

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

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| **Code assigned:** | **2020.121B** |  |
| **Short title:** Create one new genus (*Pollockvirus*) including one species moved from the genus *Ithacavirus* (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Kropinski AM, Moraru C, Wittmann J | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; liliana.cristina.moraru@uol.de; jow12@dsmz.de |

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

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  DSMZ, Germany [JW] |

**Corresponding author**

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| Johannes Wittmann |

**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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the genus “Pollockvirus” including one species, Escherichia phage Pollock based on genome-based comparisons and phylogenetic analyses of terminase and vRNA polymerase protein sequences. It was formerly classified as a member of the genus “*Ithacavirus”.* Based on DNA sequence similarity (Viridic analysis) and the threshold for creating new genera, we propose to create a genus of its own. |

**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 [1-3]. | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named after Pollock, the isolated phage, Eschericha phage Pollock, of this type. It was isolated from sewage in the US [4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Escherichia phage Pollock | NC\_027381.1 | KM236242 | 68.4 | 36 | 84 | 4 |

**Electron micrograph:** None available

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [5]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. Colours in columns 3 and 4 indicate subfamilies and genera. 

**Phylogenetic analysis** using the (A) terminase and (B) vRNA polymerase protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [6]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

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**References**

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5. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. http://kronos.icbm.uni-oldenburg.de/viridic/
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