| | | |
|---|---|---|
| **Code assigned:** | ***2011.001B*** | (to be completed by ICTV officers) |

**Short title: In the family *Fuselloviridae* create genus *Betafusellovirus* and change the name existing genus, *Fusellovirus*, to *Alphafusellovirus***

| | | | | | |
|---|---|---|---|---|---|
| **Modules attached** | **1** ☒ | **2** ☒ | **3** ☒ | **4** ☐ | **5** ☐ |
| | **6** ☐ | **7** ☐ | **8** ☒ | **9** ☒ | |

**Author(s) with e-mail address(es) of the proposer:**

Prangishvili D. (david.prangishvili@pasteur.fr)

**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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses) | |

**ICTV-EC or Study Group comments and response of the proposer:**

| | |
|---|---|
| Date first submitted to ICTV: | June 2010 |
| Date of this revision (if different to above): | June, 2012 |

## NEW SPECIES

| | |
|---|---|
| Code | ***2011.001aB*** |

**To create 6 new species within:**

| | |
|---|---|
| Genus: | ***Fusellovirus*** |
| Subfamily: | |
| Family: | ***Fuselloviridae*** |
| Order: | |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

| **And name the new species:** | **GenBank sequence accession number(s) of reference isolate:** |
|---|---|
| *Sulfolobus spindle-shaped virus 2* | [AY370762] |
| *Sulfolobus spindle-shaped virus 4* | [EU030938] |
| *Sulfolobus spindle-shaped virus 5* | [EU030939] |
| *Sulfolobus spindle-shaped virus 7* | [FJ870916] |
| *Sulfolobus spindle-shaped virus 8* | [AY388628] |
| *Sulfolobus spindle-shaped virus 9* | [AY423772] |

**Reasons to justify the creation and assignment of the new species:**

Each of the proposed species differs from the type species of the genus, *Sulfolobus spindle-shaped virus 1*, by the host range, size of the genome, its nucleotide sequence and content (see module 2011.001eB, below, and annex, Fig. 1, Fig. 2).

Species demarcation criteria in the genus *Fusellovirus*:

Sulfolobus spindle-shaped virus 1, Sulfolobus spindle-shaped virus 2, Sulfolobus spindle-shaped virus 4, Sulfolobus spindle-shaped virus 5, Sulfolobus spindle-shaped virus 7, Sulfolobus spindle-shaped virus 8, and Sulfolobus spindle-shaped virus 8, differ from each other by the host range, virion size, the length, nucleotide sequence and content of the genome (see module 2011.001eB, below, and annex, Fig. 1, Fig. 2).

## NEW SPECIES

| | |
|---|---|
| Code | ***2011.001bB*** |

**To create 2 new species within:**

| | |
|---|---|
| Genus: | ***Betafusellovirus*** (new) |
| Subfamily: | |
| Family: | ***Fuselloviridae*** |
| Order: | |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

| **And name the new species:** | **GenBank sequence accession number(s) of reference isolate:** |
|---|---|
| *Sulfolobus spindle-shaped virus 6*<br>*Acidianus spindle-shaped virus 1* | [FJ870915]<br>[FJ870917] |

**Reasons to justify the creation and assignment of the new species:**

-

The genus was created for classification of the *Sulfolobus spindle-shaped virus 6*, and *Acidianus spindle-shaped virus 1*. At present, there are no other members of the genus.

