

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

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| **Code assigned:** | ***2022.065B*** |  |
| **Short title:** Create a new family (*Pootjesviridae*) with one subfamily and five genera (*Caudoviricetes*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
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**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | April 2022 |
| Date of this revision (if different to above) | October 2022 |

**ICTV-EC comments and response of the proposer**

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| ICTV-EC: Annotate members of the family on the figures for clarity.  Proposer: done. |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| --- |
| 2022.065B.A.v2.Pootjesviridae\_nf.xlsx |

**Abstract**

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| --- |
| We have created a new family named in honour of pioneering Agrobacterium phage researcher named in honour of Christine Pootjes (1927 - 2010). On average the genomes of phages which belong to this family are 150.58 kb (49.08 mol%G+C) and encode for 253 proteins and 0-2 tRNA. At the DNA sequence level all these viruses show ≥11.2% DNA sequence similarity and share 30.5% conserved proteins. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [8]  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [8]  **Family demarcation criteria:** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (ViPTree, GRAViTy dendrogram, vConTACT2 network). Members of the family share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of members of the family). [8] | |

**Supporting evidence**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. This heatmap only shows members of the family *Pootjesviridae*, other phages show no detectable nucleotide sequence similarity.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**. The members of the *Pootjesviridae* are indicated with a **blue rectangle**.





**Phylogeny:** The phylogenetic tree was constructed using the MCPs from these and related phages with phylogeny.fr in “one click” mode [6]. 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 [7] for details." The members of the *Pootjesviridae* are indicated with a **blue rectangle**.

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**Proposals**

1. **Create a new genus, *Trinifflemingvirus* with three species**
2. **Create a new genus, *Innesvirus* with five species**
3. **Create a new subfamily, *Staniewskivirinae*, for these two genera.**
4. **Create a new genus, *Emnonavirus* with one species**
5. **Create a new genus, *Rollinsvirus* with a single species**
6. **Rename the genus *Oliverocinquevirus* to *Heverleevirus***
7. **Create a new family, *Pootjesviridae***
8. **Create a new genus** ***Trinifflemingvirus* with three species**

**Origin of the name of this taxon:** This taxon is in honor of Trinidad Figueroa Fleming (1975-2020), Professor of Botany at the Faculty of Natural Sciences, University of Salta, Argentina. She did studies on the diversity and taxonomy of the family Papilionoideae (Leguminosae) of the Salta region in Argentina. She contributed to the isolation of phages RHEph N34, I34,I46, I9, and I19, which are the subject of this proposal.



(photograph kindly provided by Angela Etcheverry, National University of Salta, Argentina)

**Historical aspects:** Lytic myophage RHph\_Y68 was isolated against a Rhizobium strain in Mexico [11-13]. Phage RHph\_N34 was isolated from agricultural soil from Argentina against Rhizobium etli. Rhizobium phage RHph\_I1\_9 is another Argentine isolate.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Rhizobium phage RHph\_Y68 | [MN988486.1](https://www.ncbi.nlm.nih.gov/nuccore/MN988486.1) | 152.76 | 49.4 | [256](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98417/1553867|Rhizobium phage RHph_Y68/viral segment/) | 100 | 100 |
| Rhizobium phage RHph\_N34 | [MN988534.1](https://www.ncbi.nlm.nih.gov/nuccore/MN988534.1) | 153.81 | 49.0 | [253](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98347/1553797|Rhizobium phage RHph_N34/viral segment/) | 75.5 | 87.5 |
| Rhizobium phage RHph\_I1\_9 | [MN988532.1](https://www.ncbi.nlm.nih.gov/nuccore/MN988532.1) | 154.21 | 48.5 | [255](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98359/1553809|Rhizobium phage RHph_I1_9/viral segment/) | 74.2 | 85.6 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

1. **Create a new genus, *Innesvirus* with five species**

**Origin of the name of this taxon:** This taxon is named in honour of the John Innes Institute (currently John Innes Centre) where the first phage of its type was isolated.

**Historical aspects:** Lytic transducing phage RL38 was isolated on Rhizobium leguminosarum was isolated by Vicky Buchanan-Wollaston, John Innes Institute, Norwich (UK) [14]. It has a relatively broad host range, infecting strains of Rhizobium leguminosarum, R. phaseoli, and R. trifolii. Rhizobium phage RL38JI DNA is resistant to cleavage by a variety of restriction endonucleases, and is only partially sensitive to digestion by pancreatic DNase I or by micrococcal nuclease, because of the presence of a modified base replacing dC [15]. Phage RL2RES was isolated by Penny R. Hirsch, IACR-Rothamsted, Harpenden, Hertfordshire (UK). It possesses an icosahedral 90 nm diameter head, a 140 nm tail, and a base plate structure, and is also capable of generalized lytic transduction [16]. These two phages were sequenced by Gunathilake et al. [17].

