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:** | ***2017.022B*** | | | | (to be completed by ICTV officers) |
| **Short title: To create one (1) new genus, *Jwalphavirus*, including two (2) new species in the family *Podoviridae*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Johannes Wittmann - Leibniz Institute DSMZ (Germany)  Andrew M. Kropinski – University of Guelph (Canada)  Manfred Rohde – Helmholtz Centre for Infection Research (Germany)  Jens H. Kuhn - National Institute of Allergy and Infectious Diseases (USA)  Evelien M. Adriaenssens – University of Liverpool (UK) | | | | | |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | ICTV Bacterial and Archaeal Viruses Subcommittee | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 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: 2017.022B.N.v1.Jwalphavirus** |

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

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

| **References:** |
| --- |
| 1. Wittmann J, Klumpp J, Moreno Switt AI, Yagubi A, Ackermann HW, Wiedmann M, Svircev A, Nash JH, Kropinski AM (2015) Taxonomic reassessment of N4-like viruses using comparative genomics and proteomics suggests a new subfamily—’’Enquar-tavirinae’’. Arch Virol. 160(12):3053–3062.  2. Wittmann J, Dreiseikelmann B, Rohde C, Rohde M, Sikorski J. Isolation and characterization of numerous novel phages targeting diverse strains of the ubiquitous and opportunistic pathogen Achromobacter xylosoxidans. Plos ONE. p. e86935. doi:10.1371/journal.pone.0086935.  3. Wittmann J, Dreiseikelmann B, Rohde M, Meier-Kolthoff JP, Bunk B et al (2014) First genome sequences of Achromobacter phages reveal new members of the N4 family. Virol J 11:14  4. Ma Y, Li E, Qi Z, Li H, Wei X, Lin W, Zhao R, Jiang A, Yang H, Yin Z, Yuan J, Zhao X (2016) Isolation and molecular characterisation of Achromobacter phage phiAxp-3, an N4-like bacteriophage. Sci Rep 6:24776.  5. 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.](http://www.ncbi.nlm.nih.gov/pubmed/21546353) Mol Biol Evol. 2011; 28(10):2731-9.  6. Sullivan MJ, Petty NK, Beatson SA (2011) Easyﬁg: a genome comparison visualizer. Bioinformatics 27:1009–1010 |

**Species demarcation:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of the proposed species differ from each other by less than 5% at the DNA level as confirmed with the BLASTN algorithm [1].

**Genus demarcation:** BLASTN (Table 1) and phylogenetic analyses (Fig. 1) indicate that the proposed genus, *Jwalphavirus*, is cohesive and distinct from other genera. On average, the genomes of members of this genus are 72.9 kb in length (54.6 mol% G+C) and encode on average 87 proteins and 0 tRNAs. OrthoVenn analysis (<http://www.bioinfogenome.net/OrthoVenn/start.php>) of phiAxp-3 with JWAlpha revealed 75% orthologous genes (Fig. 4).

Achromobacter phages JWAlpha and JWDelta were isolated from two different waste water treatment plants in Werl and Braunschweig (Germany), respectively [2]. Both phages belong to the family Podoviridae; Achromobacter phage JWAlpha produces particles that consist of icosahedral heads with diameters of about 59 nm, whereas the heads of Achromobacter phage JWDelta virions are about 72 nm in length and 67 nm in width and there by slightly longer. Particles of both phages possess short tails with an approximate length of 22 nm and several short tail fibers (Fig.2). Particles of both phages contain linear, double-stranded DNA with a length of 72329 bp and 73659 bp, respectively. Bioinformatic analysis resulted in 92 and 89 putative open reading frames for Achromobacter phages JWAlpha and JWDelta, respectively (Fig. 3) [3]. Achromobacter phage phiAxp-3 was isolated from raw hospital sewage in China [4]. Its genome consists of 72825 bp and has 80 putative open reading frames.

The type species *Achromobacter* *virus JWAlpha* was chosen because it represents the first sequenced member of this genus and the name of the new genus was based on that.

**Table 1**. Properties of the phages belonging to the genus *Jwalphavirus*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage Name | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* |
| Achromobacter phage JWAlpha | KF787095 | 72.3 | 54.4 | 92 | 0 | 100 |
| Achromobacter phage JWDelta | KF787094 | 73.7 | 54.3 | 89 | 0 | 96.0 |
| Achromobacter phage phiAxp-3 | KT321317 | 72.8 | 55.2 | 80 | 0 | 46.6 |

\* Determined using BLASTN

**Fig. 1.** Phylogenetic analysis of (A) large subunit terminase proteins, (B) major capsid proteins; and (C) virion RNA polymerases. Proteins were aligned and the phylogenetic tree was constructed using MEGA5 [5]. The members of the *Jwalphavirus* genus are boxed in **red**. The **blue arrow** indicates the only member of the *N4virus* genus; the **blue box** delineates the *Lit1virus* genus; **dark green**, *Luz7virus*; **black**, G7cvirus.

