



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:	2016.001a,bM	(to be completed by ICTV officers)
Short title: Adding one (1) new species and renaming of twelve (12) species in the genus <i>Avulavirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	1x <input type="checkbox"/> 6 <input type="checkbox"/>	2 x <input type="checkbox"/> 7 <input type="checkbox"/>
	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 x
		5 <input type="checkbox"/> 11x

Author(s):

The 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	Australia	Linfa.Wang@csiro.au

And:

Kuhn, Jens H.	Chair, ICTV <i>Mononegavirales</i> Study Group	USA	kuhnjens@mail.nih.gov
Calogero Terregino	correspondent	Italy	cterregino@izsvenezie.it

Corresponding author with e-mail address:

Rima, Bertus K: b.rima@qub.ac.uk
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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 *Paramyxoviridae* Study Group

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

Date first submitted to ICTV:

June, 2016

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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MODULE 2: **NEW SPECIES**

Code	2016.001aM	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Avulavirus</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>Avian avulavirus 13</i>	avian paramyxovirus 13 goose/Japan/Shimane67	LC041132

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 11

Two novel avulaviruses have recently been isolated from geese in Japan and Kazakhstan, respectively (1,2). The genomes of both viruses have been fully sequenced. On the basis of haemagglutination inhibition tests these isolates have been placed into a new avulavirus species. The Japanese isolate was tested against serotypes 1–7; the Kazakh isolate against serotypes 1–9. Because they were not inhibited by sera raised against these viruses in the genus, they were proposed by the authors to represent a new species. Sequence comparisons of both the F (1,2) and HN (2) proteins confirmed the high degree of identity between the two isolates, as well as their distinct nature compared to the viruses of other species in the genus. The authors did not test the cross reactivity with serotypes 10, 11, and 12. PASC analysis shows that the Japanese isolate has an identity score of 96.68% to the Kazakh isolate and only 56.03 % identity to the next most closely related virus (avian paramyxovirus 12 in the species *Avian avulavirus 12*). This score is entirely consistent with those obtained in comparisons of viruses of different established species in the genus *Avulavirus*. Furthermore, the attached tree based on RdRp sequences confirms the proposal that these new isolates represent a new species in the genus *Avulavirus*, proposed to be called *Avian avulavirus 13*.

The demarcation criteria for viruses in the genus is historically based upon hemagglutination-inhibition tests. The new species fulfils the current demarcation criteria.

MODULE 9: **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	2016.001bM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
The species names in the genus <i>Avulavirus</i>.		
Current name	Proposed name	
<i>Newcastle disease virus</i>	<i>Avian avulavirus 1</i>	
<i>Avian paramyxovirus 2</i>	<i>Avian avulavirus 2</i>	
<i>Avian paramyxovirus 3</i>	<i>Avian avulavirus 3</i>	
<i>Avian paramyxovirus 4</i>	<i>Avian avulavirus 4</i>	
<i>Avian paramyxovirus 5</i>	<i>Avian avulavirus 5</i>	
<i>Avian paramyxovirus 6</i>	<i>Avian avulavirus 6</i>	
<i>Avian paramyxovirus 7</i>	<i>Avian avulavirus 7</i>	
<i>Avian paramyxovirus 8</i>	<i>Avian avulavirus 8</i>	
<i>Avian paramyxovirus 9</i>	<i>Avian avulavirus 9</i>	
<i>Avian paramyxovirus 10</i>	<i>Avian avulavirus 10</i>	
<i>Avian paramyxovirus 11</i>	<i>Avian avulavirus 11</i>	
<i>Avian paramyxovirus 12</i>	<i>Avian avulavirus 12</i>	

