*, and all of these viruses, plus 4 newly identified ones, are monophyletic and share a unique reliance on ambisense transcription. Thus, the proposals involve effectively transferring viruses in the genus *Pefudensovirus* into the renamed genus *Ambidensovirus* (currently *Densovirus*).

Decreasing the required level of sequence similarity at the species level effectively does away with current species divisions, and in some instances results in the incorporation of several viruses currently distributed among more than one species into a single, proposed species. To avoid the contortions that would be required to accomplish this by removal of some species and renaming of others, a more straightforward approach has been taken, whereby all current species are removed and all proposed species are created afresh. The text of the proposal makes it clear where viruses in current species have ended up. The new criteria now require extensive sequence data (see below), and this has resulted in removal of a few species for the viruses in which no such data are available.

The lists in the 9th ICTV Report include, as members of the subfamilies or genera, some viruses that that have not been approved as species. Since these viruses are beyond the purview of the ICTV, they are not specified in the proposals and will be dealt with by the Study Group as a separate issue of value to the field. Note that we emphatically do not propose tampering with virus names, whether classified into species or not.

Virus discovery approaches have been instrumental in identifying several important but previously unknown parvoviral hierarchies. However, reliance on PCR typically confounds the inclusion in genome sequences of the hairpin termini, which have complex secondary structures. To accommodate these important considerations, while avoiding inclusion of viral sequence fragments integrated into host genomes or metagenomic data that lack clear host attribution, the following virus definition was employed throughout these proposals.

In order for an agent to be classified in the family *Parvoviridae*, it must be judged to be an authentic parvovirus on the basis of having been isolated and sequenced or, failing this, on the basis of having been sequenced in tissues, secretions, or excretions of unambiguous host origin, supported by evidence of its distribution in multiple individual hosts in a pattern that is compatible with dissemination by infection. The sequence must be in one piece, contain all the nonstructural (NS) and virus particle (VP) coding regions, and meet the size constraints and motif patterns typical of the family.

All viruses included in the restructured family conform to this definition.

The current and proposed taxonomy are shown overleaf. Further details are given in the individual proposals.

Current taxonomy

GENUS	SPECIES (type species in bold)
Subfamily Parvovirinae	
Amdovirus	***Aleutian mink disease virus***
Bocavirus	***Bovine parvovirus***
	Canine minute virus
Dependovirus	*Adeno-associated virus-1*
	Adeno-associated virus-2
	Adeno-associated virus-3
	Adeno-associated virus-4
	Adeno-associated virus-5
	Avian adeno-associated virus
	Bovine adeno-associated virus
	Canine adeno-associated virus
	Duck parvovirus
	Equine adeno-associated virus
	Goose parvovirus
	Ovine adeno-associated virus
Erythrovirus	***Human parvovirus B19***
	Pig-tailed macaque parvovirus
	Rhesus macaque parvovirus
	Simian parvovirus
Parvovirus	*Chicken parvovirus*
	Feline panleukopenia virus
	H-1 parvovirus
	HB parvovirus
	Kilham rat virus
	Lapine parvovirus
	LuIII virus
	Minute virus of mice
	Mouse parvovirus 1
	Porcine parvovirus
	RT parvovirus
	Tumor virus X
Subfamily Densovirinae	
Brevidensovirus	***Aedes aegypti densovirus***
	Aedes albopictus densovirus
Densovirus	*Galleria mellonella densovirus*
	Junonia coenia densovirus
Iteravirus	***Bombyx mori densovirus***
Pefudensovirus	***Periplaneta fuliginosa densovirus***

Proposed taxonomy

GENUS	SPECIES (type species in bold)
Subfamily Parvovirinae	
Amdoparvovirus	***Carnivore amdoparvovirus 1***
	Carnivore amdoparvovirus 2
Aveparvovirus	***Galliform aveparvovirus 1***
Bocaparvovirus	*Carnivore bocaparvovirus 1*
	Carnivore bocaparvovirus 2
	Carnivore bocaparvovirus 3
	Pinniped bocaparvovirus 1
	Pinniped bocaparvovirus 2
	Primate bocaparvovirus 1
	Primate bocaparvovirus 2
	Ungulate bocaparvovirus 1
	Ungulate bocaparvovirus 2
	Ungulate bocaparvovirus 3
	Ungulate bocaparvovirus 4
	Ungulate bocaparvovirus 5
Copiparvovirus	***Ungulate copiparvovirus 1***
	Ungulate copiparvovirus 2
Dependoparvovirus	***Adeno-associated dependoparvovirus A***
	Adeno-associated dependoparvovirus B
	Anseriform dependoparvovirus 1
	Avian dependoparvovirus 1
	Chiropteran dependoparvovirus 1
	Pinniped dependoparvovirus 1
	Squamate dependoparvovirus 1
Erythroparvovirus	***Primate erythroparvovirus 1***
	Primate erythroparvovirus 2
	Primate erythroparvovirus 3
	Primate erythroparvovirus 4
	Rodent erythroparvovirus 1
	Ungulate erythroparvovirus 1
Protoparvovirus	*Carnivore protoparvovirus 1*
	Primate protoparvovirus 1
	Rodent protoparvovirus 1
	Rodent protoparvovirus 2
	Ungulate protoparvovirus 1
Tetraparvovirus	*Chiropteran tetraparvovirus 1*
	Primate tetraparvovirus 1
	Ungulate tetraparvovirus 1
	Ungulate tetraparvovirus 2
	Ungulate tetraparvovirus 3
	Ungulate tetraparvovirus 4
Subfamily Densovirinae	
Ambidensovirus	*Blattodean ambidensovirus 1*
	Blattodean ambidensovirus 2
	Dipteran ambidensovirus 1

	Hemipteran ambidensovirus 1
	Lepidopteran ambidensovirus 1
	Orthopteran ambidensovirus 1
Brevidensovirus	***Dipteran brevidensovirus 1***
	Dipteran brevidensovirus 2
Hepandensovirus	***Decapod hepandensovirus 1***
Iteradensovirus	***Lepidopteran iteradensovirus 1***
	Lepidopteran iteradensovirus 2
	Lepidopteran iteradensovirus 3
	Lepidopteran iteradensovirus 4
	Lepidopteran iteradensovirus 5
Penstyldensovirus	***Decapod penstyldensovirus 1***

Correspondence between current and proposed species

CURRENT SPECIES	PROPOSED SPECIES
Subfamily Parvovirinae	
Aleutian mink disease virus	*Carnivore amdoparvovirus 1*
Bovine parvovirus	*Ungulate bocaparvovirus 1*
Canine minute virus	*Carnivore bocaparvovirus 1*
Adeno-associated virus-1	*Adeno-associated dependoparvovirus A*
Adeno-associated virus-2	*Adeno-associated dependoparvovirus A*
Adeno-associated virus-3	*Adeno-associated dependoparvovirus A*
Adeno-associated virus-4	*Adeno-associated dependoparvovirus A*
Adeno-associated virus-5	*Adeno-associated dependoparvovirus B*
Avian adeno-associated virus	*Avian dependoparvovirus 1*
Bovine adeno-associated virus	*Adeno-associated dependoparvovirus B*
Canine adeno-associated virus	*[Abolished]*
Duck parvovirus	*Anseriform dependoparvovirus 1*
Equine adeno-associated virus	*[Abolished]*
Goose parvovirus	*Anseriform dependoparvovirus 1*
Ovine adeno-associated virus	*[Abolished]*
Human parvovirus B19	*Primate erythroparvovirus 1*
Pig-tailed macaque parvovirus	*Primate erythroparvovirus 4*
Rhesus macaque parvovirus	*Primate erythroparvovirus 3*
Simian parvovirus	*Primate erythroparvovirus 2*
Chicken parvovirus	*Galliform aveparvovirus 1*
Feline panleukopenia virus	*Carnivore protoparvovirus 1*
H-1 parvovirus	*Rodent protoparvovirus 1*
HB parvovirus	*[Abolished]*
Kilham rat virus	*Rodent protoparvovirus 1*
Lapine parvovirus	*[Abolished]*
LuIII virus	*Rodent protoparvovirus 1*
Minute virus of mice	*Rodent protoparvovirus 1*
Mouse parvovirus 1	*Rodent protoparvovirus 1*
Porcine parvovirus	*Ungulate protoparvovirus 1*
RT parvovirus	*[Abolished]*
Tumor virus X	*Rodent protoparvovirus 1*
Subfamily Densovirinae	
Aedes aegypti densovirus	*Dipteran brevidensovirus 1*
Aedes albopictus densovirus	*Dipteran brevidensovirus 1*
Galleria mellonella densovirus	*Lepidopteran ambidensovirus 1*
Junonia coenia densovirus	*Lepidopteran ambidensovirus 1*
Bombyx mori densovirus	*Lepidopteran iteradensovirus 1*
Periplaneta fuliginosa densovirus	*Blattodean ambidensovirus 1*

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001aV***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Amdoparvovirus* (was *Amdovirus*)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Carnivore amdoparvovirus 1
Carnivore amdoparvovirus 2

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Amdoparvovirus*

The current species is in black italics and proposed species are in blue italics. The current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Carnivore amdoparvovirus 1 (type species)				
Aleutian mink disease virus (current type species)				
	Aleutian mink disease virus-G	M20036	(AMDV-G)	
Carnivore amdoparvovirus 2				
	Gray fox amdovirus	JN202450	(GFAV)	1

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 2).

New species containing a virus not included in previously recognized taxa:

Carnivore amdoparvovirus 2. Gray fox amdovirus was identified in the tissues of foxes in Sonoma County, California. Genome characteristics resemble those of the type species, and it similarly lacks a cognate phospholipase 2 (PLA2) domain, which is commonly used by members of the family to penetrate bilayers during cell entry (Module 9, Table 1).

Reference:

1. Li L, Pesavento PA, Woods L, Clifford DL, Luff J, Wang C, Delwart E. 2011. Novel amdovirus in gray foxes. Emerg. Infect. Dis. 17:1876-8.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001bV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Aveparvovirus* (new)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Galliform aveparvovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Aveparvovirus*

The current species is in black italics and the proposed species in blue italics. The current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Galliform aveparvovirus 1 (type species)				
Chicken parvovirus				
	Chicken parvovirus ABU-P1	GU214704	(ChPV)	1
	Turkey parvovirus-260	GU214706	(TuPV)	2, 3

The species *Chicken parvovirus* was accepted as a member of genus *Parvovirus* many years ago, but the virus turned out to be a circovirus. Later, an authentic chicken parvovirus was identified (details above) and incorrectly attributed to the vacant *Parvovirus* species in the 9th Report. The proposal is to remove the species from the genus *Parvovirus* and move the cognate virus into the new species *Galliform aveparvovirus 1* in the new genus *Aveparvovirus*.

The viruses in this species are widespread in turkeys and chickens in the United States and Europe, and are highly infectious in young poultry but of uncertain pathology. Two strains have been reported, encoding NS1 proteins that are >99% identical to each other but <30% identical to those of all other parvoviruses, indicating that they represent a single species in a new genus (Module 9, Tree 2).

