This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| --- | --- | --- |
| **Code assigned:** | ***2018.002P*** | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)**Creation of *Kitaviridae*, a new RNA virus family** |
|  |
| **Author(s):** |
| M.J. Melzer (Chair), J. Freitas-Astúa, J.C.V. Rodrigues, A. Roy, G. Wei |
| **Corresponding author with e-mail address:** |
| M. J. Melzer, melzer@hawaii.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) | ***Blunervirus*, *Cilevirus*, and *Higrevirus* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
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| Date first submitted to ICTV: | June 5th, 2018 |
| Date of this revision (if different to above): | October 20th, 2018 |

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| **ICTV-EC comments and response of the proposer:** |
| Members of the *Kitaviridae* have an RNA genome and use cognate RNA-dependent RNA polymerases (RdRps) for replication. Thus, they should be assigned to the realm *Riboviria*. |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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|  |

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module: Kitaviridae\_2018-1** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

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| The plant virus genera *Blunervirus*, *Cilevirus*, and *Higrevirus* are unassigned taxa comprised of related positive sense RNA viruses with multipartite genomes. Here we propose to create a new virus family, *Kitaviridae*, and assign these three genera to this higher taxon. The proposed name *Kitaviridae* is derived from Kitajima, the family name of Dr Elliot Watanabe Kitajima, a prominent and highly productive virologist and electron microscopist responsible for the pioneering work associated with this proposed family. Dr Kitajima has humbly agreed to this proposed nomenclature.The proposed family *Kitaviridae* will encompass all currently known plant (+) ssRNA viruses possessing a bacilliform virion. Genetically, members of these genera are most closely related to members of the plant virus family *Virgaviridae*, however, significant differences exist. These differences include virion morphology, biological vector, and predominant *in planta* movement:

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| --- | --- | --- |
| **Characteristic** | ***Kitaviridae* (proposed)** | ***Virgaviridae*** |
| Virion morphology | bacilliform\*\* | rod |
| Biological vector | mites\* | fungi/nematodes |
| Predominant *in planta* movement | localized | systemic |

\* for the species for which transmission work has been conducted\*\* for the species for which transmission electron microscopy analyses have been performedRecent reports (and GenBank accessions) of unclassified invertebrate-infecting viruses identified primarily by high-throughput sequencing (HTS) studies also appear to be closely related to members of the proposed family. The virion of these viruses, if known, appears to be spherical (Vasilakis et al. 2012), distinguishing them from members of the proposed family *Kitaviridae*. The genus name "*Negevirus*" was initially proposed (Vasilakis et al. 2012); however, the discovery of additional members by HTS suggests these viruses fall into several distinct clades, for which the genus-level names "*Nelorpivirus*" and "*Sandewavirus*" have been proposed (Kallies et al. 2014, Nunes et al. 2017). None of these viruses are currently recognized by the ICTV; however, further examination on their taxonomic relationship with members of the proposed family *Kitaviridae* is warranted. This is particularly relevant due to the apparent inability of members of the proposed family *Kitaviridae*, in most of the cases, to systemically infect their plant hosts, leading to speculation that these may primarily be arthropod/invertebrate viruses capable of only limited spread in plant tissues (Roy et al. 2015).The genera demarcation criteria are related to the number of genomic (+) ssRNAs, virion size, structural features of genome organization and sequence similarity. Major distinguishing characteristics of the three current genera that would be included into the proposed family *Kitaviridae* are outlined in the table below.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genus** | **RNAs** | **3' Structure** | **Virion (nm)** | **Replication polyprotein** | **MP\*** |
| *Blunervirus* | 4 | stem-loop/non-tRNA | n/a | RNA1 and RNA2 | 3A |
| *Cilevirus* | 2 | poly-A | 50x120 | RNA1 | 30K |
| *Higrevirus* | 3 | poly-A | 30x50 | RNA1 | TGB |

\*MP = movement proteins are of 3A, 30K, or triple gene block (TGB) typesPhylogenetic analyses using the RNA-dependent RNA polymerase amino acid sequence and both Neighbor-Joining and Maximum Likelihood algorithms place members of the genera *Blunervirus*, *Cilevirus*, and *Higrevirus* in a clade adjacent to the family *Virgaviridae* (Figure 1 and data not shown). **Figure 1.** Phylogenetic relationship among members of the three genera proposed to establish the plant virus family *Kitaviridae*, select members of the seven genera which currently comprise its sister taxon, the family *Virgaviridae* and members of the families *Closteroviridae* and *Bromoviridae*. The phylogram was generated using RNA-dependent RNA polymerase sequences in a Neighbor-Joining algorithm. Branch support is displayed in percentage and was estimated using 1000 bootstrap replications. The scale represents the number of substitutions per site for the distance displayed. An identical tree topography was generated using a Maximum Likelihood algorithm. All alignments and phylogenetic estimations were performed in MEGA-X. |
| **References:** |
| Kallies, R., Kopp, A., Zirkel, F., Estrada, A., Gillespie, TR., Drosten, C., and Junglen, S. 2014. **Genetic characterization of Goutanap virus, a novel virus related to negeviruses, cileviruses and higreviruses.** Viruses 6: 4346-4357Nunes, MRT, and 22 others. 2017. Genetic characterization, molecular epidemiology, and phylogenetic relationships of insect-specific viruses in the taxon Negevirus. Virology 504:152-167.Roy, A., Hartung, JS., Schneider, WL., Shao, J., León, MG., Melzer, M. J., Otero-Colina, G., Beard, JJ., Bauchan, GR., Ochoa, R., and Brlansky, RH. 2015. Role bending: complex relationships between viruses, hosts and mite vectors related to citrus leprosis, an emerging disease. Phytopathology 105:1013-1025. Vasilakis, N, Forrester, NL, Palacios, G, Nasar, F, Savji, N, Rossi, SL, Guzman, H, Wood, TG, Popov, V, Gorchakov, R, Gonzalez, AV, Haddow, AD, Watts, DM, da Rosa, AP, Weaver, SC, Lipkin, WI, Tesh, RB. 2013. Negevirus: a proposed new taxon of insect specific viruses with wide geographic distribution. Journal of Virology 87:2475-2488. |
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