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**

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.105B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one new species,** ***Salmonella virus SP116*** **within the *Felixounavirus* genus(renamed from *Felixo1virus* in proposal 2018.007B), *Ounavirinae* subfamily, and *Myoviridae* family** | | | |
|  | | | |
| **Author(s):** | | | |
| Hongduo Bao, JiangsuAcademy of Agricultural Sciences, China  Khashayar Shahin, University of Isfahan, Iran; JiangsuAcademy of Agricultural Sciences, China  Hui Zhang, JiangsuAcademy of Agricultural Sciences, China  Yan Zhou, JiangsuAcademy of Agricultural Sciences, China  Maoda Pang, JiangsuAcademy of Agricultural Sciences, China  Lichang Sun, JiangsuAcademy of Agricultural Sciences, China  Stefan Schmidt, University of Kwazulu- Natal, South Africa  [Ademola](http://lifesciences.ukzn.ac.za/Schoolleadershipandstaff/AdemolaOlaniran.aspx) Olaniran, University of Kwazulu- Natal, South Africa  Ran Wang, JiangsuAcademy of Agricultural Sciences, China | | | |
| **Corresponding author with e-mail address:** | | | |
| Ran Wang, [**ranwang@jaas.ac.cn**](mailto:ranwang@jaas.ac.cn) | | | |
| **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** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 2018 |
| 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:** 2018.105B.N.v1.Felixo1virus\_sp |

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:**

| 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, try to provide a tree where branch length is related to genetic distance. |

**History:**

The lytic phage, vB\_SPuM\_SP116 , belongs to *Myoviridae* family, was isolated and characterized using *Salmonella enterica* subsp*. enterica* serovar Pullorumas its host. Phage SP116 had a lytic effect on different serotypes of *Salmonella* clinical strains. The dimensions of SP116 were 64.5± 6 nm for the head diameter and 116± 10 nm for the tail length (Fig. 1). It showed a high bactericidal activity, in which it killed all pathogens in cultures containing 5×105 cfu/mL. Moreover, there was a more than 6.58 and 5.97 log unit reduction in cultures containing 5×106 cfu/mL and 5×107 cfu/mL cell, respectively. This phage is the first sequenced *S*. Pullorum phage in GenBank. Complete genome sequence analysis revealed a linear, double-stranded DNA genome of 87,510 bp with an average G+C content of 38.84%. it includes 128 predicted open reading frames (ORFs) and 22 tRNA genes. There are no bacterial virulent genes and drug-resistant genes in the genome. Among 128 ORFs, only 32 (25%) were well characterized and the rest of ORFs (96, 75%) were considered as hypothetical proteins. SP116 could be considered as a new species in the genus *Felixounavirus* (renamed from *Felixo1virus* in TaxoProp 2018.007B). However, there is a 1763 bp sequence in the genome that is not present in the currently available genome sequence of other members of the group.

E:\phd thesis\shigella\full genome sequencing\bao\2\article\fig\Fig1.tif

Fig. 1. Electron micrographs vB\_SPuM\_SP116 phage stained negatively with 2 % phosphotungstic acid (PTA) [2 % (wt/vol)].

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (bp) | GC% | Total ORFs | Number of tRNA |
| vB\_SPuM\_SP116 | KP010413 | 87510 | 38.84% | 128 | 22 |

**Genome analysis:**

The relatedness of the phage to phages taxa was confirmed using BLASTn and BLASTp (1) and, its map was drawn (Fig. 2). Finally, the phylogenic tree of the isolated phage was constructed based on the amino acid sequences of two predicted proteins: Tail fiber (ORF 91) and DNA polymerase (ORF 113). The aforementioned amino acid sequences of phage SP116 and other phages belonged to different genus of *Myoviridae* were aligned by MEGA 7.0 software using MUSCLE function. Then, unweighted pair group method with arithmetic mean (UPGMA) phylogenetic trees were constructed with a 2000 bootstrap replications (2). Tail fiber and DNA polymerase of *Shigella sonnei* phage vB\_SsoS-ISF002 (MF093736.1) (3) and *Lactococcus garvieae* phage WP-2 (KJ528544.1) (4) were used as out-groups.

We have chosen ≥95% DNA sequence identity as the criterion for demarcation of species in this genus (5). The proposed species differ from those of other species by at least 5% at the DNA level as confirmed with the BLASTN algorithm. According to Phylogenic tree (Fig. 3) and BLASTn analysis, phage SP116 can be classified as a new species in theFelix O1 virus genus.

Therefore, we propose a new species, *Salmonella virus SP116*, within the *Felixounavirus* genus (renamed from *Felixo1virus* in 2018.007B), *Ounavirinae* subfamily, and *Myoviridae* family.

E:\phd thesis\shigella\full genome sequencing\bao\2\article\fig\Fig5.tif

Fig. 2. Schematic representation of the linear dsDNA genome of phage vB\_SPuM\_SP116. A. Positions and predicted function of ORFs, B. Positions of tRNA. Each ORFs or tRNA are represented by an arrow with predicted functions.

E:\phd thesis\shigella\full genome sequencing\bao\2\article\fig\Fig6.tif

Fig. 3. Phylogenetic relationship of vB\_SPuM\_SP116. Phylogenetic trees were constructed based on amino acid sequences of the tail fiber (A) and the DNA polymerase (B). The *Shigella* phage vB\_SsoS-ISF002 (A) and *Lactococcus garvieae* phage WP-2 tail fiber (B) were used as out-groups. The numbers on the lines shows the supporting rates. The GenBank accession numbers are presented in parentheses.

| **References:** |
| --- |
| 1. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. Journal of molecular biology. 1990;215(3):403-410.  2. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular biology and evolution. 2016;33(7):1870-1874.  3. Shahin K, Bouzari M, Wang R. Isolation, characterization and genomic analysis of a novel lytic bacteriophage vB\_SsoS-ISF002 infecting *Shigella sonnei* and *Shigella flexneri*. Journal of Medical Microbiology. 2018  4. Ghasemi SM, Bouzari M, Yoon BH, Chang HI. Comparative genomic analysis of *Lactococcus garvieae* phage WP-2, a new member of *Picovirinae* subfamily of *Podoviridae*. Gene 2014;551:222–229.  5. Adriaenssens E, Brister JR. How to name and classify your phage: an informal guide. Viruses. 2017;9(4):70 |

.