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**

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| **Code assigned:** | ***2019.091B*** |  |
| **Short title:** Create eight new genera including eight new species for *Faecalibacterium* phages  |
|  |
| **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 |
| De Paepe M, Petit M-A, Cornuault JK | Marianne.depaepe@inra.fr ;marie-agnes.petit@inra.fr ;jeffrey.cornuault.1@ulaval.ca |
| **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]) |
| Micalis Institute, INRA, AgroParisTech, Université Paris-Saclay, 78350, Jouy-en-Josas, France [DPM, PMA]Département de Biochimie, Microbiologie et de Bio-Informatique, Faculté des Sciences et de Génie, Département de biochimie, de microbiologie, et de bio-informatique, Faculté des sciences et de génie, Groupe de recherche en écologie buccale, Faculté de médecine dentaire, Université Laval, Québec City, QC, G1V 0A6, Canada [JC] |

 |
| **Corresponding author** |
| Jeffrey Cornuault |
| **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: |       |
| 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:** |
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|  |

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

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| **Name of accompanying Excel module:** 2019.091B.A.v1.Faecalibacterium\_phages\_8gen8sp.xlsx |

**Supporting material:**

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| In a recent work (1) we identified a set of 23 prophages in 15 sequenced strains of *F. prausnitzii*. None of the predicted prophage had significant similarity with a viral genome of the NCBI Refseq genome database on more than 5% of its genome (using BlastN), indicating they all correspond to new viruses. Taxonomic classification of these viruses requires creation of new viral clades. Pairwise comparison at the nucleotide level with predicted prophages allows the definition of 8 viral clades (Fig. 1). Using current taxonomic metrics whereby phages within a genus share at least 40% of their proteins (Table 1), and phages of the same species have more than 95% identity on the whole genome (2,3), we defined 8 new viral genera and 18 viral species. For one representative member of each new bacterial genus (corresponding to prophages Lagaffe, Mushu, Lugh, Toutatis, Taranis, Epona, Brigit and Oengus), we searched for direct or indirect proofs of activity. For Lagaffe and Mushu, virion production was measured and detected by quantitative PCR. We also obtained a picture of Mushu by transmission electronic microscopy. It should be noted that Lagaffe was found as a prophage in the genome of the bacteria *Blautia hansenii* (Table 2), a bacterium from a different bacterial family than *F. prausnitzii,* suggesting a wide host range for Lagaffe.For other phages, we obtained indirect evidence of activity. For Lugh, Toutatis, Taranis, Epona and Brigit we found spacers targeting these phages in *F. prausnitzii* CRISPR arrays. For Oengus, Mushu and Lagaffe, we found genetically related viral contigs assembled from metagomic reads of the viral fraction of human gut microbiota. Results are shown in Table 2. The genome of the corresponding phages have been deposited on the NCBI viral database.Based on these observations, we propose the creation of the eight new viral genera (in blue) and theirs corresponding type species (in red), 6 belonging to the *Myoviridae*, and 2 to the *Siphoviridae* according to presence or not of tail sheath protein in phage genomes, and Virfam classification (Fig 1 and Table 2). * *Caudovirales – Myoviridae – Mushuvirus –* Faecalibacterium virus Mushu
* *Caudovirales – Myoviridae – Lagaffevirus –* Faecalibacterium virus Lagaffe
* *Caudovirales – Myoviridae – Taranisvirus –* Faecalibacterium virus Taranis
* *Caudovirales – Myoviridae – Eponavirus–* Faecalibacterium virus Epona
* *Caudovirales – Myoviridae – Toutatisvirus –* Faecalibacterium virus Toutatis
* *Caudovirales – Myoviridae – Brigitvirus –* Faecalibacterium virus Brigit
* *Caudovirales – Siphoviridae – Lughvirus –* Faecalibacterium virus Lugh
* *Caudovirales – Siphoviridae – Oengusvirus –* Faecalibacterium virus Oengus

