

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.005A** |  |
| **Short title:** Create one new species in the genus *Gammapleolipovirus* (*Haloruvirales*: *Pleolipoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Dyall-Smith ML, Tang S-L, Pfeiffer F, Chiang PW | mike.dyallsmith@gmail.com; [sltang@gate.sinica.edu.tw](mailto:sltang@gate.sinica.edu.tw);  fpf@biochem.mpg.de; chiangpw@gate.sinica.edu.tw |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Veterinary Biosciences, Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Australia [MD-S]  Biodiversity Research Center, Academia Sinica, Nankang, Taipei 115, Taiwan [S-LT, PWC]  Computational Biology Group, Max-Planck-Institute of Biochemistry, Martinsried, Germany [FP, MD-S] |

**Corresponding author**

|  |
| --- |
| Mike Dyall-Smith |

**List the ICTV Study Group(s) that have seen this proposal**

|  |
| --- |
| *Pleolipoviridae* SG |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | June 3, 2021 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.005A.R.Gammapleolipovirus\_1nsp.xlsx |

**Abstract**

|  |
| --- |
| We propose the creation of a new species within the genus *Gammapleolipovirus* to accommodate the virus isolate Hardyhisp2. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | The family *Pleolipoviridae* (Order *Haloruvirales*) currently has three genera with a total of 15 recognised species (https://talk.ictvonline.org/taxonomy/). The genera are *Alphapleolipovirus* (5 species), *Betapleolipovirus* (nine species) and *Gammapleolipovirus* (one species) [1, 3]. A recent publication describes a novel virus Hardyhisp2 [4] that was isolated from an Australian salt lake. The host strain is *Haloarcula hispanica*. This virus has a genome that is closely related to His2 [2], which is currently the sole representative member of the genus *Gammapleolipovirus.* Figure 1 summarises the genomic characteristics and similarities of Hardyhisp2 to the other members of the *Pleolipoviridae*. Notably, His2 and Hardyhisp2 share 80.5% nucleotide similarity while both show negligible nucleotide similarity to the other viruses. This is less than the 95% threshold for membership of the same species previously recommended for species of the genera *Pleolipoviridae* (2019.105B.A) but sufficiently high to warrant membership of the same genus.    **Figure 1.** Summary table comparing Hardyhisp2 to other members of *Pleolipoviridae,* as output from the VIRIDIC webserver [5]. Virus names are shown at the right, colour coded and labeled to indicate their membership of the *Alpha*-, *Beta*- or *Gammapleolipovirus* genera. Accession numbers are given at the lower edge. Genome length, and keys for aligned genome fraction, genome length ratio and intergenomic similarity are shown at top.  The genome of Hardyhisp2 is linear dsDNA of 16,133 bp in length, an average G+C content of 39.8%, and was annotated to possess 33 protein coding sequences [4]. The genome of Hardyhisp2 is similar in size to that of His2 (16,067 bp), as well as average G+C content (40.4%). The genomes of Hardyhisp2 and His2 carry inverted terminal repeats of a similar length (599 bp and 525 bp, respectively).  A comparison of the two genomes using the TBLASTx algorithm (translated BLAST) is shown in Figure 2, and confirms the strong similarity of the encoded proteins of the two viruses, particularly in the highly conserved genes for DNA polymerase and putative NTPase. One notable exception are the major spike proteins (VP1 spike), which share only 32% protein similarity.    **Figure 2.** Comparison of the His2 and Hardyhisp2 genomes using the translated BLAST (TBLASTx) algorithm, as output from the ViPTree [6] suite of programs available at (https://www.genome.jp/viptree). Panel A shows the dot plot and panel B shows the comparison of the gene maps, with coding sequences indicated by yellow arrows. The inverted terminal repeats are shown as grey arrows. The similarity colour key is shown at the top of panel B.  A phylogenetic tree reconstruction based on the protein sequences of the putative NTPases (Figure 3) shows the His2 and Hardyhisp2 proteins cluster closely together, and well away from the NTPase proteins of the other viruses.  **Figure 3.** Phylogenetic tree reconstruction based on NTPase proteins of pleolipoviruses. A Neighbor-joining consensus tree (100 bootstraps) was generated within the GeneiousPrime (ver 2021.1.1; <https://www.geneious.com>) . The bootstrap values are shown near branch points. Virus names (accessions) are shown. Scale bar represents 0.1 amino acid substitutions per site.  Based on the close similarity of Hardyhisp2 and His2, we propose that Hardyhisp2 represents a novel member of the same genus, i.e. *Gammapleolipovirus.* The overall nucleotide similarity is well below 95%, indicating that Hardyhisp2 should be classified into a new species in this genus, which we propose as *Gammapleolipovirus Hardyhisp2*. | |

**Supporting evidence**

**References**

1. Bamford DH, Pietila MK, Roine E, Atanasova NS, Dienstbier A, Oksanen HM, Ictv Report C (2017) ICTV Virus Taxonomy Profile: *Pleolipoviridae*. J Gen Virol 98:2916-2917. Doi:10.1099/jgv.0.000972

2. Bath C, Cukalac T, Porter K, Dyall-Smith ML (2006) His1 and His2 are distantly related, spindle-shaped haloviruses belonging to the novel virus group, Salterprovirus. Virology 350:228-239. Doi:10.1016/j.virol.2006.02.005

3. Demina TA, Oksanen HM (2020) Pleomorphic archaeal viruses: the family *Pleolipoviridae* is expanding by seven new species. Arch Virol Doi:10.1007/s00705-020-04689-1

4. Dyall-Smith M, Pfeiffer F, Chiang PW, Tang SL (2021) Genome sequence of Hardyhisp2, a gammapleolipovirus infecting *Haloarcula hispanica*. Microbiol Resour Announc 10:e00226-00221. Doi:10.1128/MRA.00226-21

5. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12:1268. Doi:10.3390/v12111268 PMCID: PMC7694805

6. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33:2379-2380. Doi:10.1093/bioinformatics/btx157