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**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.007M*** | | | | (to be completed by ICTV officers) |
| **Short title: One (1) new species in the genus *Orthobunyavirus* (*Bunyavirales*: *Peribunyaviridae*)** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Petrus Jansen van Vuren  Michael R. Wiley​  Gustavo Palacios  Nadia Storm  Jens H. Kuhn  Wanda Markotter  Monica Birkhead  Alan Kemp  Janusz T. Paweska​ | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Janusz T. Paweska​, [januszp@nicd.ac.za](mailto:januszp@nicd.ac.za) | | | | | |
| **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 *Bunyaviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| 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:** |
|  |

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

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.007M.N.v1.Orthobunyavirus\_sp** |

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

| Wolkberg virus (WBV) was described in 2017 after its discovery in wingless bat flies (*Eucampsipoda africana*) parasitizing Egyptian rousettes (*Rousettus aegyptiacus*) sampled in South Africa (Jansen van Vuren *et al*.). The virus was named after the location of the cave harbouring the parasitized bats. WBV was isolated in cell culture and fully sequenced. The phylogenetic placement of the virus, clearly indicative of the need for a novel orthobunyavirus species, is shown below in Figures 1–3 (S, M, and L segment, respectively). We propose to name the species after the virus and in line with the current bunyaviral non-Latinized binomials species name format: *Wolkberg orthobunyavirus*. |
| --- |

Figure 1

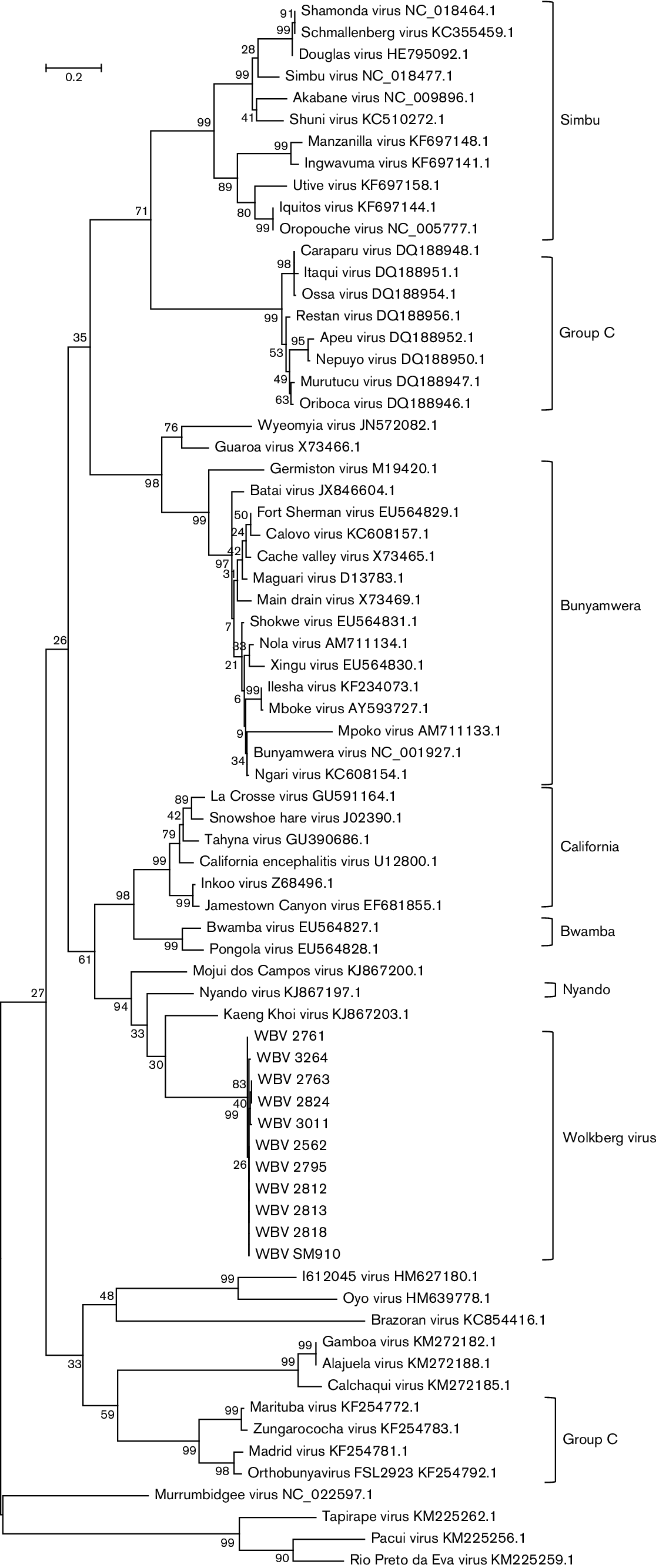
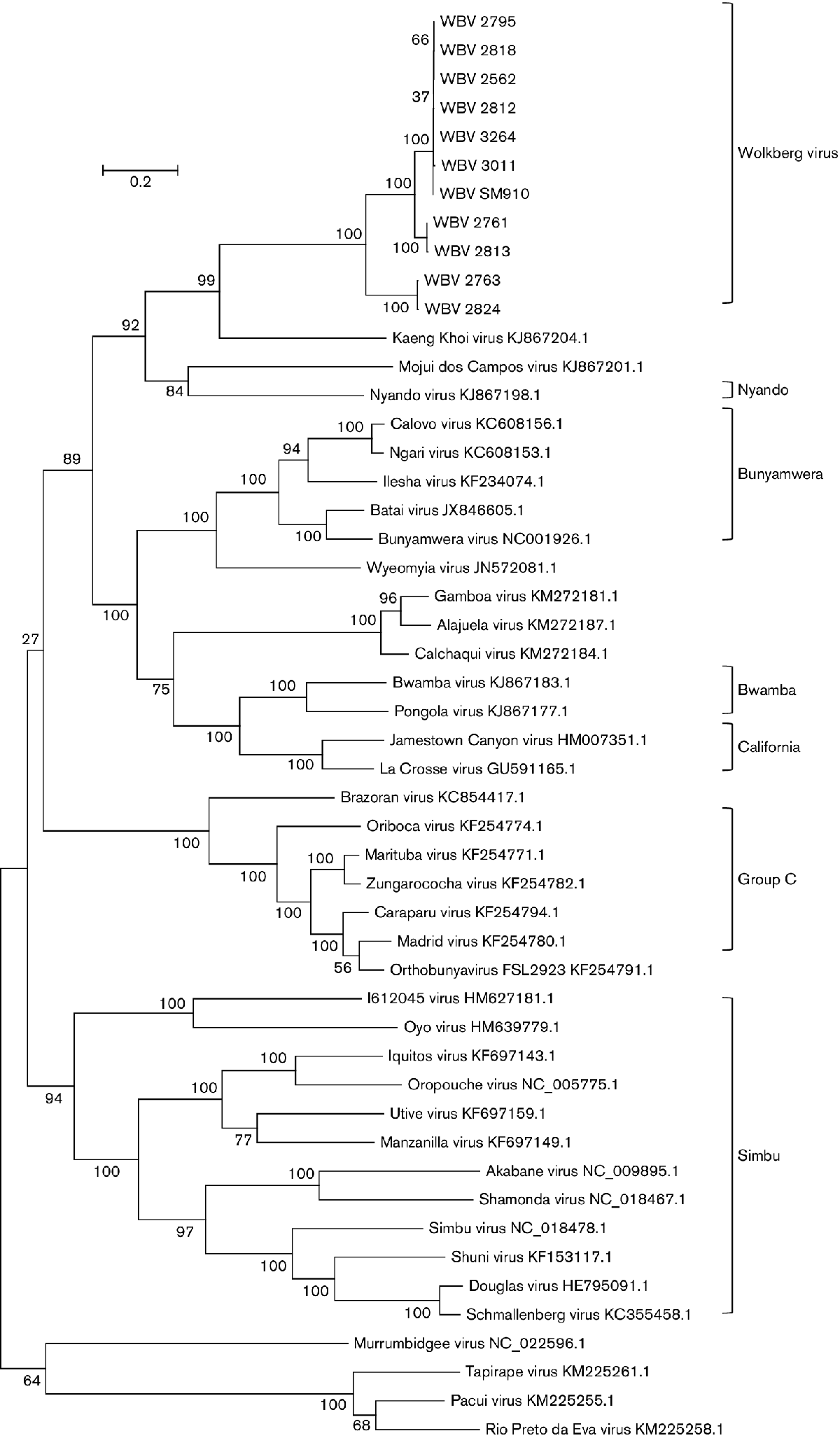