**A. Large terminase subunits**

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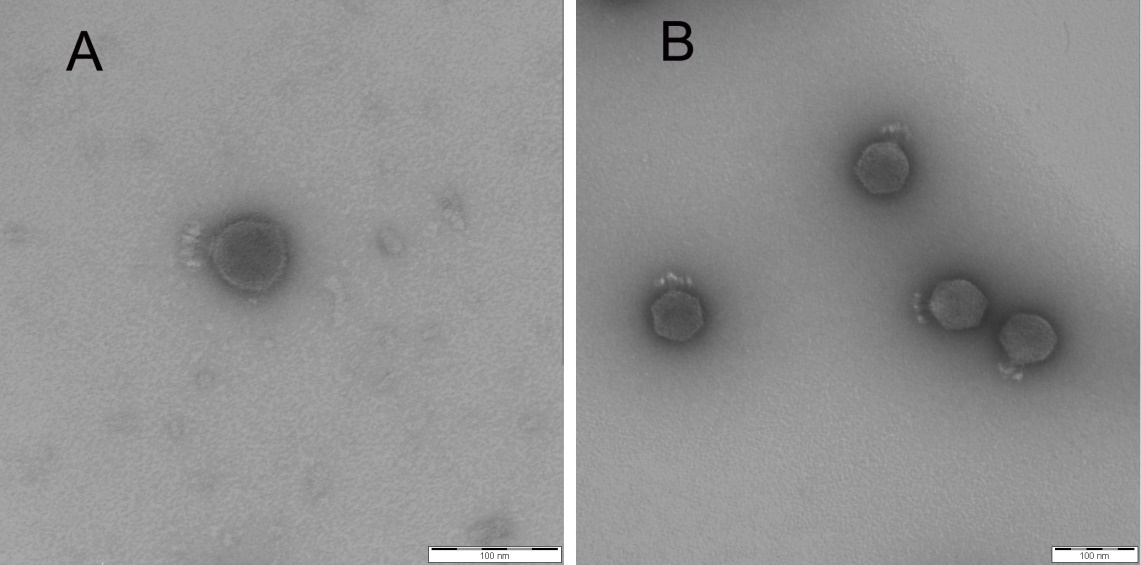
**B. Major capsid proteins**

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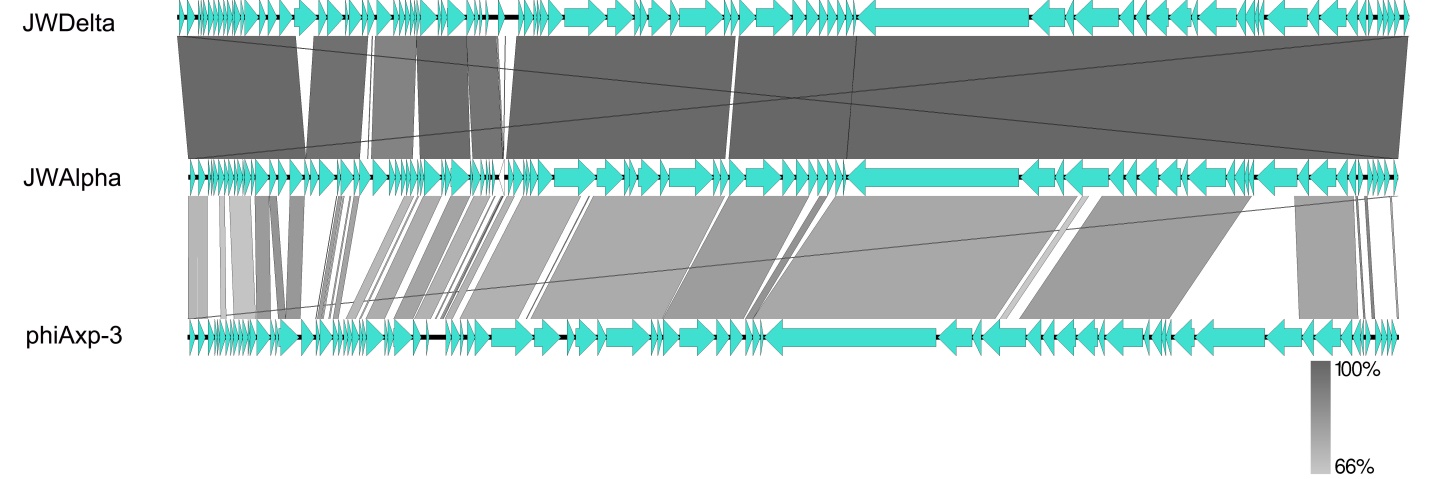
**C. virion RNA polymerases**

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**Fig 2.**  Electron micrograph of Achromobacter phage JWAlpha (A) and JWDelta (B) particles (Negative staining (4% (w/v) uranyl acetate, pH 5.0, provides by M. Rohde).

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**Fig 3.** Synteny plot of the members of the *Jwalphavirus* visualized with EasyFig [6]. The scale bar shows the level of nucleotide identity.



**Fig 4.** OrthoVenn analysis of JWAlpha and phiAxp-3

