MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2015.016aM*	(to be completed by ICTV officers)

Short title: Ten (10) new species in the genus *Rubulavirus*
(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:

EC 47 decision:
Provide phylogenetic tree and define species demarcation criteria.

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	*2015.016aM*			(assigned by ICTV officers)

To create 10 new species within:

Fill in all that apply.

Genus:	*Rubulavirus*	
Subfamily:		
Family:	*Paramyxoviridae*	
Order:	*Mononegavirales*	

- 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.

Name of new species:	Representative isolate: (only 1 per species please)	Abbreviation	GenBank sequence accession number(s)
Menangle rubulavirus	Menangle virus	Menang	JX112711
Tioman rubulavirus	Tioman virus	Tioman	AF298895
Bat mumps rubulavirus	bat mumps virus	MuV-Bat	HQ660095
Teviot rubulavirus	Teviot virus Cedar Grove isolate	Teviot	KP271124
Achimota rubulavirus 1	Achimota virus 1	Achi-1	JX051319
Achimota rubulavirus 2	Achimota virus 2	Achi-2	JX051320
Sosuga rubulavirus	Sosuga virus	Sosuga	KF774436
Tuhoko rubulavirus 1	Tuhoko virus 1	Tuhoko-1	GU128080
Tuhoko rubulavirus 2	Tuhoko virus 2	Tuhoko-2	GU128081
Tuhoko rubulavirus 3	Tuhoko virus 3	Tuhoko-3	GU128082

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

The isolation of many new viruses from bats of different species has a great effect on the organization of the genus *Rubulavirus* as many of the newly identified viruses clearly belong to this genus. Here we

propose the establishment of 10 new rubulavirus species based on references 1-6. The ten viruses proposed to be members of these 10 species fit within the *Rubulavirus* genus because their genomes encode (without co-transcriptional editing) the V protein. Co-transcriptional editing by insertion of 2G residues generates a messenger RNA encoding the P protein. A major feature of rubulavirus P proteins is that they are significantly smaller than those of the respiro- and morbilliviruses.

The oldest but as yet unclassified virus is Tioman virus (2) and has been described in 2002; the other nine viruses have been described more recently (e.g., since 2010). One of the recently isolated viruses, Sosuga virus, has been associated with an acute human febrile disease associated with rash (5). The other virus have been isolated from bats (1,2,3,4,6). A tree generated on the basis of the nucleocapsid proteins of the rubulaviruses in reference 5 (Fig 2D) by Albariño et al. showed that for example Sosuga virus is most closely related to Tuhoko virus 3, that Achimota 1 virus and Tuhoko2 virus are as closely related as are Tioman and Menangle viruses, but that Achimota 2 and Tuhoko 1 virus are quite distinct. PASC analysis further supports these classifications. There also appears to be a separation between these new viruses and classical rubulaviruses, such as human parainfluenza virus type 2 (HPIV-2), parainfluenza virus type 5 (PIV5), formerly SV5, mumps virus (MuV), porcine rubulavirus aka La-Piedad- Michoacan-Mexico Virus (LPMV), and Mapuera virus. The rubulavirus RNA dependent RNA polymerase (RdRp) probably provides the best phylogenetic picture of the relationships between these viruses. An alignment based on Clustal W in the Mega programme of the RdRp which was hand adjusted shows that:

1   there is a high degree of amino acid sequence conservation in the RdRps of members of the genus *Rubulavirus,* and many completely new conserved rubulavirus-specific motifs are present
2   the replacements that do take place between members of different rubulavirus species are often conservative
3   gaps are small and major insertion and deletions are found in the same areas as identified in alignments of all other paramyxoviruses (variable regions around amino acids 650 and 1730)
4   the relationships displayed in the tree in reference 5 based on rubulavirus nucleocapsid proteins is consistent with the ML phylogenetic tree of the RdRps shown below
5   the comparison of the level of variation between mumps virus Miyahara from clade A and mumps virus SBL1 from clade A, as well as the variation in a clade A mumps virus-derived vaccine strain show the level of variation within viruses of a rubulavirus species to be very low
6   bat mumps virus (3) is much more distinct than classical mumps viruses are from each other but is clear strongly related to the other mumps virus strains. PASC analysis gives an overall value of 76.5% identity, below the value of 80% which is used currently as a cut-off for species demarcation.
7   Teviot virus is related to Tioman virus, but is sufficiently different for it to be classified in a separate species and the same applies to Achimota viruses 1 and 2 and Tuhoko viruses 1,2, and 3.

