

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

MODULE 1. MILE, ACTIONO, CLO								
Code assigned:	2010.010aV			(to be completed by ICTV officers)				
Short title: create new species named <i>Bundibugyo ebolavirus</i> in the genus Ebolavirus, family Filoviridae (e.g. 6 new species in the genus <i>Zetavirus</i>) Modules attached $1 \times 2 \times 3 \times 4 \times 5$ (modules 1 and 9 are required) $5 \times 5 \times 5 \times 5$								
Author(s) with e-mail address(es) of the proposer:								
Jens H. Kuhn- kuhnjens@mail.nih.gov (submitting author) (ICTV Filoviridae SG member) Stephan Becker- becker@staff.uni-marburg.de (ICTV Filoviridae SG member) Hideki Ebihara- ebiharah@niaid.nih.gov (ICTV Filoviridae SG member) Thomas W. Geisbert- geisbert@bu.edu (ICTV Filoviridae SG member) Karl M. Johnson- karlmjohnson@aol.com Yoshihiro Kawaoka- kawaokay@svm.vetmed.wisc.edu (ICTV Filoviridae SG member) Sergey V. Netesov- nauka@nsu.ru (ICTV Filoviridae SG member) Stuart T. Nichol- stn1@cdc.gov (ICTV Filoviridae SG member) Clarence J. Peters- cjpeters@utmb.edu (ICTV Filoviridae SG member) Viktor E. Volchkov- viktor.volchkov@inserm.fr (ICTV Filoviridae SG member) Peter B. Jahrling- jahrlingp@niaid.nih.gov (ICTV Filoviridae SG member)								
List the ICTV study group(s) that have seen this proposal:								
http://www.ictvonline.org/subcom in doubt, contact the appropriate	ist of study groups and contacts is provided at p://www.ictvonline.org/subcommittees.asp . If doubt, contact the appropriate subcommittee air (fungal, invertebrate, plant, prokaryote or rtebrate viruses) ICTV Filoviridae Study Group							
ICTV-EC or Study Group comments and response of the proposer:								
Date first submitted to ICTV: 06/04/2010								
Date of this revision (if different		06/14/2010						

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	ode 2010.010aV		(assigned by ICTV officers)				
To create 1 new species within:							
				Fill	in all that apply.		
C	enus:	Ebolavirus		If the higher taxon has yet to be			
Subfa	Subfamily: /				reated (in a later module, below) write new) " after its proposed name.		
Fa	Family: Filoviridae			 If no genus is specified, enter 			
(Order:	Mononegavirales	"unassigned" in the genus box.				
And name the new species:				GenBank sequence accession number(s) of reference isolate:			
Bundibugyo ebolavirus					FJ217161		

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.
 - o 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

A new virus was isolated from ill humans in Uganda (Towner et al.). It has biological and molecular features consistent with members of the order *Mononegavirales* and the family *Filoviridae* as procribed in the 8th ICTV Report (Feldmann et al., Pringle et al.). Within the family *Filoviridae*, the virus should be assigned to the genus *Ebolavirus* because, as proscribed in the 8th ICTV Report (Feldmann et al.),

- it has no antigenic cross-reactivity with marburgviruses
- it forms virions with morphologies similar to virions formed by ebolaviruses
- it has a genome length fitting those of ebolaviruses (18.9 kb) vs. those of marburgviruses (19.1 kb)
- it has a genome with several gene overlaps (ebolaviruses) rather than only one gene overlap (marburgviruses)
- it expresses its glycoprotein via transcriptional editing, whereas marburgviruses express it directly
- transcription of only the first ORF of gene four yields a soluble small glycoprotein not observed with marburgviruses
- it has a protein profile distinct from marburgviruses; but is species-specific
- its glycoprotein gene nt sequence differs by more than 57% compared to marburgviruses (Towner et al.)

The virus also fulfills the newly proposed *Ebolavirus* genus inclusion criteria as recently proposed by the ICTV *Filoviridae* Study Group (Kuhn et al.):

- it has the properties of filoviruses plus
- its genome contains several gene overlaps
- its gene 4 (GP) encodes four proteins. The soluble glycoprotein (sGP) and its cleavage product Δ -peptide are the primary expression products; the spike glycoprotein (GP_{1,2}) and a secondary soluble glycoprotein (ssGP) are expressed via transcriptional editing
- it has a genome that differs from those of marburgviruses by ≥50% at the nucleotide level
- it produces virions that show almost no antigenic cross-reactivity with marburgvirions