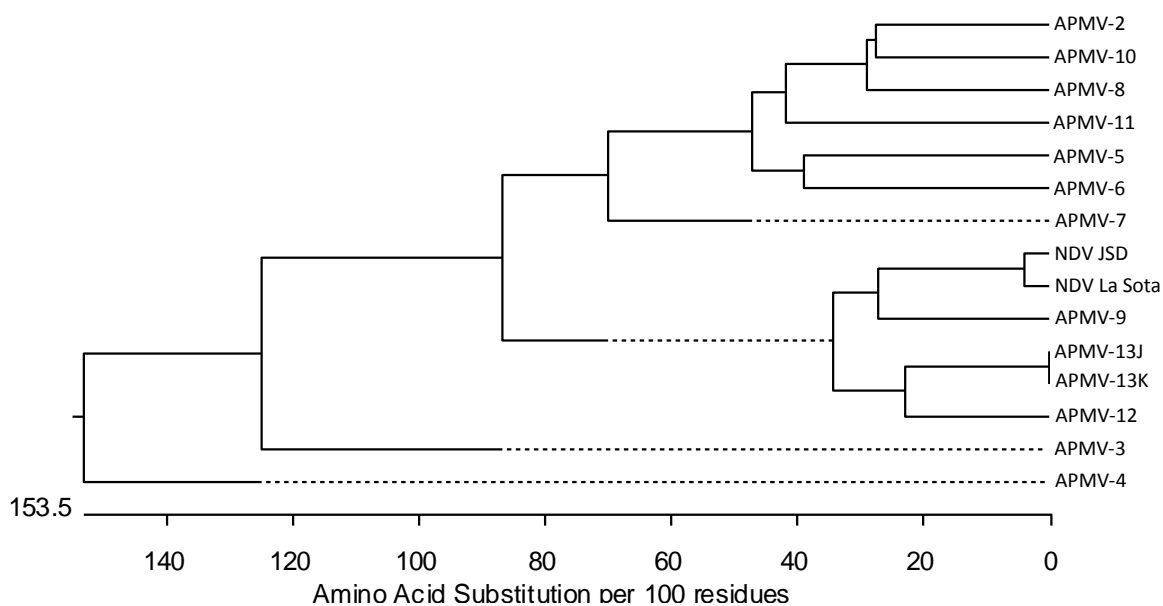
<p>Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed</p> <p>Importantly, the World Organization for Animal Health (OIE) regulates Newcastle disease virus (NDV), currently classified in the species <i>Newcastle disease virus</i> (and now proposed to be classified in the species <i>Avian avulavirus 1</i>) as follows:</p> <p>“For the purposes of the Terrestrial Code, Newcastle disease (ND) is defined as an infection of poultry by Newcastle disease virus (NDV), which is an avian paramyxovirus serotype 1 (APMV-1) that meets one of the following criteria for virulence:</p> <p>a. the virus has an intracerebral pathogenicity index (ICPI) in day-old chicks (<i>Gallus gallus</i>) of 0.7 or greater; or</p> <p>b. multiple basic amino acids have been demonstrated in the virus (either directly or by deduction) at the C-terminus of the F2 protein and phenylalanine at residue 117, which is the N-terminus of the F1 protein. The term ‘multiple basic amino acids’ refers to at least three arginine or lysine residues between residues 113 and 116. Failure to demonstrate the characteristic pattern of amino acid residues as described above would require characterisation of the isolated virus by an ICPI test.</p> <p>In this definition, amino acid residues are numbered from the N-terminus of the amino acid sequence deduced from the nucleotide sequence of the F0 gene, 113–116 corresponds to residues –4 to –1 from the cleavage site. ””</p> <p>It is therefore important to recognize that not all avian paramyxovirus serotype 1 strains (the members of the current <i>Newcastle disease</i> and in the future the members of <i>Avian avulavirus 1</i>) are Newcastle disease viruses from a regulatory standpoint (albeit they may be from a</p>

phylogenetic standpoint) and that other viruses belonging to the same serotype, such as pigeon paramyxovirus type 1, are considered separate but of the same serotype. To avoid regulatory problems due to still ongoing confusion of virus species and viruses, we propose to change the species name *Newcastle disease virus* to *Avian avulavirus 1*. *Avian avulavirus 1* will be/remain the type species of the genus, with Newcastle disease virus remaining the representative virus/isolate.

The 11 other recognized species in the genus currently follow a pseudo-non-Latinized binomial format (pseudo because there is no genus “*Paramyxovirus*”). We therefore propose to make the species naming uniform within the genus and to adopt a true non-Latinized binomial format (*paramyxovirus* → *avulavirus*).

MODULE 11: **APPENDIX**: supporting material for module 2

Phylogenetic tree of the RdRp proteins of the viruses in the genus *Avulavirus*



This tree was constructed from a Clustal W alignment using MEGA align software. The following table lists the used accession numbers:

Abbreviation	Accession number
APMV-2	EU338414
APMV-3	EU403085
APMV-4	EU877976
APMV-5	GU206351
APMV-6	EF569970
APMV-7	FJ231524
APMV-8	FJ215863
APMV-9	EU910942
APMV-10	HM147142
APMV-11	JQ886184
APMV-12	KC333050
APMV-13J	LC041132
APMV-13K	KU646513
NDV_JSD	GQ849007
NDV_La*	AF077771

*The original NDV La Sota strain sequence contains a small sequencing error in the RdRp gene, hence the exaggerated variation between the two sequences in one species. The JSD strain sequence is assumed to be correct as it contains a conserved motif present in all avulaviruses in an alternative reading frame in the sequence of the RdRp of NDV La Sota.