



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:	2015.014aM	(to be completed by ICTV officers)			
Short title: One (1) new species in the genus <i>Morbillivirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

Author(s):

The ICTV <i>Paramyxoviridae</i> Study Group:			
Rima, Bertus K.	Chair	Northern Ireland, UK	b.rima@gub.ac.uk
Collins, Peter L.	Member	USA	pcollins@niaid.nih.gov
Easton, Andrew J.	Member	UK	A.J.Easton@warwick.ac.uk
Fouchier, Ron	Member	The Netherland	r.fouchier@erasmusmc.nl
Kurath, Gael	Member	USA	gael_kurath@usgs.gov
Lamb, Bob	Member	USA	ralamb@northwestern.edu
Maisner, Andrea	Member	Germany	maisner@staff.uni-marburg.de
Randall, Rick	Member	UK	rer@st-andrews.ac.uk
Rota, Paul	Member	USA	prota@cdc.gov
Wang, Lin-Fa	Member	Australia	Linfa.Wang@csiro.au

Corresponding author with e-mail address:

Rima, Bertus K. Chair Northern Ireland, UK b.rima@gub.ac.uk

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)	
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

June 15, 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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MODULE 2: **NEW SPECIES**

creating and naming one or more 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. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2015.014aM	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Morbillivirus</i>	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.
Subfamily:		
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Feline morbillivirus</i>	feline morbillivirus 761U	JQ411014

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

In 2012, Woo *et al.* (see reference 1) isolated viruses from domestic cats in Hong Kong with tubule-interstitial nephritis. Since then, a number of other isolates of this virus have been made from cats with the same clinical phenotype in Japan (see reference 2) and the US (Duprex *et al.*, in preparation). The virus was named feline morbillivirus (FeMV) and is proposed to be a member of the *Morbillivirus* genus on the basis of the basis of sequence homology of both the FeMV genome and the encoded proteins.

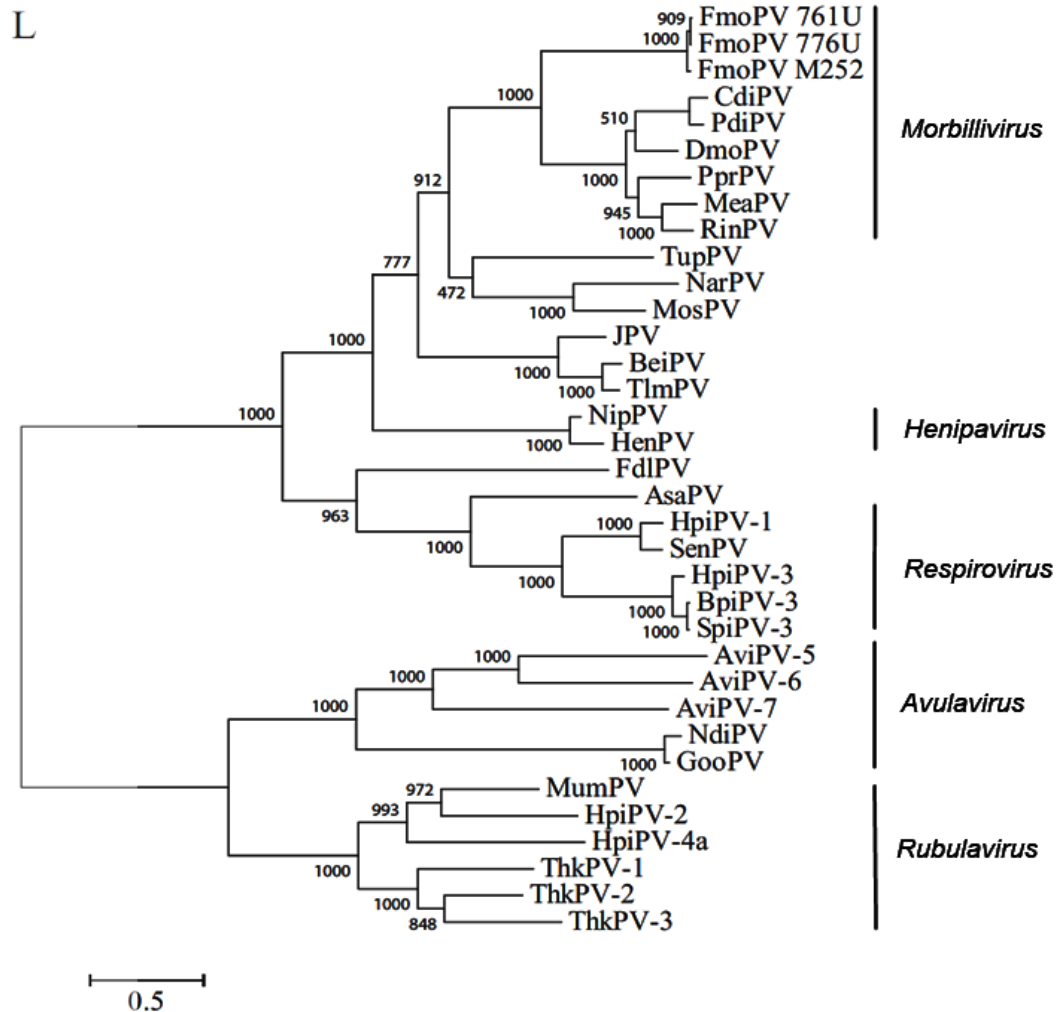
All the phylogenetic analyses in these papers (also see reference 3) indicate the close relationship between the existing morbilliviruses and FeMV. The FeMV gene order is the same as that of other morbilliviruses. The complete FeMV genome length is 16,050 nt, complying with the “rule of six.” The FeMV genome is slightly longer than those of any of the other morbilliviruses but this length difference is primarily caused by differences in the lengths of the non-coding regions: the FeMV genome-encoded proteins are all of similar size to those produced by other the morbilliviruses, and specific protein sequence motifs that are known to be conserved in the proteins of other morbilliviruses are also present in FeMV (see below for the RNA-dependent RNA polymerase (L) protein as an example).

