MODULE 1:

Code assigned:	*2015.012aM*	(to be completed by ICTV officers)

Short title: Three (3) new species in the genus *Avulavirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	1 ☒ 2 ☒ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8 ☐ 9 ☐ 10 ☒

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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 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:

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	*2015.012aM*	(assigned by ICTV officers)

To create 3 new species within:

		Fill in all that apply.
Genus:	*Avulavirus*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:	*Paramyxovirinae* [taxon proposed to be abandoned in 2015.011a-gM]	
Family:	*Paramyxoviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Mononegavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Avian paramyxovirus 10	avian paramyxovirus 10/Rockhopper Penguin/Falkland Islands/324/2007	HM147142
Avian paramyxovirus 11	avian paramyxovirus 11/Common snipe/France/100212/2010	JQ886184
Avian paramyxovirus 12	avian paramyxovirus 12/Wigeon/Italy/3920-1/2005	KC333050

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

Avian paramyxovirus 10: Supporting evidence for creation of a new species was presented in Miller PJ *et al.*, Evidence for a new avian paramyxovirus serotype 10 detected in rockhopper penguins from the Falkland Islands. J Virol. 2010 Nov; 84 (21):11496-504. The penguin virus antigen was tested for hemagglutination inhibition against reference antisera to the prototype viruses for all available avian paramyxoviruses (APMVs) and the results were negative or not sufficiently strong to comply with international standards used for serological classification of viruses. The reverse HI assay testing antiserum to the penguin virus, prepared following international serology guidelines from SPF chickens, against the 11 prototype APMV antigens showed inhibition only to the homologous penguin antigen. The virus genome sequence was highly divergent from other APMVs at the nucleotide level, and was most closely related to APMV-2 and APMV-8 viruses at the amino acid sequence level. However, genetic distance between APMV-10 and either APMV-2 or APMV-8 is large and comparable to the distances observed among other previously identified APMVs at the protein level and nucleotide level (Module 10).

Avian paramyxovirus 11: Supporting evidence for creation of a new species was presented in Briand FX et al., Complete genome sequence of a novel avian paramyxovirus. J Virol. 2012

Jul; 86(14):7710. The virus tested negative in a hemagglutination inhibition assay using reference antisera against APMV-1 to APMV-10 (except APMV-5, which was not available). An APMV-11 specific antiserum did not cross react with APMV-1 to APMV-4 and APMV-6 to APMV-10 antigens (APMV-5 was not available), whereas the homologous titer was 1024. APMV-11 was reported to rely on P gene editing in the same way as rubulaviruses; the P gene encodes V mRNA directly, and the addition of one or two non-templated G residues in the editing site produces W and P mRNA, respectively. The highest genomic nucleotide sequence identity (48.9%) was obtained with APMV-2/Chicken/ California/Yucaipa/56. These distances are comparable to the distances observed among other previously identified APMVs (Module 10).

Avian paramyxovirus 12: Supporting evidence for creation of a new species was presented in Terregino C et al., Antigenic and genetic analyses of isolate APMV/wigeon/Italy/3920-1/2005 indicate that it represents a new avian paramyxovirus (APMV-12). Arch Virol. 2013 Nov; 158(11):2233-43. Antigenic and genetic analysis between wigeon/Italy/3920-1/2005 and representative avian paramyxoviruses (APMVs) showed only a low-level relationship. Phylogenetic analysis of the whole genome and each of the six genes indicated that the strain wigeon/Italy/3920-1/2005 is rather distinct from the other APMVs. In the whole-genome analysis, wigeon/Italy/3920-1/2005 had 52.1 % nucleotide sequence identity to the closest APMV-1 virus, 50.1 % identity to the APMV-9 genome, and less than 42 % identity to representatives of the other APMVs groups. Such distances are comparable to the distances observed among other previously identified APMVs.

