



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:	2015.011a-gM	(to be completed by ICTV officers)			
Short title: Elevation of the paramyxoviral subfamily <i>Pneumovirinae</i> to family status as family <i>Pneumoviridae</i> in the order <i>Mononegavirales</i> ; and renaming of one pneumoviral genus (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 checked="" type="checkbox"/>	8 <input checked="" type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

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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 *Bornaviridae*, *Filoviridae*, *Nyamiviridae*, and *Rhabdoviridae* Study Groups

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 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) taxon/taxa to be removed or moved

Code	2015.011aM	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Orthopneumovirus</i> (new name)		
<i>Metapneumovirus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:		Fill in all that apply.
Subfamily:	<i>Pneumovirinae</i>	
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	
<p>If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right</p>		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

The ICTV *Paramyxoviridae* Study Group proposes the establishment of a new mononegaviral family to incorporate the current *Pneumovirinae* subfamily of the family *Paramyxoviridae*. This proposal is based on consideration of the phylogenetic relationships between members of the *Pneumovirinae* and *Paramyxovirinae* subfamilies and other mononegaviruses, particularly those of the family *Filoviridae*; the presence of a gene in pneumovirus genomes (M2) that encodes two unique proteins involved in the regulation of virus RNA synthesis; and the difference in the ribonucleoprotein complex structures of the members of the *Pneumovirinae* and *Paramyxovirinae* subfamilies. Members of the Study Group pointed out the similarities in viral mechanisms, biology (route of entry and primary target organ) and general conservation of the fusion F protein in members of both *Paramyxoviridae* subfamilies but the consensus was that while these factors are relevant for classification purposes they did not outweigh the considerations above.

Part (b) re-assign to a higher taxon

Code	2015.011bM	(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:		Fill in all that apply. • If the higher taxon has yet to be created write " (new) " after its proposed name and complete relevant module to create it. If no genus is specified, enter " unassigned " in the genus box.
Subfamily:		
Family:	<i>Pneumoviridae</i> (new)	
Order:	<i>Mononegavirales</i>	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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

The members of the current subfamily *Pneumovirinae* are readily distinguished from members of the subfamily *Paramyxovirinae* on the basis of: the structure of the virus RNP complex, phylogenetic distance, the presence and organization of two open reading frames in the M2 transcription unit in pneumoviruses, and the mode of expression of the M2 gene of the pneumoviruses. These differences indicate fundamental differences between the two subfamilies which justifies separation into two families.

Nucleocapsid structure

Electron microscopic analysis has demonstrated that the nucleocapsid structures of pneumoviruses and paramyxoviruses are significantly different, with the human respiratory syncytial virus and murine pneumovirus nucleocapsids having a diameter of 13.5 nm and a helical pitch 6.5 nm and the paramyxoviruses, exemplified by measles virus and human parainfluenza virus type 2, having a diameter of 17.5 to 20 nm and a helical pitch 5.0 nm, respectively (Zakstelskaya, *et al.*, 1967; Nakai and Imagawa, 1969; Joncas *et al.*, 1969; Berthiaume *et al.*, 1974). These differences have been confirmed by more recent cryo-electron microscopic analysis of nucleocapsid structures (Gutsche *et al.*, 2015).

Phylogenetic relationships

Phylogenetic analysis of a number of proteins encoded by pneumoviruses and paramyxoviruses consistently indicate that the members of the two subfamilies are well separated and, also consistently, that the members of the *Pneumovirinae* show an almost equal phylogenetic relationship with the members of the mononegaviral family *Filoviridae* as that seen with the members of the family *Paramyxovirinae*. A representative example of this is shown in the phylogenetic trees presented in the Appendix (Figure 1. Appendix, Module 10). The trees clearly demonstrate the evolutionary relationships of the *Pneumovirinae* as a group that is distinct from the *Paramyxovirinae*.

