

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.151B** |  |
| **Short title:** Create one new family *Simuloviridae* includinggenus *Yingchengvirus* (formerly *Betasphaerolipovirus*) moved from the family *Sphaerolipoviridae (Halopanivirales)* | | |
|  | | |

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

|  |  |
| --- | --- |
| Liu Y, Du S, Chen X, Krupovic M | [ying.liu@pasteur.fr](mailto:ying.liu@pasteur.fr); [ssdu@whu.edu.cn](mailto:ssdu@whu.edu.cn); [xdchen@whu.edu.cn](mailto:xdchen@whu.edu.cn); [mart.krupovic@pasteur.fr](mailto:mart.krupovic@pasteur.fr) |

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

|  |
| --- |
| Institut Pasteur (YL, MK);  Wuhan University (SD, XC) |

**Corresponding author**

|  |
| --- |
| Mart Krupovic, Xiandong Chen |

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

|  |
| --- |
| Bacterial and Archaeal Viruses Subcommittee |

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

|  |
| --- |
|  |

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

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

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 31 July 2020 |
| 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**

|  |
| --- |
| 2020.151B.R.Simuloviridae.xlsx |

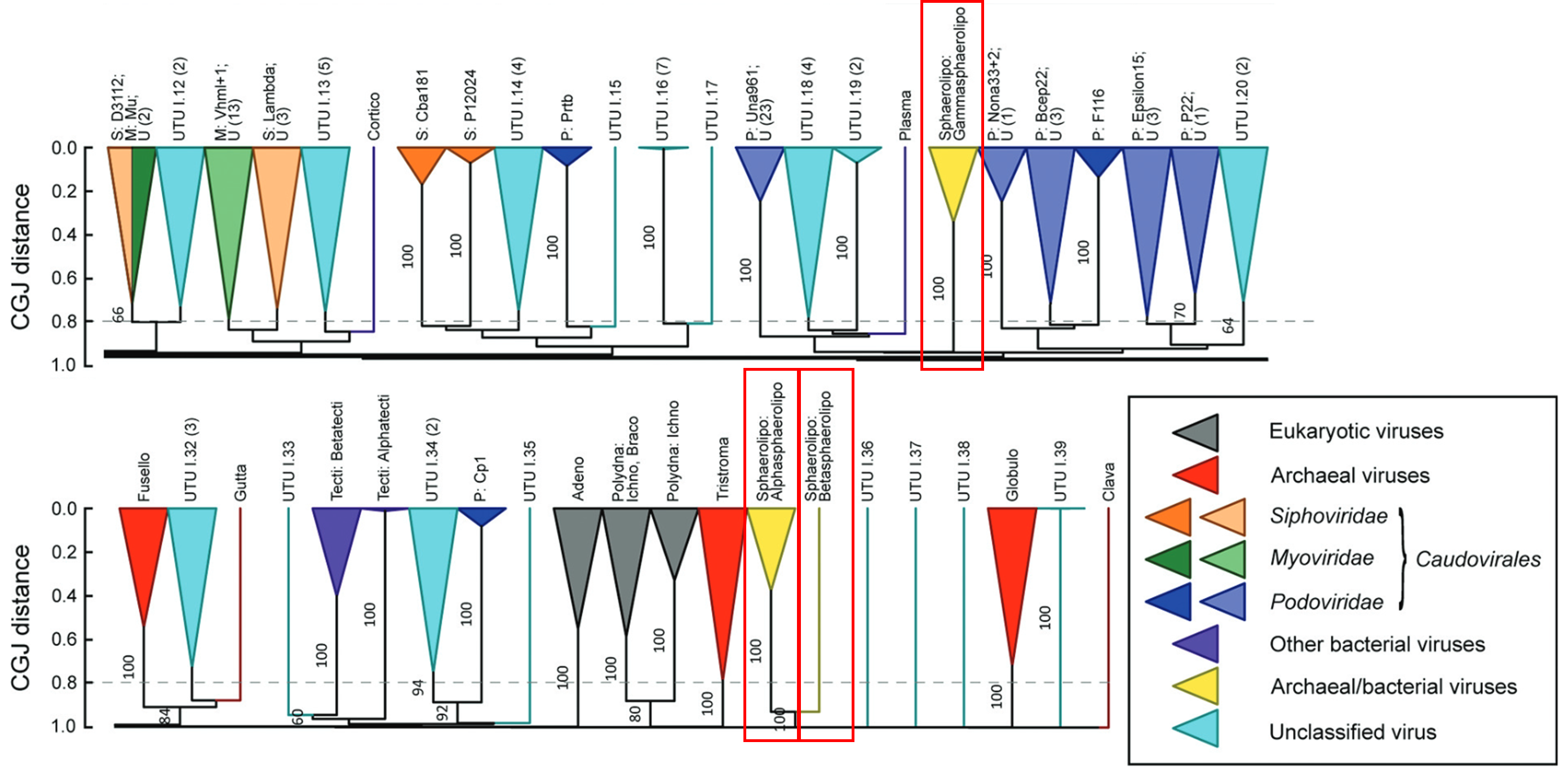
**Abstract**

|  |
| --- |
| We propose renaming genus *Betasphaerolipovirus* to *Yingchengvirus* and moving it to a new family *Simuloviridae*. In addition, we propose two new species, *Yingchengvirus NVIV1* and *Yingchengvirus HJIV1*, in the genus *Yingchengvirus* for classification of Natrinema versiforme icosahedral virus 1 and Haloterrigena jeotgali icosahedral virus 1, respectively, which have been recently discovered as episomal proviruses in halophilic archaea. |

