

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

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| **Code assigned:** | **2020.088B** |  |
| **Short title:** Create one new genus (*Lambovirus*) including five new species (*Caudovirales*: *Siphoviridae*) | | |
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**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 | 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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| 2020.088B.R.Lambovirus.xlsx |

**Abstract**

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| This proposal recognizes five distinct viruses classified by The Actinobacteriophage Database to Cluster DV as being members of a new genus, *Lambovirus*. |

**Text of proposal**

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**Supporting evidence**

**Proposal: To create a new genus, *Lambovirus* containing five species**

**History:** Lytic Gordonia phage Lambo was isolated in 2018 by Michael Lauer (University of Pittsburgh) as part of the Phage Hunters Integrating Research and Education. It was isolated from flower garden soil using *Gordonia rubripertincta* NRRL B-16540 as the host bacterium. The Actinobacteriophage Database classifies this phage and its relatives to Cluster DV.

**Source of the name of this taxon:** The name of this genus is derived from the name of the first virus of this type, Gordonia phage Lambo.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Proteins | tRNAs | Overall % DNA sequence identity (\*) | % Common proteins (\*\*) |
| Lambo | [MN234220.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234220.1) | 67.81 | 58.3 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84848/708405|Gordonia phage Lambo/viral segment/) | 0 | 100 | 100 |
| Ranch | [MN234207.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234207.1) | 66.89 | 58.3 | [101](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84870/708427|Gordonia phage Ranch/viral segment/) | 0 | 83.3 | 91.8 |
| Sadboi | [MN234232.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234232.1) | 67.49 | 58.1 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84859/708416|Gordonia phage Sadboi/viral segment/) | 0 | 82.6 | 90.8 |
| Yikes | [MN586003.1](https://www.ncbi.nlm.nih.gov/nuccore/MN586003.1) | 68.15 | 58.2 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85704/744364|Gordonia phage Yikes/viral segment/) | 0 | 79.8 | 90.8 |
| Gibbin | [MN234190.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234190.1) | 67.79 | 58.3 | [99](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84822/708379|Gordonia phage Gibbin/viral segment/) | 0 | 79.4 | 90.8 |

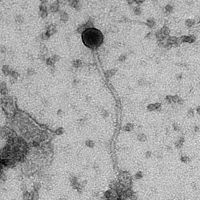
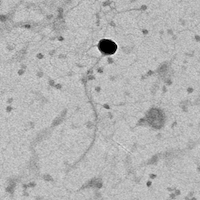
**(\*) determined using BLASTN at NCBI [1-3]**

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

**N.B. Gordonia phage GretelLyn [MN234162.1] is a strain of *Gordonia virus Sadboi.***

**BLASTN homologs:** The next most related phage based upon BLASTN analysis at NCBI [1-3] is Gordonia phage JellyBones which shares <5% DNA sequence identity with Lambo.

**Electron micrograph:** Electron micrograph of negatively stained *Gordonia* phage Gibbin (left panel) and Sadboi (right panel) (<https://phagesdb.org/phages/Gibbin/>; <https://phagesdb.org/phages/Sadboi/>) - Limited permission was granted by The Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

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

**TerL protein**

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**References**

1. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
7. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
8. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.
9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.