The unique M2 gene

A significant feature of the genomes of all members of the current *Pneumovirinae* subfamily is the presence of an M2 gene that encodes two proteins, M2-1 and M2-2, from overlapping open reading frames. The ‘architecture’ of the M2 mRNA coding potential is maintained among all pneumoviruses and is not seen in any other NSS RNA virus families (Figure 2. Appendix, Module 10). The pneumovirus M2-1 protein is unique and no homologue has been found in any other virus group. This therefore distinguishes pneumoviruses from the paramyxoviruses. The M2-1 protein sequence is well conserved among pneumoviruses and the M2-1 protein enhances virus RNA synthesis through its action as a processivity factor for the virus RNA-dependent RNA polymerase. No protein with a similar function has been described for members of the *Paramyxovirinae*, further emphasizing the differences between the two subfamilies. Expression of the second ORF M2-2 protein utilizes a unique mechanism of translation of the mRNA that is not seen among any other viruses (Ahmadian *et al.*, 2000; Gould and Easton, 2005, 2007). The M2-2 protein is involved in the switch of virus RNA synthesis from transcription to replication. No protein with a similar function has been described among members of the *Paramyxovirinae*, further emphasizing the distinction between the two subfamilies.

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) taxon/taxa to be removed or moved

Code	2015.011cM	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
The genera: <i>Aquaparamyxovirus</i> <i>Avulavirus</i> <i>Ferlavirus</i> <i>Henipavirus</i> <i>Morbillivirus</i> <i>Respirovirus</i> <i>Rubulavirus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:		Fill in all that apply.
Subfamily:	<i>Paramyxovirinae</i>	
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

A consequence of removing the genera *Pneumovirus* and *Metapneumovirus* from the *Paramyxoviridae* family (2015.011aM and 2015.011bM, above) is that the family will contain no taxa other than those in the subfamily *Paramyxovirinae*. The subfamily therefore becomes a superfluous taxonomic level, which we propose (in 2015.011eM, below) to abolish.

Part (b) re-assign to a higher taxon

Code	2015.011dM	(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:		Fill in all that apply. • If the higher taxon has yet to be created write " (new) " after its proposed name and complete relevant module to create it. If no genus is specified, enter " unassigned " in the genus box.
Subfamily:		
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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

See 2015.011cM, above. Only the taxonomic level of subfamily is being abolished. The taxa previously assigned to the subfamily *Paramyxovirinae* will remain included in the family *Paramyxoviridae*. All tentative members of the *Paramyxovirinae* will now be considered tentative members of the *Paramyxoviridae*.

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) taxon/taxa to be removed or moved

Code	2015.01eM	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
Subfamilies <i>Pneumovirinae</i> and <i>Paramyxovirinae</i>		
The present taxonomic position of these taxon/taxa:		
Genus:		Fill in all that apply.
Subfamily:		
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	
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 removal of the subfamily *Pneumovirinae* is explained in 2015.011a,bM.

The removal of the subfamily *Paramyxovirinae* is explained in 2015.011cM

Part (b) re-assign to a higher taxon

Code		(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
N/A		
Genus:		Fill in all that apply. <ul style="list-style-type: none"> • If the higher taxon has yet to be created write "(new)" after its proposed name and complete relevant module to create it. If no genus is specified, enter "unassigned" in the genus box.
Subfamily:		
Family:		
Order:		

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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

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MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	2015.011fM	(assigned by ICTV officers)
<p>To create a new family containing the subfamilies and/or genera listed below within the Order: <i>Mononegavirales</i></p> <p>If there is no Order, write “unassigned” here. If the Order has yet to be created (in Module 6) please write “(new)” after the proposed name.</p>		

Code	2015.011gM	(assigned by ICTV officers)
<p>To name the new family: <i>Pneumoviridae</i></p>		

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)
<p>To assign the following subfamilies (if any) to the new family: You may list several subfamilies here. For each subfamily, please state whether it is new or existing.</p> <ul style="list-style-type: none"> • If the subfamily is new, it must be created in Module 4 • If the subfamily already exists, please complete Module 7 to ‘REMOVE’ it from its existing family 		

Code	2015.011hM	(assigned by ICTV officers)
<p>To assign the following genera to the new family: You may list several genera here. For each genus, please state whether it is new or existing.</p> <ul style="list-style-type: none"> • If the genus is new, it must be created in Module 3 • If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to ‘REMOVE’ it from that family 		

Orthopneumovirus (new name)

Metapneumovirus

The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):**

0

Reasons to justify the creation of the new family:

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

See 2015.011aM and 2015.011bM

Origin of the new family name:

After *Pneumovirinae*, the subfamily which previously contained the genera *Pneumovirus* (proposed name *Orthopneumovirus*) and *Metapneumovirus*

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	2015.011iM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current name		Proposed name
<i>Pneumovirus</i>		<i>Orthopneumovirus</i>

Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed
The new family <i>Pneumoviridae</i> will contain two genera as currently established within the subfamily <i>Pneumovirinae</i> (to be abolished). These two genera will be named <i>Orthopneumovirus</i> and <i>Metapneumovirus</i> . The latter name is already used and accepted by the ICTV and the relevant scientific community. Renaming the current genus <i>Pneumovirus</i> <i>Orthopneumovirus</i> is logical, will provide consistency of nomenclature within the new family, and removes the ambiguity that arose from using a subfamily/family name and included genus name sharing a common word stem (both the members of the subfamily/family and genus would be called “pneumoviruses;” the word “pneumovirus” would therefore not specify whether all members of the higher taxon are meant or only the member of the one particular genus).

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Zakstelskaya, L. Y., Almeida, J. D. and Bradstreet, C. M. (1967). The morphological characterisation of respiratory syncytial virus by a simple electron microscope technique. *Acta Virologica*, **11**, 420-423.
- Nakai, M. and Imagawa, D. T. (1969). Electron Microscopy of Measles Virus Replication. *Journal of Virology*, **3**, 187-197.
- Joncas, J., Berthiaume, L. and Pavilanis, V. (1969). The structure of the respiratory syncytial virus. *Virology* **38**, 493-496.
- Berthiaume, L., Joncas, J. and Pavilanis, V. (1974). Comparative structure, morphogenesis and biological characteristics of the respiratory syncytial (RS) virus and the pneumonia virus of mice (PVM). *Archive fur die gesamte Virusforschung*, **45**, 39-51.
- Stec, D. S., Hill, M. G. and Collins, P. L. (1991). Sequence analysis of the polymerase L gene of human respiratory syncytial virus and predicted phylogeny of nonsegmented negative-strand viruses. *Virology*, **183**, 273-287.
- Randhawa, J. S., Wilson, S. D., Tolley, K. P., Cavanagh, D., Pringle, C. R. and Easton, A. J. (1996). Nucleotide sequence of the gene encoding the viral polymerase of avian pneumovirus. *Journal of General Virology*, **77**, 3047-3051.
- van den Hoogen, B. G., Bestebroer, T. M., Osterhaus, A. D. and Fouchier, R. A. (2002). Analysis of the genomic sequence of a human metapneumovirus. *Virology*, **295**, 119-132.
- Gutsche, I., Desfosses, A., Effantin, G., Ling, W. L., Haupt, M., Ruigrok, R. W., Sachse, C. and Schoehn, G. (2015). Structural virology. Near-atomic cryo-EM structure of the helical measles virus nucleocapsid. *Science*, **348**, 704-707.
- Ahmadian, G., Randhawa, J.S. and Easton, A.J. (2000). Expression of the ORF-2 protein of the human respiratory syncytial virus M2 gene is initiated by a ribosomal termination-dependent reinitiation mechanism. *EMBO Journal*, **11**, 2681-2689.
- Gould, P. S. and Easton, A. J. (2005). Coupled translation of the respiratory syncytial virus M2 ORFs requires upstream sequences. *Journal of Biological Chemistry*, **280**, 21972-21980.
- Gould, P. S. and Easton, A. J. (2007). Coupled translation of the second ORF of the M2 mRNA is sequence dependent and differs significantly in the sub family *Pneumovirinae*. *Journal of Virology*, **81**, 8488-8496.

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.