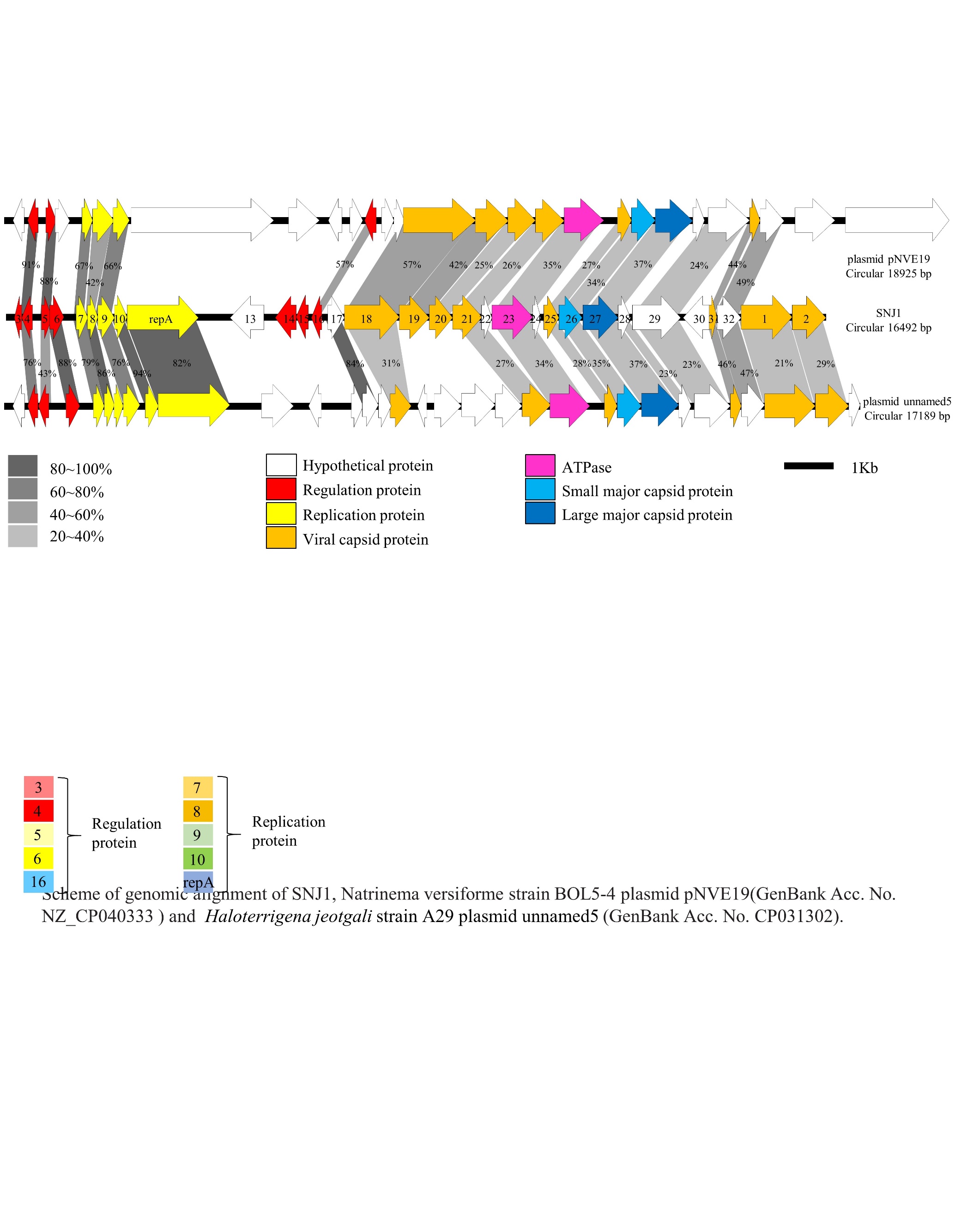
**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | The family *Sphaerolipoviridae* includes tailless dsDNA viruses with internal lipid membrane and external icosahedral capsids constructed from two single-jelly roll major capsid proteins [1-3]. The family, proposed in 2014 and ratified in 2015, currently includes three genera: *Alphaspaherolipovirus*, *Betasphaerolipovirus* and *Gammaspaherolipovirus* [4]. The latter genus has been created for classification of viruses with circular dsDNA genomes and infecting thermophilic bacteria, whereas the other two genera include haloarchaeal viruses with linear (*Alphaspaherolipovirus*) or circular (*Betasphaerolipovirus*) genomes. The similarity between sphaerolipovirids is unequivocal at the structural level [1-3], but is very remote when sequences alone are compared. Consistently, Genome Relationship Applied to Virus Taxonomy (GRAViTy) analysis, which has been designed to recognize family level groups [5], has suggested that divergence between the three genera of the *Sphaerolipoviridae* is equivalent to the divergence between most families of eukaryotic viruses [6]. To rectify this discrepancy, it has been suggested to move genus *Gammasphaerolipovirus* into a separate family, *Matsushitaviridae* (see the corresponding proposal by Oksanen et al). Here we propose renaming genus *Betasphaerolipovirus* to *Yingchengvirus* and moving it to a new family *Simuloviridae* within the existing order *Halopanivirales*.  **Etymology of the proposed names**   * *Simuloviridae*: from Latin *simulo* for *pretend*, referring to the fact that genomes of the viruses in this genus were first thought to be plasmids, i.e., viruses pretending to be plasmids) * *Yingchengvirus*: after Yingcheng city (Hubei province, China), location of the salt mine from which virus SNJ1, the first representative of the family, was isolated.   Natrinema virus SNJ1 is currently the only representative of the family. The virus has been sequenced along with the host genome and initially thought to be a plasmid [7]. However, mitomycin C treatment of *Natrinema* sp. J7-1 cells resulted in virus induction and formation of plaques on sensitive hosts *Natrinema* sp. J7-2 and CJ7, revealing that plasmid pHH205 actually represents an episomal