Maximum Likelihood Tree of the RdRp (L) proteins of rubulaviruses
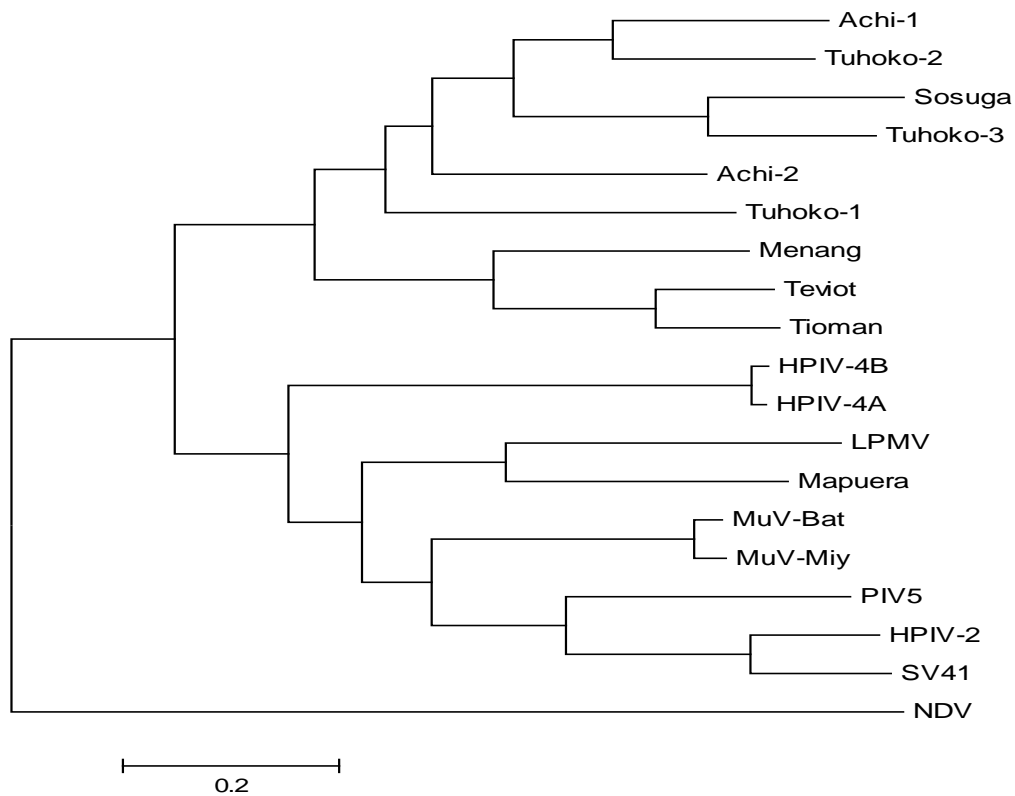
Legend of abbreviations: Ach-1, -2 are Achimota virus 1 and 2; Menang is Menangle virus; HPIV-2, -4A and -4B are human parainfluenza virus type 2, 4A and 4B; LPMV is a porcine rubulavirus; MuV-Bat is the bat isolate of a virus related to mumps virus; MuV-Miy is the Miyahara strain of mumps virus; PIV5 is parainfluenza virus type 5; SV41 is simian virus 41. NDV is Newcastle disease virus which is included as an outlier now from the *Avulavirus* genus but earlier considered a rubulavirus. The maximum likelihood tree was constructed from a Mega align of the 19 sequences of the RdRp proteins of rubulaviruses.

MODULE 10: **APPENDIX**: supporting material

References:

1   Baker KS et al. (2013). Novel, Potentially Zoonotic Paramyxoviruses from the African Straw-Colored Fruit Bat *Eidolon helvum*. J. Virol. 87(3), 1348-1358.

2   Chua KB et al. (2002). Full length genome sequence of Tioman virus, a novel paramyxovirus in the genus *Rubulavirus* isolated from fruit bats in Malaysia. Arch. Virol. 147(7), 1323-1348.

3   Drexler JF et al. (2012). Bats host major mammalian paramyxoviruses. Nat Commun 3, 796.

4   Burroughs AL et al. (2015). Complete genome sequence of Teviot paramyxovirus, a novel rubulavirus isolated from fruit bats in Australia. Genome Announc 3 (2) e00177-15

5   Albariño CG et al. (2014). Novel paramyxovirus associated with severe acute febrile disease, South Sudan and Uganda, 2012. Emerging Infect. Dis. 20 (2), 211-216.

6   Lau SK et al. (2010). Identification and complete genome analysis of three novel paramyxoviruses, Tuhoko virus 1, 2 and 3, in fruit bats from China. Virology 404, 101-116