Figure 2



| Figure 3  **C:\Users\kuhnjens\Desktop\L.gif**  Figures 1–3: “Molecular phylogenetic analysis by the maximum-likelihood method showing representative viruses from different viruses in the *Orthobunyavirus* genus using S-, M, and L-segment ORF amino acid sequences, respectively. GenBank accession numbers are indicated next to virus names (excluding WBV). Medically important serogroups, and WBV isolates, are indicated by brackets.  The mega (version 6) program was used to prepare alignments (clustal w) of nucleic acid segment sequences, deduced amino acid sequences, phylogenetic trees and pairwise distance calculations. The publicly available bunyavirus sequences used in the analysis were obtained from NCBI-Nucleotide (GenBank). Maximum-likelihood trees were prepared using amino acid sequences of all ORFs from all segments, showing the placement of WBV in the *Orthobunyavirus* genus relative to other viruses in this genus for which sequence is available on GenBank. The evolutionary histories were inferred by using the maximum-likelihood method based on the Tamura–Nei model. The trees with the highest log likelihood are 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 by applying the neighbour-joining method to a matrix of pairwise distances estimated using the maximum-composite-likelihood approach. The trees are drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in mega6. ORFs were located and deduced protein amino acid sequences prepared by using the CLC Genomics Workbench (Qiagen)” [both paragraphs are directly quoted from Jansen van Vuren *et al*.].  **References:** |
| --- |
| 1. Jansen van Vuren, P., M. R. Wiley, G. Palacios, N. Storm, W. Markotter, M. Birkhead, A. Kemp, and J. T. Paweska. 2017. Isolation of a novel orthobunyavirus from bat flies (*Eucampsipoda africana*). The Journal of general virology [Epub 2017/05/11]. PMID: 28488954. doi: 10.1099/jgv.0.000753 [eng]. |