References:

1. Kisary, J. 1985. Experimental infection of chicken embryos and day-old chickens with parvovirus of chicken origin. Avian Pathol. 14:1-7.
2. Day JM, Zsak L. 2010. Determination and analysis of the full-length chicken parvovirus genome. Virology 399:59-64.
3. Marusak RA, Guy JS, Abdul-Aziz TA, West MA, Fletcher OJ, Day JM, Zsak L, Barnes HJ. 2010. Parvovirus-associated cerebellar hypoplasia and hydrocephalus in day old broiler chickens. Avian Dis. 54:156-60.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001cV***	(assigned by ICTV officers)

To create 12 new species within:

Genus:	***Bocaparvovirus* (was *Bocavirus*)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Carnivore bocaparvovirus 1
Carnivore bocaparvovirus 2
Carnivore bocaparvovirus 3
Pinniped bocaparvovirus 1
Pinniped bocaparvovirus 2
Primate bocaparvovirus 1
Primate bocaparvovirus 2
Ungulate bocaparvovirus 1
Ungulate bocaparvovirus 2
Ungulate bocaparvovirus 3
Ungulate bocaparvovirus 4
Ungulate bocaparvovirus 5

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Bocaparvovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Carnivore bocaparvovirus 1				
Canine minute virus				
	Canine minute virus	FJ214110	(CnMV)	
Carnivore bocaparvovirus 2				
	Canine bocavirus 1	JN648103	(CBoV)	1
Carnivore bocaparvovirus 3				
	Feline bocavirus	JQ692585	(FBoV)	2
Pinniped bocaparvovirus 1				
	California sea lion bocavirus 1	JN420361	(CslBoV1)	3
	California sea lion bocavirus 2	JN420366	(CslBoV2)	3
Pinniped bocaparvovirus 2				
	California sea lion bocavirus 3	JN420365	(CslBoV3)	3
Primate bocaparvovirus 1				
	Human bocavirus 1	DQ000496	(HBoV1)	4, 5, 8, 9, 12, 13
	Human bocavirus 3	EU918736	(HBoV3)	6
	Gorilla bocavirus	HM145750	(GBoV)	10, 11
Primate bocaparvovirus 2				
	Human bocavirus 2a TU	FJ973558	(HBoV2a-TU)	7
	Human bocavirus 2b NI	FJ973560	(HBoV2b-NI)	7
	Human bocavirus 2c PK	FJ170278	(HBoV2c-PK)	7
	Human bocavirus 4 NI	FJ973561	(HBoV4-NI)	7
Ungulate bocaparvovirus 1 (type species)				
Bovine parvovirus (current type species)				
	Bovine parvovirus	DQ335247	(BPV)	
Ungulate bocaparvovirus 2				
	Porcine bocavirus 1	HM053693	(PBoV1)	14
	Porcine bocavirus 2	HM053694	(PBoV2)	14
	Porcine bocavirus A6	HQ291309	(PBoV-A6)	15
Ungulate bocaparvovirus 3				
	Porcine bocavirus SX	HQ223038	(PBoV-SX)	16
Ungulate bocaparvovirus 4				
	Porcine bocavirus H18	HQ291308	(PBoV-H18)	15
Ungulate bocaparvovirus 5				
	Porcine bocavirus 3	JF429834	(PBoV3)	17
	Porcine bocavirus 4-1	JF429835	(PBoV4-1)	17
	Porcine bocavirus 4-2	JF429836	(PBoV4-2)	17

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 2). Species with like names are numbered according to the date of their cited GenBank submission.

All of the newly proposed bocaparvoviruses have been identified predominantly in fecal and/or respiratory samples from both healthy and diseased animals, although they have also more rarely been found in serum and tissues. Epidemiological analysis suggests that they are typically widespread in their respective host populations. Among other characteristics (Module 9, Table 1), they all encode a unique type of ancillary protein, NP1, which is not found in viruses from any other genus.

New species containing viruses not previously included in recognized taxa:

Primate bocaparvovirus 1 and *Primate bocaparvovirus 2*. Human bocavirus 1 (HBoV1) was first identified using virus discovery approaches in respiratory swabs from children with lower respiratory tract infections (ref. 4). Although most commonly detected in human secretions and excretions, it can also be found less frequently in serum, cerebrospinal fluid and tonsillar tissues (ref, 5). Serology indicates that the virus is experienced by >90% of the human population, often early in life, and is present in most regions of the world. By 2010, three additional genotypes, HBoV2 to 4, had been identified in human stool samples from children with gastrointestinal illness (refs. 6 and 7). These genotypes may also be distributed globally, but their seroepidemiology has been complicated by cross-reactions (ref. 8). Although most commonly detected in association with various other viruses, overall there is significant evidence linking HBoV1 with respiratory tract infections, some data linking HBoV2 with gastroenteritis, and little evidence that the less abundant HBoV3 and 4 forms are pathogenic (ref. 9). A closely related gorilla virus was similarly first detected in stool samples from 3 groups of western gorillas (ref. 10), and seroepidemiological studies show that it is commonly experienced by wild-caught chimpanzees (73%) and gorillas (36%) in the Cameroons (ref. 11).

Although human bocaviruses have long resisted all attempts to amplify them in culture, advances in determining the sequences of HBoV1 terminal hairpins allowed development of an infectious plasmid clone, which was used to identify transfectable cell lines that are capable of generating a single burst of virus in culture (ref. 12, GenBank JQ923422). HBoV1 particles generated in such cells were then used to infect polarized primary airway epithelial cultures and shown to allow viral gene expression and replication, while also recapitulating diagnostic aspects of the human infection (ref. 13), thus opening the way for detailed laboratory study of these viruses.

Ungulate bocaparvovirus 1 through *Ungulate bocaparvovirus 5*. Multiple porcine viruses that segregate into 5 distinct species have been reported, all of which are distributed widely in geographically separated host populations (refs. 14-17). Predominantly detected in stool samples, they have also been detected more rarely in serum and lymph nodes. A sixth potential species (Module 9, Tree 2), represented by porcine bocavirus-5 JS, lacks reported epidemiological data, and is not yet proposed for classification (ref. 18).

Pinniped bocaparvovirus 1 and *Pinniped bocaparvovirus 2*. Viruses in these species were identified in fecal samples from three separate groups of Californian sea lions (ref. 3), infecting 38% of the individual animals and proving extremely abundant in ~15%. Although designated pinniped for clarity, rather than carnivore, viruses in these species cluster strongly with feline and canine bocaviruses (Module 9, Tree 2).

Carnivore bocaparvovirus 2 and *Carnivore bocaparvovirus 3.* Canine bocavirus genomes have been identified predominantly in respiratory samples (ref. 1), infecting 23% of the individual

animals tested in one study but varying from <2% to 59% depending on the animal sub-population in question. Feline bocavirus, by contrast, was found commonly in fecal samples (7.2%), occasionally in kidney (2%) and blood (0.8%), and more rarely in nasal aspirates (ref. 2). Remarkably, NS expression strategies exhibited by these viruses require splicing to generate full length forms of NS1, thus more closely resembling the human viruses identified by virus discovery approaches than the founding viruses in this genus, bovine parvovirus and canine minute virus, which have been propagated extensively in culture.

References:

1. Kapoor A, Mehta N, Dubovi EJ, Simmonds P, Govindasamy L, Medina JL, Street C, Shields S, Lipkin WI. 2012. Characterization of novel canine bocaviruses and their association with respiratory disease. J. Gen. Virol. 93:341-6
2. Lau SK, Woo PC, Yeung HC, Teng JL, Wu Y, Bai R, Fan RY, Chan KH, Yuen KY. (2012). Identification and characterization of bocaviruses in cats and dogs reveals a novel feline bocavirus and a novel genetic group of canine bocavirus J. Gen. Virol. 93:1573-82.
3. Li L, Shan T, Wang C, Cote C, Kolman J, Onions D, Gulland FM, Delwart E. 2011. The fecal viral flora of California sea lions. J. Virol. 85:9909-17.
4. Allander T, Tammi MT, Eriksson M, Bjerkner A, Tiveljung-Lindell A, Andersson B. 2005. Cloning of a human parvovirus by molecular screening of respiratory tract samples. Proc. Natl. Acad. Sci. USA 102:12891-6.
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11. Sharp CP, LeBreton M, Kantola K, Nana A, Diffo Jle D, Djoko CF, Tamoufe U, Kiyang JA, Babila TG, Ngole EM, Pybus OG, Delwart E, Delaporte E, Peeters M, Soderlund-Venermo M, Hedman K, Wolfe ND, Simmonds P. 2010. Widespread infection with homologues of human parvoviruses B19, PARV4, and human bocavirus of chimpanzees and gorillas in the wild. J. Virol. 84:10289-96.
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MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001dV***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Copiparvovirus* (new)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Ungulate copiparvovirus 1
Ungulate copiparvovirus 2

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Copiparvovirus*

Proposed species are in blue italics.

Species	Virus or strain	Accession #	Acronym	Reference/source
Ungulate copiparvovirus 1 (type species)				
	Bovine parvovirus 2	AF406966	(BPV2)	1
Ungulate copiparvovirus 2				
	Porcine parvovirus 4	GQ387499	(PPV4)	2

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 3). The genome structures and genetic organization appear similar (Table 1), but detailed protein expression profiles have yet to be determined.

New species comprising viruses not previously included in recognized taxa:

Ungulate copiparvovirus 1. Bovine parvovirus 2 was isolated in the same study as bovine parvovirus-3 (*Ungulate erythroparvovirus 1*), and was found similarly to be a common contaminant of commercial bovine serum.

Ungulate copiparvovirus 2. Porcine parvovirus 4 was isolated and cloned from pig lung samples, and shown to be present in 10% of lung lavages tested from one herd in North Carolina, but absent from pigs tested in Iowa and Kansas.

New porcine parvovirus sequences (JX896318-22) may in future contribute to the creation of a third species in this genus (not included in Module 9, Tree 3).

References:

1. Allander T, Emerson SU, Engle RE, Purcell RH, Bukh J (2001). A virus discovery method incorporating DNase treatment and its application to the identification of two bovine parvovirus species. Proc. Natl. Acad. Sci. USA 98: 11609-14.
2. Cheung AK, Wu G, Wang D, Bayles DO, Lager KM, Vincent AL. 2010. Identification and molecular cloning of a novel porcine parvovirus. Arch. Virol. 155:801-8.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001eV***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Dependoparvovirus* (was *Dependovirus*)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Adeno-associated dependoparvovirus A
Adeno-associated dependoparvovirus B
Anseriform dependoparvovirus 1
Avian dependoparvovirus 1
Chiropteran dependoparvovirus 1
Pinniped dependoparvovirus 1
Squamate dependoparvovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Dependoparvovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Adeno-associated dependoparvovirus A (type species)				
Adeno-associated virus-1				
	Adeno-associated virus-1	AF063497	(AAV1)	
	Adeno-associated virus-6	AF028704	(AAV6)	1
Adeno-associated virus-2 (current type species)				
	Adeno-associated virus-2	AF043303	(AAV2)	
	Adeno-associated virus-S17	AY695376	(AAV-S17)	
Adeno-associated virus-3				
	Adeno-associated virus-3	AF0028705	(AAV3)	
Adeno-associated virus-4				
	Adeno-associated virus-4	U89790	(AAV4)	
	Adeno-associated virus-7	AF513851	(AAV7)	2
	Adeno-associated virus-8	AF513852	(AAV8)	2
	Adeno-associated virus-9	AX753250	(AAV9)	3
	Adeno-associated virus-10	AY631965	(AAV10)	4
	Adeno-associated virus-11	AY631966	(AAV11)	4
	Adeno-associated virus-12	DQ813647	(AAV12)	5
	Adeno-associated virus-13	EU285562	(AAV13)	6
Adeno-associated dependoparvovirus B				
Adeno-associated virus-5				
	Adeno-associated virus-5	AF085716	(AAV 5)	
Bovine adeno-associated virus				
	Bovine adeno-associated virus	AY388617	(BAAV)	
	Caprine adeno-associated virus	DQ335246	(CapAAV)	7
Anseriform dependoparvovirus 1				
Duck parvovirus				
	Duck parvovirus	U22967	(DPV)	
	Goose parvovirus-PT	JF926695	(GPV2)	
Goose parvovirus				
	Goose parvovirus	U25749	(GPV)	
Avian dependoparvovirus 1				
Avian adeno-associated virus				
	Avian adeno-associated virus	AY186198	(AAAV)	
Chiropteran dependoparvovirus 1				
	Bat adeno-associated virus	GU226971	(BtAAV)	9
Pinniped dependoparvovirus 1				
	California sea lion adeno-associated virus	JN420372	(CslAAV)	8
Squamate dependoparvovirus 1				
	Snake adeno-associated virus	AY349010	(SAAV)	10

Viruses in species ***Canine adeno-associated virus***, ***Equine adeno-associated virus*** and ***Ovine adeno-associated virus*** do not meet the new criteria for inclusion in the family.

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 3). The genome structures and genetic organization of all new viruses resemble those of the virus in the type species (Module 9, Table 1).

The final term in two proposed species names is a letter rather than a number. This is to avoid any residual confusion between the species and virus designations.

New species comprising viruses not previously included in recognized taxa:

Pinniped dependoparvovirus 1. Californian sea lion adeno-associated virus sequences (ref. 1) were isolated (as protected DNA) from 6/47 (13%) of fecal samples taken from animals at 3 locations, being very abundant in some samples. The host is designated "pinniped" in the species name, rather than " carnivore", because the Study Group considered the latter potentially confusing.

Chiropteran dependoparvovirus 1. Bat adeno-associated virus (ref. 2) was similarly identified (as protected DNA) in 22.4% of fecal swabs from 19 bat species sampled in 5 provinces in China.

Squamate dependoparvovirus 1. Snake adeno-associated virus was extracted from the tissues of diseased *Python regius* and *Boa constrictor* snakes (ref. 3) and propagated in viper and iguana heart cells as a mixed culture with an adenovirus-like component. The dependoparvovirus genome was isolated and cloned in its entirety.

References:

1. Rutledge EA, Halbert CL, Russell DW. 1998. Infectious clones and vectors derived from adeno-associated virus (AAV) serotypes other than AAV type 2. J Virol. 72:309-19.
2. Gao GP, Alvira MR, Wang L, Calcedo R, Johnston J, Wilson JM. 2002. Novel adeno-associated viruses from rhesus monkeys as vectors for human gene therapy. Proc. Natl. Acad. Sci. USA 99:11854-9.
3. Gao G, Wilson JM, Alvira M. 2003. A method of detecting and/or identifying adeno-associated virus (AVV) sequences and isolating novel sequences identified thereby. Patent: EP 1310571-A2 5. 14-MAY-2003; Trustees of The University of Pennsylvania (US).
4. Mori S, Wang L, Takeuchi T, Kanda T. 2004. Two novel adeno-associated viruses from cynomolgus monkey: pseudotyping characterization of capsid protein. Virology 330:375-83.
5. Schmidt M, Voutetakis A, Afione S, Zheng C, Mandikian D, Chiorini JA. 2008. Adeno-associated virus type 12 (AAV12): a novel AAV serotype with sialic acid- and heparan sulfate proteoglycan-independent transduction activity. J. Virol. 82:1399-1406.
6. Schmidt M, Govindasamy L, Afione S, Kaludov N, Agbandje-McKenna M, Chiorini JA. 2008. Molecular characterization of the heparin-dependent transduction domain on the capsid of a novel adeno-associated virus isolate, AAV(VR-942). J. Virol. 82:8911-8916.
7. Qiu J, Cheng F, Pintel D. 2006. Molecular characterization of caprine adeno-associated virus (AAV-Go.1) reveals striking similarity to human AAV5. Virology 356:208-16.
8. Li L, Shan T, Wang C, Cote C, Kolman J, Onions D, Gulland FM, Delwart E. 2011. The fecal viral flora of California sea lions. J. Virol. 85:9909-17.
9. Li Y, Ge X, Hon CC, Zhang H, Zhou P, Zhang Y, Wu Y, Wang LF, Shi Z. 2010. Prevalence and genetic diversity of adeno-associated viruses in bats from China. J. Gen. Virol. 91:2601-9
10. Farkas SL, Zadori Z, Benko M, Essbauer S, Harrach B, Tijssen P. 2004. A parvovirus isolated from royal python (*Python regius*) is a member of the genus *Dependovirus*. J. Gen. Virol. 85:555-61.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001fV***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Erythroparvovirus* (was *Erythrovirus*)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Primate erythroparvovirus 1
Primate erythroparvovirus 2
Primate erythroparvovirus 3
Primate erythroparvovirus 4
Rodent erythroparvovirus 1
Ungulate erythroparvovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Erythroparvovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Primate erythroparvovirus 1 (type species)				
Human parvovirus B19 (current type species)				
	Human parvovirus B19-Au	M13178	(B19V-Au)	
	Human parvovirus B19-J35	AY386330	(B19V-J35)	
	Human parvovirus B19-Wi	M24682	(B19V-Wi)	
	Human parvovirus B19-A6	AY064475	(B19V-A6)	
	Human parvovirus B19-Lali	AY044266	(B19V-Lali)	
	Human parvovirus B19-V9	AJ249437	(B19V-V9)	
	Human parvovirus B19-D91	AY083234	(B19-D91	
Primate erythroparvovirus 2				
Simian parvovirus				
	Simian parvovirus (cynomolgus)	U26342	(SPV)	
Primate erythroparvovirus 3				
Rhesus macaque parvovirus				
	Rhesus macaque parvovirus	AF221122	(RhMPV)	
Primate erythroparvovirus 4				
Pig-tailed macaque parvovirus				
	Pig-tailed macaque parvovirus	AF221123	(PtMPV)	
Rodent erythroparvovirus 1				
	Chipmunk parvovirus	GQ200736	(ChpPV)	1, 2
Ungulate erythroparvovirus 1				
	Bovine parvovirus 3	AF406967	(BPV 3)	3

The viruses meet the demarcation criteria for species (Module 9, Tree 3). Also, all viruses are ~30% identical to the founder human viruses in the current genus *Erythrovirus*, and on this basis they constitute members of the proposed genus. However, the rodent and ungulate viruses are only ~24% identical to the monkey viruses, which makes the proposed genus marginally more diverse than permitted by the identity criteria. However, all of the viruses are monophyletic (Module 9, Trees 1 and 3) and share a similar genetic organization (Table 1). Therefore, we propose retaining a single genus at this stage, rather than splitting it into two.

New species comprising viruses not previously included in recognized taxa:

Rodent erythroparvovirus 1. Chipmunk parvovirus contains a single virus first detected as 22-24 nm viral particles in the serum of 4/62 Manchurian chipmunks in Korea (ref. 1). Particles contain a ~5.6 kb genome, most of which was cloned and sequenced and has been expressed in COS-7 cells in culture (ref. 2). However, the virus has yet to be propagated as a viral isolate.

Ungulate erythroparvovirus 1. Bovine parvovirus 3 was discovered as a common nuclease-protected contaminant of commercial bovine sera being used as a diluent during the development of nuclease-based virus discovery techniques (ref. 3). This virus was present in 5/8 commercial

sera tested, including two lots of fetal sera, suggesting that it is widely distributed and may cross the placenta, which is a common characteristic of parvoviruses.

References:

1. Yoo BC, Lee DH, Park SM, Park JW, Kim CY, et al. (1999) A novel parvovirus isolated from Manchurian chipmunks. Virology 253: 250-8.
2. Chen Z, Chen AY, Cheng F, Qiu J. 2010. Chipmunk parvovirus is distinct from members in the genus erythrovirus of the family *Parvoviridae*. PLoS ONE 5:e15113.
3. Allander T, Emerson SU, Engle RE, Purcell RH, Bukh J. 2001. A virus discovery method incorporating DNase treatment and its application to the identification of two bovine parvovirus species. Proc Natl Acad Sci USA 98: 11609-14.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001gV***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Protoparvovirus* (was *Parvovirus*)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Carnivore protoparvovirus 1
Primate protoparvovirus 1
Rodent protoparvovirus 1
Rodent protoparvovirus 2
Ungulate protoparvovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Protoparvovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Carnivore protoparvovirus 1				
Feline panleukopenia virus				
	Feline parvovirus FVP-3	EU659111	(FPV)	
	Canine parvovirus CPV-N	M19296	(CPV)	
	Mink enteritis virus Abashiri	D00765	(MEV)	
	Racoon parvovirus 118-A	JN867610	(RaPV)	
Primate protoparvovirus 1				
	Bufavirus 1a	JX027296	(BuPV1a)	7
	Bufavirus 1b	JX027295	(BuPV1b)	
	Bufavirus 2	JX027297	(BuPV2)	
Rodent protoparvovirus 1 **(**type species**)**				
H-1 parvovirus				
	H-1 parvovirus	X01457	(H1)	
Kilham rat virus				
	Kilham rat virus	AF321230	(KRV)	
LuIII virus				
	LuIII virus	M81888	(LuIII)	
Minute virus of mice (current type species)				
	Minute virus of mice (prototype)	J02275	(MVMp)	
	Minute virus of mice (immunosuppressive)	M12032	(MVMi)	
	Minute virus of mice (Missouri)	DQ196317	(MVMm)	1
	Minute virus of mice (Cutter)	U34256	(MVMc)	1, 2
Mouse parvovirus 1				
	Mouse parvovirus 1	U12469	(MPV1)	
	Mouse parvovirus 2	DQ196319	(MPV2)	1
	Mouse parvovirus 3	DQ199631	(MPV3)	1
	Mouse parvovirus 4	FJ440683	(MPV4)	3
	Mouse parvovirus 5	FJ441297	(MPV5)	3
	Hamster parvovirus	U34255	(HaPV)	2
Tumor virus X				
	Tumor virus X	In preparation	(TVX)	5
	Rat minute virus 1	AF332882	(RMV1)	4
Rodent protoparvovirus 2				
	Rat parvovirus 1	AF036710	(RPV1)	6
Ungulate protoparvovirus 1				
Porcine parvovirus				
	Porcine parvovirus Kresse	U44978	(PPV-Kr)	
	Porcine parvovirus NADL-2	L23427	(PPV-NADL2)	

Viruses in species ***HB parvovirus***, ***Lapine parvovirus*** and ***RT parvovirus*** do not meet the new criteria for inclusion in the family. Viruses in ***Chicken parvovirus*** are proposed for transfer to the new genus *Aveparvovirus* in the new species *Galliform aveparvovirus 1*.

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 2). Among other typical characteristics (Module 9, Table 1), they share similar genetic strategies, coding patterns, reiterated NS1-binding sites, potential classes of small non-structural proteins, and protein motifs.

New species containing only viruses that are not currently included in recognized taxa:

Rodent protoparvovirus 2. This species consists of a single virus (rat parvovirus 1). This virus is well characterized in laboratory rats, is enterotropic, and is serologically distinct.

Primate protoparvovirus 1. This species consists of three strains of bufavirus (bufavirus 1a, 1b and 2), which were identified initially by deep sequencing nuclease-protected DNA in a series of rotavirus-antigen negative cases of childhood diarrhea collected in Burkina Faso. The viral genome was then detected in 4% of individual samples from this locale and confirmed by identification of 1 case in a limited series from Tunisia. It has a highly characteristic pattern of reiterated NS1-binding sites distributed throughout its genome that currently appears to be unique to the proposed genus *Protoparvovirus*. It is most closely related to an enteric parvovirus recently identified in the serum of SIV-infected monkeys (JX627576; ref. 8), which was published after construction of the phylogenetic trees (Module 9).

