This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

## MODULE 1: TITLE, AUTHORS, etc

| | | |
|---|---|---|
| **Code assigned:** | ***2010.002a-gB*** | (to be completed by ICTV officers) |

**Short title:** create new family named Clavaviridae
(e.g. 6 new species in the genus *Zetavirus*)

| | | | | | |
|---|---|---|---|---|---|
| **Modules attached**<br>(modules 1 and 9 are required) | **1** ☒ | **2** ☒ | **3** ☒ | **4** ☐ | **5** ☒ |
| | **6** ☐ | **7** ☐ | **8** ☐ | **9** ☒ | |

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

Tomohiro Mochizuki, tomohiro.mochizuki@pasteur.fr
David Prangishvili, david.prangish@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):

## MODULE 2: NEW SPECIES

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

| | |
|---|---|
| Code | ***2010.002aB*** |

(assigned by ICTV officers)

**To create 1 new species within:**

| | |
|---|---|
| Genus: | ***Clavavirus* (new)** |
| Subfamily: | - |
| Family: | ***Clavaviridae* (new)** |
| 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: |
|---|---|
| ***Aeropyrum pernix bacilliform virus 1*** | AB537968 |

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

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

| | | |
|---|---|---|
| Code | ***2010.002bB*** | (assigned by ICTV officers) |

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | - |
| Family: | ***Clavaviridae*** |
| 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

naming a new genus

| | | |
|---|---|---|
| Code | ***2010.002cB*** | (assigned by ICTV officers) |

**To name the new genus: *Clavavirus***

Assigning the type species and other species to a new genus

| | | |
|---|---|---|
| Code | ***2010.002dB*** | (assigned by ICTV officers) |

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

***Aeropyrum pernix bacilliform virus 1***

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

***1***

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

Additional material in support of this proposal may be presented in the Appendix, Module 9

We propose classifying the *Aeropyrum bacilliform virus 1* (APBV1) infecting hyperthermophilic archaea as a first representative of a new genus because of the unique combination of exceptional morphological and genomic properties. The virion of APBV1 has rigid bacilliform morphology, about 140 x 20 nm, with one end pointed and the other rounded (Fig. 1). The genome comprises 5,278 bp, encompassing 14 ORFs, all localized on a single DNA strand, without any matches with sequences in the extent databases (Fig. 2).

The virion morphology is clearly distinct from that of any known archaeal or bacterial virus. It resembles plant viruses from the genera *Badnavirus* and *Tungrovirus* of the family *Caulimoviridae*. The members of this family replicate their genomes with a help of virus-encoded reverse transcriptase and RNAse H, resulting in the reproduction of the circular DNA molecule with a number of site-specific discontinuities, due to the fact that the priming sites are not ligated. An absence on the APBV1 genome of any recognizable gene for a reverse transcriptase, as well as lack of nicks in the circular dsDNA (as documented by the supercoiled state of viral DNA) indicates that DNA replication mechanism of the virus should be different from that of the caliumoviruses.

**Origin of the new genus name:**

From the Latin *clava*, for club, stick

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

The only species in the genus

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

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

N/A

MODULE 5: **NEW FAMILY**

creating and naming a new family

| | | |
|---|---|---|
| Code | ***2010.002eB*** | (assigned by ICTV officers) |
| **To create a new family containing the subfamilies and/or genera listed below within the Order:** unassigned<br>If there is no Order, write "**unassigned**" here.<br>If the Order has yet to be created (in Module 6) please write **"(new)"** after the proposed name. | | |

| | | |
|---|---|---|
| Code | ***2010.002fB*** | (assigned by ICTV officers) |
| **To name the new family:** ***Clavaviridae*** | | |

assigning subfamilies, genera and unassigned species to a new family

| | | |
|---|---|---|
| Code | | (assigned by ICTV officers) |
| **To assign the following subfamilies (if any) to the new family:**<br>You may list several subfamilies here. For each subfamily, please state whether it is new or existing.<br>• If the subfamily is new, it must be created in Module 4<br>• If the subfamily already exists, please complete Module 7 to 'REMOVE' it from its existing family | | |
| Code | ***2010.002gB*** | (assigned by ICTV officers) |
| **To assign the following genera to the new family:**<br>You may list several genera here. For each genus, please state whether it is new or existing.<br>• If the genus is new, it must be created in Module 3<br>• If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family | | |
| ***Clavavirus*** | | |
| The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):** | | |
| None | | |

| |
|---|
| **Reasons to justify the creation of the new family:**<br>Additional material in support of this proposal may be presented in the Appendix, Module 9 |
| |
| **Origin of the new family name:** |
| |

## MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

### References:

Mochizuki, T., T. Yoshida, R. Tanaka, P. Forterre, Y. Sako and D. Prangishvili (2010) Diversity of viruses of the hyperthermophilic archaeal genus *Aeropyrum* and isolation of the *Aeropyrum pernix* bacilliform virus 1, APBV1, the first representative of the family *Clavaviridae. Virology* **402**, 347-354.

### Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

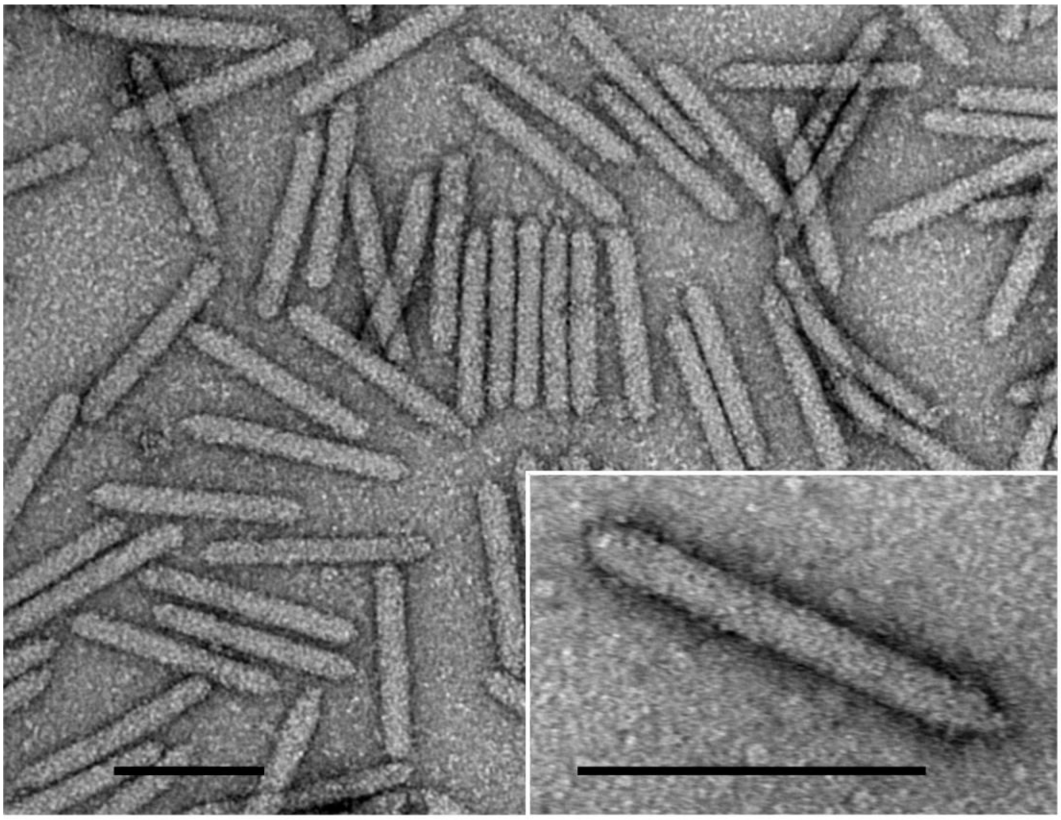

Fig. 1 Electron micrographs of APBV1 virions, negatively stained with 2% uranyl acetate. Scale bar, 100 nm.

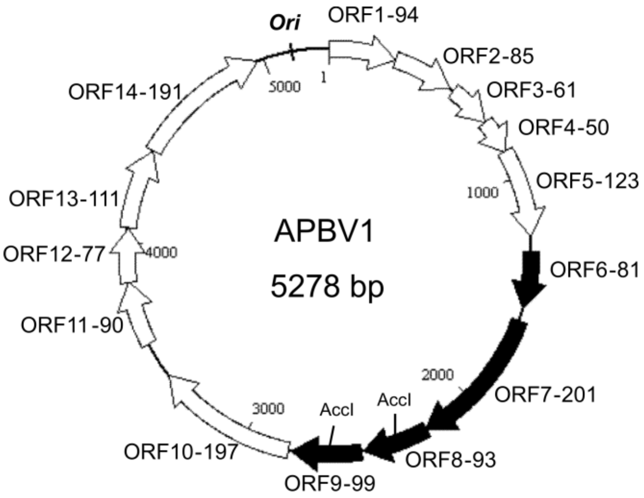

Fig. 2. Genome map of APBV1. Each ORF is designated with two numbers; the first number is the order starting from the first ORF after the putative ori, and the second reflects the number of amino acids in the encoded proteins. Black arrows indicate genes encoding virion proteins.