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:** | ***2018.001M*** | | | | (to be completed by ICTV officers) |
| **Short title:** One new genus (*Alphanemrhavirus*), including 2 new species, in the family *Rhabdoviridae*. | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Peter J. Walker  Kim R. Blasdell  Ralf G. Dietzgen  Juliana Freitas-Astúa  Hideki Kondo  Robert B. Tesh  Nikos Vasilakis  Anna E. Whitfield | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Peter J. Walker, [peter.walker@uq.edu.au](mailto: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) | | | ICTV *Rhabdoviridae* Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| The proposal is supported by a majority of Study Group members (8 supporters and 4 non-responders). | | | | | |
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| Date first submitted to ICTV: | | | | June 6, 2018 | |
| 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:** 2018.001M.N.v1.Alphanemrhavirus |

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

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| **References:** |
| 1. **Shi M, Lin XD, Tian JH, Chen LJ, Chen X, Li CX, Qin XC, Li J, Cao JP, Eden JS, Buchmann J, Wang W, Xu J, Holmes EC, Zhang YZ.** 2016. Redefining the invertebrate RNA virosphere. Nature **540:**539-543 |

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| **Annex:**  The new genus *Alphanemrhavirus* is proposed to accommodate two currently unassigned rhabdoviruses that have been detected in nematodes (1). Each virus will be assigned to a new species within the new genus.  ***Xingshan alphanemrhavirus*.** Xingshan nematode virus 4 (XsNV-4) was detected in a spirurian (subclass Spiruria) parasitic nematode in Xingshan, Hubei Province, People’s Republic of China, in 2014. Near-complete genome sequences including complete coding sequences and partial terminal sequences have been determined for XsNV-4 (1).  ***Xinzhou alphanemrhavirus*.** Xinzhou nematode virus 4(XzNV-4) and Xinzhou dimarhabdovirus 1 (XzDRV-1) were each detected in snake-associated nematodes collected in Xinzhou, Shanxi Province, People’s Republic of China, in 2014. Near-complete genome sequences including complete coding sequences and partial terminal sequences have been determined for XzNV-4 (1).  A third virus, Xinzhou dimarhabdovirus 1 (XzDRV-1), is a probable member of the genus but only a partial genome sequence is available, including complete *M*, *G* and *L* gene sequences (1). It is included here for comparative purposes but, as the coding sequence is incomplete, we do not propose formal classification at this time.  No isolates are available for any of these viruses and no other biological data are available.  The genomes range in size from approximately 11.5 kb to 11.7 kb, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 1**). The XzNV-4 genome contains an additional ORF (Mx) of 201 nt that overlaps the end of the *M* gene. It is not known if it is expressed.  Based on well-supported ML trees generated from complete L protein sequences, alphanemrhaviruses form a monophyletic clade that is distinct from all currently assigned genera and other currently unassigned rhabdoviruses (**Figure 2**). Nucleotide sequence identity (p-distance) between alphanemrhavirus genomes is relatively low (26.7% to 33.1%) (**Table 1**). Amino acid sequence identities are also relatively low (>30% in the N and G proteins and >50% in the L proteins) (**Tables 2-4**).  Four other rhabdoviruses have been detected in association with nematodes but they are phylogenetically very distant from the proposed alphanemrhaviruses, clustering with the plant rhabdoviruses (**Figure 2**). Taxonomic assignment of these other nematode viruses will be the subject of future proposals.  **Species demarcation criteria.**  Viruses assigned to different species within the genus *Alphanemrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organization 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 vertebrate hosts and or arthropod vectors.  All proposed members of the new genus meet demarcation criteria A, B, C, D and F.  **Derivation of the genus name.**  *Alphanemrhavirus* is derived from the alpha group of nematode rhabdoviruses. (Beta and gamma groups of nematode rhabdoviruses will be the subject of future proposals).  **Type species.**  *Xingshan alphanemrhavirus* is designated as the type species of the genus as the virus assigned to it (Xingshan nematode virus 4) is the genome sequence provides clearer indications of the locations of all transcription initiation sequences.    **Figure 1.** Alphanemrhavirus genome organisations. Arrows indicate the locations of long open reading frames (ORFs), each of which is located within a single transcriptional unit bounded by conserved transcription initiation and transcription termination/polyadenylation sequences. N, P, M, G and L represent ORFs encoding the canonical rhabdovirus structural protein genes. An additional ORF (shaded grey) in XzNV-4 overlaps the end of the M gene encodes a putative protein of unknown function.    **Figure 2.** The evolutionary history was inferred from a Clustal W alignment of complete L protein sequences of 126 rhabdoviruses currently assigned to species as well as the two proposed alphanemrhaviruses (Xingshan nematode virus 4 and Xinzhou nematode virus 4) and one possible member of the proposed genus (Xinzhou dimarhabdovirus 2). The data set also included three proposed caligrhaviruses (see separate proposal) and four other nematode rhabdoviruses that are currently unclassified. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 517 positions in the final dataset. The tree was inferred in MEGA by using the Maximum Likelihood method based on the Whelan And Goldman + Freq. model. The tree with the highest log likelihood (-58691.9794) is shown. 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 (1,000 iterations) are shown for each node. Asterisks (\*) indicate bootstrap support proportion >80%; the bootstrap proportions of other nodes are indicated. [Note that viruses currently assigned to the genus *Nucleorhabdovirus* are not monophyletic and so are shown together with viruses in the genus *Dichorhavirus*.]  **Table 1.** Percentage nucleotide sequence identities (p-distance) of a MUSCLE alignment of alphanemrhavirus genomes (excluding 3' and 5' terminal sequences).   |  |  |  | | --- | --- | --- | |  | XsNV-4 | XzNV-4 | | XsNV-4 |  |  | | XzNV-4 | 39.5 |  |   **Table 2.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of alphanemrhavirus N proteins.     |  |  |  | | --- | --- | --- | |  | XsNV-4 | XzNV-4 | | XsNV-4 |  |  | | XzNV-4 | 36.0 |  |   **Table 3.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of alphanemrhavirus G proteins.   |  |  |  |  | | --- | --- | --- | --- | |  | XsNV-4 | XzNV-4 | XzDRV-1 | | XsNV-4 |  |  |  | | XzNV-4 | 19.9 |  |  | | XzDRV-1 | 21.3 | 24.5 |  |   **Table 4.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of alphanemrhavirus L proteins.   |  |  |  |  | | --- | --- | --- | --- | |  | XsNV-4 | XzNV-4 | XzDRV-1 | | XsNV-4 |  |  |  | | XzNV-4 | 46.0 |  |  | | XzDRV-1 | 47.4 | 49.1 |  | |