



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:	2016.011aM	(to be completed by ICTV officers)				
Short title: Implementation of taxon-wide non-Latinized binomial species names in the family <i>Paramyxoviridae</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 type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>	
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input checked="" type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>	

Author(s):

ICTV *Paramyxoviridae* Study Group:

Rima, Bertus K.	Chair	Northern Ireland, UK	b.rima@qub.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
Rota, Paul	Member	USA	prota@cdc.gov
Wang, Lin-Fa	Member	Singapore	Linfa.Wang@duke-nus.edu.sg

and
Kuhn, Jens H., kuhnjens@mail.nih.gov

Corresponding author with e-mail address:

Rima, Bertus K. (ICTV *Paramyxoviridae* Study Group Chair), b.rima@qub.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)	ICTV <i>Paramyxoviridae</i> Study Group
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

July 18, 2016

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

Renaming one or more taxa

Code	2016.011aM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current species name	Proposed species name	Exemplar virus (abbrev ⁿ)
<i>Atlantic salmon paramyxovirus</i>	<i>Salmon aquaparamyxovirus</i>	Atlantic salmon paramyxovirus (AsaPV)
<i>Fer-de-Lance paramyxovirus</i>	<i>Reptilian ferlavivirus</i>	Fer-de-Lance virus (FDLV)
<i>Cedar henipavirus</i>	No change necessary	Cedar virus (CedV)
<i>Ghanaian bat henipavirus</i>	No change necessary	Kumasi virus (KV)
<i>Hendra virus</i>	<i>Hendra henipavirus</i>	Hendra virus (HeV)
<i>Mojiang henipavirus</i>	No change necessary	Mòjiāng virus (MojV)
<i>Nipah virus</i>	<i>Nipah henipavirus</i>	Nipah virus (NiV)
<i>Canine distemper virus</i>	<i>Canine morbillivirus</i>	canine distemper virus (CDV)
<i>Cetacean morbillivirus</i>	No change necessary	cetacean morbillivirus (CeMV)
<i>Feline morbillivirus</i>	No change necessary	feline morbillivirus (FeMV)
<i>Measles virus</i>	<i>Measles morbillivirus</i>	measles virus (MeV)
<i>Peste-des-petits-ruminants virus</i>	<i>Small ruminant morbillivirus</i>	peste-des-petits-ruminants virus (PPRV)
<i>Phocine distemper virus</i>	<i>Phocine morbillivirus</i>	phocine distemper virus (PDV)

<i>Rinderpest virus</i>	<i>Rinderpest morbillivirus</i>	rinderpest virus (RPV)
<i>Bovine parainfluenza virus</i> 3	<i>Bovine respirovirus 3</i>	bovine parainfluenza virus 3 (BPIV-3)
<i>Human parainfluenza virus</i> 1	<i>Human respirovirus 1</i>	human parainfluenza virus 1 (HPIV-1)
<i>Human parainfluenza virus</i> 3	<i>Human respirovirus 3</i>	human parainfluenza virus 3 (HPIV-3)
<i>Porcine parainfluenza virus</i> 1	<i>Porcine respirovirus 1</i>	porcine parainfluenza virus 1 (PPIV-1)
<i>Sendai virus</i>	<i>Murine respirovirus</i>	Sendai virus (SeV)
<i>Human parainfluenza virus</i> 2	<i>Human rubulavirus 2</i>	human parainfluenza virus 2 (HPIV-2)
<i>Human parainfluenza virus</i> 4	<i>Human rubulavirus 4</i>	human parainfluenza virus 4a (HPIV-4a)
<i>Mapuera virus</i>	<i>Mapuera rubulavirus</i>	Mapuera virus (MapV)
<i>Mumps virus</i> *	<i>Mumps rubulavirus</i> *	mumps virus (MuV)
<i>Parainfluenza virus 5</i>	<i>Mammalian rubulavirus 5</i>	parainfluenza virus 5 (PIV- 5)
<i>Porcine rubulavirus</i>	No change necessary	La Piedad Michoacán Mexico virus (LPMV)
<i>Simian virus 41</i>	<i>Simian rubulavirus</i>	simian virus 41 (SV-41)

*Note that the species names of the genus *Avulavirus* are addressed in a separate proposal.

Reasons to justify the renaming:

[Explain why the taxon \(or taxa\) should be renamed](#)

At the moment, numerous paramyxovirus species names are identical in spelling to the names of their virus members and only differ by presence or absence of italics and/or capitalization (e.g., the species *Hendra virus* is the taxonomic home for Hendra virus). Consequently, species and virus names are constantly confused. In other cases, pseudo-

binomial names are in use that imply the existence of genera that actually do not exist (e.g., the species name *Atlantic salmon paramyxovirus* implies the existence of a genus *Paramyxovirus*, which does not exist). To remove this ambiguity, we propose replacing the current ambiguous species names with non-Latinized binomial names distinct from virus names as proposed by van Regenmortel *et al.*, 2010, and as already implemented for six of the eight mononegaviral families (*Bornaviridae*, *Filoviridae*, *Mymonaviridae*, *Nyamiviridae*, *Rhabdoviridae*, and *Sunviridae*) and several other, non-mononegaviral families (e.g., *Arenaviridae*, *Bunyaviridae*).

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Van Regenmortel, M.H., Burke, D.S., Calisher, C.H., Dietzgen, R.G., Fauquet, C.M., Ghabrial, S.A., Jahrling, P.B., Johnson, K.M., Holbrook, M.R., Horzinek, M.C., Keil, G.M., Kuhn, J.H., Mahy, B.W., Martelli, G.P., Pringle, C., Rybicki, E.P., Skern, T., Tesh, R.B., Wahl-Jensen, V., Walker, P.J., and Weaver, S.C. (2010). A proposal to change existing virus species names to non-Latinized binomials. *Arch. Virol.* 2010 155, 1909-1919.

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.
