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:** | ***2017.002B*** | | | | (to be completed by ICTV officers) |
| **Short title:** (e.g. 6 new species in the genus *Zetavirus*) Create a new genus within a new family *Portogloboviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| David Prangishvili  Mart Krupovic | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| David Prangishvili [david.prangishvili@pasteur.fr](mailto:david.prangishvili@pasteur.fr)  Mart Krupovic [krupovic@pasteur.fr](mailto:krupovic@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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | [Bacterial and Archaeal Viruses Subcommittee](https://talk.ictvonline.org/information/w/members/441/bacterial-and-archaeal-viruses-subcommittee) | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | May, 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:** 2017.002B.N.v1.Portogloboviridae.xlsx |

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 3:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

|  |
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| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
|  |

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

| additional material in support of this proposal |
| --- |

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| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

The recently described *Sulfolobus* polyhedral virus 1 (SPV1) (Liu et al., 2017) infects hyperthermophilic archaea of the genus *Sulfolobus*. The virus condenses its circular double-stranded DNA genome in a manner not previously observed for other known viruses. The genome complexed with virion proteins is wound up sinusoidally into a spherical coil which is surrounded by an envelope and further encased by an outer icosahedral capsid (Figures 1 and 2). Lipids selectively acquired from the pool of host lipids are integral constituents of the virion (Figure 3). The SPV1 genome consists of 20,222 bp and encodes 45 open reading frames, only one fifth (nine ORFs, 20%) of which could be functionally annotated using a combination of BLASTP and HHpred analyses (Figure 4).

The virion contains four major proteins (VP1, VP2, VP3, and VP4) and five minor proteins (VP5, VP6, VP7, VP8, and VP9) (Figures 4 and 5). Virion dissociation experiments have revealed that VP4 is the constituent of the outer polyhedral shell. None of the major virion proteins of SPV1 show similarity to structural proteins of known viruses. However, minor structural proteins, which are predicted to mediate host recognition, are shared with other hyperthermophilic archaeal viruses infecting members of the order Sulfolobales.

**Proposed taxonomy**

Due to the unique genomic and architectural features of SPV1, we propose that the virus is assigned into a new species *Sulfolobus alphaportoglobovirus 1* within a new genus *Alphaportoglobovirus* in a new virus family, which we tentatively name *Portogloboviridae* (from Latin *porto*; to bear, carry, and *globus*; a ball).