A comparison of the individual NP, M, F, HN, and L open reading frames for the members of the 9 approved *Avulavirus* species and the 3 newly proposed ones is shown in module 10. This analysis shows that the maximum percentage amino acid sequence identity between the members of the newly proposed species and previously approved species is lower than between members of some of the previously approved species. The most closely related viruses are APMV-2 and APMV-8, APMV-1, and APMV-9, all of which are classified into separate species. Terregino C *et al.* (Arch Virol. 2013 Nov;158(11):2233-43) provide phylogenetic trees including viruses of all approved and proposed species, in agreement with data in module 10.

additional material in support of this proposal

References:

APMV-10: Evidence for a new avian paramyxovirus serotype 10 detected in rockhopper penguins from the Falkland Islands. Miller PJ, Afonso CL, Spackman E, Scott MA, Pedersen JC, Senne DA, Brown JD, Fuller CM, Uhart MM, Karesh WB, Brown IH, Alexander DJ, Swayne DE. J Virol. 2010 Nov;84(21):11496-504. doi: 10.1128/JVI.00822-10. Epub 2010 Aug 11.
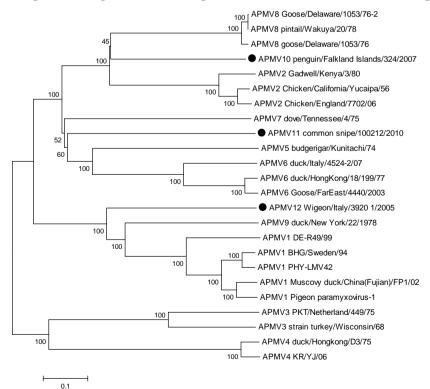
APMV-11: Complete genome sequence of a novel avian paramyxovirus. Briand FX, Henry A, Massin P, Jestin V. J Virol. 2012 Jul;86(14):7710. doi: 10.1128/JVI.00946-12.

APMV-12: Antigenic and genetic analyses of isolate APMV/wigeon/Italy/3920-1/2005 indicate that it represents a new avian paramyxovirus (APMV-12). Terregino C, Aldous EW, Heidari A, Fuller CM, De Nardi R, Manvell RJ, Beato MS, Shell WM, Monne I, Brown IH, Alexander DJ, Capua I. Arch Virol. 2013 Nov;158(11):2233-43. doi: 10.1007/s00705-013-1735-2. Epub 2013 May 25.

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. Phylogenetic analysis using the Neighbor-joining method with 1,000 bootstrap replicates based on the full genome sequences of APMV-1 to APMV-12. Evolutionary distances were computed using the Kimura 2-parameter substitution model (tree provided by F.X. Briand).

Tables 1-5. Percentage amino acid sequence identity between the five major open reading frames (nucleoprotein, matrix protein, fusion protein, hemagglutinin-neuraminidase, polymerase protein) of avian paramyxovirus 1 through 12. Highlighted in yellow are the maximum percentages identity between members of previously approved species (most similar are APMV-2 to APMV-8 and APMV-1 to APMV-9), and for members of each of the proposed new species. Sequence identity between members of newly proposed species and approved species is in the same range (or lower) as between members of approved species.

NP ORF	APMV2	APMV3	APMV4	APMV5	APMV6	APMV7	APMV8	APMV9	APMV10	APMV11	APMV12
APMV1	0.087	0.067	0.084	0.058	0.062	0.079	0.086	0.057	0.098	0.070	0.058
APMV2		0.367	0.376	0.516	0.508	0.539	0.707	0.360	0.726	0.577	0.367
APMV3			0.511	0.358	0.366	0.349	0.352	0.347	0.352	0.359	0.359
APMV4				0.362	0.375	0.355	0.350	0.335	0.341	0.341	0.361
APMV5					0.613	0.516	0.532	0.348	0.520	0.520	0.354
APMV6						0.527	0.493	0.350	0.508	0.523	0.376
APMV7							0.549	0.374	0.524	0.557	0.373
APMV8								0.391	0.727	0.547	0.379
APMV9									0.364	0.380	0.553
APMV10										0.565	0.373
APMV11											0.369