## NEW GENUS

| | | |
|---|---|---|
| Code | ***2011.001cB*** | (assigned by ICTV officers) |

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | |
| Family: | ***Fuselloviridae*** |
| Order: | |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

| | | |
|---|---|---|
| Code | ***2011.001dB*** | (assigned by ICTV officers) |

**To name the new genus: *Betafusellovirus***

Assigning the type species and other species to a new genus

| | | |
|---|---|---|
| Code | ***2011.001eB*** | (assigned by ICTV officers) |

**To designate the following as the type species of the new genus**

***Sulfolobus spindle-shaped virus 6***

**Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

**2 species**

**Reasons to justify the creation of a new genus:**

The known species of the family *Fuselloviridae* can be divided into two groups mainly differing in the shape of the virions, its attachment structures and genomic sequences. During discussions at EC43 in Sapporo it was decided to classify the two groups in different genera, and thus to introduce two genera, *Alphafusellovirus* and *Betafusellovirus* in the family *Fuselloviridae*. Virions of members of the genus *Alphafusellovirus,* although slightly pleomorphic, have obvious spindle-shaped morphology. Multiple thin tail fibers are attached to one of the pointed ends of the virion (annex, Fig. 1). The virions have a tendency to stick to each other with their fiber-carrying ends, to form “rosette”-like structures. Virion shapes, as well as attachment structures of members of the genus *Betafusellovirus* differ from those of the members of the *Alphafusellovirus* (annex, Fig. 1). They are pleomorphilic in shape, assuming shapes ranging from thin-cigar-like to pear-like, with tail fibers at the end corresponding to where the pear “stalk” would be. Moreover, instead of multiple thin fibers of the alphafuselloviruses, these virions carry 3 or 4 thicker and slightly curved fibers. They appear to be less sticky than their thin counterparts in the other genus and formation of the characteristic “rosette”-like structures was never observed. Despite pronounced morphological differences, the genomes of members of the two genera are closely related. The similarities are evident, both in terms of overall gene syntheny and sequence similarity (annex, Fig. 2), and 13 genes are conserved in all nine sequenced fiselloviruses. The most striking genomic difference between the genomes of the two genera of the *Fuselloviridae* is the “replacement” of the module SSV1-C792 highly conserved in all alphafuselloviruses with the SSV6_B1232 module, characteristic of the batafusellovirus genomes (annex, Fig. 2C). This observation suggests a pghenotype-genotype link, with the SSV1-C792 module being responsible for adsorption filament of the *Alphavirus* members and the SSV6_B1232 module responsible for their conterparts in the *Batafusellovirus*.

**Origin of the new genus name:**

Derived from the name of the family.

**Reasons to justify the choice of type species:**

*Sulfolobus spindle-shaped virus 6* is produced by the host strain in high amount, facilitating its further characterization. Another member of the genus, *Acidianus spindle-shaped virus 1*, is produced in very low amounts.

**Species demarcation criteria in the new genus:**

*Sulfolobus spindle-shaped virus 6,* and *Acidianus spindle-shaped virus 1* differ from each other by the host range, the length, nucleotide sequence, and content of the genome (see annex, Figures 1 and 2).

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

| | | |
|---|---|---|
| Code | ***2011.001fB*** | (assigned by ICTV officers) |
| **Title of proposal:** Change the name of the genus *Fusellovirus* to *Alphafusellovirus* | | |

**Text of proposal:**

| **Change the name of the genus *Fusellovirus* to *Alphafusellovirus*** |
|---|
| **Reasons to justify proposal:** |
| The proposed new name, *Alphafusellovirus*, complements that of the new genus *Betafusellovirus* |

**APPENDIX**: supporting material

**References**:

Fröls, S., Gordon, P.M., Panlilio, M.A., Schleper, C., and Sensen, C.W. (2007) Elucidating the transcription cycle of the UV-inducible hyperthermophilic archaeal virus SSV1 by DNA microarrays. *Virology*, 365, 48-59. Krupovic, M., White, M. F., Forterre, P., and Prangishvili, D. (2012). Postcards from the edge: structural genomics of archaeal viruses. *Adv.Virus Res.*, **82**, 33-62.

Muskhelishvili, .G, Palm, P., and Zillig, W. (1993) SSV1-encoded site-specific recombination system in *Sulfolobus shibatae. Mol. Gen. Genet.*, **237**,334-342.

