

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

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| **Code assigned:** | **2020.068B** |  |
| **Short title:** Rename the genus *Halcyonevirus* (formerly *Trippvirus*) and create four new species *(Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Jakub Barylski |

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

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| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**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)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 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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| 2020.068B.R.Halcyonevirus.xlsx |

**Abstract**

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| We have identified four new species in the genus *Trippvirus,* which we propose to rename *Halcyonevirus* in keeping with the taxonomy proposed by Dr. Tsourkas. |

**Text of proposal**

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| |  | | --- | | **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 | |

**Supporting evidence**

**History:** The genus *Trippvirus* was proposed/ratified through TaxoProp 2018.102B with a single species. DNA sequence analysis using VIRIDIC [1] reveals numerous new species and strains which have been deposited to GenBank since 2015. We intend to rename it *Halcyonevirus* in keeping with the wishes of Dr. Tsourkas [2,3].

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The phage name which has been highlighted in **blue** corresponds to the existing species recognized by ICTV.

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**N.B. Paenibacillus phages Heath, Ash and Lev are strains in this genus**

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| **Phage name** | **Accession** | **Belongs to species** |
| Paenibacillus phage Heath | MH460826 | *Paenibacillus virus Halcyone* |
| Paenibacillus phage Ash | MH454076 | *Paenibacillus virus C7Cdelta* |
| Paenibacillus phage Lev | MH454080 | *Paenibacillus virus C7Cdelta* |

**References**

1. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>
2. Stamereilers C, Fajardo CP, Walker JK, Mendez KN, Castro-Nallar E, Grose JH, Hope S, Tsourkas PK. Genomic Analysis of 48 *Paenibacillus larvae* Bacteriophages. Viruses. 2018 Jul 19;10(7):377. doi: 10.3390/v10070377. PMID: 30029517; PMCID: PMC6070908.
3. Tsourkas PK. *Paenibacillus larvae* bacteriophages: obscure past, promising future. Microb Genom. 2020 Feb;6(2):e000329. doi: 10.1099/mgen.0.000329. PMID: 32111267; PMCID: PMC7067210.