genome of a temperate virus, subsequently renamed to SNJ1 [8]. Recently, two more proviruses related to SNJ1 were discovered [9], both residing as circular plasmids in *Natrinema versiforme* strain BOL5-4 (18,925 bp; plasmid pNVE19; CP040333) and *Haloterrigena jeotgali* A29 (17,189 bp; plasmid unnamed5; CP031302), respectively. The two plasmids are generally collinear with the SNJ1 genome and display extensive gene content similarity, including genes encoding the two characteristic major capsid proteins and the genome packaging ATPase (Figure 2). Accordingly, plasmids pNVE19 and unnamed5 were deposited as Third Party Annotations in GenBank under names Natrinema versiforme icosahedral virus 1 (NVIV1) and Haloterrigena jeotgali icosahedral virus 1 (HJIV1), respectively.  Species demarcation criteria have not been previously proposed, due to scarcity of available representatives. We propose to use a 95% global genome identity as a species demarcation criterion, to be consistent with the thresholds used for other prokaryotic viruses. At the nucleotide level, the similarity between SNJ1, NVIV1 and HJIV1 are low: NVIV1 shows 82.9% identity to SNJ1 over 31% of the genome, whereas HJIV1 displays 87.9% identity to SNJ1 over 46% of the genome. NVIV1 and HJIV1 are 80% identical over 67% of the genome.  We propose classifying NVIV1 and HJIV1 into two new species, *Yingchengvirus NVIV1* and *Yingchengvirus HJIV1*, respectively, within the *Yingchengvirus* genus in the family *Simuloviridae*. | |

**Supporting evidence**



**Figure 1.** Dendrogram of classified and unclassified dsDNA viruses (Baltimore group I) based on composite generalised Jaccard (CGJ) distances. Tips are labelled with genus for members of Caudovirales (abbreviated as S: *Siphoviridae*; M: *Myoviridae*; P: *Podoviridae*), with family/genus for other bacterial, eukaryotic and archaeal viruses or with accession number codes for unclassified viruses. The scale bar for CGJ distance is shown at the left of each line and the 0.8 threshold that corresponds to eukaryotic family groupings is shown as a grey dotted line. Groupings including the three genera of the *Sphaerolipoviridae* are highlighted with red boxes. The figure is reproduced from Aiewsakun et al. [6]; only portion of the original figure relevant to this proposal is shown.