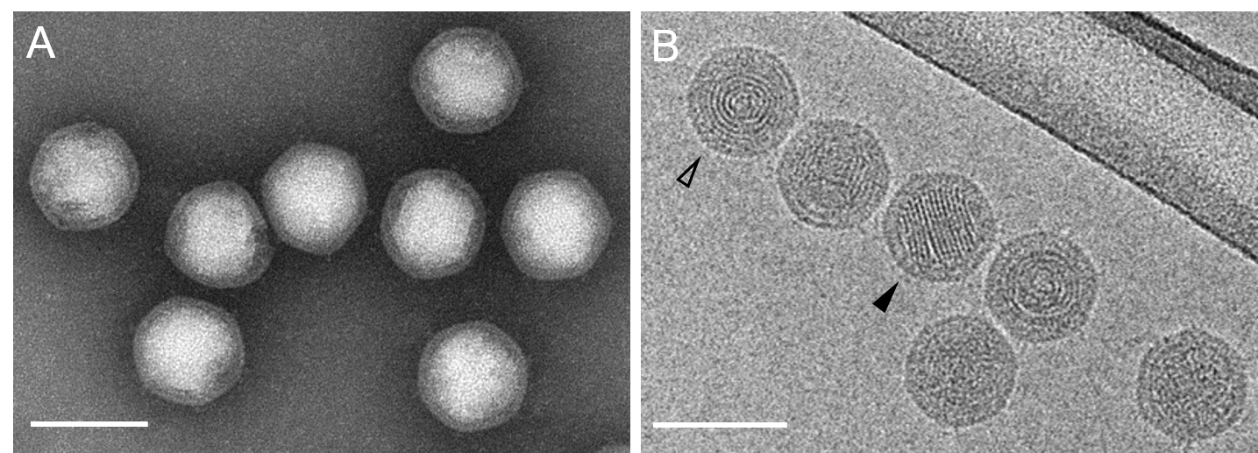
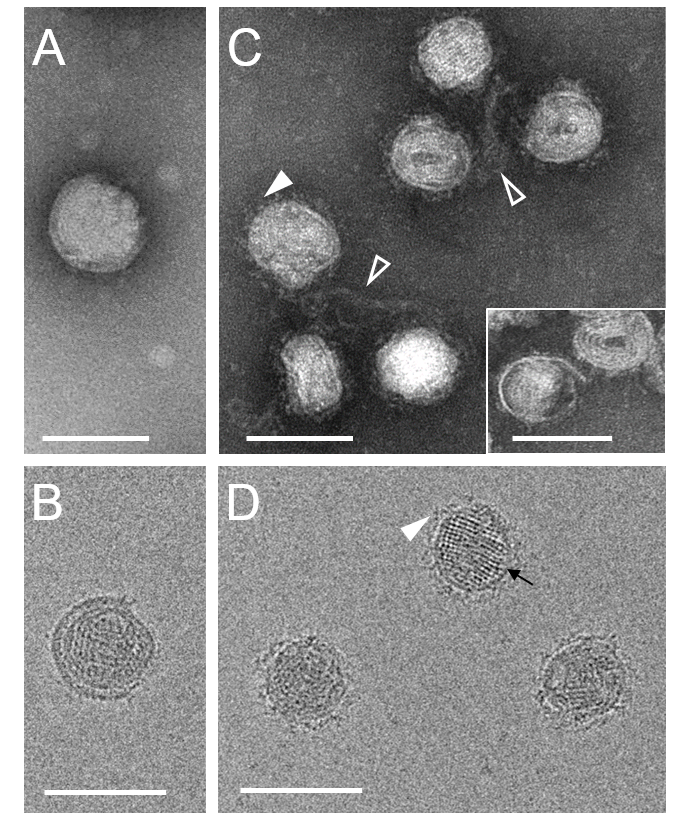


Figure 1. Electron micrographs of SPV1 virions. (A) Negatively stained with 2% (wt/vol) uranyl acetate. (B) Sample embedded in vitreous ice. The open arrowhead points to the projection in the axial view, the filled arrowhead points to the projection in the side view. Scale bars, 100 nm.

 Figure 2. Electron micrographs of partially disrupted virions of SPV1. (A, B) Particles partially devoid of outer shell. (C, D) Particles completely devoid of the outer shell. The filled arrowheads point to the protrusions on the surface of the inner core; the black arrow indicates the envelope of the inner core; open arrowheads point to the nucleoprotein filament released from the core. (A, C*)* Negative staining with 2% (wt/vol) uranyl acetate. (B, D) Samples embedded in vitreous ice. Scale bars, 100 nm.

T:\Prangish's Documents\PAPER\Portogloboviridae\Submission\Figure 6.tifFigure 3. Thin-layer chromatography of lipids extracted from purified SPV1 virions and uninfected cells of *Sulfolobus* sp. S38A. The filled arrowhead points the main lipid type of the SPV1 virion, and the open arrowheads point to the main lipid types of the host cell.