References:

1. Besselsen DG, Romero MJ, Wagner AM, Henderson KS, Livingston RS. 2006. Identification of novel murine parvovirus strains by epidemiological analysis of naturally infected mice. J. Gen. Virol. 87:1543-56.
2. Besselsen DG, Pintel DJ, Purdy GA, Besch-Williford CL, Franklin CL, Hook RR Jr, Riley LK. 1996. Molecular characterization of newly recognized rodent parvoviruses. J. Gen. Virol. 77:899-911.
3. Henderson, KS, Jennings, SM, Hayes, BJ, Perkins, CL. 2008. Identification of mouse parvoviruses 4 and 5. Unpublished.
4. Wan CH, Soderlund-Venermo M, Pintel DJ, Riley LK. 2002 Molecular characterization of three newly recognized rat parvoviruses. J. Gen. Virol. 83:2075-83.
5. Vollmers E, Tattersall P. 2013. Complete coding sequence of the orphan parvovirus Tumor virus X (TVX). Unpublished.
6. Ball-Goodrich LJ, Leland SE, Johnson EA, Paturzo FX, Jacoby RO. 1998. Rat parvovirus type 1: the prototype for a new rodent parvovirus serogroup. J. Virol. 72:3289-99.
7. Phan TG, Vo NP, Bonkoungou IJ, Kapoor A, Barro N, O'Ryan M, Kapusinszky B, Wang C, Delwart E. 2012. Acute diarrhea in West African children: diverse enteric viruses and a novel parvovirus genus. J. Virol. 86:11024-30.
8. Handley SA, Thackray LB, Zhao G, et al. 2012. Pathogenic simian immunodeficiency virus infection is associated with expansion of the enteric virome. Cell 151:253-66.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001hV***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Tetraparvovirus* (new)**
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Chiropteran tetraparvovirus 1
Primate tetraparvovirus 1
Ungulate tetraparvovirus 1
Ungulate tetraparvovirus 2
Ungulate tetraparvovirus 3
Ungulate tetraparvovirus 4

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Tetraparvovirus*

Proposed species are in blue italics.

Species	Virus or strain	Accession #	Acronym	Reference/source
Chiropteran tetraparvovirus 1				
	Eidolon helvum (bat) parvovirus	JQ037753	(Ba-PARV4)	9
Primate tetraparvovirus 1 (type species)				
	Human parvovirus 4 G1	AY622943	(PARV4G1)	1, 2
	Human parv4 G2 (C25-5)	DQ873391	(PARV4G2)	3
	Human parv4 G3 (NG-OR)	EU874248	(PARV4G3)	4
	Chimpanzee parv4	HQ113143	(Ch-PARV4)	5
Ungulate tetraparvovirus 1				
	Bovine hokovirus 1	EU200669	(B-PARV4-1)	6
	Bovine hokovirus 2	JF504697	(B-PARV4-2)	7
Ungulate tetraparvovirus 2				
	Porcine hokovirus	EU200677	(P-PARV4)	6
Ungulate tetraparvovirus 3				
	Porcine Cnvirus	GU938300	(CnP-PARV4)	8
Ungulate tetraparvovirus 4				
	Ovine hokovirus	JF504699	(O-PARV4)	7

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 3). Genome structures and organization appear similar (Module 9, Table 1), but to date none of the viruses has been successfully propagated in culture.

New species comprising viruses not previously included in recognized taxa:

Primate tetraparvovirus 1. This proposed species contains three genotypes of the founder human virus, PARV4, plus a chimpanzee virus. First identified in nuclease-digested plasma from patients with acute viral infection syndrome (ref. 1), and rediscovered, with genotype 2, in pooled plasma used to manufacture blood products (ref. 3), these viruses are widely distributed in blood from injecting drug users in the USA and Europe, particularly in co-infections with HIV. Although relatively rare in the general population, the virus has also been detected in lymphoid tissue, bone marrow and liver samples from people at high risk for parenteral infection, and such people are also commonly seropositive for the virus. A third genotype was identified in bone marrow and lymphoid tissue of AIDS patients in Africa (ref. 4). The chimpanzee virus was also detected in plasma, with blood from 63% of chimpanzees and 18% of gorillas from a group of 73 wild-caught apes sampled in the Cameroons testing seropositive for antibodies.

Ungulate tetraparvovirus 1, *Ungulate tetraparvovirus 2*, *Ungulate tetraparvovirus 3* and *Ungulate tetraparvovirus 4*. Viruses in these proposed species have been detected repeatedly in the serum and tissues of livestock.

Chiropteran tetraparvovirus 1. This proposed species contains a PARV4-like virus detected at high concentration in blood samples and tissues from *Eidolon helvum* bats in Africa (Ghana). High titers of these viruses were particularly apparent in samples from spleen and kidney,

suggesting these organs as likely sites for viral replication.

References:

1. Jones MS, Kapoor A, Lukashov VV, Simmonds P, Hecht F, Delwart E. 2005. New DNA viruses identified in patients with acute viral infection syndrome. J. Virol. 79:8230-6.
2. Lou S, Xu B, Huang Q, Zhi N, Cheng F, Wong S, Brown K, Delwart E, Liu Z, Qiu J. 2012. Molecular characterization of the newly identified human parvovirus 4 in the family *Parvoviridae*. Virology 422:59-69.
3. Fryer JF, Delwart E, Bernardin F, Tuke PW, Lukashov VV, Baylis SA. 2007. Analysis of two human parvovirus PARV4 genotypes identified in human plasma for fractionation. J. Gen. Virol. 88:2162-7.
4. Simmonds P, Douglas J., Bestetti G, Longhi E, Antinori S, Parravicini C, Corbellino M. 2008. A third genotype of the human parvovirus PARV4 in sub-Saharan Africa. J. Gen. Virol. 89:2299-302.
5. Sharp CP, Lebreton M, Kantola K, Nana A, Diffo Jle D, Djoko CF, Tamoufe U, Kiyang JA, Babila TG, Ngole EM, Pybus OG, Delwart E, Delaporte E, Peeters M, Soderlund-Venermo M, Hedman K, Wolfe ND, Simmonds P. 2010. Widespread infection with homologues of human parvoviruses B19, PARV4, and human bocavirus of chimpanzees and gorillas in the wild. J. Virol. 84:10289-96.
6. Lau SK, Woo PC, Tse H, Fu CT, Au WK, Chen XC, Tsoi HW, Tsang TH, Chan JS, Tsang DN, Li KS, Tse CW, Ng TK, Tsang OT, Zheng BJ, Tam S, Chan KH, Zhou B, Yuen KY. 2008. Identification of novel porcine and bovine parvoviruses closely related to human parvovirus 4. J. Gen. Virol. 89:1840-8.
7. Tse H, Tsoi HW, Teng JL, Chen XC, Liu H, Zhou B. Zheng B.J, Woo PC, Lau SK, Yuen KY. 2011. Discovery and genomic characterization of a novel ovine partetravirus and a new genotype of bovine partetravirus. PLoS ONE 6:E25619.
8. Wang F, Wei Y, Zhu C, Huang X., Xu Y, Yu L, Yu X. 2010. Novel parvovirus sublineage in the family of *Parvoviridae*. Virus Genes 41:305-8.
9. Canuti M, Eis-Huebinger AM, Deijs M, de Vries M, Drexler JF, Oppong SK, Muller MA, Klose SM, Wellinghausen N, Cottontail VM, Kalko,EK, Drosten C, van der Hoek L. 2011. Two novel parvoviruses in frugivorous New and Old World bats. PLoS ONE 6:E29140.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001iV***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Ambidensovirus* (was *Densovirus*)**
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Blattodean ambidensovirus 1
Blattodean ambidensovirus 2
Dipteran ambidensovirus 1
Hemipteran ambidensovirus 1
Lepidopteran ambidensovirus 1
Orthopteran ambidensovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Ambidensovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Blattodean ambidensovirus 1				
Periplaneta fuliginosa densovirus (current type species of genus *Pefudensovirus*)				
	Periplaneta fuliginosa densovirus	AF192260	(PfDV)	
Blattodean ambidensovirus 2				
	Blattella germanica densovirus 1	AY189948	(BgDV1)	7
Dipteran ambidensovirus 1				
	Culex pipens densovirus	FJ810126	(CpDV)	5, 6
Hemipteran ambidensovirus 1				
	Planococcus citri densovirus	AY032882	(PcDV)	9
Lepidopteran ambidensovirus 1 (type species)				
	Diatraea saccharalis densovirus	AF036333	(DsDV)	2
Galleria mellonella densovirus				
	Galleria mellonella densovirus	L32896	(GmDV)	
	Helicoverpa armigera densovirus	JQ894784	(HaDV1)	4
Junonia coenia densovirus (current type species of genus *Densovirus*)				
	Junonia coenia densovirus	S47266	(JcDV)	
	Mythimna loreyi densovirus	AY461507	(MlDV)	3
	Pseudoplusia includens densovirus	JX645046	(PiDV)	1
Orthopteran ambidensovirus 1				
	Acheta domesticus densovirus	HQ827781	(AdDV)	8

This proposal seeks to merge the viruses in the genera *Densovirus* and *Pefudensovirus* because the phylogeny of 5 new isolates indicates that the existing division is not sustainable (see Module 9, Trees 1 and 4). This merger requires renaming of the current genus *Densovirus* to *Ambidensovirus*, removal of current genus *Pefudensovirus*, and transfer of viruses in the current genus *Pefudensovirus* into the genus *Ambidensovirus*.

The viruses in the new genus are monophyletic, and they share a wide range of characteristics including a complex rearrangement that allows them to co-ordinate bidirectional transcription. The viruses meet the demarcation criteria for species (Module 9, Trees 1 and 4). However, the genus demarcation criteria (Module 9) will not strictly accommodate the proposed expansion, since certain pairs of viruses fall outside the demarcation limit. The average p-distance for NS1 proteins within the proposed genus is 0.56, compared to average internal values of, for example, 0.53 for genus *Bocaparvovirus* and 0.44 for genus *Erythroparvovirus*, while average external p-distances (between viruses in the proposed genus and all other members of the family) are 0.89 (for *Ambidensovirus)*, 0.84 (for *Bocaparvovirus*) and 0.83 (for *Erythroparvovirus*), yielding similar internal/external ratios of 0.63, 0.63 and 0.52, respectively. Thus, overall, the diversity within the proposed genus only modestly exceeds the standard parameters.

Sufficient sequence data (JQ320376) are available for an additional virus, Blattella germanica densovirus-like virus 2 (ref. 10), but the material was environmental in origin and classification is not proposed at this stage.

References:

1. Huynh OT, Pham HT, Yu Q, Tijssen P. 2012. Pseudoplusia includens Densovirus Genome Organization and Expression Strategy. J. Virol. 86:13127-8.
2. Boublik Y, Kouassi KN, Cavallaro C, Bergoin M. 1997. Complete nucleotide sequence and genome organization of an infectious clone of Diatraea saccharalis densovirus (DsDNV). Unpublished.
3. Fediere G, El-Far M, Li Y, Bergoin M, Tijssen P. 2004. Expression strategy of densonucleosis virus from Mythimna loreyi. Virology 320:181-9.
4. El-Far M, Szelei J, Yu Q, Fediere G, Bergoin M, Tijssen P. 2012. Organization of the Ambisense genome of the Helicoverpa armigera densovirus. J. Virol. 86:7024.
5. Jousset FX, Baquerizo E, Bergoin M. 2000. A new densovirus isolated from the mosquito *Culex pipiens* (Diptera: Culicidae). Virus Res. **67:**11-6.
6. Baquerizo-Audiot E, Abd-Alla A, Jousset FX, Cousserans F, Tijssen P, Bergoin M. 2009. Structure and expression strategy of the genome of Culex pipiens densovirus, a mosquito densovirus with an ambisense organization. J. Virol. 83:6863-73.
7. Mukha DV, Chumachenko AG, Dykstra MJ, Kurtti TJ, Schal C. 2006. Characterization of a new densovirus infecting the German cockroach, Blattella germanica. J. Gen. Virol. 87:1567-75.
8. Szelei J, Woodring J, Goettel MS, Duke G, Jousset FX, Liu KY, Zadori Z, Li Y, Styer E, Boucias DG, Kleespies RG, Bergoin M, Tijssen P. 2011. Susceptibility of North-American and European crickets to Acheta domesticus densovirus (AdDNV) and associated epizootics. J. Invertebr. Pathol. 106:394-9.
9. Thao M.L, Wineriter S, Buckingham G, Baumann P. 2001. Genetic characterization of a putative Densovirus from the mealybug Planococcus citri. Curr. Microbiol. 43:457-8.
10. Ge X, Li Y, Yang X, Zhang H, Zhou P, Zhang Y, Shi, Z. 2012. Metagenomic analysis of viruses from bat fecal samples reveals many novel viruses in insectivorous bats in China. J. Virol. 86:4620-30.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001jV***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Brevidensovirus***
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Dipteran brevidensovirus 1
Dipteran brevidensovirus 2

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Brevidensovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Dipteran brevidensovirus 1 (type species)				
Aedes aegypti densovirus (current type species)				
	Aedes aegypti densovirus 1	M37899	(AaeDV1)	
Aedes albopictus densovirus				
	Aedes albopictus densovirus 1	AY095351	(AalDV1)	
	Culex pipiens pallens densovirus	EF579756	(CppDV)	1
	Anopheles gambiae densovirus	EU233812	(AgDV)	2
	Aedes aegypti densovirus 2	FJ360744	(AaeDV2)	3
Dipteran brevidensovirus 2				
	Aedes albopictus densovirus 2	X74945	(AalDV2)	4
	Aedes albopictus densovirus 3	AY310877	(AalDV3)	5
	Haemagogus equinus densovirus	AY605055	(HeDV)	6

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 4). The phylogeny suggests that the forerunner of this genus may have segregated from an ancestral form prior to separation of all other genera in the two subfamilies *Parvovirinae* and *Densovirinae*. However, the viruses are included in the subfamily *Densovirinae* to accommodate host range constraints and to reflect the fact that the branches are deep and the tree topology dependent on the particular rooting method used. The viruses have small (~ 4 kb), monosense, homotelomeric genomes that lack discernable PLA2 motifs (Module 9, Table 2).

References:

1. Zhai YG, Lv XJ, Sun XH, Fu SH, Gong ZD, Fen Y, Tong SX, Wang ZX, Tang Q, Attoui H, Liang GD. 2008. Isolation and characterization of the full coding sequence of a novel densovirus from the mosquito Culex pipiens pallens. J. Gen. Virol. 89:195-9.
2. Ren X, Hoiczyk E, Rasgon JL. 2008. Viral paratransgenesis in the malaria vector Anopheles gambiae. PLoS Pathog. 4:e1000135.
3. Sivaram A, Barde PV, Kumar SR, Yadav P, Gokhale MD, Basu A, Mourya DT. 2009. Isolation and characterization of densonucleosis virus from *Aedes aegypti* mosquitoes and its distribution in India. Intervirology 52:1-7.
4. Boublik Y, Jousset FX, Bergoin M. 1994. Complete nucleotide sequence and genomic organization of the Aedes albopictus parvovirus (AaPV) pathogenic for *Aedes aegypti* larvae. Virology 200:752-63.
5. Afanasiev BN, Carlson JO. 2003. A new mosquito densovirus from Peru: genomic sequence and in vitro growth characteristics of wild type and hybrid viruses. Microbiology, Colorado State University, Fort Collins, CO 80523, USA. Unpublished.
6. Paterson A., Robinson E., Suchman E., Afanasiev B, Carlson J. 2005. Mosquito densonucleosis viruses cause dramatically different infection phenotypes in the C6/36 *Aedes albopictus* cell line. Virology 337: 253-61.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001kV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Hepandensovirus* (new)**
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Decapod hepandensovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Hepandensovirus*

The proposed species is in blue italics.

Species	Virus or strain	Accession #	Acronym	Reference/source
Decapod hepandensovirus 1 (type species)				
	Penaeus monodon hepandensovirus 1	DQ002873	(PmoHDV1)	1
	Penaeus chinensis hepandensovirus	AY008257	(PchDV)	2
	Penaeus monodon hepandensovirus 2	EU247528	(PmoHDV2)	3
	Penaeus monodon hepandensovirus 3	EU588991	(PmoHDV3)	3
	Penaeus merguiensis hepandensovirus	DQ458781	(PmeDV)	4
	Penaeus monodon hepandensovirus 4	FJ410797	(PmoHDV4)	5
	Fenneropenaeus chinensis hepandensovirus	JN082231	(FchDV)	6

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 4). The viruses are monophyletic and all have relatively large (~6.3 kb), monosense, heterotelomeric genomes that lack discernable PLA2 motifs (Module 9, Table 2).

The viruses were known previously as hepatopancreatic parvovirus [HPV] of prawns and shrimp. They are widespread and highly pathogenic in nature, causing hepatopancreatic disease, and can constitute an economic threat in cultured shrimp populations on rare occasions when larvae from wild-caught shrimp are introduced.

References:

1. Sukhumsirichart W, Attasart P, Boonsaeng V, Panyim S. 2006. Complete nucleotide sequence and genomic organization of hepatopancreatic parvovirus (HPV) of *Penaeus monodon*. Virology 346:266-77.
2. Bonami JR, Mari J, Poulos BT Lightner DV. 1995. Characterization of hepatopancreatic parvo-like virus, a second unusual parvovirus pathogenic for penaeid shrimps. J. Gen. Virol. 76:813-7.
3. Tang KFJ, Pantoja CR, Lightner DV. 2008. Nucleotide sequencing of a Madagascar hepatopancreatic parvovirus (HPV) and the comparison of genetic variation among geographic isolates. Unpublished.
4. La Fauce KA, Elliman J, Owens L. 2007. Molecular characterisation of hepatopancreatic parvovirus (PmergDNV) from Australian *Penaeus merguiensis*. Virology 362:397-403.
5. Safeena MP, Tyagi A, Rai P, Karunasagar I, Karunasagar I. 2010. Complete nucleic acid sequence of Penaeus monodon densovirus (PmDNV) from India. Virus Res. 150:1-11.
6. Jeeva S, Kang SW, Lee YS, Jang IK, Seo HC, Choi TJ. 2012. Complete nucleotide sequence analysis of a Korean strain of hepatopancreatic parvovirus (HPV) from *Fenneropenaeus chinensis*. Virus Genes 44:89-97.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001lV***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Iteradensovirus* (was *Iteravirus*)**
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Lepidopteran iteradensovirus 1
Lepidopteran iteradensovirus 2
Lepidopteran iteradensovirus 3
Lepidopteran iteradensovirus 4
Lepidopteran iteradensovirus 5

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Iteradensovirus*

Current species are in black italics and proposed species in blue italics. All current species will be removed from the genus.

Species	Virus or strain	Accession #	Acronym	Reference/source
Lepidopteran iteradensovirus 1 (type species)				
Bombyx mori densovirus (current type species)				
	Bombyx mori densovirus	AY033435	(BmDV)	
Lepidopteran iteradensovirus 2				
	Casphalia extranea densovirus	AF375296	(CeDV)	1
	Sibine fusca densovirus	JX020762	(SfDV)	2
Lepidopteran iteradensovirus 3				
	Dendrolimus punctatus densovirus	AY665654	(DpDV)	3
Lepidopteran iteradensovirus 4				
	Papilio polyxenes densovirus	JX110122	(PpDV)	4
Lepidopteran iteradensovirus 5				
	Helicoverpa armigera densovirus	HQ613271	(HaDV2)	5

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 4). Among other characteristics (Module 9, Table 2), they share similar genetic strategies, coding patterns, homotelomeric termini, and typical VP1-encoded PLA2 domains.

References:

1. Fediere G, Li Y, Zadori Z, Szelei J, Tijssen P. 2002. Genome organization of Casphalia extranea densovirus, a new iteravirus. Virology 292:299-308.
2. Yu Q, Fediere G, Abd-Alla A, Bergoin M, Tijssen P. 2012. Iteravirus-like genome organization of a densovirus from *Sibine fusca* Stoll. J. Virol. 86:8897-98.
3. Wang J, Zhang J, Jiang H, Liu C, Yi F, Hu Y. 2005. Nucleotide sequence and genomic organization of a newly isolated densovirus infecting *Dendrolimus punctatus*. J. Gen. Virol. 86:2169-73.
4.Yu Q, Hajek AE, Bergoin M, Tijssen P. 2012. Papilio polyxenes Densovirus has an iteravirus-like genome organization J. Virol. 86:9534-5.
5. Xu P, Cheng P, Liu Z, Li Y, Murphy RW, Wu K. 2012. Complete genome sequence of a monosense densovirus infecting the cotton bollworm, *Helicoverpa armigera*. J. Virol. 86:10909.

MODULE 2: **NEW SPECIES**

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2013.001mV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Penstyldensovirus* (new)**
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:

Decapod penstyldensovirus 1

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see Module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Proposed species in genus *Penstyldensovirus*

The proposed species is in blue italics.

Species	Virus or strain	Accession #	Acronym	Reference/source
Decapod penstyldensovirus 1 (type species)				
	Penaeus stylirostris penstyldensovirus 1	AF273215	(PstDV1)	1, 2
	Penaeus monodon penstyldensovirus 1	GQ411199	(PmoPDV1)	4
	Penaeus monodon penstyldensovirus 2	AY124937	(PmoPDV2)	3
	Penaeus stylirostris penstyldensovirus 2	GQ475529	(PstDV2)	5

The viruses meet the demarcation criteria for species and genus (Module 9, Trees 1 and 4). The viruses are monophyletic and all have small (~4 kb), monosense, homotelomeric genomes that lack discernable PLA2 motifs (Module 9, Table 2).

The viruses were known previously as infectious hypodermal and hematopoietic necrosis virus [IHHNV] of prawns and shrimp. They were first identified as pathogens responsible for an economically significant and virulent disease in farmed shrimp (infectious hypodermal and hematopoietic necrosis), are widespread in nature, but are no longer a major economic problem because tolerant shrimp populations have been developed.

References:

1. Lightner DV, Redman RM, Bell TA. 1983. Infectious hypodermal and hematopoietic necrosis, a newly recognized virus disease of penaeid shrimp. J. Invertebr. Pathol. 42:62-70.
2. Shike H, Dhar AK, Burns JC, Shimizu C, Jousset FX, Klimpel KR, Bergoin M. 2000. Infectious hypodermal and hematopoietic necrosis virus of shrimp is related to mosquito brevidensoviruses. Virology 277:167-77.
3. Tang KF, Poulos BT, Wang J, Redman RM, Shih HH, Lightner DV. 2003. Geographic variations among infectious hypodermal and hematopoietic necrosis virus (IHHNV) isolates and characteristics of their infection. Dis. Aquat. Org. 53:91-9.
4. Rai P, Safeena MP, Karunasagar I. 2011. Complete nucleic acid sequence of Penaeus stylirostris densovirus (PstDNV) from India. Virus Res. 158:37-45.
5. Saksmerprome V, Puiprom O, Noonin C, Flegel TW. 2010. Detection of infectious hypodermal and haematopoietic necrosis virus (IHHNV) in farmed Australian *Penaeus monodon* by PCR analysis and cDNA sequencing. Aquaculture 298:190-3.

MODULE 3: **NEW GENUS**

Ideally, a genus should be placed within a higher taxon.

Code	***2013.001nV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

Code	***2013.001oV***	(assigned by ICTV officers)

To name the new genus: *Aveparvovirus*

Code	***2013.001pV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus :

Galliform aveparvovirus 1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The viruses meet the demarcation criteria for a genus (Module 9). They occupy a branch of the phylogenetic tree that is well separated from branches giving rise to other genera, with secure posterior probability scores (Module 9, Trees 1 and 2), and have similar characteristics (Table 1).

