This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.018B*** | | | | (to be completed by ICTV officers) |
| **Short title: To create one (1) new genus, *Sp58virus*, including three (3) new species in the family *Podoviridae*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Johannes Wittmann - Leibniz Institute DSMZ (Germany)  Andrea I. Moreno Switt, Universidad Andrés Bello, (Chile)  Andrew M. Kropinski – University of Guelph (Canada)  Jens H. Kuhn - National Institute of Allergy and Infectious Diseases (USA)  Evelien M. Adriaenssens – University of Liverpool (UK) | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Johannes Wittmann, jow12@dsmz.de | | | | | |
| **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 Bacterial and Archaeal Viruses Subcommittee | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.018B.N.v1.Sp58virus** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| 1. Wittmann J, Klumpp J, Moreno Switt AI, Yagubi A, Ackermann HW, Wiedmann M, Svircev A, Nash JH, Kropinski AM (2015) Taxonomic reassessment of N4-like viruses using comparative genomics and proteomics suggests a new subfamily—’’Enquar-tavirinae’’. Arch Virol. 160(12):3053–3062.  2. Andrea I. Moreno Switt, Henk C. den Bakker, Kitiya Vongkamjan, Karin Hoelzer, Lorin D. Warnick, Kevin J. Cummings, and Martin Wiedmann. *Salmonella* bacteriophage diversity reflects host diversity on dairy farms. Food Microbiology, 2013, 36: 275–285  3. Andrea I. Moreno Switt, Renato H. Orsi, Henk C. den Bakker, Kitiya Vongkamjan, Craig Altier, and Martin Wiedmann. Genomic characterization provides new insight into *Salmonella* phage diversity. BMC Genomics, 2013, 14:481 4. [Patel](https://www.ncbi.nlm.nih.gov/pubmed/?term=Patel%20RS%5BAuthor%5D&cauthor=true&cauthor_uid=25635029), RS, [Lessor](https://www.ncbi.nlm.nih.gov/pubmed/?term=Lessor%20LE%5BAuthor%5D&cauthor=true&cauthor_uid=25635029), LE, [Hernandez](https://www.ncbi.nlm.nih.gov/pubmed/?term=Hernandez%20AC%5BAuthor%5D&cauthor=true&cauthor_uid=25635029), AC and [Kuty Everett](https://www.ncbi.nlm.nih.gov/pubmed/?term=Kuty%20Everett%20GF%5BAuthor%5D&cauthor=true&cauthor_uid=25635029), GF. Complete Genome Sequence of Enterotoxigenic *Escherichia coli* N4-Like Podophage Pollock. Genome Announc., 2015, Jan-Feb; 3(1): e01431-14. 5. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. [MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.](http://www.ncbi.nlm.nih.gov/pubmed/21546353) Mol Biol Evol. 2011; 28(10):2731-9.  6. Sullivan MJ, Petty NK, Beatson SA (2011) Easyﬁg: a genome comparison visualizer. Bioinformatics 27:1009–1010 |

**Species demarcation:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of the proposed species differ from each other by less than 5% at the DNA level as confirmed with the BLASTN algorithm [1].

**Genus demarcation:** BLASTN (Table 1) and phylogenetic analyses (Fig. 1) indicate that the proposed genus, *Sp58virus*, is cohesive and distinct from other genera. On average, the genomes of members of this genus are 70.9 kb in length (38.4 mol% G+C) and encode approximately 85 proteins and 4–9 tRNAs.

Salmonella phages FSL SP-058 and FSL SP-076 were isolated from Moreno Switt *et al*. [2] from the environment of two different dairy farms in Central New York, USA, in the year 2008. Both phages infected up to six different *Salmonella* serovars. Salmonella phages FSL SP-058 and FSL SP-076 were sequenced [3]. Both phages belong to the *Podoviridae* and produce particles with an icosahedral head and short tail (Fig. 2). The genome lengths of Salmonella phages SP-058 and SP-076 are 72394 bp and 72098 bp, respectively. Bioinformatic analysis resulted in 87 and 83 putative open reading frames for Salmonella phages FSL SP-058 and FSL SP-076, respectively (Fig. 3).

Escherichia phage Pollock was isolated from sewage collected in College Station, TX [4]. Its genome length is 68365 bp, including 84 predicted coding sequences, a G+C content of 36%, and a coding density of 93%.

The type species *Salmonella virus FSL SP-058* was chosen because it represents the first sequenced member of this genus and the name of the new genus was based on that.

