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:** | ***2017.018M*** | | | | (to be completed by ICTV officers) |
| **Short title: 1 new species in the genus *Orthoreovirus*** | | | | | |
| **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  Stewart McCulloch  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 *Reoviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| supported | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 21, 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: 2017.018M.N.v1.Orthoreovirus\_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

| Figures 1-3, citing from Reference 1:  “A Maximum Likelihood tree, constructed with nucleic acid sequence data for the RNA-dependent RNA polymerase (RdRp) encoding segments of representative viruses from the different genera within Reoviridae shows the placement of two isolates of MAHLV amongst other orthoreoviruses in the family. Maximum Likelihood trees were prepared using the deduced amino acid sequences from the open reading frames (ORF’s) of all the virus’ segments and those of other viruses in the Orthoreovirus genus. A distinct clade is formed by MAHLV, Bush viper reovirus, Baboon orthoreovirus and Broome virus within the genus. The above-mentioned clade is visibly distinct from others composed of bat-associated viruses; the Nelson Bay orthoreovirus and bat-derived mammalian orthoreoviruses. The closest relative of MAHLV, based on sequence homology of a conserved core protein, is Bush viper reovirus (Lambda B nucleic acid identity—63.7%; RdRp amino acid identity—66.3%) while the closest bat-associated virus is Broome virus (LambdaB nucleic acid identity—60.7%; RdRp amino acid identity—58.0%). Homology of the divergent major outer capsid protein of MAHLV to known orthoreoviruses is much lower: Sigma B nucleic acid identity—28.7%–41.9%; amino acid identity—5.6%–24.3%.  The genome segments of MAHLV were named according to the nucleotide length, which is consistent with the nomenclature of other orthoreoviruses. The total genome size is 23,200 nucleotides and predicted to encode eleven proteins, seven of which are structural. All ten genome segments of MAHLV contain an identical 3' terminal sequence, UCAUC-3', which is conserved between all known species of Orthoreovirus, and an identical 5' terminal sequence, 5'-GGUCA which is unique to MAHLV. Non-coding regions (NCRs) are present at both ends of the genome segments, with the 5' NCRs being shorter in nucleotide length than 3' CRs. The nucleotide sequences of the two isolates of MAHLV, 2511 and 06-24, are not identical. Nucleotide homology of the RdRp encoding segment between the two isolates is 93.5% (99.8% deduced amino acid sequence), and 80.4% (89.0% deduced amino acid sequence) for the Sigma B encoding segment.  Members of a species within the Orthoreovirus genus are usually identified by a number of characteristics: amino acid and nucleotide sequence identity, organization of the polycistronic genome segment and host species. For conserved core proteins, an amino acid identity >85% for homologous proteins indicates that two viruses belong to the same species, while identity <65% indicates a possible new species. When comparing the amino acid sequence of more divergent outer capsid proteins, >55% identity indicates one species and <35% indicates different species. Nucleic acid sequence identity of homologous segments of >75% indicates the same species and <60% a new species. The nature of conserved genome segment termini sequences of orthoreoviruses is also useful for virus classification. The divergence of MAHLV sequence from other known orthoreoviruses combined with a unique conserved 5’ genome segment end and a unique host species, suggests that this is a new virus species in this genus.” |
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| **References:** |
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| 1. Jansen van Vuren P, Wiley M, Palacios G, Storm N, Mcculloch S, Markotter W, Birkhead M, Kemp A, Paweska JT. Isolation of a novel fusogenic Orthoreovirus from Eucampsipoda africana bat flies in South Africa. Viruses 2016;8:65. |