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:** | ***2019.009G*** | |  |
| **Short title:** (e.g. “Create six new species in the genus *Zetavirus”*)  Correction of an administrative error resulting in an incorrect taxonomy of the realm *Riboviria* | | | |
|  | | | |
| **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 | |
| Gorbalenya AE, Krupovic M, Siddell S, Varsani A, Kuhn JH. | | a.e.gorbalenya@lumc.nl; krupovic@pasteur.fr; stuart.siddell@bristol.ac.uk; Arvind.Varsani@asu.edu;  kuhnjens@niaid.nih.gov | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | |  | | | | |
| **Corresponding author** | | | |
| Stuart Siddell | | | |
| **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 Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | July 2019 |
| Date of this revision (if different to above): | | |  |

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

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

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

| **Text of proposal:** |
| --- |
| This correction rectifies the erronous inclusion of two viroid families, the *Asunviroidae* and the *Pospiviroidae*, and the genus *Deltavirus* in the realm *Riboviria*. This clerical error occurred as data from the original submission was transfered into a simplified format Excel spreadsheet, 2017.006G.U.v3. Riboviria prior to the 2018 EC meeting. At no time was the inclusion in the realm *Riboviria* of viroid families, or the viroid-like hepatitis delta virus, proposed or intended by the authors, or discussed by the EC or its subcommittees. Indeed the criteria for inclusion in the realm Ribovira, namely "**RNA viruses** that use cognate **RNA-dependent RNA polymerases** (RdRps) for replication", precludes the inclusion of viroids and HDV, which both use host cell enzymes to replicate their genomes. |

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

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| --- |
| **Name of accompanying Excel module:** 2019.009G.A.v1\_Riboviria\_corrections.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

| **References:** |
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