

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

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| **Code assigned:** | **2020.058B** |  |
| **Short title:** Create six new genera including five new speciesin the genus *Muminvirus,* six new species in the genus *Lillamyvirus*, one new species in the genus *Hattifnattvirus*,two new species in the genus *Pippivirus,* one new species in the genus *Tantvirus* one new species in the genus *Labanvirus* (*Caudovirales*) | | |
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**Author(s) and email address(es)**

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| --- | --- |
|  |  |
| Nilsson E, Holmfeldt K | emelie.nilsson@lnu.se; karin.holmfeldt@lnu.se |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Linnaeus University, Kalmar, Sweden |

**Corresponding author**

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| --- |
| Karin Holmfeldt |

**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial and archaeal viruses subcommittee |

**ICTV study group comments and response of proposer**

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| * You used an old version of the template, copy over the submission to the new.   + We have not moved the data to the new templates. * Can you please add the accession numbers of the genomes to the Excel part of the submission.   + We have added these. * In the Excel file, per genus there should be only one type species (designated with a “1” in the column “Type species”. The drop down menu further on should be changed accordingly, i.e. use “create new, assign type species” only once per genus, for the other new species select “create new”.   + This has been corrected. * Double-check that all members of the same genus share at least 60% preferably 70% DNA identity.   + We went through our Gegenees results and decided to split the large “mumin”-genus into three smaller since our previous suggestion did lump together phages with as little as 57% similarity. Now the members of each genus share at least 72% nucleotide identity to the type phage. |

**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | January 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.058B.R.Flavobacterium\_phages.xlsx |

**Abstract**

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| Based on whole genome sequencing and morphological analyses, we propose to group 39 newly isolated and characterized phages into six new genera within the order *Caudovirales.* The two largest genera (*Muminvirus* and *Lillamyvirus*) contain 5 and 6 species, respectively, that share at least 72% nucleotide identity to the type phage. The third genus (*Hattifnattvirus*) contains one species consisting of only one isolate, but it is less than 70% similar to the two first genera and therefore split into its own genus. The last three genera share no similarity with the three mentioned. The fourth genus (*Pippivirus*) contain two species that are more than 90% similar to each other, and the two last genera (*Tantvirus* and *Labanvirus*) contain one species each. |

**Text of proposal**

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| |  | | --- | | **Species:**  To define the species within these genera, 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 16 species consist of a total of 39 isolates that have been submitted to NCBI genbank and each species is named after the type-phage. The phage isolates are named Flavobacterium phage vB\_FspM/S followed by the name for the particular species and a number that indicate which *Flavobacterium* sp. strain (LMO**6**, LMO**8** or LMO**9**) that the isolate was isolated on and an arbitrary number (1-7) to differentiate between isolates of the same species isolated on the same host. The species are described in the paper “Diversity and host interactions among virulent and temperate Baltic Sea *Flavobacterium* phages” [3]. All isolates and which species they belong to are discussed in the paper, but also reported in table 2.  **Genus:**  The proposed genera contain species that share at least 70% nucleotide identity with their type phage and are distinct from references investigated. The genera are named after different characters from children books, and the species with most associated isolates is suggested as type species for each genus.  The new proposed genera *Muminvirus, Lillamyvirus, Hattifnattvirus* and *Pippivirus* form separate and distinct clusters from each other and 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 one representative of *Tantvirus*, tant8-1, clustered together with *Flavobacterium phage Fpv5* but was otherwise alone and separate from the other clusters (figure 1). Still, they do not share any nucleotide similarities and only 24-25% amino acid identity to each other (table 3), and we therefore do not propose to place this reference genome within *Tantvirus*. Similarly, the only representative of *Labanvirus,* laban6-1, did not cluster with the other phages discussed in this proposal, but it is placed within the same genus according to VICTOR as a potential prophage in *Flavobacterium psychrophilum* JIP02/86 and the potential temperate phages Flavobacterium phage 23T, Flavobacterium phage 6H, Flavobacterium phage 2A and Flavobacterium phage 1H. However, laban6-1 does not share any nucleotide similarity and only 20-23% amino acid identity to these references and we therefore propose to place laban6-1 in a genus of its own.  Based on how phages are taxonomically assigned as of now, we propose that *Muminvirus, Lillamyvirus, Hattifnattvirus, Tantvirus* and *Labanvirus* should be placed in *Siphoviridae* and *Pippivirus* should be placed in *Myoviridae* based on the morphology of the type phages (figure 2). The proposed names for the novel genera are based upon the type phages, Flavobacterium phage vB\_FspS\_mumin9-1, Flavobacterium phage vB\_FspS\_lillamy9-1, Flavobacterium phage vB\_FspS\_hattifnatt9-1, Flavobacterium phage vB\_FspS\_tant8-1, Flavobacterium phage vB\_FspS\_laban6-1 and Flavobacterium phage vB\_FspM\_pippi8-1. | |

**Supporting evidence**

Table 1. The sixteen proposed species divided in boxes for the genus, compared to each other and the type phage (in bold) of the respective genus (mumin9-12, hattifnatt9-1, lillamy9-1, tant8-1, pippi8-1, laban6-1). 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% amino acid identity.