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Rhizobium phage P9VFCI | [MT778839.1](https://www.ncbi.nlm.nih.gov/nuccore/MT778839.1) | 156.5 | 49.9 | [257](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94223/979297|Rhizobium phage P9VFCI/viral segment/) | 100 | 100 |
| Rhizobium phage vB\_RleM\_P10VF | [KM199770.1](https://www.ncbi.nlm.nih.gov/nuccore/KM199770.1) | 156.45 | 49.9 | [257](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/34497/460955|Rhizobium phage vB_RleM_P10VF/viral segment Unknown/) | 91.3 | 93.0 |
| Rhizobium phage AF3 | [MT778837.1](https://www.ncbi.nlm.nih.gov/nuccore/MT778837.1) | 156.19 | 50.1 | [258](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94221/979295|Rhizobium phage AF3/viral segment/) | 92.9 | 93.8 |
| Rhizobium phage RL38J1 | [MN549360.1](https://www.ncbi.nlm.nih.gov/nuccore/MN549360.1) | 158.58 | 49.8 | [270](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86430/751406|Rhizobium phage RL38J1/viral segment/) | 82.8 | 91.4 |
| Rhizobium phage RL2RES | [MN549361.1](https://www.ncbi.nlm.nih.gov/nuccore/MN549361.1) | 156.88 | 50.0 | [261](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86428/751404|Rhizobium phage RL2RES/viral segment/) | 82.3 | 88.7 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

1. **Create a new subfamily, *Staniewskivirinae*, for these two genera.**

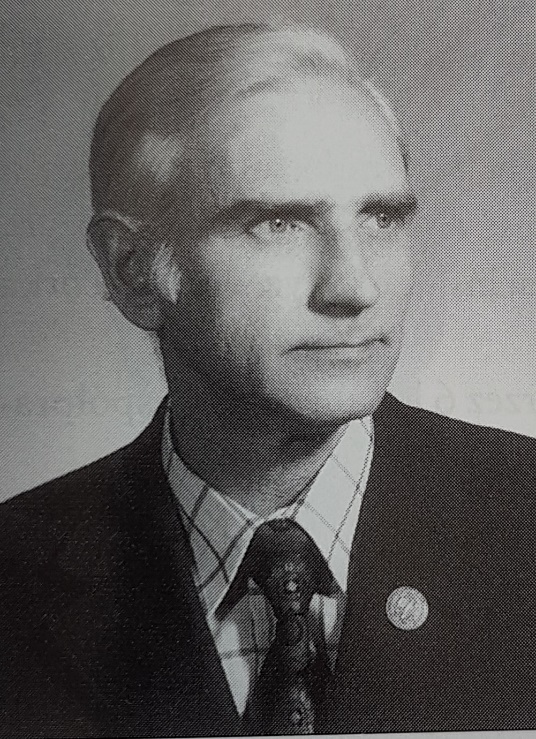
**Origin of the name of this taxon:** This taxon is named in honour of Dr Ryszard Staniewski who was born on January 2nd, 1927 in Zdołbunów in Wołyń (now Ukraine), where he graduated from primary school. In 1945, he and his family were repatriated to Chełm Lubelski (Poland), where he graduated from high school. In 1950, he began biological studies at the Faculty of Mathematics and Natural Sciences of UMCS, which he completed in 1955 with a diploma in general microbiology. The supervisor of his Master thesis was prof. Władysław Kunicki-Goldfinger.

In 1954 he was employed at the Department of General Microbiology of UMCS. In 1966 he obtained a doctoral degree in natural sciences in the field of microbiology on the basis of dissertation entitled “Typing of Rhizobium with the use of phages” (the supervisor of his doctoral dissertation was Prof. Jadwiga Marszewska-Ziemięcka), and was promoted to the position of assistant professor.

The subject of Dr. Staniewski's research work concerned pioneering research on phages of bacteria forming symbiosis with legumes, competition of these bacteria for the infection of a host plant, and the phenomenon of phage DNA transfection. He was the author/co-author of over 30 original papers, he completed scientific internships in Poland and abroad (Institute of Microbiology, Medical Academy in Szeged, Hungary), presented results of his research at national and international scientific symposia.

