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:** | ***2016.043a-dB*** | (to be completed by ICTV officers) |
|---|---|---|

**Short title:** To create one (1) new genus, *Rslunavirus*, including one (1) new species, within the *Myoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

| **Modules attached** (modules 1 and 11 are required) | | | | | |
|---|---|---|---|---|---|
| | **1** ☒ | **2** ☒ | **3** ☒ | **4** ☐ | **5** ☐ |
| | **6** ☐ | **7** ☐ | **8** ☐ | **9** ☐ | **10** ☒ |

**Author(s):**


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**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 Bacterial and Archaeal Viruses Subcommittee |

**ICTV Study Group comments (if any) and response of the proposer:**

Date first submitted to ICTV: June 2016
Date of this revision (if different to above):

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

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 | ***2016.043aB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 1 new species within:**

| | |
|---|---|
| Genus: | ***Rslunavirus*** |
| Subfamily: | |
| Family: | ***Myoviridae*** |
| Order: | ***Caudovirales*** |

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.

| **Name of new species:** | **Representative isolate: (only 1 per species please)** | **GenBank sequence accession number(s)** |
|---|---|---|
| ***Ralstonia virus RSL1*** | **Ralstonia phage phiRSL1** | **AB366653.2** |

**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 11

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

| Code | ***2016.043bB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | |
| Family: | ***Myoviridae*** |
| Order: | ***Caudovirales*** |

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 | ***2016.043cB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new genus: *Rslunavirus***

Assigning the type species and other species to a new genus

| Code | ***2016.043dB*** | (assigned by ICTV officers) |
|---|---|---|

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

| |
|---|
| ***Ralstonia virus RSL1*** |

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 11

Ralstonia phage phiRSL1 lytically infects the phytopathogen *Ralstonia solanacearum*. The phage particles have icosahedral heads of 123 nm in diameter (T=27) and contractile tails 105 nm in length and 24.5 nm in diameter [5]. The phage genome is linear, circularly permuted, and terminally redundant; and >200 kb in length. It encodes a number of interesting proteins involved in lipid (acyl carrier protein and CDP-diacylglycerol-glycerol-3-phosphotransferase) and carbohydrate metabolism (glucosyltransferases, nucleotidyl transferase/lipopolysaccharide biosynthesis protein, nucleoside-diphosphate-sugar pyrophosphorylase-like/capsular polysaccharide). This virus has no close relatives; indeed it was not possible to identify the large subunit terminase or major capsid protein-encoding genes on the basis of BLASTP searches. The tail sheath protein (YP_001950015) is most closely related to that of another giant virus, Pseudomonas phage Lu11.

**Origin of the new genus name:**

Ralstonia phage RSL1. We have chosen to name the genus Rslunavirus instead of Rsl1virus, because the letter "l" is often confused with the number "1".

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

This was the first and only sequenced member of this 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.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**


1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.

2. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140. doi: 10.1186/1756-0500-6-140.

3. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008; 36(Web Server issue):W465-9.

4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107.

5. Yamada T, Satoh S, Ishikawa H, Fujiwara A, Kawasaki T, Fujie M, Ogata H. A jumbo phage infecting the phytopathogen *Ralstonia solanacearum* defines a new lineage of the *Myoviridae* family. Virology. 2010;398(1):135-47.

6. Effantin G, Hamasaki R, Kawasaki T, Bacia M, Moriscot C, Weissenhorn W, Yamada T, Schoehn G. Cryo-electron microscopy three-dimensional structure of the jumbo phage ΦRSL1 infecting the phytopathogen *Ralstonia solanacearum*. Structure. 2013 ;21(2):298-305.


**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 micrograph of negatively stained (2% ammonium molybdate pH 7.5) Ralstonia phage phiRSL1 (provided by: Dr. Takashi Yamada, Department of Molecular Biotechnology, Graduate School of Advanced Sciences of Matter, Hiroshima University, 1-3-1 Kagamiyama, Higashi-Hiroshima, 739-8530, Japan).