**Table 1**. Properties of the phages belonging to the genus *Sp58virus*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage Name | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* |
| Salmonella phage FSL SP-058 | KC139517 | 72.4 | 39.6 | 87 | 9 | 100 |
| Salmonella phage FSL SP-076 | KC139520 | 72.1 | 39.5 | 83 | 9 | 88.2 |
| Escherichia phage Pollock | KM236242 | 68.4 | 36.0 | 84 | 4 | 59.7 |

\* Determined using BLASTN

**Fig. 1.** Phylogenetic analysis of (A) large subunit terminase proteins, (B) major capsid proteins; and, (C) virion RNA polymerases. Proteins were aligned and the phylogenetic tree was constructed using MEGA5 [5]. The members of the *Sp58virus* genus are boxed in red.

**A. Large terminase subunits**

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**B. Major capsid proteins**

****

**C. virion RNA polymerases**



**Fig 2.** Electron micrographs of Salmonella phage FSL SP-058 particles.

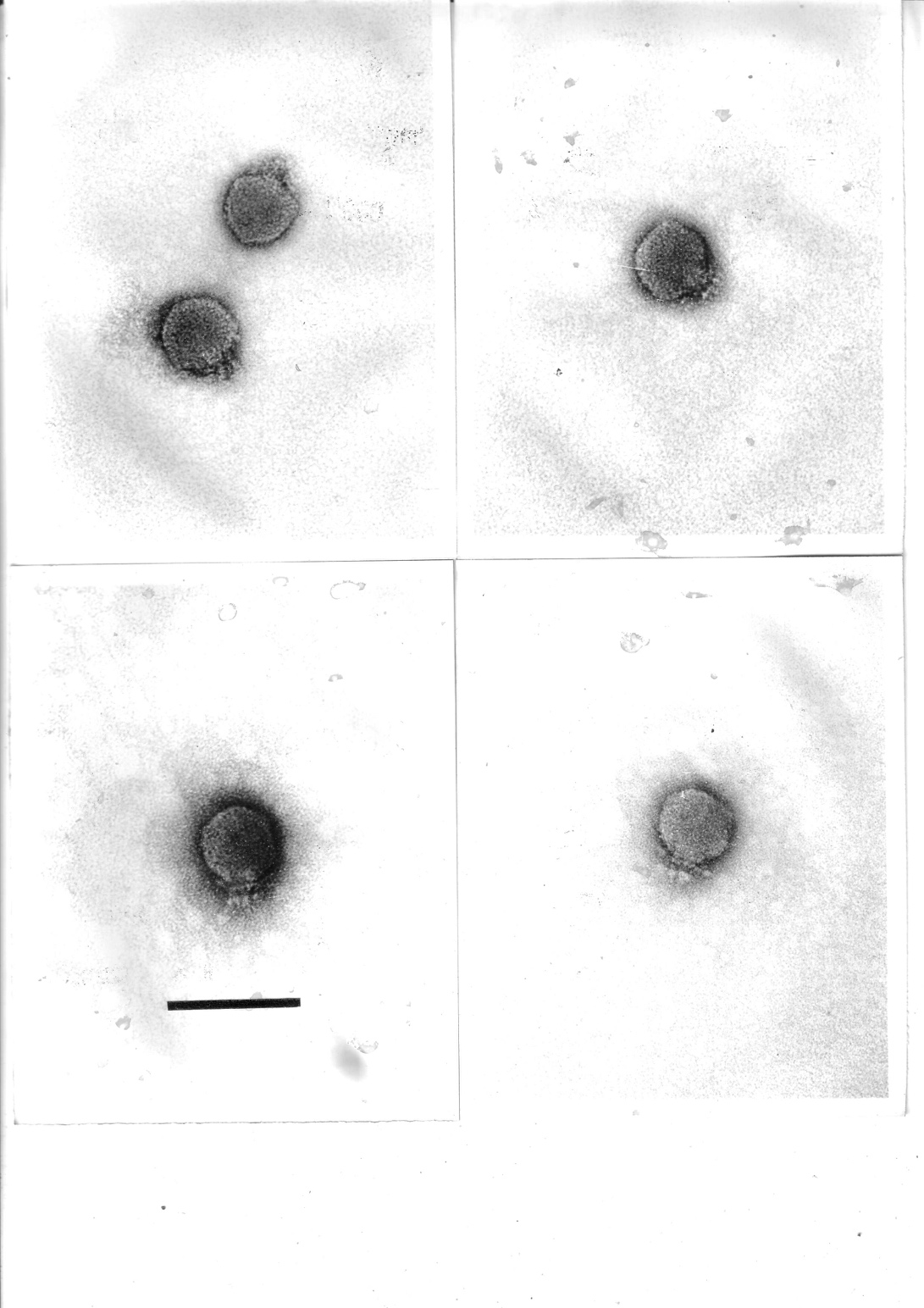


Fig 3. Synteny plot of the three species visualized with EasyFig [6]. The scale bar shows the level of nucleotide identity.