He conducted classes and seminars in the field of general and medical microbiology, and immunology. The students were particularly interested in his original lectures of food bacteriology. He was the promoter and supervisor of several dozen of master theses, and co-author of the academic textbook on microbiology. He was member of the Polish Society of Microbiologists, the Polish Genetic Society, he was the treasurer of the Nicolaus Copernicus Nature Society. For his research and teaching activities, he was awarded by the Rector of UMCS and the Secretary of the Polish Academy of Sciences, he also received other Orders and National Distinction, including the Golden Cross of Merit, the Knight's Cross of the Order of Polonia Restituta, and the Medal of the National Education Commission.

He died at the age of 91 on November 1st, 2018.



(kindly provided by dr hab. Andrzej Mazur, Uniwersytet Marii Curie-Skłodowskiej w Lublinie, Poland)

**Data supporting the creation of this taxon:** At the DNA sequence level Rhizobium phage P9VFCI and Rhizobium phage RHph\_Y68 share 62.1% DNA sequence similarity, while at the protein level they share 205 common proteins (80.1% homologous proteins). These values are in line with the creation of a subfamily.

1. **Create a new genus, *Emnonavirus* with one species**

**Origin of the name of this taxon:** The name of this taxon is derived from that of phage phiM9.

**Historical aspects:** Phage PhiM9 was isolated from commercial alfalfa inoculants manufactured in the United States (K. LeMieux, M.S. thesis, Northeastern University, Boston, Mass.; quoted in [18]). Structurally, ΦM9 has a T=16 capsid formed from repeating units of an extended gp23-like subunit that assemble through interactions between one subunit and the adjacent E-loop insertion domain [19]. It was sequenced by Kathryn M Jones’s group at Florida State University, Tallahassee, Florida, USA.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Sinorhizobium phage phiM9 | [KP881232.1](https://www.ncbi.nlm.nih.gov/nuccore/KP881232.1) | 149.22 | 49.8 | [271](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42131/461842|Sinorhizobium phage phiM9/viral segment Unknown/) | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

1. **Create a new genus, *Rollinsvirus* with a single species.**

**Origin of the name of this taxon:** This taxon is named after the location (1201 Rollins Street) where in the Informatics Research Core Facility, University of Missouri, Agrobacterium phage Atu\_ph04 was isolated and sequenced.

**Historical aspects:** Agrobacterium tumefaciens myophage Atu\_ph04 was isolated from waste water in Columbia, MO (USA). The average capsid head diameter of Atu\_ph04 is 84.7 nm and its tail length is 79.8 nm [20].

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Agrobacterium phage Atu\_ph04 | [MF403007.1](https://www.ncbi.nlm.nih.gov/nuccore/MF403007.1) | 143.35 | 49.4 | [223](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63796/466417|Agrobacterium phage Atu_ph04/viral segment/) | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

1. **Rename *Oliverocinquevirus* to *Heverleevirus***

**Historical aspects:** The genus *Oliverocinquevirus* was created through Taxonomy Proposal 2021.058B. The authors have requested a name change. Heverlee is a borough of the city of Leuven where at KULeuven Agrobacterium phage OLIVR5 was isolated and sequenced.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Agrobacterium phage OLIVR5 | [MT234342.1](https://www.ncbi.nlm.nih.gov/nuccore/MT234342.1) | 151.07 | 46.9 | [259](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/100265/1598843|Agrobacterium phage OLIVR5/viral segment/) | 2 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

1. **Create a new family, *Pootjesviridae***

**Origin of the name of this taxon:** This taxon is named in honour of Dr. Christine Pootjes (b. 1927, Clifton, N.J., d. 2010, Hershey PA). She received her PhD from Rutgers before taking up an academic position in the Department of Microbiology at Pennsylvania State University. A recipient of the Excellence in Advising award in 1987, she was on the University Senate from 1978 to 1981. She retired in 1990. Dr. Pootjes was one of the first scientist to study Agrobacterium phages. (pronounced Poh-jez)



(reproduced from : <https://www.legacy.com/us/obituaries/centredaily/name/christine-pootjes-obituary?id=14717222>)

**Logic for creation of this taxon:** At the DNA sequence level this group of phages shares ≥11.2% sequence identity. Using the Bidirectional Best Hit algorithm in CoreGenes 5.0 (<https://coregenes.ngrok.io/>) phages Agrobacterium phage OLIVR5 (MT234342.1), Sinorhizobium phage phiM9 (KP881232.1), Rhizobium phage P9VFCI (MT778839.1) and Rhizobium phage RHph\_Y68 (MN988486.1) share 76 homologs. The latter include: UDP-galactopyranose mutase, sliding clamp DNA polymerase accessory protein, sliding clamp loader subunit, clamp loader subunit, DNA polymerase, N-acetylmuramoyl-L-alanine amidase, dCMP deaminase, DNA polymerase III subunit epsilon, DNA ligase, topoisomerase II medium subunit, DNA gyrase, DNA helicase, large and small terminases, DNA end protector protein, ribonucleoside-diphosphate reductase, tail tube and sheath proteins, portal, major capsid, neck proteins, thymidylate synthase, RNaseH, and a number of baseplate proteins. Based upon an average of 248 proteins this corresponds to 30.5% conserved proteins in this taxon.

