

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

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| **Code assigned:** | **2020.007B** |  |
| **Short title:** Create one new genus (*Agmunavirus*) with a single species (*Caudovirales*: *Siphoviridae*) | | |
|  | | |

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

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**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 | July 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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| 2020.007B.R.Agmunavirus |

**Abstract**

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| The only classified Brevibacterium virus is LuckyBarnes which belongs to the genus *Luckybarnesvirus*. This proposal creates another genus. |

**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**

**Source of the name of this taxon:** The name of this genus is derived directly from that of the type phage Brevibacterium phage AGM1.

**History**: “Brevibacterium aurantiacum is among the most important bacterial species used as a surface ripening culture for such cheeses. Various cheese and environmental samples were collected between 2013 and 2016 from three manufacturing sites in Canada, where flavour and colour defects were observed in washed rind cheeses. One phage isolate, named AGM1, was randomly selected for measurements and is made of an isometric capsid of 57 ± 3 nm in diameter and a long non-contractile flexible tail of 315 ± 12 nm long and 8 ± 1 nm wide. The analysis showed that all 16 of the B. aurantiacum phages analysed are cos-type phages that possess 30 overhang cos-sites that are nine nucleotides long (5’-CGCCGGAGA-3’)” [de Melo AG et al. 2020].This manuscript describes these phages as virulent (obligately lyric) but the annotation indicates integrase and repressor homologs.

**Specific Reference:** de Melo AG, Rousseau GM, Tremblay DM, Labrie SJ, Moineau S. DNA tandem repeats contribute to the genetic diversity of Brevibacterium aurantiacum phages [published online ahead of print, 2020 Jun 8]. Environ Microbiol. 2020;10.1111/1462-2920.15113.

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Brevibacterium phage AGM1 | MN023176 | 36.03 | 60.77 | 53 | 0 |

**List of strains:**

|  |  |  |
| --- | --- | --- |
| [**Phage Name**](https://blast.ncbi.nlm.nih.gov/Blast.cgi) | **Accession** | **Belongs to species** |
| [Brevibacterium phage AGM16](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698232215) | [MN023191.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023191.1?report=genbank&log$=nucltop&blast_rank=1&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM15](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698232161) | [MN023190.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023190.1?report=genbank&log$=nucltop&blast_rank=2&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM6](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231672) | [MN023181.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023181.1?report=genbank&log$=nucltop&blast_rank=3&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM12](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231999) | [MN023187.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023187.1?report=genbank&log$=nucltop&blast_rank=5&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM2](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231455) | [MN023177.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023177.1?report=genbank&log$=nucltop&blast_rank=6&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM8](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231782) | [MN023183.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023183.1?report=genbank&log$=nucltop&blast_rank=7&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM5](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231618) | [MN023180.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023180.1?report=genbank&log$=nucltop&blast_rank=8&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM3](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231510) | [MN023178.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023178.1?report=genbank&log$=nucltop&blast_rank=9&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM7](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231727) | [MN023182.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023182.1?report=genbank&log$=nucltop&blast_rank=10&RID=HXJW7MCS014) | *Brevibacterium virus AGM9* |
| [Brevibacterium phage AGM14](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698232107) | [MN023189.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023189.1?report=genbank&log$=nucltop&blast_rank=11&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM9](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231836) | [MN023184.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023184.1?report=genbank&log$=nucltop&blast_rank=12&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM4](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231564) | [MN023179.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023179.1?report=genbank&log$=nucltop&blast_rank=13&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM13](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698232053) | [MN023188.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023188.1?report=genbank&log$=nucltop&blast_rank=14&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM11](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231945) | [MN023186.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023186.1?report=genbank&log$=nucltop&blast_rank=15&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |
| [Brevibacterium phage AGM10](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1698231890) | [MN023185.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN023185.1?report=genbank&log$=nucltop&blast_rank=16&RID=HXJW7MCS014) | *Brevibacterium virus AGM1* |

**BLASTN homologs:** Genomic orphans [1-3].

**Electron micrograph:** Negative stained AGM1 (kindly provide by Sylvain Moineau O.C., O.Q., Ph.D., MSRC, Professeur titulaire, Chaire de recherche du Canada sur les bacteriophages, Curateur du Centre de référence pour virus bactériens Félix d'Hérelle. Département de biochimie, de microbiologie et de bio-informatique, Université Laval, Québec, Canada, G1V 0A6)

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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of AGM1 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."

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**References**

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