

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

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| **Code assigned:** | **2020.100B** |  |
| **Short title:** Create one new family (*Matsushitaviridae*) including one renamed genus (*Hukuchivirus* – formerly *Gammasphaerolipovirus*) moved from the family *Sphaerolipoviridae* (*Halopanivirales*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| **ICTV Bacterial and Archaeal Viruses Subcommittee Chair** |

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

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

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Matsushitaviridae* | Isao Matsushita | Y |
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**Submission dates**

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| Date first submitted to SC Chair | July 29, 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.100B.R.Matsushitaviridae.xlsx |

**Abstract**

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| We propose to rename the genus *Gammasphaerolipovirus* to *Hukuchivirus* and move it from the family *Sphaerolipoviridae* to a new family *Matsushitaviridae*. We also propose to rename species *Thermus virus P23-77* and *Thermus virus IN93* to *Hukuchivirus P23-77* and *Hukuchivirus IN93*, respectively. *Matsushitaviridae* is a family of tailless, icosahedral, internal membrane-containing bacterial viruses with double-stranded DNA genomes and two vertical single jelly-roll MCPs forming pseudohexameric double jelly-roll MCPs. The family includes one genus, *Hukuchivirus*, with two species *Hukuchivirus P23-77* and *Hukuchivirus IN93*. The family *Matsushitaviridae* belongs to the order *Halopanivirales* with the family *Sphaerolipoviridae*. |

**Text of proposal**

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| |  | | --- | | Thermus phages P23-77 [1] and IN93 [2] are tailless, icosahedral, internal membrane-containing bacterial viruses with circular double-stranded DNA genomes. They infect thermophilic bacterium *Thermus* *thermophilus*. The corresponding species *Thermus virus P23-77* and *Thermus virus IN93* are members of the genus *Gammasphaerolipovirus* in the family *Sphaerolipoviridae* [3] (Figure 1). Other species in the family *Sphaerolipoviridae* include archaeal viruses SH1, PH1, HHIV-2, HCIV-1, and SNJ1 [4-5]. Genera *Alphasphaerolipovirus* have four species: *Haloarcula hispanica virus SH1, Haloarcula hispanica virus PH1, Haloarcula hispanica icosahedral virus 2,* and *Haloarcula virus HCIV1*. *Natrinema virus SNJ1* in the only species in the genus *Betasphaerolipovirus*. These viruses form a group of tailless icosahedral viruses with two types of vertical single jelly roll major capsid proteins (MCP) encoded by two genes, vertex penton protein and putative genome packaging ATPase of FtsK-HerA superfamily [6-9] (Figure 2). The capsids are organized in *T* = 28 lattice made of pseudo-hexameric double-jelly roll capsomers formed of two single jelly-roll MCPs. The MCPs of alphasphaerolipoviruses SH1, PH1, HHIV-2, and HCIV-1 and gammasphaerolipoviruses P23-77 and IN93 share low sequence similarities (24%–29% [4]), but based on the solved structures [5-8] the fold of their MCPs and overall virion architecture are conserved. The family *Sphaerolipoviridae* belongs to the kingdom *Helvetiavira* in the realm *Varidnaviria*.  Further analysis of sequence relatedness of prokaryotic viruses by genomics-based method (Genome Relationship Applied to Virus Taxonomy; GRAViTy) showed that the members of the genus *Gammasphaerolipovirus* (P23-77 and IN93) are grouped completely separately from other members in the family *Sphaerolipoviridae* that infect archaea [10] (Figure 3).  Because P23-77 and IN93 are sufficiently different from all other known viruses, we propose to rename the genus *Gammasphaerolipovirus* to *Hukuchivirus* and move it from the *Sphaerolipoviridae* to a new family *Matsushitaviridae*.  The species including P23-77 and IN93 are currently called *Thermus virus P23-77* and *Thermus virus IN93*. We propose to rename the species to *Hukuchivirus P23-77* and *Hukuchivirus IN93*.  *Matsushitaviridae* is a family of tailless, icosahedral, internal membrane-containing bacterial viruses with double-stranded DNA genomes and two vertical single jelly-roll MCPs forming pseudohexameric double jelly-roll MCPs. The family includes one genus, *Hukuchivirus*, with two species *Hukuchivirus P23-77* and *Hukuchivirus IN93*. *Hukuchivirus P23-77* is the type species of the family. The order *Halopanivirales* includes two families *Matsushitaviridae* and *Sphaerolipoviridae*.  Origin of names:  *Matsushitaviridae*: after Isao Matsushita, who was one of the persons isolating the first virus of this taxon Thermus phage IN93 in 1995.  *Hukuchivirus*: after a hot spring in Hukuchi, Gifu prefecture, Japan, from which Thermus phage IN93 was isolated.    **Figure 1.** Maximum likelihood phylogenetic trees of conserved proteins of viruses in the family *Sphaerolipoviridae* and related proviruses (marked with asterisks). Viruses in the genus *Alphasphaerolipovirus*, *Betasphaerolipovirus*, and *Gammasphaerolipovirus* (the proposed genus *Hukuchivirus*) and their related proviruses are shown in yellow, purple, and blue, respectively. (A) Putative genome packaging ATPase. (B) Large MCP. (C) Small MCP. Evolutionary analysis was conducted using the JTT amino acid substitution model and 1,000 bootstrap values in MEGA 5.05. The bar (0.1) indicates the inferred number of substitutions per site. The figure is adapted from [4].    **Figure 2.** Genomes of Thermus phages P23-77 (NC\_013197) and IN93 (NC\_004462). Circular genomes are presented here in linear forms. Transcriptional units are indicated in brackets below the IN93 genome. Genes (arrows) are shown in color if their gene products have been identified as structural components of the virus (VP = virion protein) or if a function is assigned according to experimental data or hits in BLAST searches. Genes encoding viral core proteins: a putative packaging ATPase, and the two major capsid proteins (small and large MCPs), are marked in italics and bold-framed arrows. The figure is adapted from [3].    **Figure 3.** Heat map and dendrogram showing the genome relationships of archaeal viruses and other related viruses using pairwise composite generalized Jaccard (CGJ) distances. Branches and labels were colour coded by their hosts - *Podoviridae*: blue; other bacterial: purple; archaeal: red; dual host (archaea and bacteria): yellow (*Sphaerolipoviridae*); eukaryotic: black. The order of taxa in the heat map followed the phylogeny of the den-drogram and was not therefore constrained by ICTV family assignments. Bootstrap support is shown above branches in the dendrogram (values of >70 % are shown). The figure is adapted from [10]. | |

**References**

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