Peng, X. (2008) Evidence for the horizontal transfer of an integrase gene from a fusellovirus to a pRN-like plasmid within a single strain of Sulfolobus and the implications for plasmid survival. *Microbiology*, **154**, 383–391.

Prangishvili, D., Garrett, R. A., and Koonin, E. V. (2006). Evolutionary genomics of archaeal viruses: unique viral genomes in the third domain of life. *Virus Res.*, 117, 52-67.

Redder, P., Peng, X., Brügger, K., Shah, S. A., Roesch, F., Greve, B., She, Q., Schleper, C., Forterre, P., Garrett, R. A. and Prangishvili, D. (2009)**.** Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible inter-viral recombination mechanism. *Environ. Microbiol.*, **11**, 2849–2862.

Schleper, C., Kubo, K., and Zillig. W. (1992) The particle SSV1 from the extremely thermophilic archaeon Sulfolobus is a virus: demonstration of infectivity and of transfection with viral DNA. *Proc Natl Acad Sci U S A*, **89**, 7645-7649.

Stedman, K.M., She, Q., Phan, H., Arnold, H.P., Holz, I., Garrett, R.A. and Zillig, W. (2003). Relationships between fuselloviruses infecting the extremely thermophilic archaeon *Sulfolobus*: SSV-1 and SSV-2. *Res. Microbiol*., **154**, 295-302.

Wiedenheft, B., Stedman, K;, Roberto, F., Willits, D., Gleske, A.-K., Zoeller, L., Snyder, J., Douglas, T. and Young, M. (2004) Comparative genomic analysis of hyperthermophiluic archaeal Fuselloviridae viruses. *J. Virol.*, **78**, 1954-1961.

Zillig, W., Prangishvili, D., Schleper, C., Elferink, M., Holz, I., Albers, S., Janekovic, D., and Götz, D. (1996) Viruses, plasmids and other genetic elements of thermophilic and hyperthermophilic Archaea. *FEMS Microbiol Rev.*, **18**, 225-36.

Zillig W, Arnold HP, Holz I, Prangishvili D, Schweier A, Stedman K, She Q, Phan H, Garrett R, Kristjansson JK. (1998) Genetic elements in the extremely thermophilic archaeon *Sulfolobus*.Extremophiles. 2:131-140.

