This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.



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.

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

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| **Code assigned:** | ***2019.033M*** | | | | (to be completed by ICTV officers) |
| **Short title:** Create one new species in the genus *Almendravirus,* family *Rhabdoviridae* | | | | | |
| **Modules attached** | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Peter J. Walker  Kim R. Blasdell  Ralf G. Dietzgen  Juliana Freitas-Astúa  Hideki Kondo  Gael Kurath  Ivan V. Kuzmin  Robert B. Tesh  Noel Tordo  Nikos Vasilakis  Anna E. Whitfield | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| peter.walker@uq.edu.au | | | | | |
| **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) | | | *Rhabdoviridae* Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| Supported by 11 of 13 SG members with limited corrections related to formatting and spelling errors. There were two non-responders. | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | |  | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

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| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:**  2019.033M.A.v1.Menghai\_almendravirus\_1sp.xlsx |

**Part 4:** **APPENDIX**: supporting material

| **References:** |
| --- |
| 1. **Sun Q, Zhao Q, An X, Guo X, Zuo S, Zhang X, Pei G, Liu W, Cheng S, Wang Y, Shu P, Mi Z, Huang Y, Zhang Z, Tong Y, Zhou H, Zhang J.** 2017. Complete genome sequence of Menghai rhabdovirus, a novel mosquito-borne rhabdovirus from China. Archives of Virology **162:**1103-1106.  2. **Roche S, Bressanelli S, Rey FA, Gaudin Y.** 2006. Crystal structure of the low-pH form of the vesicular stomatitis virus glycoprotein G. Science **313:**187-191.  3. **Walker PJ, Kongsuwan K.** 1999. Deduced structural model for animal rhabdovirus glycoproteins. Journal of General Virology **80:**1211-1220. |