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|  | genomes | **mumin9-1** | mymlan6-1 | tooticki6-1 | filifjonk9-1 | snusmum6-1 | **hattifnatt9-1** | **lillamy9-1** | morran9-1 | hemulen6-1 | stinky9-1 | sniff9-1 | snork6-1 | **tant8-1** | **pippi8-1** | lotta8-1 | **laban6-1** | prot.1 | %shared prot.2 | | |
|  | **mumin9-1** | **100** | **93.1** | **81.9** | **77.3** | **75.6** | **62.8** | 60.9 | 58.3 | 64.9 | 59.3 | 67.2 | 66.5 | 0 | 0 | 0 | 0 | **67** | **100** |  |
|  | mymlan6-1 | 92.8 | 100 | 78.0 | 71.9 | 78.9 | 60.7 | 64.0 | 61.4 | 67.4 | 62.3 | 65.1 | 69.7 | 0 | 0 | 0 | 0 | 68 | 94.1 |  |
|  | tooticki6-1 | 85.0 | 81.1 | 100 | 87.7 | 64.2 | 70.5 | 71.8 | 67.2 | 78.3 | 71.7 | 78.5 | 78.2 | 0 | 0 | 0 | 0 | 65 | 86.2 |  |
|  | filifjonk9-1 | 79.1 | 73.3 | 85.5 | 100 | 61.7 | 67.6 | 77.5 | 72.0 | 72.5 | 70.8 | 78.7 | 74.3 | 0 | 0 | 0 | 0 | 68 | 75 |  |
|  | snusmum6-1 | 72.9 | 75.7 | 59.7 | 58.3 | 100 | 72.9 | 60.0 | 57.3 | 58.2 | 57.7 | 58.7 | 59.9 | 0 | 0 | 0 | 0 | 72 | 62.5 |  |
|  | **hattifnatt9-1** | 61.2 | 58.7 | 66.3 | 64.8 | 73.3 | **100** | 64.4 | 59.9 | 60.8 | 60.3 | 68.2 | 64.2 | 0 | 0 | 0 | 0 | **76** | **100** |  |
|  | **lillamy9-1** | 61.0 | 63.9 | 69.4 | 76.7 | 61.8 | 65.2 | **100** | **93.3** | **78.8** | **79.0** | **87.4** | **87.9** | 0 | 0 | 0 | 0 | **73** | **100** |  |
|  | morran9-1 | 58.5 | 61.3 | 64.8 | 71.3 | 58.8 | 60.3 | 93.1 | 100 | 77.1 | 77.1 | 82.6 | 82.8 | 0 | 0 | 0 | 0 | 73 | 87.7 |  |
|  | hemulen6-1 | 64.4 | 66.7 | 73.7 | 71.0 | 58.5 | 60.6 | 76.7 | 75.2 | 100 | 88.9 | 81.5 | 86.4 | 0 | 0 | 0 | 0 | 70 | 74.3 |  |
|  | stinky9-1 | 59.4 | 62.3 | 69.1 | 70.2 | 59.4 | 60.9 | 78.3 | 76.9 | 89.6 | 100 | 79.4 | 80.9 | 0 | 0 | 0 | 0 | 69 | 75.4 |  |
|  | sniff9-1 | 67.6 | 65.2 | 75.8 | 77.9 | 60.6 | 69.6 | 87.4 | 83.0 | 83.2 | 80.3 | 100 | 93.7 | 0 | 0 | 0 | 0 | 74 | 81.1 |  |
|  | snork6-1 | 66.3 | 69.1 | 75.0 | 72.8 | 61.5 | 65.3 | 87.2 | 83.0 | 87.9 | 81.2 | 93.2 | 100 | 0 | 0 | 0 | 0 | 73 | 80.8 |  |
|  | **tant8-1** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **100** | 0 | 0 | 0 | **62** | **100** |  |
|  | **pippi8-1** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **100** | **94.3** | 0 | **53** | **100** |  |
|  | lotta8-1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 93.5 | 100 | 0 | 53 | 90.6 |  |
|  | **laban6-1** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **100** | **57** | **100** |  |
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1Number of predicted proteins in each proposed species.

2The proportion of predicted genes in each species that are shared with the type phage for the genus that species belongs to.

Table 2. All isolates that belong to the sixteen proposed species within the six proposed genera, *Pippivirus, Tantvirus, Muminvirus, Hattifnattvirus, Lillamyvirus* and *Labanvirus*. Their length, predicted number of proteins, GC-content, as well as which species and genera they belong to and which genbank number that has been assigned to them.