**Annex:**

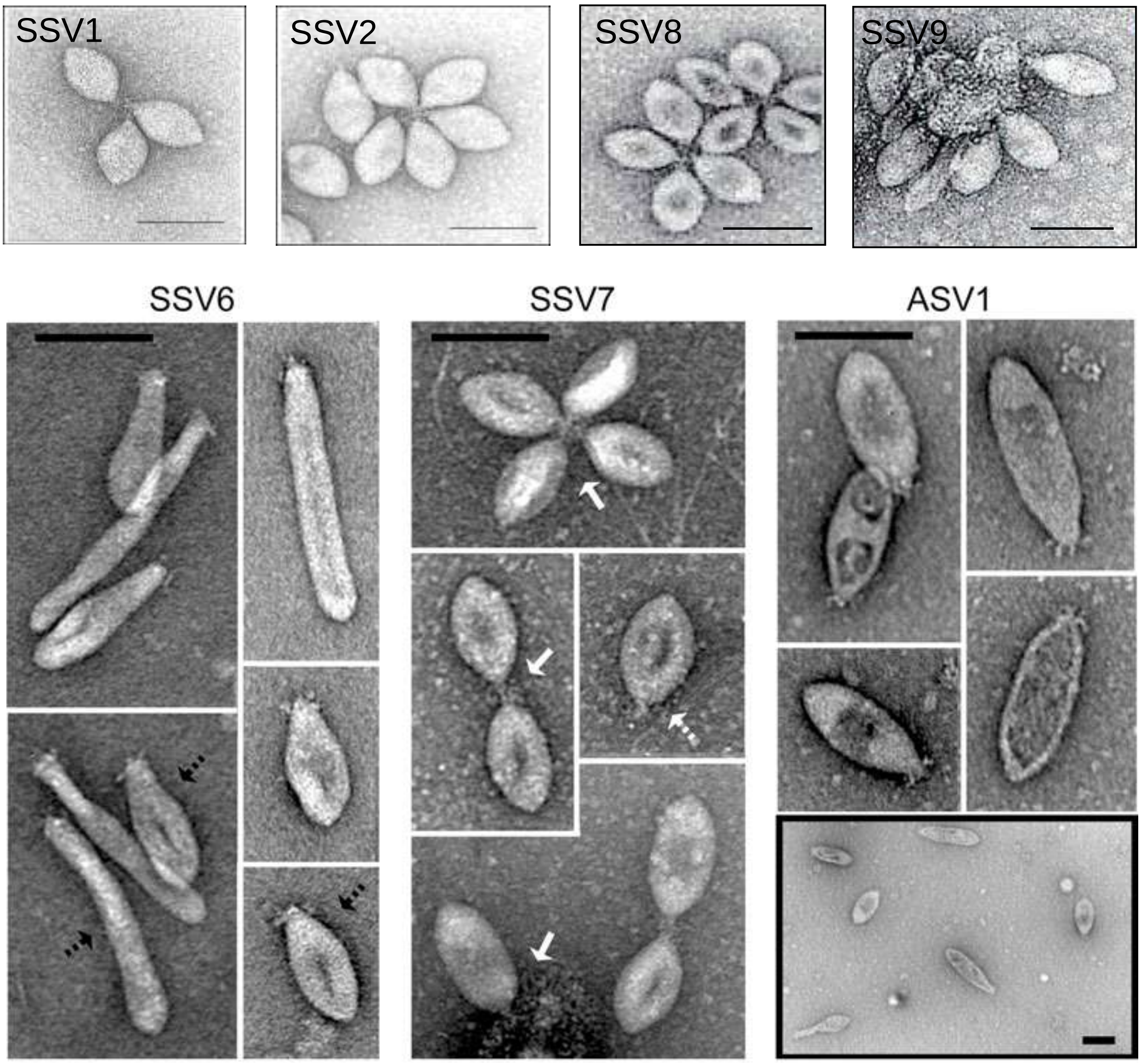

**Fig. 1.** Negative contrast electron micrographs of the species from the two proposed genera of the family *Fuselloviridae*. Members of the proposed genus *Alphafusellovirus* are: *Sulfolobus spindle-shaped virus 1* (SSV1), *Sulfolobus spindle-shaped virus 2* (SSV2), *Sulfolobus spindle-shaped virus 7* (SSV7), *Sulfolobus spindle-shaped virus 8* (SSV8), and *Sulfolobus spindle-shaped virus 9* (SSV9). Members of the proposed genus *Betafusellovirus* are: *Sulfolobus spindle-shaped virus 6* (SSV6), and *Acidianus spindle-shaped virus 1* (ASV1). The bars represent 100 nm.

