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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.023M*** | |  |
| **Short title:** Remove one species (*Rotavirus E*)from genus *Rotavirus,* family *Reoviridae* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Matthijnssens E, Johne R, Patton J, Bányai K | | [jelle.matthijnssens@kuleuven.be](mailto:jelle.matthijnssens@kuleuven.be); [Reimar.Johne@bfr.bund.de](mailto:Reimar.Johne@bfr.bund.de); [jtpatton@iu.edu](mailto:jtpatton@iu.edu); bkrota@hotmail.com | |
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| Jelle Matthijnssens; [jelle.matthijnssens@kuleuven.be](mailto:jelle.matthijnssens@kuleuven.be) | | | |
| **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:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 19, 2019 |
| Date of this revision (if different to above): | | |  |

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

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

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| --- |
| **Name of accompanying Excel module:** 2019.023M.A.v1.Rem1sp\_Rotavirus\_E.xlsx |

**Supporting material:**

Rotavirus species (often referred to as groups) were historically defined based on: 1) serological assays, primarily targeting the inner capsid protein VP6, 2) genome profiling, contrasting the migration patterns of genomic dsRNAs on polyacrylamide gels, and 3) fingerprinting analysis of terminal regions of genomic dsRNAs. These techniques were used in 1986 to define two novel rotavirus species, representing viruses isolated from a chicken and a pig (Rotavirus D and Rotavirus E, respectively) (1). In 2012, sequence-based species demarcation criteria, based on phylogenetic analyses and pairwise identify profiles of the VP6 encoding gene were introduced, resulting in a 53% amino acid cut-off value to distinguish rotaviruses assigned to different species (2).

Unfortunately, for the reported porcine RVE strain, no sequence data were ever produced and the original sample could not be retrieved despite several attempts (personal communication with Dr. Ulrich Desselberger). No other reports on RVE-like strains are known to the authors of this proposal. This issue has also been discussed during the 7th Rotavirus Classification Working Group (RCWG) meeting in October 2015 in Goa (minutes of this meeting: <https://rega.kuleuven.be/cev/viralmetagenomics/virus-classification/minutes-of-the-7th-rcwg-meeting>). The consensus was that due to the complete lack of sequence data or an isolate of this virus the species *Rotavirus E* should be removed from the official ICTV taxonomy.

| **References:** |
| --- |
| 1. Pedley S, Bridger JC, Chasey D, McCrae MA. Definition of two new groups of atypical rotaviruses. J Gen Virol. 1986 Jan;67 (Pt 1):131-7. 2. Matthijnssens J, Otto PH, Ciarlet M, Desselberger U, Van Ranst M, Johne R. VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. Arch Virol. 2012 Jun;157(6):1177-82. |