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:** | ***2018.074B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Ionavirus* containing one (1) new species in the family *Myoviridae*** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph  Hans-Wolfgang Ackermann, Université Laval  Evelien 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): | | |  |

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| **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: 2018.074B.N.v1.Ionavirus** |

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:** Named after Iona Island in Richmond, British Columbia, Canada, where this bacteriophage was identified in the late1960s.

**History:** In 1967, Andrew Kropinski using raw sewage from the Iona Island wastewater treatment plant (Richmond, BC, Canada) and Delftia (Pseudomonas) acidovorans strain #14 from Roger Stanier’s culture collection at the University of California, Berkeley isolated phage ΦW-14.

It was fully characterized with respect to its host range, adsorption rate constant (1.9 x 10-9 mL/min), one-step growth curve (latent period, 63 min; burst size, 300), and sensitivity to pH, temperature, sonication and UV irradiation. It spontaneously generates and unusually high number of plaque morphology variants and can enter into a carrier state with its host. The most exciting aspect of this research was the observation of a major discrepancy between the mol% G+C calculated on the basis of Tm measurements (71.9%) and that from CsCl buoyant density determinations (6%). Hydrolysis of the DNA with formic acid, but not perchloric acid, revealed five UV-adsorbing spots on paper chromatograms. Spectrophotometric quantitation of the resolved bases indicated that the mol%G+C was in fact 54.8 and that approximately 50% of the thymine content was replaced by the fifth base. The structure of this hypermodified base was elucidated through chemical analysis and NMR spectroscopy revealing it to be 5-(4-aminobutylaminomethyl)uracil, now commonly called alpha-putrescinylthymine (PutThy) [1,2].

**Electron microscopy:** The most recent electron micrographic analysis of this phage (Fig. 1) revealed that the phage head is icosahedral as indicated by the observation of pentagonal and hexagonal particles, and the tail contractile. The diameter of the capsid is about 81 nm while the tail is 150 nm in the extended state, and 80 x 23 nm in the contracted state. A 7 nm neck but no collar was observed; and, the tail was terminated by a 33 nm baseplate to which indistinct 12 nm fibres were attached.



**Fig. 1.** Electron micrograph of 2% uranyl acetate stained phage ΦW-14.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| RefSeq | INSDC | Size (Kb) | GC% | Protein | Gene | Pseudogene | tRNA |
| NC\_013697.1 | GQ357915.1 | 157.49 | 56.3 | 236 | 238 | 2 | 0 |

**BLASTN homologs:** None (genomic orphan, singleton)

**Phylogeny:** Phylogenetic analysis, using phylogeny.fr, of the major capsid proteins (Fig. 2) and synthases (right panel) of *Delftia* phage ΦW-14 reveal a peripheral relationship to viruses belonging to the *Ackermannviridae* family.



Fig 2.

| **References:** |
| --- |
| 1. Kropinski, A.M.; Bose, R.J.; Warren, R.A. 5-(4-Aminobutylaminomethyl)uracil, an unusual pyrimidine from the deoxyribonucleic acid of bacteriophage fW-14. Biochemistry 1973, 12, 151-157.  2. Kropinski, A.M.B. The Physico-Chemical Properties of Bacteriophage ΦW-14 Deoxyribonucleic Acid. University of British Columbia, Vancouver, B.C., Canada, 1973. |