



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:	2016.012aM	(to be completed by ICTV officers)				
Short title: Implementation of taxon-wide non-Latinized binomial species names in the family <i>Pneumoviridae</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 (currently also responsible for the family *Pneumoviridae*):

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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)	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	2016.012aM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current species name	Proposed species name	Member virus names and abbreviations (unchanged)
<i>Avian metapneumovirus</i>	no change necessary	avian metapneumovirus (AMPV)
<i>Human metapneumovirus</i>	no change necessary	human metapneumovirus (HMPV)
<i>Bovine respiratory syncytial virus</i>	<i>Bovine orthopneumovirus</i>	bovine respiratory syncytial virus (BRSV)
<i>Human respiratory syncytial virus</i>	<i>Human orthopneumovirus</i>	human respiratory syncytial virus (HRSV)
<i>Murine pneumonia virus</i>	<i>Murine orthopneumovirus</i>	murine pneumonia virus (MPV)

Reasons to justify the renaming:

Explain why the taxon (or taxa) should be renamed

At the moment, three accepted orthopneumovirus 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 *Human respiratory syncytial virus* is the taxonomic home for human respiratory syncytial virus). Consequently, species and virus names are constantly confused. 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*, *Myxonaviridae*, *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.
