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:** | ***2016.078a-dB*** | (to be completed by ICTV officers) |

**Short title:** To create a new genus, *Ea92virus*, including 2 (two) new species within the family *Podoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

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

**Author(s):**


Johannes Wittmann – Leibniz Institute DSMZ (Germany)
Julianne H. Grose - Brigham Young University (USA)
Abdelbaset I. Yagubi - Brock University (Canada)
Antonet M. Svircev - Agriculture and Agri-Food Canada (Canada)
Andrew M. Kropinski – University of Guelph (Canada)


**Corresponding author with e-mail address:**


Johannes Wittmann jow12@dsmz.de


**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) | Bacterial & Archaeal Virus Subcommittee |

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

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

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

Currently in GenBank there are over 40 fully sequenced N4-like phage genomes, which while displaying similar genome length; and, the presence of a high molecular weight virion-associated RNA polymerase; are poorly related at the phylogenetic (Fig. 1), genomic and proteomic levels. At this time we do not want to propose higher orders, until a firm molecular basis can be proposed to define these.

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 | ***2016.078aB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 2 new species within:**

| | |
|---|---|
| Genus: | ***Ea92virus*** |
| Subfamily: | |
| Family: | ***Podoviridae*** |
| 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)** |
|---|---|---|
| *Erwinia virus Ea9-2*<br>*Erwinia virus Frozen* | *Erwinia phage Ea9-2*<br>*Erwinia phage vB_EamP_Frozen* | KF806588<br>KX098389 |
| | | |

**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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with 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 | ***2016.078bB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | |
| Family: | ***Podoviridae*** |
| 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 | ***2016.078cB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new genus: *Ea92virus***

Assigning the type species and other species to a new genus

| Code | ***2016.078dB*** | (assigned by ICTV officers) |
|---|---|---|

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

| |
|---|
| ***Erwinia virus Ea9-2*** |

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:**

***2***

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

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

Phages addressed in this taxonomic proposal are specific for *Erwinia amylovora*. Phage Ea9-2 was isolated from soil adjacent to infected trees while phage vB_EamP_Frozen was isolated from blossoms and branches. No publication quality electron micrographs exists for members of this genus.
Ea9-2 and vB_EamP_Frozen revealed a genome length of 75,568 bp and 75,147, respectively. Both phages share about 94% similarity at the nucleotide level (query coverage x sequence identity)(Table 1)(Fig 2).
BLASTN, CoreGenes and phylogenetic analyses (Fig. 1) all indicate that the proposed genus, *Ea92virus*, is distinct from other genera in the N4-superfamily of viruses.

**Origin of the new genus name:**

*Erwinia* phage Ea9-2

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

The first virus of its type that was sequenced.

**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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

1. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol. 2011 Oct; 28(10):2731-9.

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.

3. Sullivan MJ, Petty NK, Beatson SA (2011) Easyfig: a genome comparison visualizer. Bioinformatics 27:1009–1010

**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. The virion RNA polymerases of several N4-like phages were aligned and the phylogenetic tree was constructed using MEGA5 (1). The members of the *Ea92virus* genus are boxed in red.

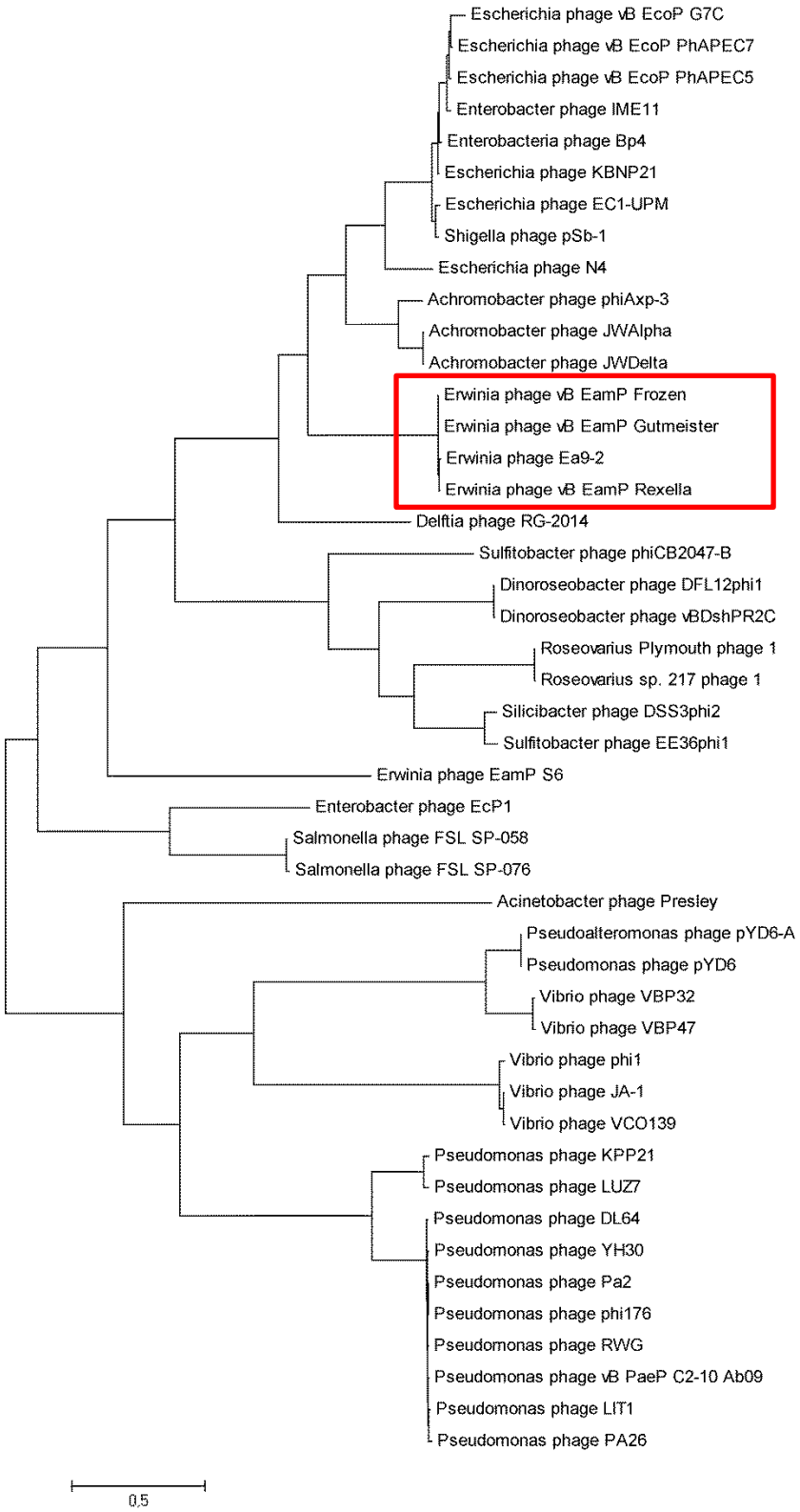
Escherichia phage vB EcoP G7C
Escherichia phage vB EcoP PhAPEC7
Escherichia phage vB EcoP PhAPEC5
Enterobacter phage IME11
Enterobacteria phage Bp4
Escherichia phage KBNP21
Escherichia phage EC1-UPM
Shigella phage pSb-1
Escherichia phage N4
Achromobacter phage phiAxp-3
Achromobacter phage JWAlpha
Achromobacter phage JWDelta
Erwinia phage vB EamP Frozen
Erwinia phage vB EamP Gutmeister
Erwinia phage Ea9-2
Erwinia phage vB EamP Rexella
Delftia phage RG-2014
Sulfitobacter phage phiCB2047-B
Dinoroseobacter phage DFL12phi1
Dinoroseobacter phage vBDshPR2C
Roseovarius Plymouth phage 1
Roseovarius sp. 217 phage 1
Silicibacter phage DSS3phi2
Sulfitobacter phage EE36phi1
Erwinia phage EamP S6
Enterobacter phage EcP1
Salmonella phage FSL SP-058
Salmonella phage FSL SP-076
Acinetobacter phage Presley
Pseudoalteromonas phage pYD6-A
Pseudomonas phage pYD6
Vibrio phage VBP32
Vibrio phage VBP47
Vibrio phage phi1
Vibrio phage JA-1
Vibrio phage VCO139
Pseudomonas phage KPP21
Pseudomonas phage LUZ7
Pseudomonas phage DL64
Pseudomonas phage YH30
Pseudomonas phage Pa2
Pseudomonas phage phi176
Pseudomonas phage RWG
Pseudomonas phage vB PaeP C2-10 Ab09
Pseudomonas phage LIT1
Pseudomonas phage PA26
0.5

Fig 2. Synteny plot of several Ea92viruses visualized with EasyFig [3]. The scale bar shows the level of nucleotide identity.

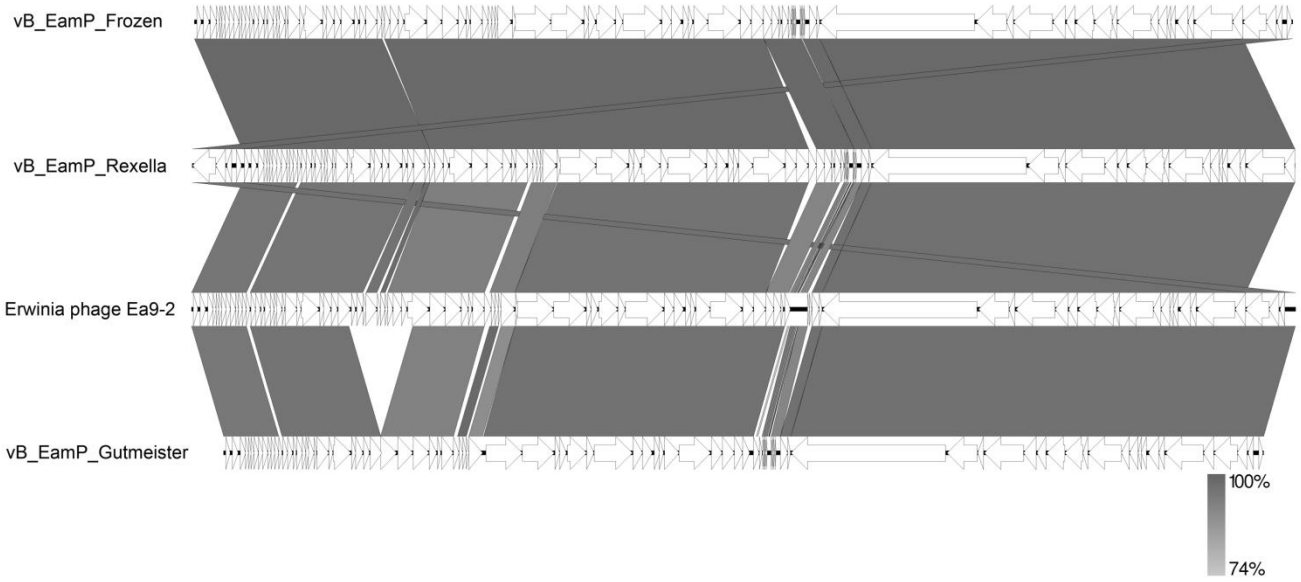


Table 1. Properties of the two phages belonging to the *Ea92virus* and the genomic orphan N4

| Phage | GenBank acc. no. | Genome length (kb) | No. CDS | No. tRNAs | DNA (% sequence identity)* | Proteome (% homologous proteins)** |
|---|---|---|---|---|---|---|
| Ea9-2 | KF806588 | 75,568 | 89 | 7 | 100 | 100 |
| vB_EamP_Frozen | KX098389 | 75,147 | 99 | 8 | 94 | 95.7 |
| | | | | | | |
| N4 | EF056009 | 70,153 | 72 | 3 | 20 | 53.2 |

* Determined using BLASTN; ** Determined using CoreGenes (2); Erwinia phage vB_EamP_Gutmeister (KX098391) and Erwinia phage vB_EamP_Rexella (KX098390) should be considered strains in this genus.