Origin of the new genus name:

Founding viruses in this genus infect birds (Aves). The "s" is omitted to ensure correct pronounciation of "parvovirus".

Reasons to justify the choice of type species:

First species classified in the genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

MODULE 3: **NEW GENUS**

Ideally, a genus should be placed within a higher taxon.

Code	***2013.001qV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

Code	***2013.00rV***	(assigned by ICTV officers)

To name the new genus: *Copiparvovirus*

Code	***2013.001sV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Ungulate copiparvovirus 1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:

2

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The viruses meet the demarcation criteria for a genus (Module 9). They occupy a branch of the phylogenetic tree that is well separated from branches giving rise to other genera, with secure posterior probability scores (Module 9, Trees 1 and 3), and have similar characteristics (Table 1).

Origin of the new genus name:

Sigla for cow and pig, which were the hosts of the first two species identified.

Reasons to justify the choice of type species:

First virus identified in the genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

See Module 9.

MODULE 3: **NEW GENUS**

Ideally, a genus should be placed within a higher taxon.

Code	***2013.001tV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

Code	***2013.001uV***	(assigned by ICTV officers)

To name the new genus: *Tetraparvovirus*

Code	***2013.00vV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Primate tetraparvovirus 1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:

6

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The viruses meet the demarcation criteria for a genus (Module 9). They occupy a branch of the phylogenetic tree that is well separated from branches giving rise to other genera, with secure posterior probability scores (Module 9, Trees 1 and 3), and have similar characteristics (Table 1).

Origin of the new genus name:

From the name of the founder virus, human parvovirus 4 (PARV4), using Latin "tetra" in place of the numeral 4.

Reasons to justify the choice of type species:

This species includes the most intensely studied viruses and contains the founder virus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

See Module 9.

MODULE 3: **NEW GENUS**

Ideally, a genus should be placed within a higher taxon.

Code	***2013.001wV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

Code	***2013.001xV***	(assigned by ICTV officers)

To name the new genus: *Hepandensovirus*

Code	***2013.001yV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Decapod hepandensovirus 1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Aligned amino acid sequences of the NS1 proteins of all viruses in this genus are <30% identical to all other members of the Parvoviridae, qualifying them a distinct genus. They occupy a branch of the phylogenetic tree that is well separated from branches giving rise to other genera, as detailed in Module 9, Trees 1 and 4, and share a group of genomic characteristics, as listed in Table 2.

Origin of the new genus name:

From hepatopancreatic parvovirus (HPV), their original name.

Reasons to justify the choice of type species:

First virus identified in the genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

MODULE 3: **NEW GENUS**

Ideally, a genus should be placed within a higher taxon.

Code	***2013.001zV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

Code	***2013.001aaV***	(assigned by ICTV officers)

To name the new genus: *Penstyldensovirus*

Code	***2013.001bbV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Decapod penstyldensovirus 1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Aligned amino acid sequences of the NS1 proteins of all viruses in this genus are <30% identical to those of all other members of the family, qualifying them a distinct genus. They occupy a branch of the phylogenetic tree that is well separated from branches giving rise to other genera, as detailed in Module 9, Trees 1 and 4, and have similar characteristics, as listed in Table 2.

Origin of the new genus name:

Sigla for Penaeus stylirostris, the host, and name, of the founding member of this species.

Reasons to justify the choice of type species:

First virus identified in the genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001ccV***	(assigned by ICTV officers)
To remove the following species from their present position:		
Aleutian mink disease virus		
The present taxonomic position of these taxon/taxa:		
Genus:	***Amdovirus***	Fill in all that apply.
Subfamily:	***Parvovirinae***	
Family:	***Parvoviridae***	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		**YES**

Reasons to justify the removal: Explain why the taxon (or taxa) should be removed
The species in the current genus is removed and the virus therein placed in a new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001ddV***	(assigned by ICTV officers)
To remove the following species from their present position:		
Bovine parvovirus *Canine minute virus*		
The present taxonomic position of these taxon/taxa:		
Genus:	***Bocavirus***	Fill in all that apply.
Subfamily:	***Parvovirinae***	
Family:	***Parvoviridae***	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		**YES**

Reasons to justify the removal: Explain why the taxon (or taxa) should be removed
All species in the current genus are removed and the viruses therein are grouped into new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001eeV***	(assigned by ICTV officers)

To remove the following species from their present position:

Adeno-associated virus-1
Adeno-associated virus-2
Adeno-associated virus-3
Adeno-associated virus-4
Adeno-associated virus-5
Avian adeno-associated virus
Bovine adeno-associated virus
*Canine adeno-associated virus**
Duck parvovirus
*Equine adeno-associated virus**
Goose parvovirus
*Ovine adeno-associated virus**

The present taxonomic position of these taxon/taxa:

Genus:	***Dependovirus***
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

All species in the current genus are removed and the viruses therein are grouped into new species. No sequence data are available for viruses in species marked by asterisks, making it impossible to incorporate them into new species using standard criteria (Module 9).

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001ffV***	(assigned by ICTV officers)

To remove the following species from their present position:

Human parvovirus B19
Pig-tailed macaque parvovirus
Rhesus macaque parvovirus
Simian parvovirus

The present taxonomic position of these taxon/taxa:

Genus:	***Erythrovirus***
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

All species in the current genus are removed and the viruses therein are grouped into new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001ggV***	(assigned by ICTV officers)

To remove the following species from their present position:

Chicken parvovirus
Feline panleukopenia virus
H-1 parvovirus
*HB parvovirus**
Kilham rat virus
*Lapine parvovirus**
LuIII virus
Minute virus of mice
Mouse parvovirus 1
Porcine parvovirus
*RT parvovirus**
Tumor virus X

The present taxonomic position of these taxon/taxa:

Genus:	***Parvovirus***
Subfamily:	***Parvovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

All species in the current genus are removed and the viruses therein are grouped into new species. No sequence data are available for viruses in species marked by asterisks, making it impossible to incorporate them into new species using standard criteria (Module 9).

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001hhV***	(assigned by ICTV officers)

To remove the following species from their present position:

Aedes aegypti densovirus
Aedes albopictus densovirus

The present taxonomic position of these taxon/taxa:

Genus:	***Brevidensovirus***
Subfamily:	***Densovirinae***
Family:	***Parvoviridae***
Order:	

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

All species in the current genus are removed and the viruses therein are grouped into new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001iiV***	(assigned by ICTV officers)
To remove the following species from their present position:		
Galleria mellonella densovirus *Jujonia coenia densovirus*		
The present taxonomic position of these taxon/taxa:		
Genus:	***Densovirus***	Fill in all that apply.
Subfamily:	***Densovirinae***	
Family:	***Parvoviridae***	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		**YES**

Reasons to justify the removal: Explain why the taxon (or taxa) should be removed
All species in the current genus are removed and the viruses therein are grouped into new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001jjV***	(assigned by ICTV officers)
To remove the following species from their present position:		
Bombyx mori densovirus		
The present taxonomic position of these taxon/taxa:		
Genus:	***Iteravirus***	Fill in all that apply.
Subfamily:	***Densovirinae***	
Family:	***Parvoviridae***	
Order:		

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal: Explain why the taxon (or taxa) should be removed
The species in the current genus is removed and the virus therein placed in a new species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a)

Code	***2013.001kkV***	(assigned by ICTV officers)
To remove the following species from their present position:		
Periplaneta fuliginosa densovirus		
The present taxonomic position of these taxon/taxa:		
Genus:	***Pefudensovirus***	Fill in all that apply.
Subfamily:	***Densovirinae***	
Family:	***Parvoviridae***	
Order:		

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal: Explain why the taxon (or taxa) should be removed
The species in the current genus is removed and the virus therein placed in a new species.

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by Modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

Code	***2013.001llV*** - ***2013.001rrV*** See individual codes, below	(assigned by ICTV officers)
Title of proposal: Modification of current genus names		

Text of proposal:

Taxon names in the family *Parvoviridae* generally lack cohesion and transparency, making individual taxa appear unrelated. The proposal is to extend current genus names to include the subfamily designations "parvo" or "denso", as indicated below. This proposal also includes modification of the current genus names *Parvovirus* and *Densovirus*, to avoid the confusion that currently results from viruses in both the genus and the subfamily being described as parvo- or densoviruses.

Revised genus names are in bold.

Current genus name	Proposed genus name	Type species
Code	***2013.001llV***	
Amdovirus	***Amdoparvovirus***	*Carnivore amdoparvovirus 1*
Code	***2013.001mmV***	
Bocavirus	***Bocaparvovirus***	*Ungulate bocaparvovirus 1*
Code	***2013.001nnV***	
Dependovirus	***Dependoparvovirus***	*Adeno-associated dependoparvovirus A*
Code	***2013.001ooV***	
Erythrovirus	***Erythroparvovirus***	*Primate erythroparvovirus 1*
Code	***2013.001ppV***	
Parvovirus	***Protoparvovirus***	*Rodent protoparvovirus 1*
Code	***2013.001qqV***	
Densovirus	***Ambidensovirus***	*Lepidopteran ambidensovirus 1*
Code	***2013.001rrV***	
Iteravirus	***Iteradensovirus***	*Lepidopteran iteradensovirus 1*

For sections ***2013.001ssV*** - ***2013.001aaa***, please see the **ADDENDUM** at the end of this proposal

MODULE 9: **APPENDIX**: supporting material

Index

Taxon demarcation criteria

The two subfamilies, *Parvovirinae* and *Densovirinae*, remain distinguished primarily by their ability to infect vertebrate versus arthropod hosts. This distinction is supported by Bayesian phylogeny, although segregation of viruses in the genus *Brevidensovirus* appears to precede the recognized schism under the rooting procedure used (Tree 1).

Previously, genera were defined largely by non-quantifiable criteria, including helper-virus requirements and genome characteristics, which provided little taxonomic structure. The proposals add the requirement that all viruses in a genus should be monophyletic and encode NS1 proteins that are generally >30% identical to each other at the amino acid sequence level but <30% identical to those of other genera. Within the subfamily *Parvovirinae*, these criteria work well to separate all current and proposed genera, with the minor exception of the proposed genus *Erythroparvovirus*, where marginally greater divergence is evident for some members. However, in the subfamily *Densovirinae*, attributable sequences are only available for a small number of economically significant viruses, which may reflect poorly the diverse nature of viruses infecting this immense host phylum. Accordingly, the >30% identity requirement is applied less rigorously within this subfamily, in order to allow clustering of monophyletic viruses with conspicuously similar characteristics from host orders separated by large evolutionary distances.