M ORF	APMV2	APMV3	APMV4	APMV5	APMV6	APMV7	APMV8	APMV9	APMV10	APMV11	APMV12
APMV1	0.290	0.261	0.264	0.318	0.255	0.323	0.272	0.542	0.266	0.271	0.507
APMV2		0.289	0.295	0.424	0.384	0.420	0.520	0.272	0.560	0.373	0.286
APMV3			0.328	0.282	0.239	0.284	0.269	0.236	0.284	0.240	0.231
APMV4				0.274	0.274	0.279	0.284	0.247	0.287	0.270	0.241
APMV5					0.510	0.448	0.413	0.286	0.403	0.422	0.302
APMV6						0.404	0.352	0.264	0.368	0.344	0.280
APMV7							0.428	0.332	0.425	0.444	0.324
APMV8								0.297	0.555	0.373	0.281
APMV9									0.308	0.283	0.508
APMV10										0.378	0.270
APMV11											0.274

F ORF	APMV2	APMV3	APMV4	APMV5	APMV6	APMV7	APMV8	APMV9	APMV10	APMV11	APMV12
APMV1	0.387	0.296	0.307	0.387	0.380	0.380	0.390	0.551	0.357	0.319	0.544
APMV2		0.283	0.319	0.457	0.477	0.363	0.624	0.362	0.544	0.393	0.369
APMV3			0.316	0.282	0.290	0.270	0.299	0.273	0.251	0.295	0.288
APMV4				0.312	0.315	0.282	0.333	0.277	0.283	0.312	0.303
APMV5					0.523	0.359	0.442	0.356	0.405	0.370	0.362
APMV6						0.347	0.474	0.364	0.431	0.384	0.371
APMV7							0.367	0.343	0.336	0.336	0.351
APMV8								0.368	0.547	0.397	0.361
APMV9									0.344	0.312	0.518
APMV10										0.356	0.337
APMV11											0.318

HN ORF	APMV2	APMV3	APMV4	APMV5	APMV6	APMV7	APMV8	APMV9	APMV10	APMV11	APMV12
APMV1	0.335	0.327	0.338	0.328	0.297	0.347	0.336	0.611	0.338	0.342	0.534
APMV2		0.293	0.299	0.412	0.377	0.405	0.471	0.313	0.489	0.394	0.307
APMV3			0.392	0.316	0.286	0.314	0.300	0.345	0.309	0.320	0.324
APMV4				0.290	0.292	0.335	0.318	0.340	0.294	0.340	0.315
APMV5					0.533	0.417	0.405	0.306	0.412	0.418	0.294
APMV6						0.403	0.360	0.289	0.372	0.390	0.295
APMV7							0.404	0.325	0.395	0.405	0.300
APMV8								0.327	0.502	0.390	0.297
APMV9									0.323	0.326	0.543
APMV10										0.399	0.321
APMV11											0.314

L ORF	APMV2	APMV3	APMV4	APMV5	APMV6	APMV7	APMV8	APMV9	APMV10	APMV11	APMV12
APMV1	0.373	0.328	0.325	0.370	0.385	0.384	0.377	0.614	0.377	0.384	0.573
APMV2		0.328	0.330	0.411	0.420	0.425	0.579	0.369	0.595	0.470	0.367
APMV3			0.405	0.334	0.352	0.351	0.338	0.324	0.335	0.350	0.326
APMV4				0.321	0.329	0.342	0.329	0.307	0.333	0.340	0.321
APMV5					0.499	0.441	0.428	0.370	0.421	0.452	0.369
APMV6						0.438	0.428	0.388	0.436	0.457	0.381
APMV7							0.447	0.380	0.448	0.470	0.389
APMV8								0.379	0.589	0.482	0.382
APMV9									0.382	0.382	0.528
APMV10										0.480	0.375
APMV11											0.394