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| --- | --- | --- | --- | --- | --- | --- |
| Isolate | Species | Genus | Length (bp) | Predicted proteins | % GC | Genbank accession number |
| **vB\_FspM\_pippi8-1** | ***Flavobacterium virus Pippi*** | ***Pippivirus*** | **34711** | **53** | **37.6** | **MN812205** |
| **vB\_FspM\_lotta8-1** | ***Flavobacterium virus Lotta*** | *Pippivirus* | 34751 | 53 | 37.6 | MN812203 |
| vB\_FspM\_lotta8-2 | *Flavobacterium virus Lotta* | *Pippivirus* | 34627 | 53 | 37.8 | MN812204 |
| **vB\_FspS\_tant8-1** | ***Flavobacterium virus Tant*** | ***Tantvirus*** | **40542** | **62** | **34.4** | **MN812239** |
| **vB\_FspS\_morran9-1** | ***Flavobacterium virus Morran*** | *Lillamyvirus* | 38385 | 73 | 29.5 | MN812219 |
| **vB\_FspS\_hemulen6-1** | ***Flavobacterium virus Hemulen*** | *Lillamyvirus* | 39039 | 70 | 29.5 | MN812208 |
| vB\_FspS\_hemulen6-2 | *Flavobacterium virus Hemulen* | *Lillamyvirus* | 39030 | 70 | 29.7 | MN812209 |
| vB\_FspS\_hemulen9-1 | *Flavobacterium virus Hemulen* | *Lillamyvirus* | 38901 | 70 | 29.7 | MN812210 |
| **vB\_FspS\_tooticki6-1** | ***Flavobacterium virus Tooticki*** | *Muminvirus* | 36912 | 65 | 29.3 | MN812240 |
| vB\_FspS\_tooticki9-1 | *Flavobacterium virus Tooticki* | *Muminvirus* | 36912 | 65 | 29.5 | MN812241 |
| **vB\_FspS\_filifjonk9-1** | ***Flavobacterium virus Filifjonk*** | *Muminvirus* | 38028 | 68 | 29.8 | MN812206 |
| **vB\_FspS\_hattifnatt9-1** | ***Flavobacterium virus Hattifnatt*** | *Hattifnattvirus* | 39262 | 76 | 29.2 | MN812207 |
| **vB\_FspS\_lillamy9-1** | ***Flavobacterium virus Lillamy*** | *Lillamyvirus* | 38268 | 73 | 29.4 | MN812212 |
| vB\_FspS\_lillamy9-2 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 38268 | 73 | 29.6 | MN812213 |
| vB\_FspS\_lillamy9-3 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 38268 | 73 | 29.3 | MN812214 |
| vB\_FspS\_lillamy9-4 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 38268 | 73 | 29.6 | MN812215 |
| vB\_FspS\_lillamy9-5 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 38268 | 73 | 29.4 | MN812216 |
| vB\_FspS\_lillamy9-6 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 38007 | 71 | 29.7 | MN812217 |
| vB\_FspS\_lillamy9-7 | *Flavobacterium virus Lillamy* | *Lillamyvirus* | 37531 | 70 | 29.7 | MN812218 |
| **vB\_FspS\_sniff9-1** | ***Flavobacterium virus Sniff*** | *Lillamyvirus* | 38134 | 74 | 29.4 | MN812229 |
| vB\_FspS\_sniff9-2 | *Flavobacterium virus Sniff* | *Lillamyvirus* | 37907 | 73 | 29.6 | MN812230 |
| **vB\_FspS\_stinky9-1** | ***Flavobacterium virus Stinky*** | *Lillamyvirus* | 38502 | 69 | 29.4 | MN812238 |
| **vB\_FspS\_mymlan6-1** | ***Flavobacterium virus Mymlan*** | *Muminvirus* | 38501 | 68 | 29.2 | MN812227 |
| vB\_FspS\_mymlan6-2 | *Flavobacterium virus Mymlan* | *Muminvirus* | 38372 | 68 | 29.2 | MN812228 |
| **vB\_FspS\_snork6-1** | ***Flavobacterium virus Snork*** | *Lillamyvirus* | 38214 | 73 | 29.5 | MN812231 |
| vB\_FspS\_snork6-2 | *Flavobacterium virus Snork* | *Lillamyvirus* | 37732 | 71 | 29.7 | MN812232 |
| vB\_FspS\_snork9-1 | *Flavobacterium virus Snork* | *Lillamyvirus* | 38084 | 73 | 29.8 | MN812233 |
| **vB\_FspS\_snusmum6-1** | ***Flavobacterium virus Snusmum*** | *Muminvirus* | 39365 | 72 | 29.1 | MN812234 |
| vB\_FspS\_snusmum6-2 | *Flavobacterium virus Snusmum* | *Muminvirus* | 39365 | 73 | 29.2 | MN812235 |