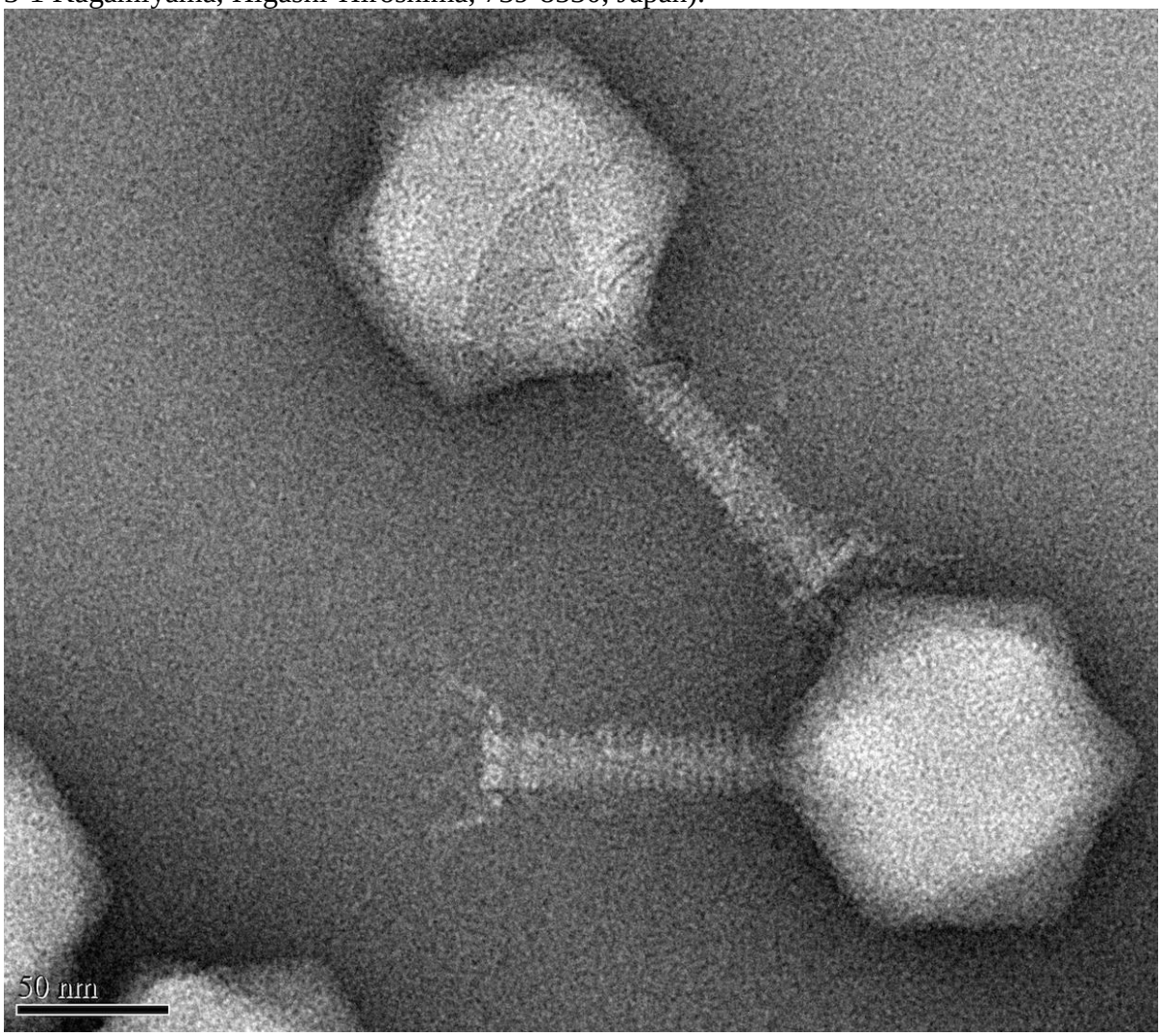


**Table 1**. Properties of the only member of the genus *Rslunavirus.*

| Ralstonia phage | GenBank Accession No. | RefSeq No. | Genome length (kb) | Genome (mol%G+C) | No. CDS | No. tRNAs |
|---|---|---|---|---|---|---|
| phiRSL1 | AB366653.2 | NC_010811.2 | 231.26 | 58.0 | 343 | 2 |