**References**

1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870
2. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. <http://kronos.icbm.uni-oldenburg.de/viridic/>
3. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. <https://www.genome.jp/viptree/>
4. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423
5. 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.
6. 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.
7. 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.
8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.
9. 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.
10. Olsen NS, Hendriksen NB, Hansen LH and Kot W. A New High-Throughput Screening Method for Phages: Enabling Crude Isolation and Fast Identification of Diverse Phages with Therapeutic Potential. Phage (New Rochelle) 1 (3), 137-148 (2020) <https://www.liebertpub.com/doi/10.1089/phage.2020.0016>
11. Santamaría RI, Bustos P, Van Cauwenberghe J, González V. Hidden diversity of double-stranded DNA phages in symbiotic Rhizobium species. Philos Trans R Soc Lond B Biol Sci. 2022 Jan 17;377(1842):20200468. doi: 10.1098/rstb.2020.0468. Epub 2021 Nov 29. PMID: 34839703; PMCID: PMC8628074.
12. Van Cauwenberghe J, Santamaría RI, Bustos P, Juárez S, Ducci MA, Fleming TF, Etcheverry AV, González V. Correction to: Spatial patterns in phage-Rhizobium coevolutionary interactions across regions of common bean domestication. ISME J. 2021 Jul;15(7):2167. doi: 10.1038/s41396-021-00963-5. Erratum for: ISME J. 2021 Jul;15(7):2092-2106. PMID: 33854191; PMCID: PMC8245540.
13. Van Cauwenberghe J, Santamaría RI, Bustos P, Juárez S, Ducci MA, Figueroa Fleming T, Etcheverry AV, González V. Spatial patterns in phage-Rhizobium coevolutionary interactions across regions of common bean domestication. ISME J. 2021 Jul;15(7):2092-2106. doi: 10.1038/s41396-021-00907-z. Epub 2021 Feb 8. Erratum in: ISME J. 2021 Apr 14;: PMID: 33558688; PMCID: PMC8245606.
14. Buchanan-Wollaston V. Generalized Transduction in Rhizobium leguminosarum. J. Gen Microbiol 112: 135-142 (1979). <https://doi.org/10.1099/00221287-112-1-135>
15. Swinton D, Hattman S, Benzinger R, Buchanan-Wollaston V, Beringer J. Replacement of the deoxycytidine residues in Rhizobium bacteriophage RL38JI DNA. FEBS Lett. 1985 May 20;184(2):294-8. doi: 10.1016/0014-5793(85)80625-6. PMID: 2987032.
16. Mendum TA, Clark IM, Hirsch PR. Characterization of two novel Rhizobium leguminosarum bacteriophages from a field release site of genetically-modified rhizobia. Antonie Van Leeuwenhoek. 2001 Jun;79(2):189-97. doi: 10.1023/a:1010238412538. PMID: 11520005.
17. Gunathilake KMD, Bhat SV, Yost CK, Hynes MF. Genome Sequences of vB\_RleM\_RL38JI and vB\_RleM\_RL2RES, Two Virulent Rhizobium leguminosarum Transducing Phages. Microbiol Resour Announc. 2020 Mar 12;9(11):e01589-19. doi: 10.1128/MRA.01589-19. PMID: 32165392; PMCID: PMC7067960.
18. Finan TM, Hartweig E, LeMieux K, Bergman K, Walker GC, Signer ER. General transduction in Rhizobium meliloti. J Bacteriol. 1984 Jul;159(1):120-4. doi: 10.1128/jb.159.1.120-124.1984. PMID: 6330024; PMCID: PMC215601.
19. Johnson MC, Tatum KB, Lynn JS, Brewer TE, Lu S, Washburn BK, Stroupe ME, Jones KM. Sinorhizobium meliloti Phage ΦM9 Defines a New Group of T4 Superfamily Phages with Unusual Genomic Features but a Common T=16 Capsid. J Virol. 2015 Nov;89(21):10945-58. doi: 10.1128/JVI.01353-15. Epub 2015 Aug 26. PMID: 26311868; PMCID: PMC4621102.
20. Attai H, Brown PJB. Isolation and Characterization T4- and T7-Like Phages that Infect the Bacterial Plant Pathogen Agrobacterium tumefaciens. Viruses. 2019 Jun 7;11(6):528. doi: 10.3390/v11060528. PMID: 31181591; PMCID: PMC6630229.