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:** | ***2019.004B*** | |  |
| **Short title:** Create one new genus (*Barbavirus*) including five new species in the family *Myoviridae* | | | |
|  | | | |
| **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 | |
| Nilsson E, Adriaenssens EM, Kropinski AM, Holmfeldt K | | [emelie.nilsson@lnu.se](mailto:emelie.nilsson@lnu.se); [Evelien.adriaenssens@quadram.ac.uk](mailto:Evelien.adriaenssens@quadram.ac.uk); [phage.canada@gmail.com](mailto:phage.canada@gmail.com); [karin.holmfeldt@lnu.se](mailto:karin.holmfeldt@lnu.se) | |
| **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]) | | **Linnaeus University, Sweden [EN, KH]**  **Quadram Institute Bioscience, UK [EMA]**  **University of Guelph, Canada [AMK]** | | | | |
| **Corresponding author** | | | |
| Karin Holmfeldt | | | |
| **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) | | **Bacterial and Archaeal Viruses Subcommittee**  **Caudovirales Study Group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | |  |
| Date of this revision (if different to above): | | |  |

|  |
| --- |
| **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:** |
| --- |
|  |

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

|  |
| --- |
| **Name of accompanying Excel module:** 2019.004B.A.v1.Barbavirus.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.  **Species demarcation criteria:** To define the species within this genus, we have used 95% DNA sequence identity, i.e. species differ with more than 5% nucleotide identity according to BLASTn comparison made with Gegenees [1] (Table 1). They are also placed as separate species according to VICTOR [2] (Figure 1). The five species consist of a total of 54 isolates that have been submitted to NCBI GenBank and each species is named after the type-phage. The phage isolates are named Rheinheimera phage vB\_RspM-Barba followed by numbers indicating the order of isolation and A or S, representing the time of sampling (August or September). The species are described in the submitted paper “Genomic and seasonal variations among aquatic phages infecting the Baltic Sea Gammaproteobacteria *Rheinheimera* sp. BAL341” [3]. All isolates and which species they belong to are discussed in the paper, but also seen in Table 2.  **Higher taxa:** The new proposed genus form a separate and distinct cluster from relevant reference genomes (chosen since they shared some gene similarity based on blastp searches to NCBI nr) according to the FastME tree produced by VICTOR [2] (figure 1). The genus is placed within *Myoviridae* since the type phage showed myovirus-morphology (figure 2). The name for the novel genus is proposed to be Barbavirus, this is based on the host of the isolates – Baltic Sea *Rheinheimera* sp. BAL341. The type species for the genus is *Rheinheimera virus Barba18A* since most isolates belonged to this species.  **Supporting evidence**:  Table 1. The five proposed species compared to the type virus of the proposed genus (Barba18A). Average nucleotide identity (nt. id.) is determined with BLASTN comparisons through Gegenees [1] and shared proteins has been calculated with roary [4] with a similarity cut-off of 70%.   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Species name | GenBank number | Size (kb) | % GC | Proteins | % average nt. id. | % shared proteins | | Rheinheimera virus Barba18A | MK719729 | 80.34 | 38.2 | 136 | - | - | | Rheinheimera virus Barba21A | MK719733 | 80.36 | 38.3 | 140 | 94.5 | 95.0 | | Rheinheimera virus Barba5S | MK719710 | 82.74 | 38.2 | 145 | 93.2 | 91.7 | | Rheinheimera virus Barba8S | MK719714 | 82.00 | 38.3 | 141 | 92.8 | 92.2 | | Rheinheimera virus Barba19A | MK719730 | 84.61 | 38.2 | 143 | 74.0 | 73.4 |   Table 2. List of all the strains identified which belong to the genus *Barbavirus*. Their length, % GC content, predicted number of proteins as well as which species they belong to and which GenBank number has been assigned to them are listed.   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | Isolate | Length (bp) | % GC | Predicted proteins | Species | Genbank accession number | | Rheinheimera phage vB\_RspM-Barba10A | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719716 | | Rheinheimera phage vB\_RspM-Barba10S | 80469 | 38.2 | 138 | *Rheinheimera virus Barba18A* | MK719717 | | Rheinheimera phage vB\_RspM-Barba11S | 80353 | 38.2 | 138 | *Rheinheimera virus Barba18A* | MK719718 | | Rheinheimera phage vB\_RspM-Barba12A | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719719 | | Rheinheimera phage vB\_RspM-Barba12S | 80342 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719720 | | Rheinheimera phage vB\_RspM-Barba13A | 80342 | 38.2 | 137 | *Rheinheimera virus Barba18A* | MK719721 | | Rheinheimera phage vB\_RspM-Barba14A | 80332 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719722 | | Rheinheimera phage vB\_RspM-Barba14S | 80312 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719723 | | Rheinheimera phage vB\_RspM-Barba15S | 80303 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719725 | | Rheinheimera phage vB\_RspM-Barba16S | 80226 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719726 | | Rheinheimera phage vB\_RspM-Barba17A | 80342 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719727 | | Rheinheimera phage vB\_RspM-Barba17S | 81537 | 38.3 | 141 | *Rheinheimera virus Barba18A* | MK719728 | | Rheinheimera phage vB\_RspM-Barba1A | 80281 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719701 | | Rheinheimera phage vB\_RspM-Barba1S | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719702 | | Rheinheimera phage vB\_RspM-Barba20A | 80342 | 38.2 | 137 | *Rheinheimera virus Barba18A* | MK719731 | | Rheinheimera phage vB\_RspM-Barba20S | 81477 | 38.2 | 140 | *Rheinheimera virus Barba18A* | MK719732 | | Rheinheimera phage vB\_RspM-Barba21S | 80785 | 38.2 | 137 | *Rheinheimera virus Barba18A* | MK719734 | | Rheinheimera phage vB\_RspM-Barba22A | 80342 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719735 | | Rheinheimera phage vB\_RspM-Barba22S | 80342 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719736 | | Rheinheimera phage vB\_RspM-Barba23A | 83415 | 38.4 | 140 | *Rheinheimera virus Barba18A* | MK719737 | | Rheinheimera phage vB\_RspM-Barba23S | 80342 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719738 | | Rheinheimera phage vB\_RspM-Barba24S | 80340 | 38.2 | 134 | *Rheinheimera virus Barba18A* | MK719739 | | Rheinheimera phage vB\_RspM-Barba25A | 80284 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719740 | | Rheinheimera phage vB\_RspM-Barba25S | 80355 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719741 | | Rheinheimera phage vB\_RspM-Barba26A | 82164 | 38.4 | 140 | *Rheinheimera virus Barba18A* | MK719742 | | Rheinheimera phage vB\_RspM-Barba26S | 80342 | 38.2 | 134 | *Rheinheimera virus Barba18A* | MK719743 | | Rheinheimera phage vB\_RspM-Barba27S | 80341 | 38.2 | 134 | *Rheinheimera virus Barba18A* | MK719744 | | Rheinheimera phage vB\_RspM-Barba28A | 80270 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719745 | | Rheinheimera phage vB\_RspM-Barba28S | 81595 | 38.4 | 138 | *Rheinheimera virus Barba18A* | MK719746 | | Rheinheimera phage vB\_RspM-Barba29A | 80342 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719747 | | Rheinheimera phage vB\_RspM-Barba29S | 81390 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719748 | | Rheinheimera phage vB\_RspM-Barba2A | 80352 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719703 | | Rheinheimera phage vB\_RspM-Barba2S | 80341 | 38.2 | 135 | *Rheinheimera virus Barba18A* | MK719704 | | Rheinheimera phage vB\_RspM-Barba30A | 80237 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719749 | | Rheinheimera phage vB\_RspM-Barba32A | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719751 | | Rheinheimera phage vB\_RspM-Barba33A | 80336 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719752 | | Rheinheimera phage vB\_RspM-Barba34A | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719753 | | Rheinheimera phage vB\_RspM-Barba35A | 80206 | 38.1 | 136 | *Rheinheimera virus Barba18A* | MK719754 | | Rheinheimera phage vB\_RspM-Barba3A | 81004 | 38.2 | 139 | *Rheinheimera virus Barba18A* | MK719705 | | Rheinheimera phage vB\_RspM-Barba3S | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719706 | | Rheinheimera phage vB\_RspM-Barba4A | 80327 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719707 | | Rheinheimera phage vB\_RspM-Barba4S | 80400 | 38.2 | 137 | *Rheinheimera virus Barba18A* | MK719708 | | Rheinheimera phage vB\_RspM-Barba5A | 80236 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719709 | | Rheinheimera phage vB\_RspM-Barba6A | 80332 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719711 | | Rheinheimera phage vB\_RspM-Barba7A | 80341 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719712 | | Rheinheimera phage vB\_RspM-Barba8A | 80236 | 38.2 | 136 | *Rheinheimera virus Barba18A* | MK719713 | | Rheinheimera phage vB\_RspM-Barba9A | 80203 | 38.1 | 138 | *Rheinheimera virus Barba18A* | MK719715 | | Rheinheimera phage vB\_RspM-Barba15A | 82059 | 38.2 | 143 | *Rheinheimera virus Barba5S* | MK719724 | | Rheinheimera phage vB\_RspM-Barba31A | 84615 | 38.3 | 143 | *Rheinheimera virus Barba19A* | MK719750 |     Figure 1. Phylogenomic genome BLAST distance phylogeny (GBDP) tree created by FastME, as a part of VICTOR [2]. The numbers above branches are GBDP pseudo-bootstrap support values from 100 replications, and the branch lengths are scaled in terms of the D0 distance formula used, according to VICTOR. The proposed genus is marked in purple, and the different species are marked with green in case of more than one isolate or an asterisk in case of only one isolate present. The multi-strain species Barba18A is represented with two isolates.    Figure 2. TEM of Barba18A with myovirus morphology with a capsid that was measured to 72.1 nm (sd ±2.7 nm) and the tail length to 88.7 nm (sd ±2.2 nm) and width to 18.8 nm (sd ±1.5 nm). Scale bar 100 nm. |

| **References:** |
| --- |
| 1. Ågren J, Sundström A, Håfström T, Segerman B.2012. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One 7:e39107  2. Meier-Kolthoff JP, Göker M.2017. VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics 33:3396-3404.  3. Nilsson E, Li K, Fridlund J, Šulčius S, Bunse C, Karlsson CMG, Lindh M, Lundin D, Pinhassi J, Holmfeldt K. Submitted. Genomic and seasonal variations among aquatic phages infecting the Baltic Sea Gammaproteobacteria *Rheinheimera* sp. BAL341. Applied and Environmental Microbiology.  4. Page AJ, Cummins CA, Hunt M, Wong VK, Reuter S, Holden MT, Fookes M, Falush D, Keane JA, Parkhill J.2015. Roary: rapid large-scale prokaryote pan genome analysis. Bioinformatics 31:3691-3693. |