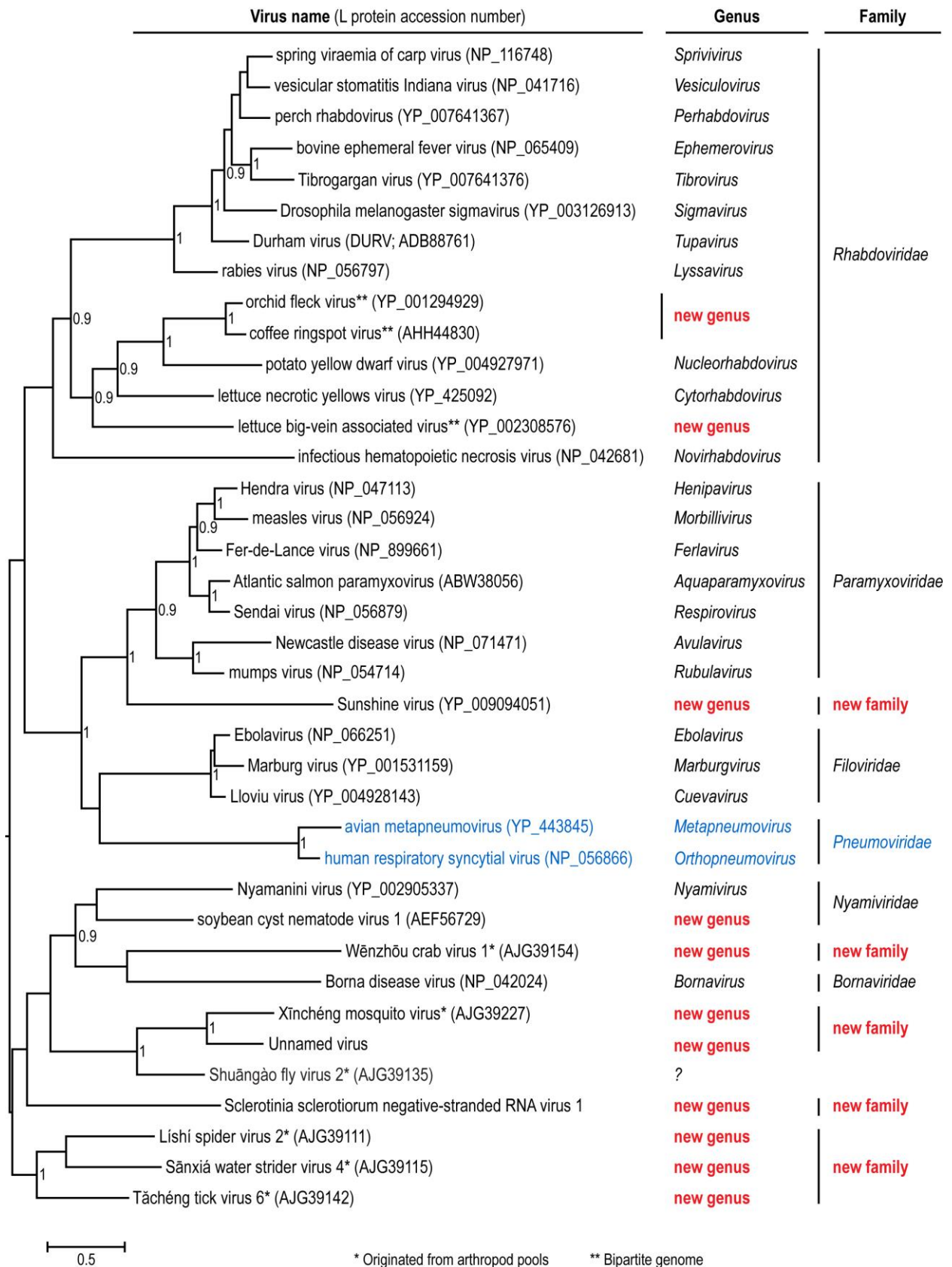


Figure 1A. Phylogenetic relationships of selected mononegaviruses.