**Figure 2.** Genome alignment of SNJ1 and the two proviruses residing as circular plasmids in *Natrinema versiforme* BOL5-4 (plasmid pNVE19; NZ\_CP040333) and *Haloterrigena jeotgali* A29 (plasmid unnamed5; CP031302). For convenience of presentation, the circular genome of SNJ1 was linearized between ORFs 2 and 3. Gene encoding transcription regulators and those involved in genome replication are indicated with red or yellow arrows, respectively. Capsid proteins identified by mass spectrometric in SNJ1 virion [8] are shown in orange. The two major capsid proteins are shown in blue, whereas the putative genome packaging ATPase is shown in pink. Homologous ORFs are connected with grey shading, with the numbers representing the percentages of protein identities. The figure is reproduced from [9].

**References**

1. Santos-Pérez I, Charro D, Gil-Carton D, Azkargorta M, Elortza F, Bamford DH, Oksanen HM, Abrescia NGA. Structural basis for assembly of vertical single β-barrel viruses. Nat Commun. 2019; 10(1):1184. doi: 10.1038/s41467-019-08927-2. PMID: 30862777
2. De Colibus L, Roine E, Walter TS, Ilca SL, Wang X, Wang N, Roseman AM, Bamford D, Huiskonen JT, Stuart DI. Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. Nat Commun. 2019; 10(1):1456. doi: 10.1038/s41467-019-09451-z. PMID: 30926810
3. Rissanen I, Grimes JM, Pawlowski A, Mäntynen S, Harlos K, Bamford JK, Stuart DI. Bacteriophage P23-77 capsid protein structures reveal the archetype of an ancient branch from a major virus lineage. Structure. 2013; 21(5):718-26. doi: 10.1016/j.str.2013.02.026. PMID: 23623731
4. Pawlowski A, Rissanen I, Bamford JK, Krupovic M, Jalasvuori M. Gammasphaerolipovirus, a newly proposed bacteriophage genus, unifies viruses of halophilic archaea and thermophilic bacteria within the novel family Sphaerolipoviridae. Arch Virol. 2014; 159(6):1541-54. doi: 10.1007/s00705-013-1970-6. PMID: 24395078
5. Aiewsakun P, Simmonds P. The genomic underpinnings of eukaryotic virus taxonomy: creating a sequence-based framework for family-level virus classification. Microbiome. 2018; 6(1):38. doi: 10.1186/s40168-018-0422-7. PMID: 29458427
6. Aiewsakun P, Adriaenssens EM, Lavigne R, Kropinski AM, Simmonds P. Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. J Gen Virol. 2018; 99(9):1331-1343. doi: 10.1099/jgv.0.001110. PMID: 30016225
7. Ye X, Ou J, Ni L, Shi W, Shen P. Characterization of a novel plasmid from extremely halophilic Archaea: nucleotide sequence and function analysis. FEMS Microbiol Lett. 2003; 221(1):53-7. doi: 10.1016/S0378-1097(03)00175-7. PMID: 12694910
8. Zhang Z, Liu Y, Wang S, Yang D, Cheng Y, Hu J, Chen J, Mei Y, Shen P, Bamford DH, Chen X. Temperate membrane-containing halophilic archaeal virus SNJ1 has a circular dsDNA genome identical to that of plasmid pHH205. Virology. 2012; 434(2):233-41. doi: 10.1016/j.virol.2012.05.036. PMID: 22784791
9. Chen B, Chen Z, Wang Y, Gong H, Sima L, Wang J, Ouyang S, Gan W, Krupovic M, Chen X, Du S. ORF4 of the temperate archaeal virus SNJ1 governs the lysis-lysogeny switch and superinfection immunity. J Virol. 2020 Jun 10:JVI.00841-20. doi: 10.1128/JVI.00841-20. PMID: 32522850