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:** | ***2017.009M*** | | | | (to be completed by ICTV officers) |
| **Short title: One (1) new species in the genus *Ledantevirus* (*Mononegavirales*: *Rhabdoviridae*)** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Tony L. Goldberg, Andrew J. Bennett, Robert Kityo, Jens H. Kuhn, Colin A. Chapman | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Tony L. Goldberg, [tony.goldberg@wisc.edu](mailto:tony.goldberg@wisc.edu) | | | | | |
| **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 *Rhabdoviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: “Mononegavirales 2 TP new ledantevirus species”** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

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

| A novel putative ledantevirus, Kanyawara virus (KYAV), was characterized in 2016 by next-generation sequencing in an unclassified nycteribiid bat fly parasitizing a Ugandan unclassified pteropodid bat, all of which were sampled in 2010 (Goldberg *et al*.). The coding-complete genome sequence of KYAV was determined and deposited into GenBank. The closest known relative of KYAV appears to be Mount Elgon bat virus.  Figure A. Maximum likelihood phylogenetic tree of rhabdoviruses. The rhabdovirus phylogeny is based on concatenated codon-based alignments (8,256 positions) of nucleotide sequences of the canonical rhabdovirus nucleoprotein (*N*), phosphoprotein (*P)*, matrix (*M*), glycoprotein (*G*), and RNA-dependent RNA polymerase (*L*) genes of 15 viruses of the subgroups A–C of the genus *Ledantevirus* with vesicular stomatitis Indiana virus (genus *Vesiculovirus*) as the outgroup. Circles on nodes indicate statistical confidence based on 1,000 bootstrap replicates of the data (closed circles = 100%; open circles ≥75%); scale bars indicate nucleotide substitutions per site.  Viruses assigned to different species within the genus Ledantevirus have several of the following characteristics: A) minimum amino acid sequence divergence of 7% in L proteins; B) minimum amino acid sequence divergence of 15% in G proteins; C) significant differences in genome organization as evidenced by numbers and locations of ORFs; D) can be distinguished in serological tests; and E) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors. All current members clearly meet criteria A and B (see Annex).  The viruses each meet the other criteria to varying extents based on available data. KYAV fulfills criterion A and B; it has the same genomic organization as other ledanteviruses; and it occupies a novel ecological niche (E).  **References:** |
| --- |
| Goldberg TL, Bennett AJ, Kityo R, Kuhn JH, Chapman CA. 2017. Kanyawara Virus: A Novel Rhabdovirus Infecting Newly Discovered Nycteribiid Bat Flies Infesting Previously Unknown Pteropodid Bats in Uganda. Sci Rep, in press. |

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| **Annex:**  L protein distance matrix: |

G protein distance matrix:

