

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

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| **Code assigned:** | **2020.021M** |  |
| **Short title:** Create one new species (*Bughendera ledantevirus*) in the genus *Ledantevirus* (*Mononegavirales:* *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Rhabdoviridae* Study Group |

**ICTV study group comments and response of proposer**

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| Approved by all responding members of the study group (11 of 14). |

**Submission dates**

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| Date first submitted to SC Chair | July 31, 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.021M.R.Ledantevirus\_1nsp |

**Abstract**

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| The new species *Bughendera ledantevirus* is proposed for Bughendera virus (BUGV), detected in louse flies infesting fruit bats in Uganda. Based on large (L) protein sequences, BUGV clusters phylogenetically with other ledanteviruses and meets demarcation criteria for assignment to a new species in the genus. |

**Text of proposal**

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| |  | | --- | | Bughendera virus (BUGV; isolate BF402) was detected in nycteribiid bat flies (*Dipseliopoda* sp.) parasitizing Angolan soft-furred bats (Pteropodidae: *Lissonycteris angolensis ruwenzorii* Bocage, 1898) sampled in the Bundibugyo District of Uganda in 2017 [1]. The near-complete genome sequence (10,895 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini [1]. We propose the assignment of BUGV to a new species (*Bughendera ledantevirus*) in the genus *Ledantevirus*.  **Genome organization**  The BUGV genome contains the five canonical rhabdovirus structural protein genes (N, P, M, G, and L). The genome is similar in organization to the genomes of all other ledanteviruses comprising phylogroup C (**Figure 1**).  **Phylogeny and amino-acid sequence relationships**  Based on maximum likelihood (ML) trees generated from complete large (L) protein sequences, BUGV clusters with the viruses forming the genus *Ledantevirus*. It falls within genogroup C and is most closely related to Kanyawara virus (KYAV; species *Kanyawara ledantevirus*) (**Figure 2**). Amino-acid sequence identities estimated from pair-wise alignments (p-distances) confirm that BUGV is most closely related to KYAV (72.7% identity in the G protein and 72.2 % identity in the L protein) (**Table 1** and **Table 2**).  **Ecology**  BUGV falls within ledantevirus phylogroup C, which comprises only viruses isolated from louse flies (Diptera: Hippoboscoidea), hard ticks (Ixodida: Ixodidae) or bats (Chiroptera) from Africa or Asia. KYAV was first detected in an unclassified nycteribiid bat fly parasitizing an unclassified pteropodid bat in Uganda [2]. KYAV has subsequently been detected in bat flies infesting bats in the same roost in Uganda at the same time as BUGV [1]. BUGV and KYAV appear to share similar ecological relationships.  **Species demarcation criteria**  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; B) minimum amino-acid sequence divergence of 15% in G; C) significant differences in genome organization, as evidenced by numbers and locations of open reading frames (ORFs); D) can be distinguished in serological tests; and E) occupy different ecological niches, as evidenced by differences in hosts and/or arthropod vectors.  BUGV meets demarcation criteria A and B. BUGV has a similar genome organization to other viruses comprising phylogroup C (criterion C). Serological tests (criterion D) have not been conducted, as no BUGV isolate is currently available. BUGV appears to occupy the same ecological niche or a similar niche to KYAV (criterion E). | |

**Supporting evidence**

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**Figure 1.** Ledantevirus genome organizations. N, P, M, G, and L represent open reading frames (ORFs) encoding the structural proteins. The U1 ORFs of Kern Canyon virus, Keuraliba virus, Le Dantec virus, and Vaprio virus (red) and the Mx ORF of Fukuoka virus (blue) are indicated.

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**Figure 2.** The evolutionary history was inferred from multiple alignment (performed with ClustalW) of complete L protein sequences of 167 animal rhabdoviruses currently assigned or recently proposed for assignment to species and Bughendera virus. Phylogenetically informative sites were selected from the alignment using Gblocks, resulting in 961 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 (-138036.61) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial trees for the heuristic search were obtained automatically by applying Neighbor-Joining 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.

**Table 1.** Percentage amino-acid sequence identities (p-distance) of a ClustalW alignment of ledantevirus G proteins.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | NKOV | BARV | FUKV | NISV | YTV2 | KCV | KEUV | LDV | VAPV | MEBV | WLFV5 | KRV | OITAV | FKRV | KOLEV | KYAV | BUGV |
| NKOV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BARV | 50.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 49.9 | 85.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 52.8 | 80.5 | 80.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YTV2 | 41.5 | 40.9 | 43.1 | 40.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 34.3 | 35.9 | 37.0 | 35.7 | 38.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 34.7 | 33.1 | 33.9 | 33.9 | 35.7 | 52.0 |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 33.5 | 34.1 | 34.5 | 33.5 | 35.1 | 52.0 | 73.3 |  |  |  |  |  |  |  |  |  |  |
| VAPV | 36.6 | 36.3 | 36.3 | 35.7 | 38.0 | 55.0 | 60.0 | 61.8 |  |  |  |  |  |  |  |  |  |
| MEBV | 30.0 | 27.9 | 29.0 | 28.7 | 32.0 | 32.9 | 30.2 | 32.4 | 33.3 |  |  |  |  |  |  |  |  |
| WLFV5 | 32.9 | 30.2 | 30.4 | 30.6 | 30.6 | 32.2 | 31.8 | 31.0 | 32.4 | 46.0 |  |  |  |  |  |  |  |
| KRV | 24.6 | 25.7 | 26.7 | 25.9 | 26.1 | 28.3 | 26.7 | 27.1 | 26.9 | 27.5 | 26.3 |  |  |  |  |  |  |
| OITAV | 28.1 | 26.5 | 26.3 | 26.9 | 29.0 | 27.1 | 27.1 | 25.5 | 28.5 | 29.6 | 30.6 | 35.5 |  |  |  |  |  |
| FKRV | 27.3 | 26.1 | 25.3 | 25.9 | 27.5 | 26.5 | 27.9 | 28.5 | 29.0 | 33.7 | 30.0 | 34.5 | 46.2 |  |  |  |  |
| KOLEV | 28.7 | 27.7 | 27.7 | 27.5 | 28.5 | 28.5 | 28.7 | 29.6 | 28.7 | 30.8 | 31.8 | 35.7 | 41.5 | 52.8 |  |  |  |
| KYAV | 30.8 | 30.6 | 30.4 | 30.6 | 30.4 | 32.4 | 32.6 | 32.2 | 32.4 | 49.7 | 45.2 | 28.7 | 31.0 | 31.6 | 33.7 |  |  |
| BUGV | 32.0 | 30.4 | 32.0 | 30.6 | 30.8 | 34.3 | 32.6 | 32.9 | 34.9 | 48.5 | 43.9 | 27.7 | 30.4 | 30.0 | 31.2 | 72.7 |  |

**Table 2.** Percentage amino-acid sequence identities (p-distance) of a ClustalW alignment of ledantevirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | NKOV | BARV | FUKV | NISV | YTV2 | KCV | KEUV | LDV | VAPV | MEBV | WLFV5 | KRV | OITAV | FKRV | KOLEV | KYAV | BUGV |
| NKOV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BARV | 62.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 62.5 | 92.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 61.8 | 87.9 | 89.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YTV2 | 55.2 | 54.5 | 54.6 | 54.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 51.5 | 50.7 | 51.2 | 51.3 | 51.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 51.7 | 51.1 | 51.9 | 51.9 | 50.9 | 63.8 |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 51.2 | 50.7 | 50.9 | 50.6 | 50.8 | 63.5 | 81.6 |  |  |  |  |  |  |  |  |  |  |
| VAPV | 51.5 | 51.6 | 51.4 | 51.4 | 49.9 | 64.1 | 70.7 | 70.0 |  |  |  |  |  |  |  |  |  |
| MEBV | 49.4 | 49.3 | 49.3 | 49.5 | 47.9 | 49.4 | 49.5 | 49.4 | 50.3 |  |  |  |  |  |  |  |  |
| WLFV5 | 48.2 | 48.2 | 48.2 | 48.6 | 47.1 | 49.0 | 49.7 | 49.7 | 50.7 | 62.3 |  |  |  |  |  |  |  |
| KRV | 47.8 | 48.2 | 48.1 | 47.6 | 48.7 | 49.1 | 49.3 | 49.3 | 50.6 | 56.2 | 55.9 | # |  |  |  |  |  |
| OITAV | 48.4 | 48.4 | 48.4 | 48.1 | 47.3 | 49.2 | 48.3 | 48.1 | 50.4 | 54.9 | 55.9 | 63.9 |  |  |  |  |  |
| FKRV | 47.5 | 48.1 | 48.0 | 48.1 | 47.1 | 48.8 | 48.4 | 47.6 | 49.4 | 55.3 | 54.3 | 62.6 | 62.8 |  |  |  |  |
| KOLEV | 48.5 | 47.7 | 48.4 | 48.2 | 48.5 | 49.6 | 50.1 | 49.0 | 50.3 | 55.7 | 54.7 | 63.5 | 63.0 | 75.9 |  |  |  |
| KYAV | 48.6 | 49.1 | 49.2 | 49.0 | 48.9 | 48.9 | 48.8 | 48.0 | 49.3 | 64.6 | 59.8 | 55.3 | 53.9 | 53.7 | 55.0 |  |  |
| BUGV | 47.7 | 47.1 | 47.5 | 47.4 | 47.5 | 48.2 | 48.3 | 47.8 | 48.0 | 63.6 | 57.8 | 54.3 | 53.0 | 52.9 | 53.9 | 72.2 |  |

**References**

1. Bennett AJ, Paskey AC, Kuhn JH, Bishop-Lilly KA, Goldberg TL (2020) Diversity, transmission, and cophylogeny of ledanteviruses (*Rhabdoviridae*: *Ledantevirus*) and nycteribiid bat flies parasitizing Angolan soft-furred fruit bats in Bundibugyo District, Uganda. Microorganisms 8:e750. PMID: 32429498 DOI: 10.3390/microorganisms8050750

2. 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. Scientific Reports 7:e5287. PMID: **28706276** DOI: 10.1038/s41598-017-05236-w