A maximum-likelihood tree was constructed using PhyML 3.0 (<http://www.atgc-montpellier.fr/phyml/>) based on a multiple amino acid sequence alignment of the entire L polymerase. Ambiguously aligned regions were removed using Gblocks 0.91b

(http://molevol.cmima.csic.es/castresana/Gblocks_server.html) with the all options of less stringent selection. The best-fit model LG+I +G+F was selected using ProtTest ver. 2.4 (http://darwin.uvigo.es/software/protest2_server.html). Virus names (the members of type species or others) and GenBank/Refseq accession numbers are shown. The name of the proposed family is highlighted in blue. Numbers at the nodes represent aLRT values derived using an SH like calculation (only values greater than 0.9 are shown). (Figure created by Dr. Hideki Kondo, Okayama University, Japan)

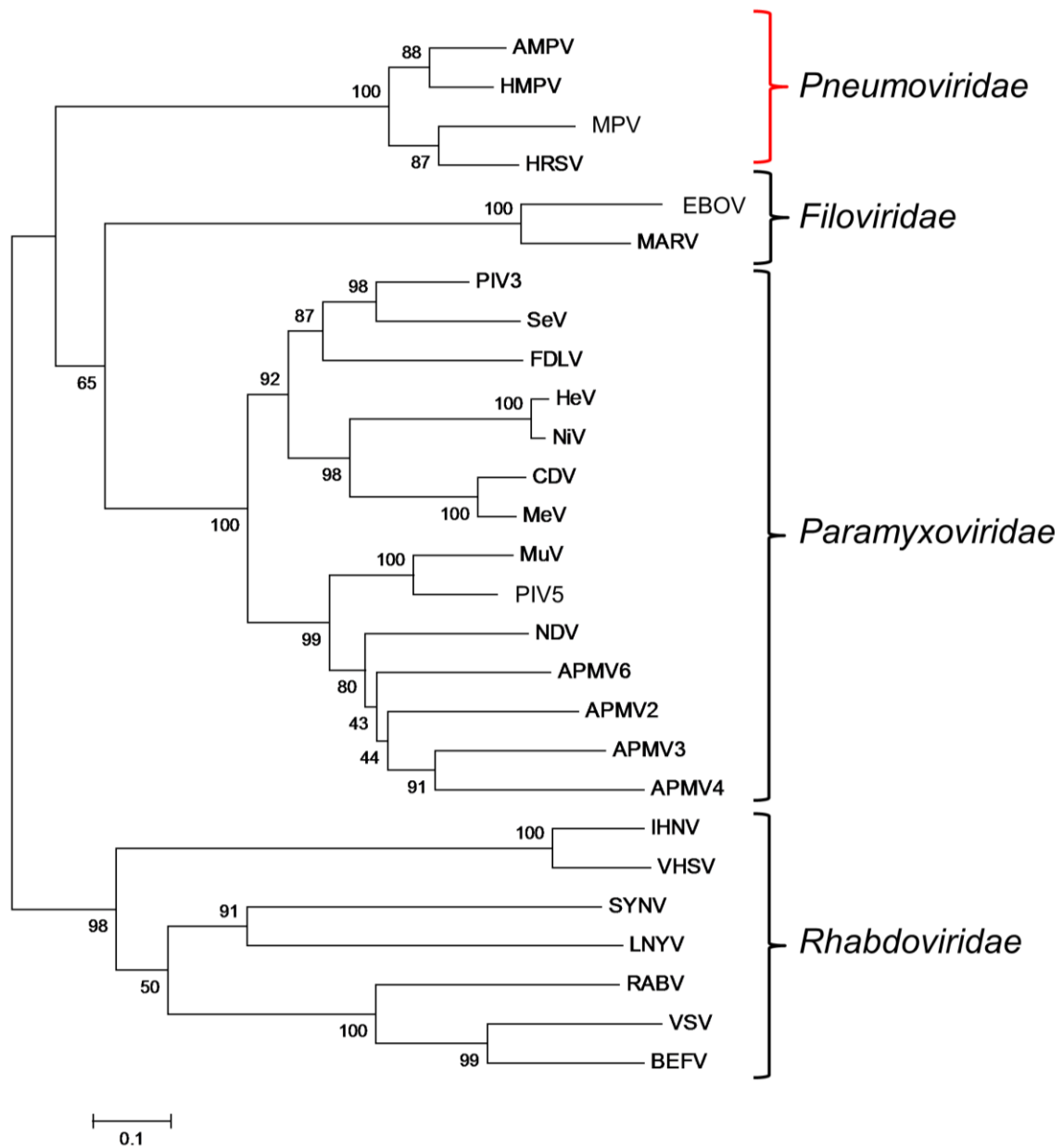


Figure 1B. Neighbour-joining phylogenetic tree of the 200 amino acid core region of the *Mononegavirales* polymerase protein.

