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:	***2015.013aM***	(to be completed by ICTV officers)

Short title: Three (3) new species in the genus *Henipavirus*
(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: 15 June 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	***2015.013aM***	(assigned by ICTV officers)

To create 3 new species within:

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

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Cedar henipavirus	Cedar virus (CedV)	JQ001776
Ghanaian bat henipavirus	Kumasi virus (KV-GH-M74a)	HQ660129
Mòjiāng henipavirus[1]	Mòjiāng virus (MojV)	KF278639

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

Cedar virus (CedV)

In 2012, Marsh et al. (see reference 1) isolated a new virus from Australian pteropid bats.

CedV should be assigned to the genus *Henipavirus* because:

- Sequence analysis and phylogenic analyses indicate the close relationship with the two pathogenic henipaviruses Nipah virus (NiV) and Hendra virus (HeV) (Figures 1 and 2).
- The complete CedV genome length is 18,162 nt, similar to that of HeV, also complying with the "rule of six."
- CedV has a 3-nt intergenic sequence of CTT absolutely conserved at all seven positions and highly conserved gene start and stop signals similar to those present in HeV and NiV.
- CedV is antigenically related to the current henipaviruses as shown by antisera cross-reactivity.

[1] [1] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics and apostrophes in taxon names. In case TaxoProp 2015.001aG.v1.Diacritics is ratified, the diacritical mark in the species name in this proposal will simply be dropped (resulting in ***Mojiang henipavirus***). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

- Similar to NiV and HeV, CedV can use human ephrin-B2 as entry receptor.

CedV has to be assigned to a new species within the genus *Henipavirus* because:
- Amino acid sequences of all viral proteins differ from HeV and NiV by ≥ 40%
- Sequence alignment of the P gene suggest that CedV lacks both the functional V mRNA/protein and the coding capacity for the RNA editing site and ORF V
- In contrast to NiV and HeV, CedV cannot use human ephrin-B3 as cell entry receptor
- There is no cross-neutralization: NiV/HeV-specific antisera did not neutralize CedV and vice versa.

Kumasi virus (KV-GH-M74a)

In 2009, Drexler et al. (see reference 2a) isolated RNA from a straw-colored fruit bat (*Eidolon helvum*) in Ghana. As described in reference 2b, the full-length genome could be sequenced from RNA samples and was provisionally named BatPV/Eid hel/GH-M74a/GHA/2009 (GH-M74a). Live, replicative virus could not be isolated so far.

GH-M74a should be assigned to the genus *Henipavirus* because:
- Sequence analysis and phylogenic analyses indicate a close relationship with Nipah virus (NiV) and Hendra virus (HeV) (Figures 1 and 2).
- As with NiV and HeV, the complete GH-M74a genome length is unusually long for a member of the *Paramyxoviridae* family (18,530 nt) and contains the typical long intergenic untranslated regions between genes.
- Studies on plasmid-encoded surface glycoproteins revealed that GH-M74a can interact with the human henipavirus receptor ephrin-B2 (reference 2c).

GH-M74a has to be assigned to a new species because:
- It has a completely different geographic origin (Africa)
- GH-M74a was isolated from a different bat reservoir (genus *Eidolon*) compared to NiV, CedV, and HeV (originating from bats of the genus *Pteropus*)
- Amino acid sequences of all viral proteins differ from HeV and NiV by at least 37%
- Within the L protein, GH-M74a contains the catalytic motif GDNQ, as typical for members of the order *Mononegavirales*, whereas HeV and NiV have an atypical GDNE motif.

Mòjiāng virus (MojV)