Without doubt this virus belongs to the morbilliviruses though phylogenetically it is slightly more distant from the other morbilliviruses than the hitherto very closely related CDV/PDV, MV/RPV, CeMV and PPRV virus groups.

This looser connection is also evident from the phylogenetic tree of the L proteins of the Paramyxoviridae shown in module 10.

MODULE 10: **APPENDIX**: supporting material

The attached tree shows the relationships between amino acid sequences of the L or RdRp proteins of the *Paramyxovirinae*. It demonstrates that Feline morbillivirus clearly belongs to the genus *Morbillivirus* and is distinct from the other genera in the subfamily. It also shows that the feline morbillivirus is closer to the other morbilliviruses than to the hitherto unassigned Tupaia, Nariva and Mossman viruses.



Legend

FmoPV = feline morbillivirus; CdiPV = canine distemper virus; PdiPV = phocine distemper virus; DmoPV = dolphin morbillivirus (belonging to the species cetacean morbillivirus); PprPV = peste-des-petits ruminants virus; MeaPV = measles virus; RinPV = rinderpest virus; TupPV = Tupaia paramyxovirus; NarPV = Nariva virus; MosPV = Mossman virus; JPV = J virus; BeiPV = Beilong virus; TlmPV = Tailam virus; NipPV = Nipah virus; HenPV = Hendravirus; FdIPV = Fer-de lance virus; AsaPV = Atlantic salmon paramyxovirus; HpiPV-1 = human paramyxovirus type 1; SenPV = Sendai virus; HpiPV-3 = human paramyxovirus type 3; BpiPV-3 = bovine paramyxovirus type 3; SpiPV-3 = swine para-influenzavirus type 3; AviPV-5 = avian paramyxovirus type 5; AviPV-6 = avian paramyxovirus type 6; AviPV-7 = avian paramyxovirus type 7; NdiPV = Newcastle disease virus; GooPV = Goose paramyxovirus; mumPV = mumps virus; HpiPV-2 = human paramyxovirus type 2; HpiPV-4a = human paramyxovirus type 4a; ThkPV-1 = Tuhoko virus type 1; ThkPV-2 = Tuhoko virus type 2 and ThkPV-3 = Tuhoko virus type 3.

With permission from reference 1 Woo et al. Fig 2. Table S5 in the same reference documents the accession numbers used.

additional material in support of this proposal

References:

1 Woo, P.C., Lau, S.K., Wong, B.H., Fan, R.Y., Wong, A.Y., Zhang, A.J., Wu, Y., Choi, G.K., Li, K.S., Hui, J., Wang, M., Zheng, B.J., Chan, K.H.

additional material in support of this proposal

References:

and Yuen, K.Y.

TITLE Feline morbillivirus, a previously undescribed paramyxovirus associated with tubulointerstitial nephritis in domestic cats
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 109 (14), 5435-5440 (2012)
PUBMED [22431644](#)

2 Furuya, T., Sassa, Y., Omatsu, T., Nagai, M., Fukushima, R., Shibutani, M., Yamaguchi, T., Uematsu, Y., Shiota, K. and Mizutani, T.

TITLE Existence of feline morbillivirus infection in Japanese cat populations
JOURNAL Arch. Virol. 159 (2), 371-373 (2014)
PUBMED [23929233](#)

3 Park, E.S., Suzuki, M., Kimura, M., Maruyama, K., Mizutani, H., Saito, R., Kubota, N., Furuya, T., Mizutani, T., Imaoka, K. and Morikawa, S.

TITLE Identification of a natural recombination in the F and H genes of feline morbillivirus.

JOURNAL Virology 468-470C, 524-531 (2014)
PUBMED [25262470](#)

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