The core region of the polymerase proteins of human respiratory syncytial virus (HRSV), murine pneumovirus (MPV), human metapneumovirus (HMPV), avian metapneumovirus (AMPV), Ebola virus (EBOV), Marburg virus (MARV), human parainfluenza virus type 3 (HPIV3), Sendai virus (SeV), Fer-de-Lance virus (FDLV), Hendra virus (HeV), Nipah virus (NiV), canine distemper virus (CDV), measles virus (MeV), mumps virus (MuV), parainfluenza virus type 5 (PIV5), Newcastle disease virus (NDV), avian paramyxovirus type 2 (APMV2), avian paramyxovirus type 3 (APMV3), avian paramyxovirus type 4 (APMV4), avian paramyxovirus type 26 (APMV6), infectious hemopoetic necrosis virus (IHNV), viral hemorrhagic septicaemia virus (VHSV), sonchus yellow net virus (SYNV), lettuce necrotic yellows virus (LNYV), rabies virus (RABV), vesicular stomatitis Indiana virus (VSV) and bovine ephemeral fever virus (BEFV) were analysed and the tree assembled using the MEGA software. Bootstrap values are indicated.

A The Family *Paramyxoviridae*

Sub-family *Paramyxovirinae*

Genus *Respirovirus*: Sendai virus, Parainfluenza virus 1 and 3



Genus *Morbillivirus*: Measles virus, Rinderpest virus



Genus *Henipavirus*: Hendra virus, Nipah virus



Genus *Rubulavirus*: Mumps virus



Genus *Avulavirus*: Newcastle disease virus, Avian paramyxoviruses 2-9

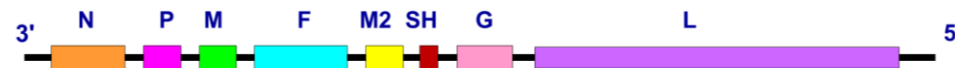


Sub-family *Pneumovirinae*

Genus *Pneumovirus*: Respiratory syncytial virus, pneumonia virus of mice



Genus *Metapneumovirus*: Avian pneumovirus, human metapneumovirus



B The organization of the M2 gene of the *Pneumoviridae*

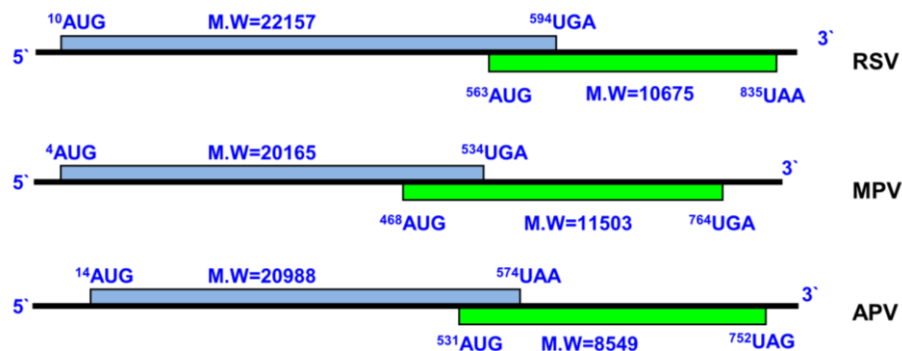


Figure 2. Diagram of the genome organization of the Family *Paramyxoviridae*. A. the genome organisation of representative members of the *Paramyxovirinae* and *Pneumovirinae* sub-families (not to scale). The M2 gene is found only in the *Pneumovirinae*. B. the organization of the M2 gene of members of the *Pneumovirus* and *Metapneumovirus* genera of the *Pneumovirinae*.