Members of species of the genus *Ebolavirus*, according to the criteria proscribed by the 8th ICTV Report, "may be distinguished on the basis of glycoprotein gene sequence differences (more than 30% aa difference), cross-protection data (where available) and differences in geographic origins" (Feldmann et al.). The new virus fulfills these criteria (Towner et al.). According to the ebolavirus species demarcation criteria recently proposed by the ICTV *Filoviridae* Study Group (Kuhn et al.), the new virus, which we suggest to be named Bundibugyo virus (BDBV-Bundibugyo), has to be assigned to a new species because it

- is endemic in the Republic of Uganda (different from members of all other ebolavirus species with the exception of those of the species *Sudan ebolavirus*)
- has a genome with three gene overlaps: VP35/VP40, GP/VP30, VP24/L (different from members of the species *Reston ebolavirus*)
- has a full-length genomic sequence different from the "type virus" of the type species of the genus *Ebolavirus* (Ebola virus) by ≥30%

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Feldmann H, Geisbert TW, Jahrling PB, Klenk H-D, Netesov SV, Peters CJ, Sanchez A, Swanepoel R, Volchkov VE (2005) Family Filoviridae. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) Virus Taxonomy - Eighth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, San Diego, California, USA, pp 645-653

Kuhn JH, Becker S, Ebihara H, Geisbert TW, Jahrling PB, Kawaoka Y, Netesov, SV, Nichol ST, Peters CJ, Volchkov V, Ksiazek TG (2010) Marburgvirus and Ebolavirus Taxonomy – Classification, Names of Taxa and Viruses, and Virus Abbreviations. Submitted to Arch Virol [and forwarded to the ICTV Executive Committee for further information on the taxonomix changes proposed here]

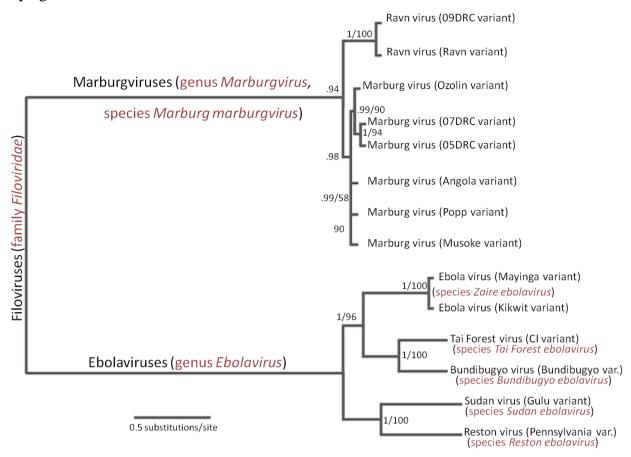
Pringle CR (2005) Order Mononegavirales. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) Virus Taxonomy - Eighth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, San Diego, California, USA, pp 609-614

Towner JS, Sealy TK, Khristova ML, Albarino CG, Conlan S, Reeder SA, Quan PL, Lipkin WI, Downing R, Tappero JW, Okware S, Lutwama J, Bakamutumaho B, Kayiwa J, Comer JA, Rollin PE, Ksiazek TG, Nichol ST (2008) Newly discovered ebola virus associated with hemorrhagic fever outbreak in Uganda. PLoS Pathog 4:e1000212

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.

Phylogenetic tree modified from Towner et al.:



Approved Taxonomy (Eighth ICTV Report) Proposed New Taxonomy Order Mononegavirales Order Mononegavirales Family Filoviridae Family Filoviridae Genus Marburgvirus Genus Marburgvirus Species: Lake Victoria marburgvirus Species Marburg marburgvirus Virus: Lake Victoria marburgvirus (MARV) Virus 1: Marburg virus (MARV) Virus 2: Ravn virus (RAVV) Genus Ebolavirus Genus Ebolavirus Species: Cote d'Ivoire ebolavirus [sic] Species Tai Forest ebolavirus Virus: Cote d'Ivoire ebolavirus (CIEBOV) Virus: Tai Forest virus (TAFV) Species: Reston ebolavirus Species Reston ebolavirus Virus: Reston ebolavirus (REBOV) Virus: Reston virus (RESV) Species: Sudan ebolavirus Species Sudan ebolavirus Virus: Sudan ebolavirus (SEBOV) Virus: Sudan virus (SUDV) Species: Zaire ebolavirus Species Zaire ebolavirus

Virus: Ebola virus (EBOV) Species *Bundibugyo ebolavirus*

Virus: Bundibugyo virus (BDBV)

Virus: Zaire ebolavirus (ZEBOV)