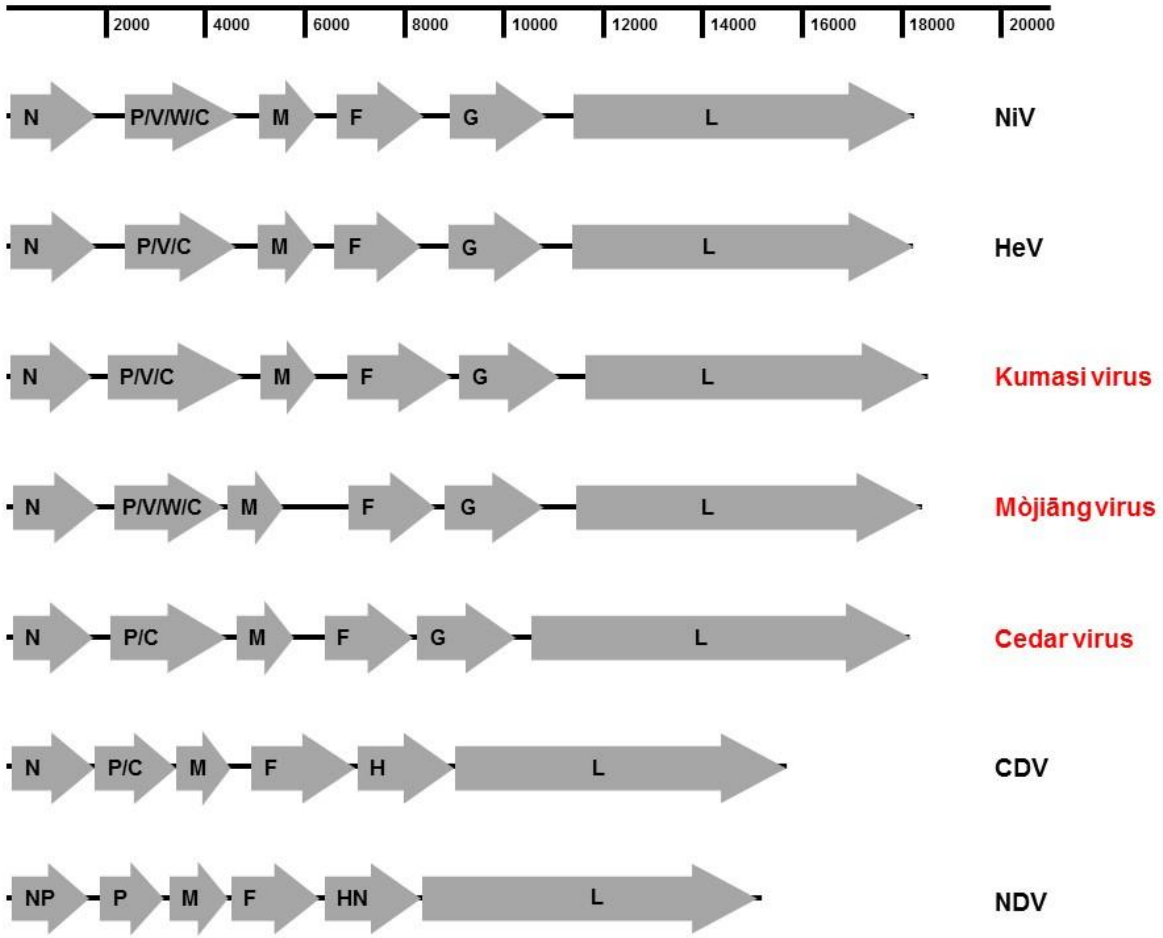
In June 2012, in Mòjiāng (China) Wu et al. isolated a novel henipavirus-like virus in RNA samples from rats (*Rattus flavipectus*). The the full-length genome was sequenced and the virus was provisionally named Mojiang paramyxovirus (MojV; see reference 3).

MojV should be assigned to the genus *Henipavirus* because:
- Sequence analysis and phylogenic analyses indicate a close relationship with NiV and HeV (Figures 1 and 2)
- MojV shares similar features with known henipaviruses, such as the genome length of 18,404 nt, and the characteristic henipavirus gene order: 3′-N (539 aa); P/V/W/C (694/464/434/177 aa); M (340 aa); F (545 aa); G (625 aa); and L (2,277 aa)-5′.
- In the P gene, MojV encodes a RNA editing site (AAAAGG) for the processing of V and W proteins conserved in the P genes of NiV and HeV.

MojV has to be assigned to a new species because:

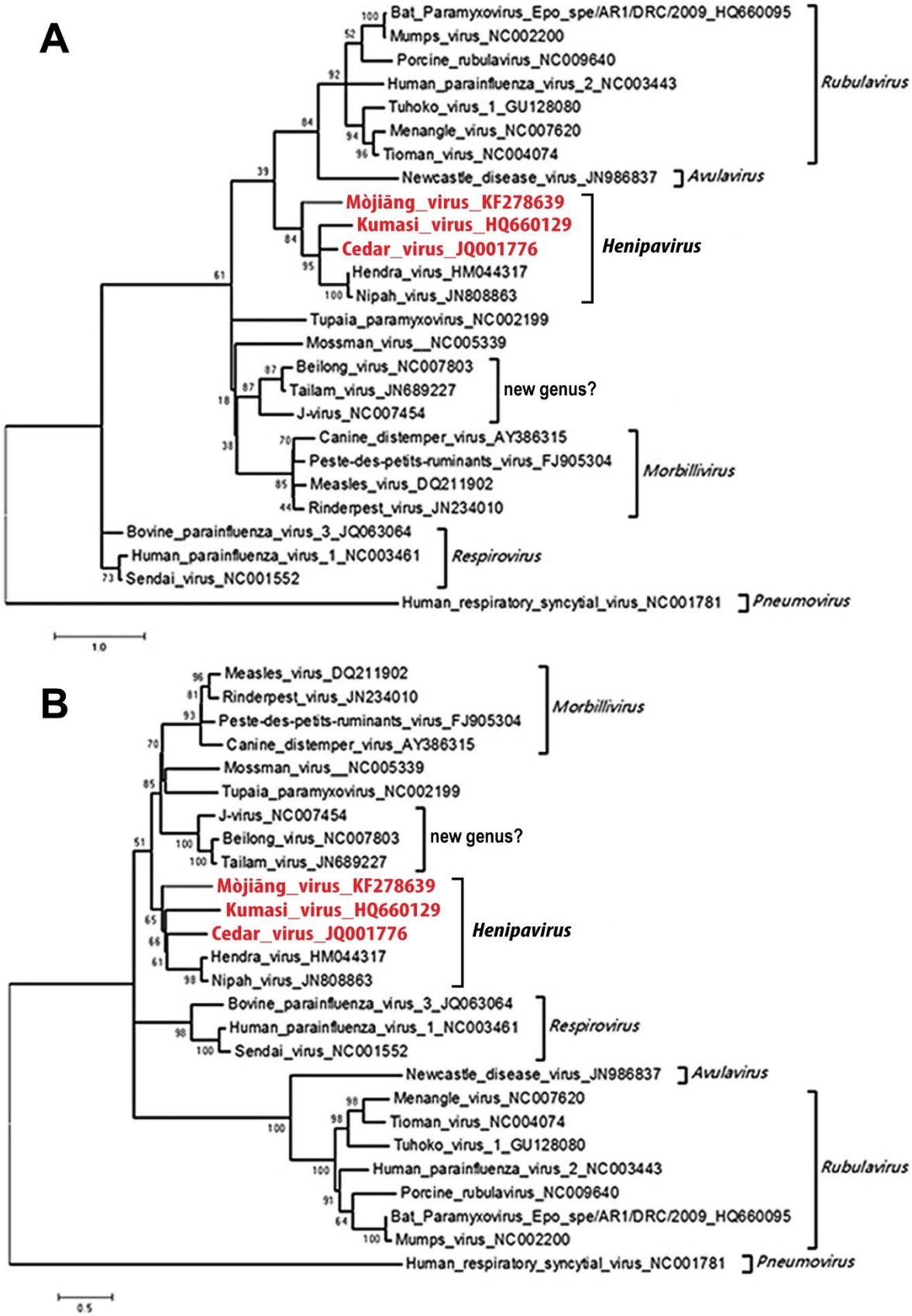
- In contrast to all other members of the genus *Henipavirus*, MojV was isolated from rodents that must be assumed to represent the virus reservoir.
- MojV is of different geographic origin (China)
- The nucleotide identities of predicted MojV genes differ from genes of known henipaviruses by at least 36%

Figure 1



Shown is the genomic organization of henipaviruses (NiV, Nipah virus; HeV, Hendra virus; Kumasi virus; Mòjiāng virus; Cedar virus), a representative morbillivirus (CDV, canine distemper virus), and a representative avulavirus (NDV, Newcastle disease virus), drawn to scale. The viruses addressed in this proposal are printed in red.