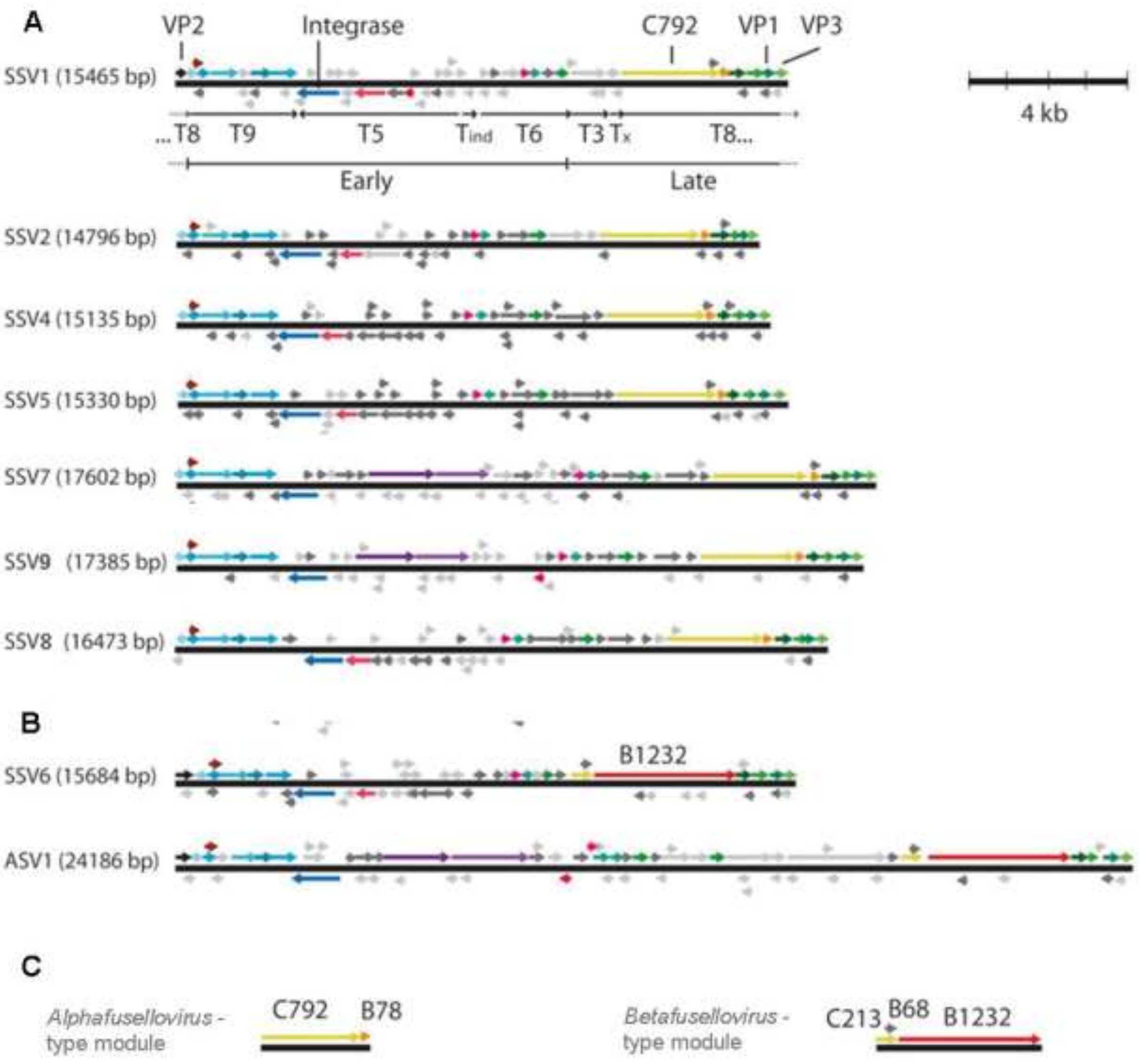

**Fig. 2.** Graphical alignment of the genomes of members of the family *Fuselloviridae*. (A) Members of the proposed genus *Alphafusellovirus*; (B) members of the proposed genus *Betafusellovirus*; (C) the two different putative end-filament modules. Arrows indicate ORFs. Black: 13 “core” genes of all members of the family. Dark grey: ORFs found in two or more fuselloviruses. Light grey: ORFs only found in one fusellovirus. Green: VP2. Yellow: SSV1_C792-homologs, both full length and partial. Red: SSV6_B1232-homologs. Orange: SSV1_B78-homologs. Purple: SSV1_D224-homologs associated with the Integrase operon in all but ASV1 and SSVk1. Dark blue, light blue: Rad3-like helicase and Msed_2283-homologs substituting for a large part of the Integrase operon in ASV1, SSV7 and SSVk1. Brown: SSV1_F93-homologs. Pink: Highly conserved SSV1_C84-homolog overlapping with some of the other “core” genes.