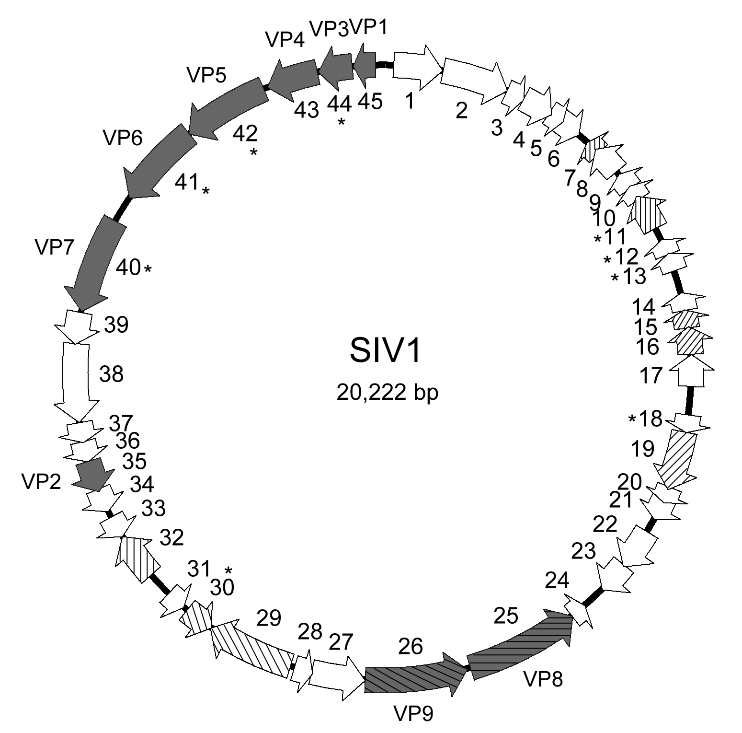


Figure 4. Genome map of SPV1. The ORFs are represented with arrows that indicate the direction of transcription. Genes identified as structural proteins are shown in grey. Homologs to other ORFs of Sulfolobales viruses are shaded by lines. ORFs encoding predicted membrane proteins are indicated by asterisks. GenBank data base acc. no.KY780159.

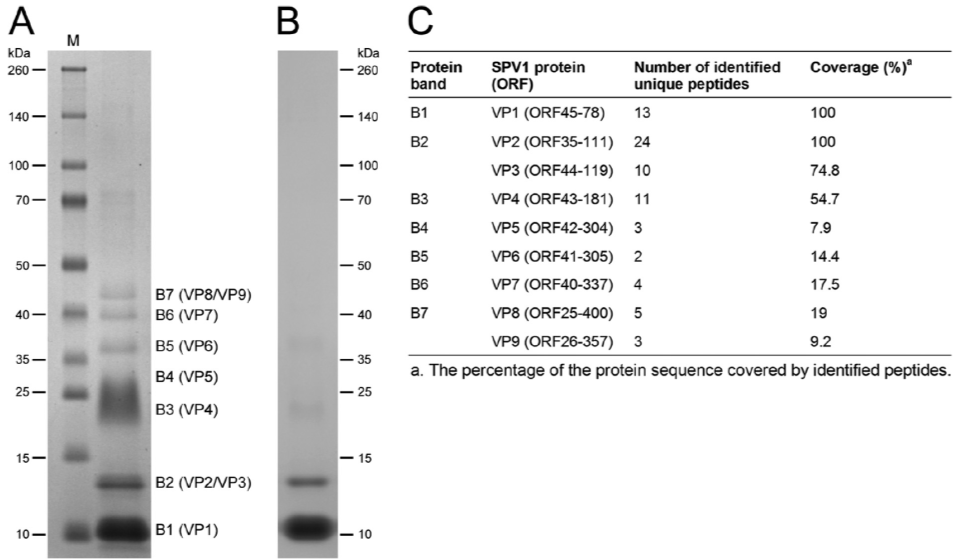


Figure 5. Characterization of SPV1 proteins. (A) SDS-PAGE of proteins in intact virions; (B) SDS-PAGE of proteins in virions with detached outer shell; (C) Identification of the genes encoding proteins in intact virions by LC-MS/MS. B1-B7, protein bands of proteins with identified genes. M, molecular mass standards.

| **References:** |
| --- |
| Liu Y., Ishino S., Ishino Y., Pehau-Arnaudet G., Krupovic M., Prangishvili D. 2017. A novel type of polyhedral viruses infecting hyperhtermophilic archcaea. *J. Virol. doi*: 10.1128/JVI.00589-17 |