The name of each species come from the infected bacterial genera, plus either a Celtic god’s name (Taranis, Epona, Toutatis, Brigit, Lugh, Oengus), the Franquin’s character (Lagaffe) or a Disney ‘s character (Mushu, it’s a word game related to the fact that the phage belongs to the former *Saltoviridae* viral family, usually called Mu phages). New phage genera are named after the name of the type species. **Figure 1** : Whole genome dot plot of the 23 F. prausnitzii prophages and 7 homologous sequences retrieved from the nr/nt database define six clades and two singletons (Brigit and Oengus, last lanes). Braces group similar prophages, which correspond to the same phage species found in different bacterial genomes. Names beginning “VC” (underlined) correspond to metagenomic viral contigs, and names in italic correspond to prophages in non-*F. prausnitzii* bacterial species**Table 1**: Similarity matrices of phage proteins within each proposed genus. For each pair of phages, the percentage of shared proteins as well as their mean amino acid identity is indicated. For each proposed genus, the closest known phage was included in the analysis, and its host is indicated. Numbers in brackets indicate the number of ORF per genome, and most of the variability within a group is due to annotation errors. Numbers in bold indicate highly homologous prophages, which were considered to correspond to the same species.

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| **Proposed genus**  | **Classification (Virfam)** | **Bacterial hosts**  | **Proposed species**  | **Prophage** **name** | **Evidence of activity** |
| **CRISPR spacers \*** | **Viral contig** |
| ‘Lagaffevirus’ | MyoviridaeType 1, cluster 6 | *F. prausnitzii**B. hansenii*CM62/1 | ‘Faecalibacterium virus Lagaffe’  | Lagaffe |  | Yes |
| ‘FPmushuvirus’ | MyoviridaeType1, Cluster 8‘Saltoviridae’ | *F. prausnitzii* | ‘Faecalibacterium virus Mushu’ | Mushu |  | Yes |
| ‘FPlughvirus’ | SiphoviridaeType1, Cluster 1 | *F. prausnitzii* | ‘Faecalibacterium virus Lugh’ | Lugh | CNCM-4544 |  |
| ‘FPtaranisvirus’ | MyoviridaeType1, cluster 6 | *F. prausnitzii* | ‘Faecalibacterium virus Taranis’ | Taranis | CNCM-4541(2), L2/6 |  |
| ‘FPeponavirus’ | MyoviridaeType1, cluster 6 | *F. prausnitzii*  | ‘Faecalibacterium virus Epona’ | Epona | CNCM-4541, CNCM-4575 |  |
| ‘FPtoutatisvirus’ | MyoviridaeType1, cluster 6 | *F. prausnitzii* | ‘Faecalibacterium virus Toutatis’ | Toutatis | CNCM-4541 |  |
| ‘FPbrigitvirus’ | MyoviridaeType 1, cluster7 | *F. prausnitzii* | ‘Faecalibacterium virus Brigit’ | Brigit | CNCM-4541 |  |
| ‘FPoengusvirus’ | SiphoviridaeType1, cluster 2 | *F. prausnitzii*  | ‘Faecalibacterium virus Oengus’ | Oengus |  | Yes |

**Table 2**: Main characteristics of the eight proposed *F. prausnitzii* phage genera and species.  |

| **References:** |
| --- |
| 1. Cornuault JK, Petit M-A, Mariadassou M, Benevides L, Moncaut E, Langella P, et al. Phages infecting Faecalibacterium prausnitzii belong to novel viral genera that help to decipher intestinal viromes. Microbiome. 2018;6:65. doi: 10.1186/s40168-018-0452-1

(2)Lavigne R, Seto D, Mahadevan P, Ackermann HW, Kropinski AM. Unifying classical and molecular taxonomic classification: analysis of the Podoviridae using BLASTP-based tools. Res Microbiol. 2008;159(5):406–14.(3) Adriaenssens E, Brister JR. How to name and classify your phage: an informal guide. Viruses. 2017;9(4) |