Figure 2


A
Bat_Paramyxovirus_Epo_spe/AR1/DRC/2009_HQ660095
Mumps_virus_NC002200
Porcine_rubulavirus_NC009640
Human_parainfluenza_virus_2_NC003443
Tuhoko_virus_1_GU128080
Menangle_virus_NC007620
Tioman_virus_NC004074
Rubulavirus
Newcastle_disease_virus_JN986837
Avulavirus
Mòjiāng_virus_KF278639
Kumasi_virus_HQ660129
Cedar_virus_JQ001776
Hendra_virus_HM044317
Nipah_virus_JN808863
Henipavirus
Tupaia_paramyxovirus_NC002199
Mossman_virus__NC005339
Beilong_virus_NC007803
Tailam_virus_JN689227
J-virus_NC007454
new genus?
Canine_distemper_virus_AY386315
Peste-des-petits-ruminants_virus_FJ905304
Measles_virus_DQ211902
Rinderpest_virus_JN234010
Morbillivirus
Bovine_parainfluenza_virus_3_JQ063064
Human_parainfluenza_virus_1_NC003461
Sendai_virus_NC001552
Respirovirus
Human_respiratory_syncytial_virus_NC001781
Pneumovirus
1.0
B
Measles_virus_DQ211902
Rinderpest_virus_JN234010
Peste-des-petits-ruminants_virus_FJ905304
Canine_distemper_virus_AY386315
Morbillivirus
Mossman_virus__NC005339
Tupaia_paramyxovirus_NC002199
J-virus_NC007454
Beilong_virus_NC007803
Tailam_virus_JN689227
new genus?
Mòjiāng_virus_KF278639
Kumasi_virus_HQ660129
Cedar_virus_JQ001776
Hendra_virus_HM044317
Nipah_virus_JN808863
Henipavirus
Bovine_parainfluenza_virus_3_JQ063064
Human_parainfluenza_virus_1_NC003461
Sendai_virus_NC001552
Respirovirus
Newcastle_disease_virus_JN986837
Avulavirus
Menangle_virus_NC007620
Tioman_virus_NC004074
Tuhoko_virus_1_GU128080
Human_parainfluenza_virus_2_NC003443
Porcine_rubulavirus_NC009640
Bat_Paramyxovirus_Epo_spe/AR1/DRC/2009_HQ660095
Mumps_virus_NC002200
Rubulavirus
Human_respiratory_syncytial_virus_NC001781
Pneumovirus
0.5

Phylogenetic trees established with MEGA5 based on the nucleocapsid (N) proteins (A) and RNA-dependent RNA polymerases (L) (B) of Kumasi virus; Mòjiāng virus; Cedar virus (in bold red) and other previously reported paramyxoviruses. Scale bars indicate nucleotide substitutions per site. Modified from (3).

References:

1) Marsh,G.A., de Jong,C., Barr,J.A., Tachedjian,M., Smith,C., Middleton,D., Yu,M., Todd,S., Foord,A.J., Haring,V., Payne,J., Robinson,R., Broz,I., Crameri,G., Field,H.E. and Wang,L.F. "Cedar virus: a novel henipavirus isolated from Australian bats". PLoS Pathog. 8 (8), E1002836 (2012).

2a) Drexler, J. F., Corman, V. M., Gloza-Rausch, F., Seebens, A., Annan, A., Ipsen, A., Drosten, C. "Henipavirus RNA in African Bats." *PLoS ONE*. 4(7):e6367 (2009).

2b) Drexler,J.F., Corman,V.M., Muller,M.A., Maganga,G.D., Vallo,P., Binger,T., Gloza-Rausch,F., Rasche,A., Yordanov,S., Seebens,A., Oppong,S., Sarkodie,Y.A., Pongombo,C., Lukashev,A.N., Schmidt-Chanasit,J., Stocker,A., Carneiro,A.J., Erbar,S., Maisner,A., Fronhoffs,F., Buettner,R., Kalko,E.K., Kruppa,T., Franke,C.R., Kallies,R., Yandoko,E.R., Herrler,G., Reusken,C., Hassanin,A., Kruger,D.H., Matthee,S., Ulrich,R.G., Leroy,E.M. and Drosten,C. "Bats host major mammalian paramyxoviruses". Nat Commun 3, 796 (2012)

2c) Lee, B., Pernet, O., Ahmed, A. A., Zeltina, A., Beaty, S. M., & Bowden, T. A. "Molecular recognition of human ephrinB2 cell surface receptor by an emergent African henipavirus." *Proceedings of the National Academy of Sciences of the United States of America*, *112*(17), E2156–E2165 (2015).

3) Wu,Z., Yang,L., Yang,F., Ren,X., Jiang,J., Dong,J., Sun,L., Zhu,Y., Zhou,H. and Jin,Q. "Novel Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012". Emerging Infect. Dis. 20 (6), 1064-1066 (2014).

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.