

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

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| **Code assigned:** | **2020.125B** |  |
| **Short title:** Create one new genus (*Pseudotevenvirus*) including nine species in the subfamily *Tevenvirinae* (*Caudovirales*: *Myoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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

**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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| 2020.125B.R.Pseudotevenvirus.xlsx |

**Abstract**

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| The species *Escherichia virus RB43* is an orphan species in the subfamily *Tevenvirinae*. This proposal creates a genus, *Pseudotevenvirus*, for this an eight new species. |

**Text of proposal**

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**Supporting evidence**

**Historical aspects:** Based upon the scientific literature the Pseudo T-Even Bacteriophages group is comprised on *Escherichia* phages Lw1, RB16, RB43, RB49, *Klebsiella* phages KP15 and KP27 and *Cronobacter* phage vB\_CsaM\_GAP161 [1-3]. We have subsequently placed RB49 in the genus *Krishvirus*, and the Klebsiella phages in genus *Slopekvirus*. ICTV recognizes RB43 as an unclassified member of the *Tevenvirinae* (2009.007a-rB)

**Proposal: To transfer *Escherichia virus RB43* to the genus *Pseudotevenvirus* and add eight (8) new species.**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage RB43 |  | AY967407.1 | 180.50 | 43.2 | 292 | 1 | 100 | 100 |
| Citrobacter phage Margaery | [NC\_028755.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028755.1) | [KT381880.1](https://www.ncbi.nlm.nih.gov/nuccore/KT381880.1) | 178.18 | 44.9 | [280](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/54577/464247|Citrobacter phage Margaery/viral segment/) | 1 | 76.7 | 86.6 |
| Cronobacter phage vB\_CsaM\_leB |  | [KX431559.1](https://www.ncbi.nlm.nih.gov/nuccore/KX431559.1) | 177.91 | 44.9 | [280](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62997/465620|Cronobacter phage vB_CsaM_leB/viral segment/) | 1 (\*\*\*) | 75.9 | 85.6 |
| Cronobacter phage vB\_CsaM\_GAP161 | [NC\_019398.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019398.1) | [JN882287.1](https://www.ncbi.nlm.nih.gov/nuccore/JN882287.1) | 178.19 | 44.5 | [275](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15411/459748|Cronobacter phage vB_CsaM_GAP161/viral segment Unknown/) | 2 | 75.6 | 85.3 |
| Cronobacter phage vB\_CsaM\_leE |  | [KX443552.1](https://www.ncbi.nlm.nih.gov/nuccore/KX443552.1) | 181.57 | 44.7 | [284](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62984/465607|Cronobacter phage vB_CsaM_leE/viral segment/) | 1 (\*\*\*) | 74.0 | 85.3 |
| Citrobacter phage IME-CF2 | [NC\_029013.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_029013.1) | [KR869820.1](https://www.ncbi.nlm.nih.gov/nuccore/KR869820.1) | 177.69 | 43.2 | [263](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42421/462004|Citrobacter phage IME-CF2/viral segment Unknown/) | 2 | 88.7 | 82.9 |
| Citrobacter phage Miller | [NC\_025414.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_025414.1) | [KM236237.1](https://www.ncbi.nlm.nih.gov/nuccore/KM236237.1) | 178.17 | 43.1 | [277](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/37168/461404|Citrobacter phage Miller/viral segment Unknown/) | 1 | 89.1 | 88.0 |
| Escherichia phage RB16 | [NC\_014467.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_014467.1) | [HM134276.1](https://www.ncbi.nlm.nih.gov/nuccore/HM134276.1) | 176.79 | 43.5 | [270](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4037/455906|Escherichia phage RB16/viral segment Unknown/) | 2 | 82.2 | 86.6 |
| Escherichia phage Lw1 | [NC\_021344.2](https://www.ncbi.nlm.nih.gov/nuccore/NC_021344.2) | [KC801932.2](https://www.ncbi.nlm.nih.gov/nuccore/KC801932.2) | 176.23 | 43.5 | [273](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/17877/460077|Escherichia phage Lw1/viral segment Unknown/) | 1 | 81.0 | 85.3 |

**(\*) determined using VIRIDIC [4]**

**(\*\*) determined using CoreGenes 3.5 [6]**

**(\*\*\*) None indicated in replicon Indo; discovered using tRNAscan-SE [5]**

**The following should be considered strains in this genus:** Citrobacter phage Maroon **[**MH823906.1], Cronobacter phage vB\_CsaM\_leN [KX431560.1], and Citrobacter phage vB\_CfrM\_CfP1 [KX245890.1]

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. The black boxes delineate strains

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**Specific Reference: 2009.007a-rB**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of RB43 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."



**Strain table**

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| **Phage name** | **Accession** | **Belongs to species** |
| Citrobacter phage Maroon | MH823906.1 | *Citrobacter virus Margaery* |
| Cronobacter phage vB\_CsaM\_leN | KX431560.1 | *Cronobacter virus leB* |
| Citrobacter phage vB\_CfrM\_CfP1 | KX245890.1 | *Citrobacter virus Miller* |

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