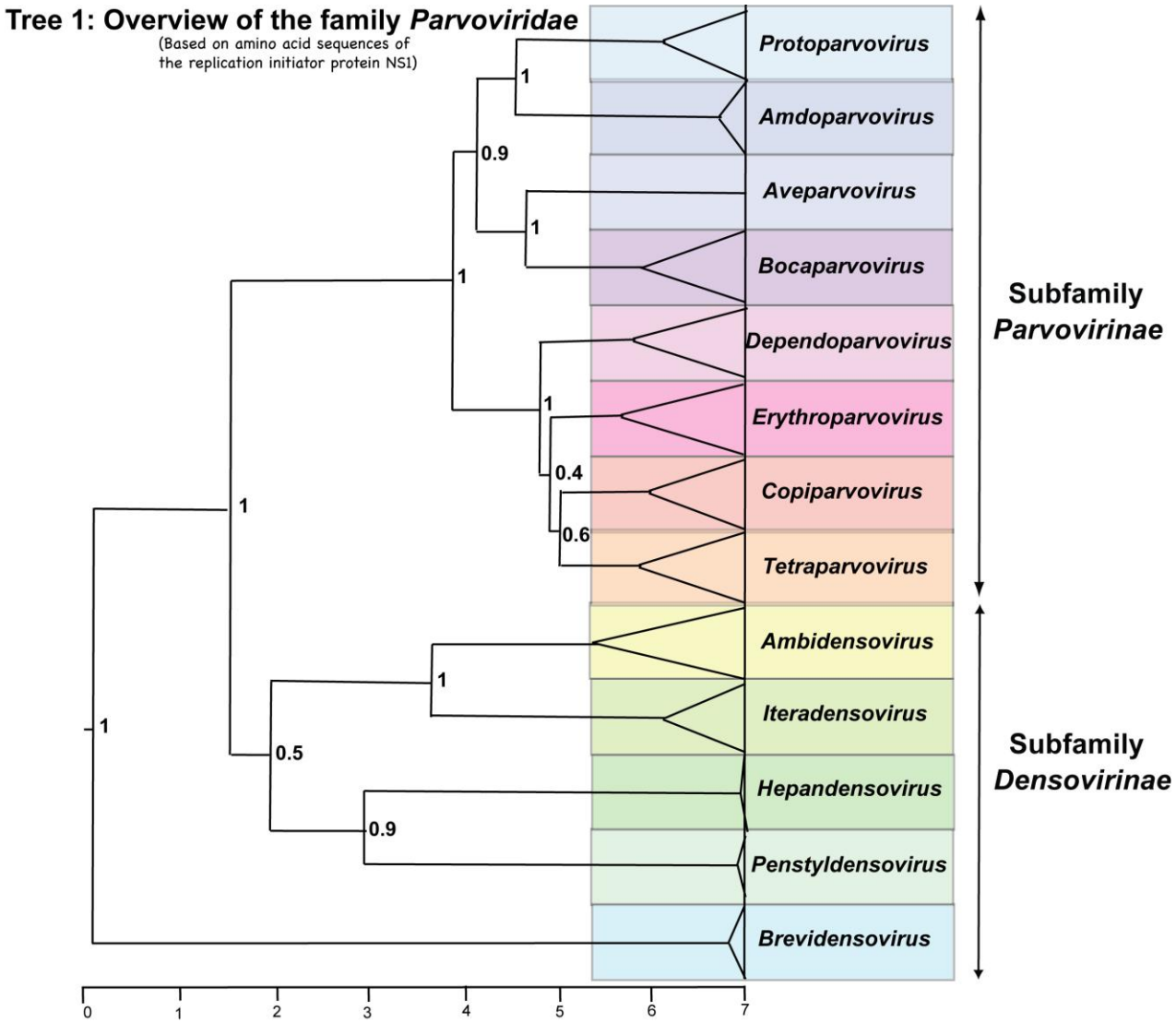
Previously, species were generally required to be >95% related in the NS1 DNA sequence, which is so high a level that many current species consist of single isolates. These proposals will decrease the species demarcation level significantly, requiring viruses in a species to encode NS1 proteins that show >85% amino acid sequence identity, while diverging by >15% from viruses in other species. This adjustment add useful structure within the genera by permitting a species to contain a greater diversity of viruses than is currently the case. Other criteria, such as host, antigenic properties, and genome characteristics are still considered.

In addition, the current nomenclature system causes confusion between species and virus names, which, except for the use of italics in the former, are generally identical. We propose a system in which species names are emphatically different from virus names, typically consisting of a host taxon, a genus affiliation, and a distinguishing numeral or letter. These terms indicate the range of viruses included and their branch within the family, and allow for facile addition of new species.

Also, since the proposed species distinguish major branches within a genus, they will provide taxonomic names for groups of viruses that are already commonly represented in the literature. Lastly, we propose expanding the names of genera to include a subfamily affiliation, thus providing those in the field with a more self-explanatory framework and greater precision when using taxonomically derived terms.

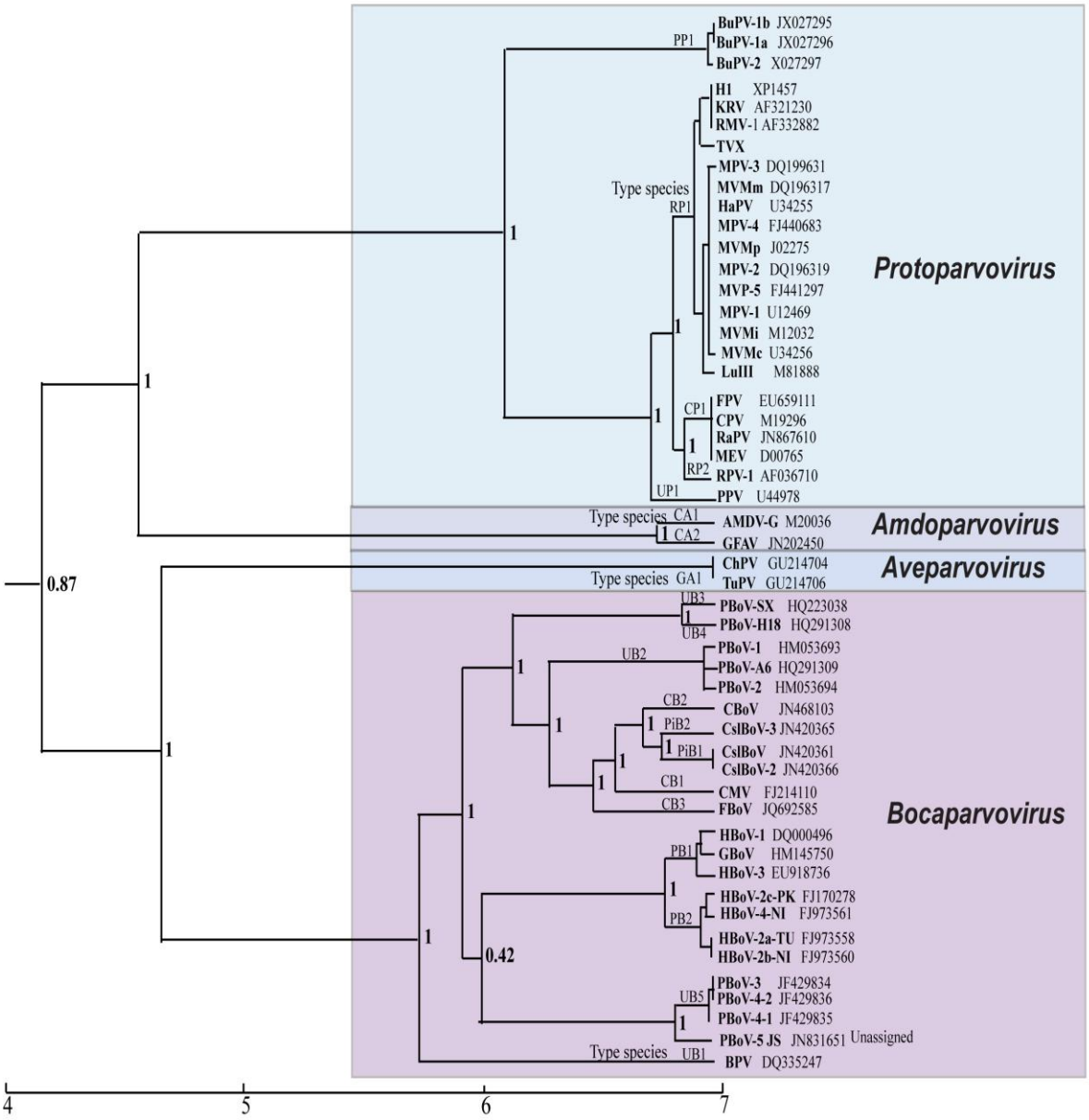
Phylogenetic trees

The phylogenetic analyses described below are based on the amino acid sequence of the viral replication initiator protein, NS1, which contains a conserved AAA+ helicase domain corresponding to the Parvo_NS1 Pfam domain: http://pfam.sanger.ac.uk/family/Parvo_NS1. Accordingly, this region was aligned by incorporating insights from structural biology using the ehmmalign application in EMBASSY(ref. 1), while sequences flanking the Pfam domain were aligned using the modification of the Needleman-Wunsch local alignment method (ref. 2) as implented in MOE-Align (http://www.chemcomp.com). Pairwise p-distance matrices were constructed from this alignment using MEGA version 5.10 (ref. 3), and variously color-coded to explore potential taxon identity criteria. Bayesian trees were calculated over one billion iterations using BEAST (ref. 4), using a Yule model of speciation and an exponential relaxed molecular clock (ref. 5). Trees were viewed in FigTree (part of BEAST) in ultrametric format on an arbitrary scale, with posterior probability scores indicated at statistically significant nodes.



