This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.011M*** | (to be completed by ICTV officers) |
| **Short title:** Create one new genus including one new species in the mononegaviral family *Filoviridae* |
|  |
| **Author(s):** |
| Wáng, Línfā (王林发); linfa.wang@duke-nus.edu.sg Shí, Zhènglì (石正丽); zlshi@wh.iov.cnYáng Xìnglóu (扬兴娄); yangxl@wh.iov.cnKuhn, Jens H.; kuhnjens@mail.nih.gov |
| **Corresponding authors with e-mail addresses:** |
| Wáng, Línfā (王林发); linfa.wang@duke-nus.edu.sg Shí, Zhènglì (石正丽); zlshi@wh.iov.cn  |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | **ICTV *Filoviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
| No objections from any member of the ICTV *Filoviridae* Study Group. |
|  |
| Date first submitted to ICTV: | 01/13/2019 |
| Date of this revision (if different to above): |       |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.011M.A.v1.Mengla\_dianlovirus.xlxs |

In 2015, a new filovirus, Měnglà virus (MLAV; previously designated “BtFilo9447”) was discovered by next generation sequencing in liver tissue of an unspecified Rousettus bat sampled in Měnglà County, Yúnnán Province, China (Yang *et al*., 2017; Yang *et al*., 2019). A coding-complete, 18,330-nt-long viral genome sequences was determined and deposited into GenBank; isolation of MLAV has not been reported (Yang *et al*., 2019). Akin to cuevaviruses, marburgviruses, and ebolaviruses, MLAV encodes seven structural proteins from the standard set of seven filovirus genes (3'-*NP-VP35-VP40-GP-VP30-VP24-L*-5'). However, the MLAV genome differs from the genomes of cuevaviruses, marburgviruses, and ebolaviruses in the number of gene overlaps (4 versus 5 [cuevaviruses], 2-3 [ebolaviruses], and 1 [marburgviruses]) and transcriptional termination sequence. In contrast to cuevaviruses and ebolaviruses, and similar to marburgviruses, MLAV only encodes a single product from the *GP* gene (Yang *et al*., 2019).

Phylogenetic analysis clearly places MLAV into a novel lineage of filoviruses more closely related to marburgviruses than to other filoviruses (Figs. 1 and 2).

**Figure 1.** Neighbor-joining phylogenetic tree based on deduced amino acid sequences of

filovirus RNA-dependent RNA polymerase (L) protein. Sequences were aligned using ClustalW using Geneious software 10.0.2. The tree was built using MEGA7 (bootstrap value = 1,000). Evolutionary distances were computed using the Poisson correction method and are in depicted as units of the number of amino acid substitutions per site. BDBV, Bundibugyo virus; EBOV, Ebola virus; HUJV, Huángjiāo virus; LLOV, Lloviu virus; MLAV, Měnglà virus; RAVN, Ravn virus; RESTV, Reston virus; SUDV, Sudan virus; TAFV, Taï Forest virus; XILV, Xīlăng virus (Yang *et al*., 2019).



 **Figure 2. Phylogenetic tree of filoviruses based on genomic sequences**. Sequence alignment was performed using ClustalW in Geneioussoftware 10.0.2. The tree was built using MEGA7 using the neighbor-joining method with p-distance model (bootstrap value = 1,000). Thescale bar represents the units of the number of base differences per site. BDBV, Bundibugyo virus; EBOV, Ebola virus; HUJV, Huángjiāo virus; LLOV, Lloviu virus; MLAV, Měnglà virus; RAVN, Ravn virus; RESTV, Reston virus; SUDV, Sudan virus; TAFV, Taï Forest virus; XILV, Xīlăng virus. GenBank accession numbers: NC014372 for TAFV1994; NC014373 for BDBV2007; NC002549 for EBOV1976; FJ968794 for SUDV1976; NC004161 for RESTV1989; NC016144 for LLOV2003; Z29337 for MARV1967; FJ750958 for RAVV2007; MG599980 for XILV2017; MG599981 for HUJV2017 (Yang *et al*., 2019).



In 2017, the ICTV *Filoviridae* Study Group established filovirus taxon demarcation criteria based on the US National Center for Biotechnology Information (NCBI) Pairwise Sequence Comparison (PASC) tool. Genus demarcation was set at the 55–58% sequence diversity threshold range and species demarcation was set at the 23–36% sequence diversity threshold. Using RefSeq “type” filovirus genome sequences, an algorithm was established for streamlined filovirus classification (Fig. 3).

**Figure 3.** Algorithm/flow chart for filovirus classification based on genomics sequence information and PASC-derived sequence demarcation criteria established by the ICTV *Filoviridae* Study Group (Bào *et al*.). A putative filovirus genome of interest is compared to the type filovirus RefSeq genome sequence (i.e., that of Marburg virus/H.sapiens-tc/KEN/1980/Mt. Elgon-Musoke) and then sequentially moved through the process until its proper taxonomic placement is revealed or the need to create novel taxa is obvious.

****

PASC analysis using the complete genome sequences of MLAV revealed that MLAV is most closely related to Marburg virus (43.86% sequence identity) (Fig. 4).

