This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2018.020B*** | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)**To create one (1) new genus, *Galaxyvirus*, containing two (2) species in the family *Siphoviridae*** |
|  |
| **Author(s):** |
| Andrew M. Kropinski, University of GuelphEvelien M. Adriaenssens, University of Liverpool |
| **Corresponding author with e-mail address:** |
| Andrew M. Kropinski Phage.Canada@gmail.com |
| **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** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | May 2018 |
| Date of this revision (if different to above): |       |

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

**Part 2:** **NON-STANDARD**

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

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module: 2018.020B.N.v1.Galaxyvirus** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

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

**Species demarcation 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.

**Source of the name of this taxon:** The name is directly taken from the first isolated member of this type of phage, Arthrobacter phage Galaxy [1].

**History:** Temperate phage Galaxy was isolated in 2013 by Yein Christina Park from Harmony, PA USA as part of the Phage Hunters Integrating Research and Education program, using Arthrobacter sp. ATCC 21022 as the host bacterium. It is classified to subcluster AS1 in The Actinobacteriophage Database (<http://phagesdb.org/phages/Galaxy/>). The genome possesses 10 bp overhanging ends but it is not known whether they are 5’ or 3’ extensions.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | tRNA | Overall DNA sequence identity |
| Galaxy | KU160644 | 37.81 | 68.4 | 65 | 0 | 100% |
| Abidatro | MF140397 | 39.12 | 68.5 | 66 | 0 | 90 |

**BLASTN homologs:** see above

**Electron micrograph:** Electron micrograph of negatively stained Arthobacter phage Galaxy (http://phagesdb.org/phages/Galaxy/) - Limited permission was granted by The

Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this

electron micrograph for this taxonomy proposal; it cannot be reused without permission of The

Actinobacteriophages Database.

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**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the major capsid protein homologs of these and related phages.



| **References:** |
| --- |
| 1: Klyczek KK, Bonilla JA, Jacobs-Sera D, Adair TL, Afram P, Allen KG,Archambault ML, Aziz RM, Bagnasco FG, Ball SL, Barrett NA, Benjamin RC, Blasi CJ,Borst K, Braun MA, Broomell H, Brown CB, Brynell ZS, Bue AB, Burke SO, Casazza W,Cautela JA, Chen K, Chimalakonda NS, Chudoff D, Connor JA, Cross TS, Curtis KN,Dahlke JA, Deaton BM, Degroote SJ, DeNigris DM, DeRuff KC, Dolan M, Dunbar D,Egan MS, Evans DR, Fahnestock AK, Farooq A, Finn G, Fratus CR, Gaffney BL,Garlena RA, Garrigan KE, Gibbon BC, Goedde MA, Guerrero Bustamante CA, HarrisonM, Hartwell MC, Heckman EL, Huang J, Hughes LE, Hyduchak KM, Jacob AE, Kaku M,Karstens AW, Kenna MA, Khetarpal S, King RA, Kobokovich AL, Kolev H, Konde SA,Kriese E, Lamey ME, Lantz CN, Lapin JS, Lawson TO, Lee IY, Lee SM, Lee-Soety JY, Lehmann EM, London SC, Lopez AJ, Lynch KC, Mageeney CM, Martynyuk T, Mathew KJ,Mavrich TN, McDaniel CM, McDonald H, McManus CJ, Medrano JE, Mele FE, MenningerJE, Miller SN, Minick JE, Nabua CT, Napoli CK, Nkangabwa M, Oates EA, Ott CT,Pellerino SK, Pinamont WJ, Pirnie RT, Pizzorno MC, Plautz EJ, Pope WH, Pruett KM,Rickstrew G, Rimple PA, Rinehart CA, Robinson KM, Rose VA, Russell DA, Schick AM,Schlossman J, Schneider VM, Sells CA, Sieker JW, Silva MP, Silvi MM, Simon SE,Staples AK, Steed IL, Stowe EL, Stueven NA, Swartz PT, Sweet EA, Sweetman AT,Tender C, Terry K, Thomas C, Thomas DS, Thompson AR, Vanderveen L, Varma R,Vaught HL, Vo QD, Vonberg ZT, Ware VC, Warrad YM, Wathen KE, Weinstein JL, Wyper JF, Yankauskas JR, Zhang C, Hatfull GF. Tales of diversity: Genomic andmorphological characteristics of forty-six Arthrobacter phages. PLoS One. 2017Jul 17;12(7):e0180517. |