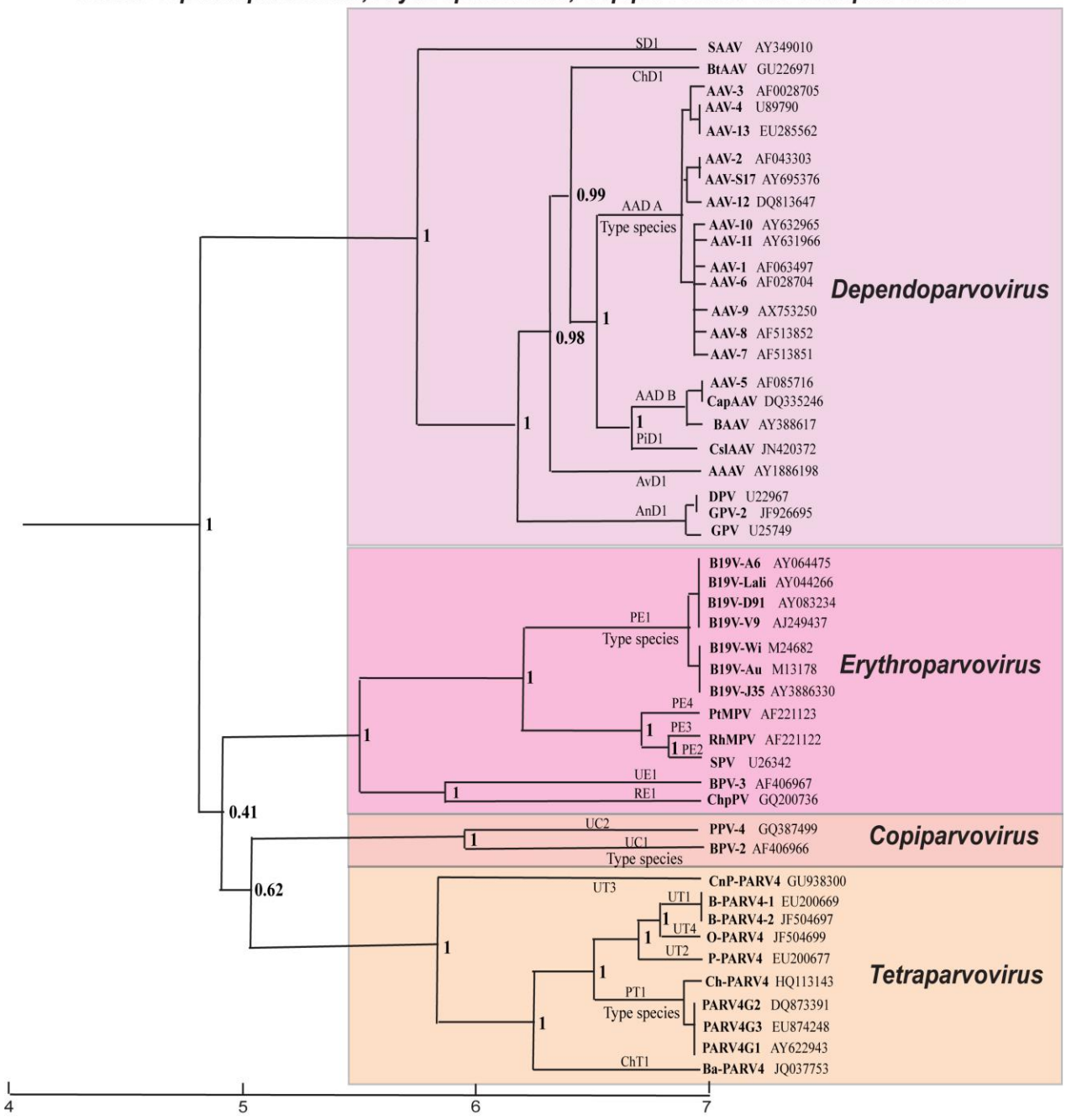
Tree 2: Subfamily *Parvovirinae*

Genus *Protoparvovirus, Amdoparvovirus, Aveparvovirus* and *Bocaparvovirus*

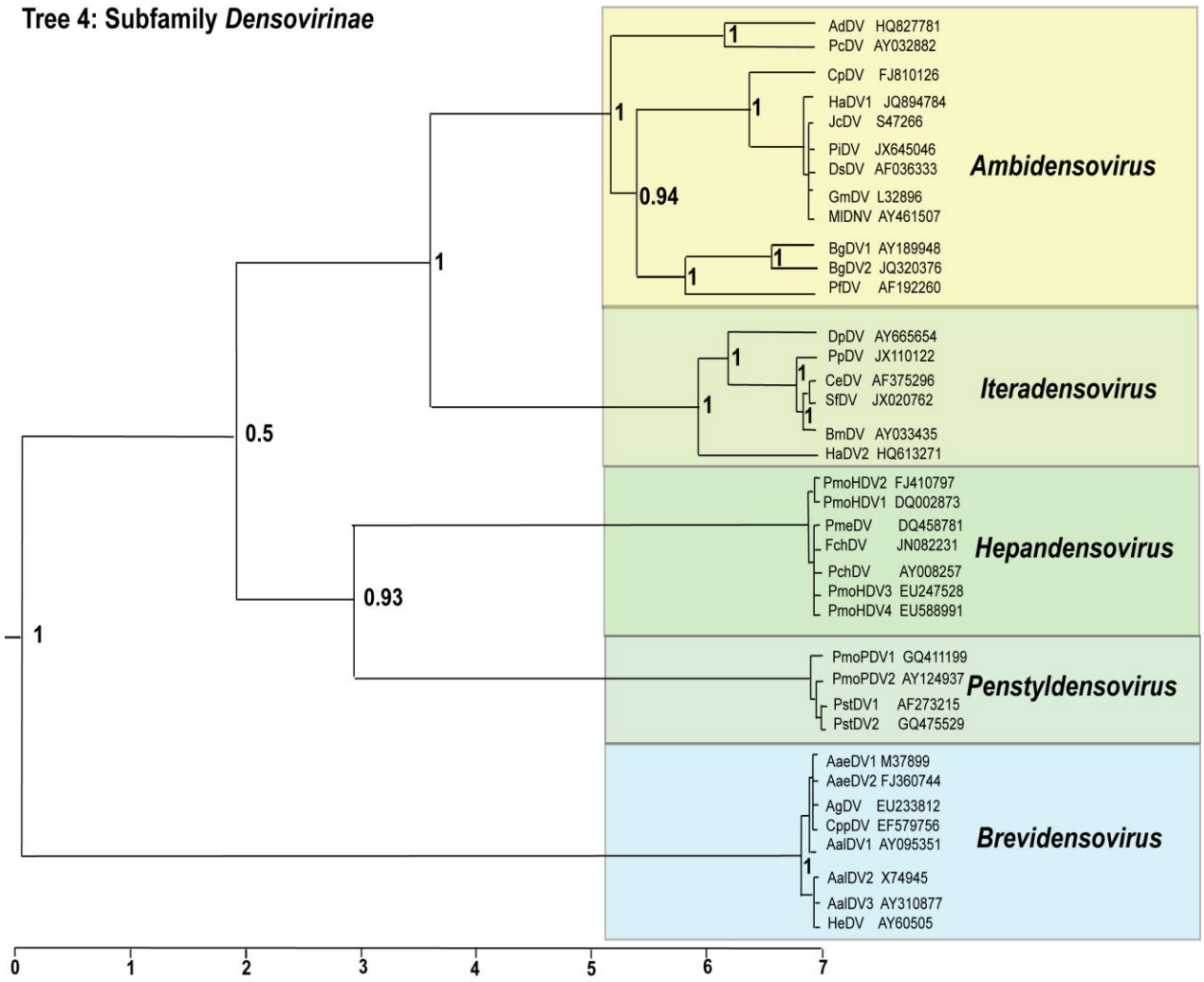


Viruses are represented by their acronyms and GenBank accession numbers. Species names are indicated on the final branches as acronyms, where the first letter indicates host taxon (C = carnivore; G = galliform; P = primate; Pi = pinniped; R= rodent; U = ungulate), and the second indicates genus affiliation.

Tree 3: Subfamily *Parvovirinae*:
Genus Dependoparvovirus, Erythroparvovirus, Copiparvovirus* and *Tetraparvovirus



Viruses are represented by their acronyms and GenBank accession numbers. Species names are indicated on the final branches as acronyms, where the first letter(s) indicates host taxon or helper-virus requirements (AA = adeno-associated, An = anseriform, Av = avian, Ch = chiropteran, P = primate, Pi = pinniped, R= rodent, S = squamate, U = ungulate), and the next indicates genus affiliation. Posterior probability scores are indicated at significant nodes.



Viruses are represented by their acronyms and GenBank accession numbers. Posterior probability scores are indicated at important nodes.

Table 1: Characteristics associated with genera in the subfamily *Parvovirinae*

Genus	Type species	Genome size (kb) and sense	Termini	Left terminus	Right terminus	Promoters (mu)	PLA2 in capsid	Ancilliary proteins	Helper virus independent
Amdoparvovirus	*Carnivore amdoparvovirus 1*	~4.8, "-"	Different HPs	~116nt	~240nt	1, at mu 4	no	NS2, SAT	yes
Aveparvovirus	*Galliform aveparvovirus 1*	~5.3,"+/-"	ITRs, similar HPs	206nt ITR 39nt HP	206nt ITR 39nt HP	2, at mu 5 and 56	no	uk	yes
Bocaparvovirus	*Ungulate bocaparvovirus 1*	~5.5, "-"	Different hairpins	~140-180nt	~180-200nt	1, at mu ~6	yes	NP1	yes
Copiparvovirus	*Ungulate copiparvovirus 1*	~5.6,uk	uk	uk	uk	uk	Motifs present	uk	yes
Dependoparvovirus	*Adeno-associated dependoparvovirus 1*	~4.7 "+/-"	ITRs, similar HPs	~145nt	~145nt	3, at mu 5,19, and 40; rarely 2 at mu 5 and 40	yes	Rep 40, AAP	Typically no; rarely yes
Erythroparvovirus	*Primate erythroparvovirus 1*	~5.6 "+/-"	ITRs, similar HPs	~385nt	~385nt	1, at mu ~6	yes	11k, 7.5k	yes
Protoparvovirus	*Rodent protoparvovirus 1*	~5.1, "-"	Different HPs	~120nt	~250nt	2, at mu ~4 and 40	yes	NS2, SAT	yes
Tetraparvovirus	*Primate tetraparvovirus 1*	~5.3, uk	uk	uk	uk	2. at mu 6 and 38.	Motifs present	uk	yes

Table 2: Characteristics associated with viruses in the subfamily *Densovirinae*

Genus	Type species	Genome size (kb) and sense	Termini	Coding sense	Left terminus	Right terminus	NS ORFs	VP ORF	PLA2 in capsid
Ambidensovirus	*Lepidopteran ambidensovirus 1*	~5.5-6.0 "+/-"	ITRs, similar HPs	Ambi-sense	200-550nt	200-550nt	three	contiguous or split	yes
Brevidensovirus	*Dipteran brevidensovirus 1*	~4, "-"	Different HPs	mono	~135nt	~180nt	two	one	no
Hepandensovirus	*Decapod hepandensovirus 1*	~6.3, "-"	Different HPs	mono	136-220nt	152-214nt	two	one	no
Iteradensovirus	*Lepidopteran iteradensovirus 1*	~5, "+/-"	ITRs, similar HPs	mono	~250nt	~250nt	two	one	yes
Penstyldensovirus	*Decapod penstyldensovirus 1*	~4 "+/-"	TRs	mono	uk	uk	two	one	no

In "genome" columns "-" = packaged strands predominantly negative sense, and "+/-" = approximately equimolar positive and negative strands. Abbreviations: uk = unknown, HPs = hairpins, TR = terminal repeat, ITR = inverted terminal repeat, mu = map unit and PLA2 = phospholipase A2.
Additional note: The sequence and predicted structures of the terminal hairpins can be very different among genera, but are typically conserved within genera, making them highly diagnostic of genus affiliation. However, these convoluted hairpin elements can be difficult to capture as stable inserts in bacterial plasmids or to copy with polymerases, so are typically the last sequence elements identified for any given virus.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Eddy SR. Accelerated Profile HMM Searches. 2011. PLoS Comput Biol. 7:e1002195.
2. Needleman SB, Wunsch CD.1970. A General Method Applicable to the Search for Similarities in the Amino Acid Sequences of Two Proteins. J. Mol. Biol. 48: 443–453.
3.Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. 2011. MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Method. Mol. Biol. and Evo. 28: 2731-2739.
4. Drummond AJ, Rambaut A. 2007. BEAST: Bayesian evolutionary analysis by sampling trees. BMC Evolutionary Biology 7; 214.
5. Drummond AJ, Ho SYW, Phillips MJ, Rambaut A. 2006. Relaxed Phylogenetics and Dating with Confidence. PLoS Biol. 4; e88

ADDENDUM

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by Modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

Code	***2013.001ssV*** - ***2013.001aaaV*** See individual codes, below	(assigned by ICTV officers)
Title of proposal: Additional taxonomic changes requiring formal proposals		

Text of proposal:

Note from the officers: Following approval and ratification of version 3 of this proposal (2013.001a-rrV.v3), we have identified nine taxonomic changes, hitherto missing from the proposal, which are also involved in the proposed restructuring of the taxonomy of the *Parvoviridae* family. Each of these nine steps is needed to complete the conversion of the old taxonomic structure to the new one. The changes, are as follows:

Code	***2013.001ssV***
designate *Carnivore amdoparvovirus 1* as type species of genus *Amdoparvovirus* (previous name, *Amdovirus*)	
Code	***2013.001ttV***
designate *Ungulate bocaparvovirus 1* as type species of genus *Bocaparvovirus* (previous name, *Bocavirus*)	
Code	***2013.001uuV***
designate *Adeno-associated dependoparvovirus A* as type species of genus *Dependoparvovirus* (previous name, *Dependovirus*)	
Code	***2013.001vvV***
designate *Primate erythroparvovirus 1* as type species of genus *Erythroparvovirus* (previous name, *Erythrovirus*)	
Code	***2013.001wwV***
designate *Rodent protoparvovirus 1* as type species of genus *Protoparvovirus* (new)	
Code	***2013.001xxV***
designate *Dipteran brevidensovirus 1* as type species of genus *Brevidensovirus*	
Code	***2013.001yyV***
designate *Lepidopteran ambidensovirus 1* as type species of genus *Ambidensovirus* (previous name, *Densovirus*)	
Code	***2013.001zzV***
designate *Lepidopteran iteradensovirus 1* as type species of genus *Iteradensovirus* (previous name, *Densovirus*)	
Code	***2013.001aaaV***
remove genus *Pefudensovirus* from subfamily *Densovirinae*, family *Parvoviridae*	