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| **Annex:**  Menghai rhabdovirus (MRV) was isolated from mosquitoes (*Aedes albopictus*) collected at Menghai County in southern Yunnan Province, China, in 2010 (1).  The complete genome sequence (10,744 nt) has been determined (1). In a well-supported Maximum Likelihood tree inferred from complete L protein sequences of currently classified and recently proposed animal rhabdoviruses, MRV falls with the almendraviruses in a unique monophyletic clade; it is most closely related to Coot Bay virus (CBV; *Coot Bay almendravirus*) (**Figure 1**).  Like other almendraviruses, the MRV genome contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G*, and *L*) and an additional gene (U1) between the *G* gene and *L* gene (**Figure 2**); the *U1* gene encode a small viroporin-like protein (**Figure 3**).  A ClustalX amino acid sequence alignment indicates that the MRV G protein has a similar arrangement of conserved cysteine residues in the ectodomain to CBV. Other almendraviruses, feature all 12 G protein disulphide bridge-forming cysteine residues (CI**–**CXII) that occur in vesicular stomatitis Indiana virus (VSIV) (2) and two additional cysteine residues in the C-terminal regions that are likely to form an additional, unique disulphide bridge (**Figure 4**). MRV, like CBV, lacks the CVI and CVII which form a disulphide bridge in VSIV (2). Shared and unique patterns of disulphide bridge formation occur commonly for viruses assigned to individual genera of *Rhabdoviridae* (3).  Amino acid sequence identities between the N, G and L proteins of MRV and other almendraviruses are relatively low (<35% in the N, <40% in the G proteins and <60% in the L proteins). MRV is most closely related to CBV by amino acid sequence identity (**Tables 1–3**).  MRV has been reported to have been passaged only in mosquito (C6/36 cells) (1). Other almendraviruses were isolated from mosquitoes collected in Peru, Colombia, Panama and Florida, and have been passaged successfully only in mosquito cells.  **Species demarcation criteria**  Viruses assigned to different species within the genus *Almendravirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N; B) minimum sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% in G; D) significant differences in genome organisation as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  MRV meets species demarcation criteria A, B, C and F. No data are available on cross-neutralisation of MRV and other almendraviruses (criterion E).    **Figure 1.** The evolutionary history was inferred from a Clustal W alignment of complete L protein sequences of Menghai rhabdovirus and 112 animal rhabdoviruses currently assigned or recently proposed to be assigned to species. Phylogenetically informative sites were selected from the alignment using GBLOCKS resulting in 1072 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan And Goldman + Freq. model. The tree with the highest log likelihood (-104695.9075) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.    **Figure 2.** Genome organisations of almendraviruses. The U1 ORFs (yellow) each encode class 1A viroporin-like proteins.  MRV U1 MMEILLLVCQLISFILLIYLVFRVIKLESMTKNIRTILSDFILRQKIAKDIGEDKKGFYYSRIDGPIMN  CBV U1 MEIIDILILIVLSVLSITLIFYILKTNSLRDILCESIKKLDIIVKNVNVKKDDYFSKLI  PTAMV U1 MNDKSDSNNNNTLLILEIIEFILIILIICMMIYLWYQSRRQSNKLCTKVNMVYNVIENLEKYIMTKCNSSLDSRTVSKWV  ABTV U1 MDSLTILSIIEIFFLIVIIILLIYRIYIDKNYFKHWKSYIASMYSKLNNTINNQRYKKDDCHESDRLTVSKWV  RCHV U1 MDVISVILWTIADIILFAIFIIILFFYKNHRKDETETTVPYKRHPTTSSYY  BALV U1 MSWENIINNILLMFVVIILIVILLKLKTISDTPIKVRMPVYRMDSKSDIANNKVSEKKYAVSKHDPAWNSRL  **Figure 3.** Almendravirus class 1A viroporin-like U1 proteins. Predicted transmembrane domains (grey shade) and clusters of basic residues in the C-terminal domain (shaded black) are shown.  **CI CII**  ABTV MIAHKLILPLVILTSFQRIKREDITCPVYNHKNVNVSSQSLLQFDMRQVSFNSGEEIINHNPLVTGYLCRKLSYET  PTAMV MITHKYILPIIVLSNFMPVKRDDLTCPIYNHQNVEFVNTTITYIRLNSVLLQSKSLELKQMPYVRGHICQKIRYIT  CBV M---HVILPVVLLTSFKLINFHELICPPDNVIDHDLEGLNMLHEYKTKEYVLKEG--ALDVFSLSGYDCTKVRMKT  MRV MIT-----------AFKAINFNELLCPDGKEIKVDESNFGLLNKYMAPEYEIDEE--SLNPYEIKGRDCYSAVFKT  RCHV M--SYYIFPVILLSAFRPAGLEDVTCPSLN----HDHKVDMSEYREYDWGMVDNSILNNDLYSVSGYDCHYVKLTT  BALV MF--FTILPTLLLGNWTLVNITDITCPHYKDYTIHPEAIN----HKLSLYEVTDEDYNEYNNVLFGRDCSKLTLST  \* :: : :: \*\* : . : \* \* \*  **CIII CIV CV**  ABTV SCYANLFTSNTVEYKLKILPITKKECATGSNSQVKSFPTPICNWSMFGSNTVKETKQYIEYEQRSYKLDMVSGKLK  PTAMV TCKANLFTSNEIFYKKEYLTVTKNDCEMKAVHETGEYPAPICTWSLFGSNLHNEEIIVTEIQSHDYHYDLFNGKIK  CBV GCKFHFFAKNDIINEMEMIPIDNRTCQNLS-NKVLKYPEPECISGIFNNDYHYVSREESLSQSRTYLFNPTTNEVI  MRV GCKFHYFGSNDIIQVIEKKTTDKKNCNQVS-TDVLTFPEANCVSGLFDNSYHYKEIEYIVTKPRNYMYDPSTGELV  RCHV SCQANLLSKNVITYTKKIINAPIDQCQSLKEDKLAEYPLPQCEWNMFGSSITENSMQYMVTKERTYRLNPVTGNIV  BALV KCKAHLMASNEIEYEEIYESPDITDCNSLKMDNMIKYPESNCRWNLFDNGYISNNETTIKINDKSFLLDVHTGLIV  \* : : .