**Figure 4.** Screenshot of the US National Center for Biotechnology Information (NCBI) Pairwise Sequence Comparison (PASC) tool result after comparing distinct near-complete, coding-complete or complete filovirus genome sequences. Shown is the PASC results for MLAV. Brown bars represent genome pairs assigned to (the three established) different filovirus genera; yellow bars represent genome pairs assigned to (the seven established) separate filovirus species; and green bars represent genome pairs assigned to the same established filovirus species. BLAST: Basic Local Alignment.



|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| BLAST-based alignments |  |  |  |  |  |
| 1 |   | [43.86%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=0) |   | [gi|361584214|gb|JN408064.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=361584214) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269)|[Lake Victoria marburgvirus - Leiden](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1126254) |  |
| [2](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=1&scale=Linear) |   | [43.76%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=1) |   | [gi|409194014|gb|JX458851.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409194014) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [3](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=2&scale=Linear) |   | [43.71%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=2) |   | [gi|254688075|gb|FJ750958.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=254688075) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [4](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=3&scale=Linear) |   | [43.65%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=3) |   | [gi|409193806|gb|JX458825.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409193806) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [5](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=4&scale=Linear) |   | [43.63%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=4) |   | [gi|34304751|gb|AY358025.2|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=34304751) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [6](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=5&scale=Linear) |   | [43.6%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=5) |   | [gi|499104175|gb|KC545387.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=499104175) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [7](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=6&scale=Linear) |   | [43.59%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=6) |   | [gi|91177759|gb|DQ447651.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=91177759) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269)|[Lake Victoria marburgvirus - DRC1999](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=378831) |  |
| [8](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=7&scale=Linear) |   | [43.53%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=7) |   | [gi|409194070|gb|JX458858.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409194070) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [9](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=8&scale=Linear) |   | [43.49%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=8) |   | [gi|409194030|gb|JX458853.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409194030) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [10](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=9&scale=Linear) |   | [43.49%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=9) |   | [gi|91177751|gb|DQ447650.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=91177751) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269)|[Lake Victoria marburgvirus - DRC1999](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=378831) |  |
| [11](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=10&scale=Linear) |   | [43.48%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=10) |   | [gi|254688067|gb|FJ750957.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=254688067) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [12](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=11&scale=Linear) |   | [43.36%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=11) |   | [gi|409194054|gb|JX458856.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409194054) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [13](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=12&scale=Linear) |   | [43.34%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=12) |   | [gi|777861532|gb|KP985768.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=777861532) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [14](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=13&scale=Linear) |   | [43.29%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=13) |   | [gi|409193822|gb|JX458827.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=409193822) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269) |  |
| [15](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=14&scale=Linear) |   | [43.2%](https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=pa2txt&jobkey=JSID_01_2704339_130.14.22.10_9000_Pasc&idx=14) |   | [gi|151564214|gb|EF446132.1|](https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=151564214) [Marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=186537)|[Marburg marburgvirus](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=11269)|[Lake Victoria marburgvirus - Ci67](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=448086) |  |  |  |  |  |

Together, these results indicate that MLAV is a representative of a novel filovirus genus and species, here proposed to be named *Dianlovirus* and *Mengla dianlovirus*, respectively.

Etymology:

* Měnglà virus: named after **勐腊**县 (**Měnglà**xiàn/Měnglà County) in 云南省 (Yúnnán sheng/Yúnnán Province), China
* *Dianlovirus*: named after ancient **滇**王国 (**Diān**wángguó/Diān Kingdom) located in today’s Yúnnán Province
* *Mengla dianlovirus*: after Měnglà virus and *Dianlovirus*

| **References:** |
| --- |
| Bào Y, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, Dolnik O, Dye JM, Ebihara H, Formenty P, Hewson R, Kobinger GP, Leroy EM, Mühlberger E, Netesov SV, Patterson JL, Paweska JT, Smither SJ, Takada A, Towner JS, Volchkov VE, Wahl-Jensen V, Kuhn JH. [Implementation of Objective PASC-Derived Taxon Demarcation Criteria for Official Classification of Filoviruses.](https://www.ncbi.nlm.nih.gov/pubmed/28492506) Viruses. 2017 May 11;9(5). pii: E106. doi: 10.3390/v9050106. PMID: 28492506.Yang X-L, Zhang Y-Z, Jiang R-D, Guo H, Zhang W, Li B, Wang N, Wang L, Waruhiu C, Zhou J-H, Li S-Y, Daszak P, Wang L-F, Shi Z-L. [Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015.](https://www.ncbi.nlm.nih.gov/pubmed/28221123) Emerg Infect Dis. 2017 Mar;23(3):482-486. doi: 10.3201/eid2303.161119. PMID: 28221123Yang X-L, Tan CW, Anderson DE, Jiang R-D, Li B, Zhang W, Zhu Y, Lim XF, Zhou P, Liu X-L, Guan W, Zhang L, Li S-Y, Zhang Y-Z, Wang L-F, Shi Z-L. [Characterization of a novel filovirus (Měnglà virus) from *Rousettus* bats in China.](https://www.ncbi.nlm.nih.gov/pubmed/30150734) Nat Microbiol. 2019 https://doi.org/10.1038/s41564-018-0328-y. |