| vB\_FspS\_snusmum6-3 | *Flavobacterium virus Snusmum* | *Muminvirus* | 39365 | 72 | 29.1 | MN812236 |
| vB\_FspS\_snusmum9-1 | *Flavobacterium virus Snusmum* | *Muminvirus* | 38743 | 71 | 29.2 | MN812237 |
| **vB\_FspS\_mumin9-1** | ***Flavobacterium virus Mumin*** | ***Muminvirus*** | **38527** | **67** | **29.2** | **MN812224** |
| vB\_FspS\_mumin9-2 | *Flavobacterium virus Mumin* | *Muminvirus* | 38527 | 67 | 29.4 | MN812225 |
| vB\_FspS\_mumin9-3 | *Flavobacterium virus Mumin* | *Muminvirus* | 38398 | 67 | 29.4 | MN812226 |
| vB\_FspS\_mumin6-1 | *Flavobacterium virus Mumin* | *Muminvirus* | 38527 | 67 | 29.4 | MN812220 |
| vB\_FspS\_mumin6-2 | *Flavobacterium virus Mumin* | *Muminvirus* | 38185 | 67 | 29.1 | MN812221 |
| vB\_FspS\_mumin6-3 | *Flavobacterium virus Mumin* | *Muminvirus* | 37682 | 66 | 29.4 | MN812222 |
| vB\_FspS\_mumin6-4 | *Flavobacterium virus Mumin* | *Muminvirus* | 37532 | 66 | 29.3 | MN812223 |
| **vB\_FspS\_laban6-1** | ***Flavobacterium virus Laban*** | ***Labanvirus*** | **43236** | **57** | **31.1** | **MN812211** |
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Table 3. Comparison (blastn and tblastx with gegenees [1]) of laban6-1 and tant8-1 against the reference genomes that they cluster with according to the VICTOR analysis (Fig 1). The values in each comparison is first based on nucleotide level and then on amino acid level, i.e. the number before the semicolon is % nucleotide identity, and the number after the semicolon is % amino acid identity.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genomes | Flavobacterium phage 1H | Flavobacterium phage 6H | Flavobacterium phage 23T | Flavobacterium phage 2A | Flavobacterium psychrophilum | laban6-1 | tant8-1 | Flavobacterium phage Fpv5 |
| Flavobacterium phage 1H | 100; 100 | 94.4; 93.9 | 87.0; 87.4 | 88.0; 89.8 | 73.7; 74.1 | 0; 21.6 | 0; 6.1 | 0; 6.3 |
| Flavobacterium phage 6H | 80.2; 79.7 | 100; 100 | 89.1; 87.4 | 86.4; 86.7 | 75.6; 75.8 | 0; 20.4 | 0; 6.1 | 0; 6.3 |
| Flavobacterium phage 23T | 81.2; 81.6 | 96.3; 94.7 | 100; 100 | 92.0; 92.0 | 77.7; 76.9 | 0; 20.2 | 0; 6.1 | 0; 6.3 |
| Flavobacterium phage 2A | 74.3; 76.7 | 85.1; 85.8 | 83.4; 84.0 | 100; 100 | 76.1; 78.0 | 0; 21.4 | 0; 6.1 | 0; 6.3 |
| Flavobacterium psychrophilum | 72.5; 73.7 | 85.4; 84.2 | 80.5; 81.2 | 88.5; 89.9 | 100; 100 | 0; 21.0 | 0; 6.1 | 0; 6.2 |
| laban6-1 | 0; 20.7 | 0; 21.7 | 0; 20.6 | 0; 22.9 | 0; 20.2 | 100; 100 | 0; 6.1 | 0; 6.2 |
| tant8-1 | 0; 6.0 | 0; 6.1 | 0; 6.0 | 0; 6.0 | 0; 6.0 | 0; 6.1 | 100; 100 | 0; 25.0 |
| Flavobacterium phage Fpv5 | 0; 6.1 | 0; 6.2 | 0; 6.2 | 0; 6.2 | 0; 6.1 | 0; 6.0 | 0; 24.2 | 100; 100 |



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 (only values above 50 are reported), and the branch lengths are scaled in terms of the D0 distance formula used, according to VICTOR. The proposed genus *Muminvirus* is in orange, *Hattifnattvirus* is in grey, *Lillamyvirus* is in dark blue, *Pippivirus* is in pink, *Tantvirus* is in green and *Labanvirus* is light blue.



Figure 2. Negatively stained transmission electron micrographs of a. tant8-1 (siphovirus morphology), b. pippi8-1 (myovirus morphology), c. mumin9-1 (siphovirus morphology), and d. laban6-1 (siphovirus morphology). Scale bars are 100 nm.

**References**

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