\* : \* . :\* . \* .:\*... : : : : .. :  **CVI CVII CVIII CIX**  ABTV HVEEIFDKCYEEYCVLKDNSGYWIRDD--QDEKKYCPKLEDQ-----KIPAKLKVIDQFEYLEVAQHIYDMQELCA  PTAMV DSEYLFEHCTLMYCKLREHKGYWIKSE--PTKNDICPIVQDD-----EIVAELKFYNENHFLKINHHLYSTEEVCK  CBV NYHDIFESKVDNVYKYKNNRGYWIAQN--NEKKMECDHYEEHGSSDLKIKIYEKEKDK--FISVNGKIYSVDNVCK  MRV DYNNIFDKKVDNVYHYRDNKGYWTIDE--TQPATTCETFKQHESSEIEVKVWKSRMNNKSLIDLGGKIYDVDEICY  RCHV NEHIIFDSCSELHCVYKNSKGYFVKKP--RSSKIDCSNHNIITVS--NMKAATGKVNNHPAIQVMNRTMMIDDVCM  BALV NQDKIFNHCDEHMCEYKNNRGFWLRSKDINTEKELCTHLKNTTHLN-KQEGYLSVYQNNKFLYIENNPVHYDDMCT  . . :\*: :: \*:: . \* : : :: : : . :::\*  **CX CXI CXII**  ABTV LEVCGNMLIHIPDIGNFIGD---DRFMKKLKKCKSLPSLRNAIENNSEDITGNEKCLDFRLKMLGNPDKSIKYHDI  PTAMV IKYCNNSLLFFKDIGFFNIKSTLQKMDKIFKKCTKIEDLRYIIHDNVEKIDNLNDCLNFKLNVLTNKDRTIAYHDI  CBV INFCGLSLATTKDRIFFKLP-----PKVDIKTC-IDEVSTPSKSDMVKVDNFYKECEENRMELISAKR--FNYQQL  MRV HDHCGVKIAVTKDHVYFKLP-----TNLDIKKCNLDYKRVYLQSEIIQEKSELKDCLEAKIDMAWMKS--INYEDL  RCHV IDRCGVKLVYLSDFQIFKVP-----HELKFKNCEEDHVQIKPEIALFTDLRDSIDCSILVERLLVRKE--VKYADI  BALV IKRCNNLILTIKNFKKYVIK-----SSGLFQECKTDNIHYLNKEESFNEVEDHILCANKLVKVIKEKK--LNYYDL  . \*. : : : :: \* \* : . \* ::  ABTV RNLHPRSPGINRVYRLGENNTLESAIAYYGSTGLDKISKKLNYWVNCTEDKVCSYNGYMGKDKLHLRSKLDSETYQ  PTAMV RKLHPKGTGINRIYRLNGNNTLESAIAYYGSVESNETKIYLDYWNDCSKTHTCTYNGYMGKKGLNIRARLNIDLFQ  CBV MKFMPQTMGIHHVYRINSNKTLEMAIGRYGMVNLDTLNGTEH-WIECGLETKCTYNGIMRP---------LTNKTS  MRV KKFNPSSSGIHPVYKLNNNKTLMRALAKYSEVNTTELHKYLE-WVRCGNKTKCTYNGVIKAD--------LVEVYG  RCHV KALHPTSIGINNVYRYKNG-TLEVALAYYSRIDKVELMKHSNRWIDCGPKANCSYNGWIEPK---------ERLDS  BALV KYFHPTRIGLHNIYRLNEDKKLEKNIAYYSKVDSDKDEVKVK-SVACGTKVNCLYNGKHKIN----------SEKE  : \* \*:: :\*: . .\* :. \*. . \* \* \*\*\*  ABTV DIFEVDDELIVYQPTRNISESFYKDVIHYELLDKMTQNFSIFNSNYYSKIIYALLIILAVFFIYKIMKLLTLRCFK  PTAMV EVYEEDSSLLIYNGTTDLSTGTIGELTKGDANVTFTTKEWIPHISNYIIIIVFCLLSGAVFIIMINIYNRIMVMKR  CBV IEIDFNQLIKHHEEIKNGIYVY--DNVYNQYYDETTTIYKTQNTLLTGLYMMLPWIAESVIILLIVFILIKRLVKR  MRV QRLTEKDFAVHVDELKVGIKAYPRDIISHSDHTEEKIYLKSDNSFVSLFFIAAPWISEGVLILIIFCILIKYIKPK  RCHV KMLDVKDYEEFVSTIASTITTKLAGSFD-QMVEEEISKKVIDSTITGFIQRNWIWAGEIISIIIICVIVFKFIIKS  BALV FNVDIKEYKIYKDEVEKGFIIEDSMYIPYEKTEIEFERNAITFDFDEIYKFGMGLLIIALILLILVCVVTKCKSRN  .. . . : ::  ABTV NQSKFGKFYQISTNKSQELDMMRKDISQWK  PTAMV NRKAF---------YNRENDNRVIYVNDWK  CBV RKNKR----------RRESD---IKMGTW-  MRV NKRHRDI-------LLRRNN---QDFESW-  RCHV IKKKE----------DKILYLPSTRSNYY-  BALV NIKSRKS--------LKRFEEKASFLNI--  :  **Figure 4.** Clustal X alignment of almendravirus G proteins. Conserved cysteine residues are highlighted (black shading) with twelve conserved cysteine (CI to CXII) residues that form six disulphide bridges in VSIV shown. The signal domains (N-terminus) and transmembrane domains (C-terminus) are also shown (grey shading).   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | **Table 1.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of almendravirus N proteins.   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | |  | ABTV | PTAMV | RCHV | BALV | CBV | MRV | | ABTV |  |  |  |  |  |  | | PTAMV | 62.2 |  |  |  |  |  | | RCHV | 23.4 | 25.5 |  |  |  |  | | BALV | 26.5 | 25.5 | 32.8 |  |  |  | | CBV | 22.9 | 23.1 | 25.8 | 26.3 |  |  | | MRV | 25.8 | 23.1 | 28.2 | 28.9 | 34.7 |  |   **Table 2.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of almendravirus G proteins.   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | |  | ABTV | PTAMV | RCHV | BALV | CBV | MRV | | ABTV |  |  |  |  |  |  | | PTAMV | 37.1 |  |  |  |  |  | | RCHV | 24.6 | 23.1 |  |  |  |  | | BALV | 21.7 | 22.9 | 25.3 |  |  |  | | CBV | 21.9 | 22.9 | 25.8 | 22.9 |  |  | | MRV | 23.9 | 22.2 | 25.1 | 23.4 | 36.9 |  |   **Table 3.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of almenrdavirus L proteins.   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | |  | ABTV | PTAMV | RCHV | BALV | CBV | MRV | | ABTV |  |  |  |  |  |  | | PTAMV | 74.6 |  |  |  |  |  | | RCHV | 46.7 | 46.6 |  |  |  |  | | BALV | 44.7 | 46.0 | 55.1 |  |  |  | | CBV | 42.2 | 42.8 | 43.4 | 43.1 |  |  | | MRV | 41.9 | 42.0 | 45.3 | 44.6 | 58.7 |  | | |