

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

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| **Code assigned:** | **2021.059B** |  |
| **Short title:** Create one new genus (*Oliverunavirus*) including one new species (*Schitoviridae*) | | |
|  | | |

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

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

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**Corresponding author**

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| Jeroen Wagemans |

**List the ICTV Study Group(s) that have seen this proposal**

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

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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 | May 2021 |
| Date of this revision (if different to above) |  |

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

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

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

**Name of accompanying Excel module**

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| 2021.059B.R.Oliverunavirus |

**Abstract**

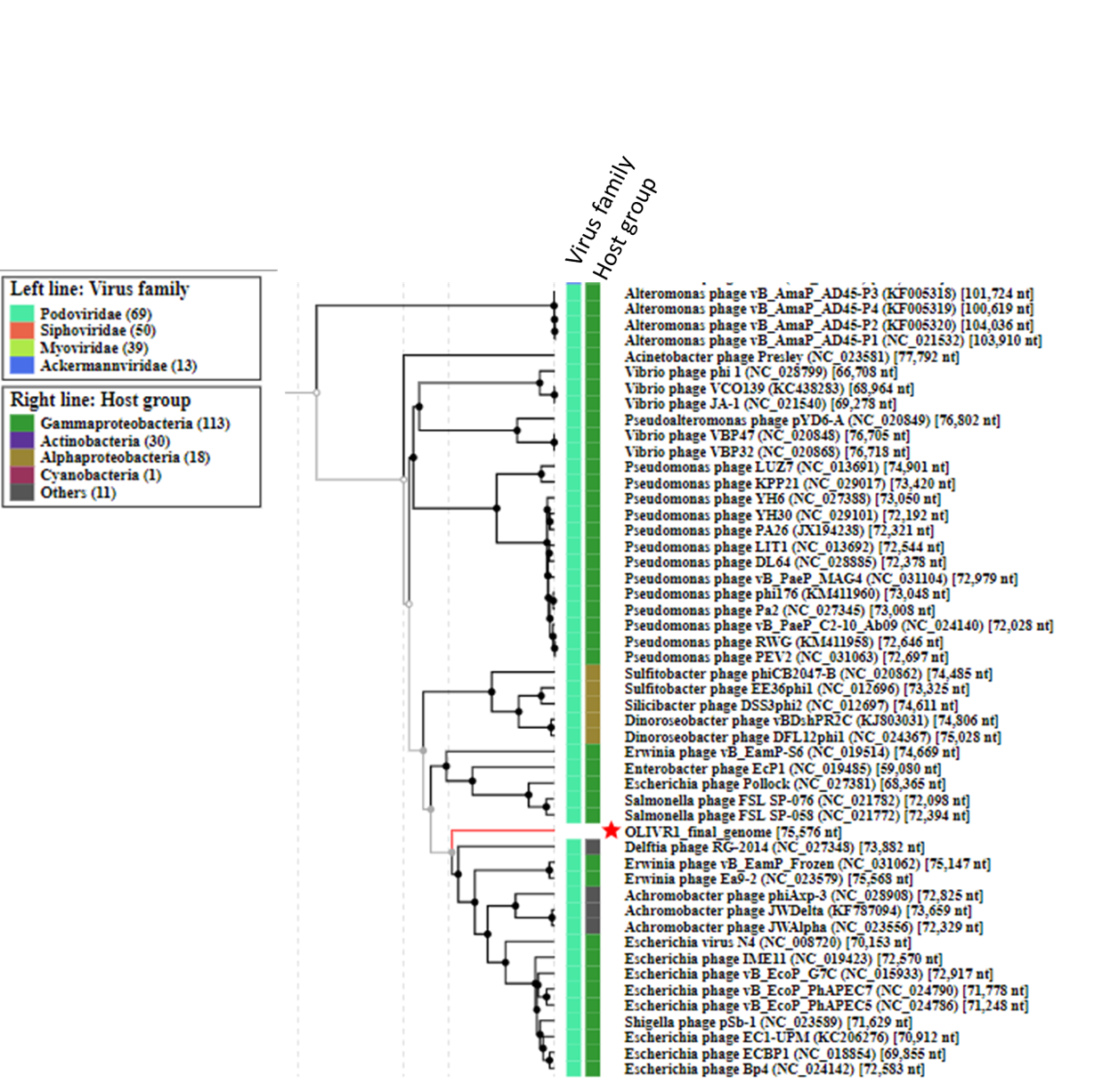
|  |
| --- |
| *Agrobacterium* phages OLIVR1, OLIVR2 and OLIVR3, members of the *Schitoviridae*, are orphan phages. Multidimensional analyses show that these phages make up a new genus, *Oliverunavirus.* The phages belong to the same species and have an average genome size of 75.5 kb with a G+C content of 45.4%. The genomes on average encode 107 proteins and 4 tRNAs. The closest phages according to a VipTree analysis share less than 20% sequence identity. According to phylogenetic analyses based on the virion-associated RNA polymerase and the major capsid protein, the phages cluster together. Combined, this evidence demonstrates that these phages make up a new species in a new genus. |

**Text of proposal**

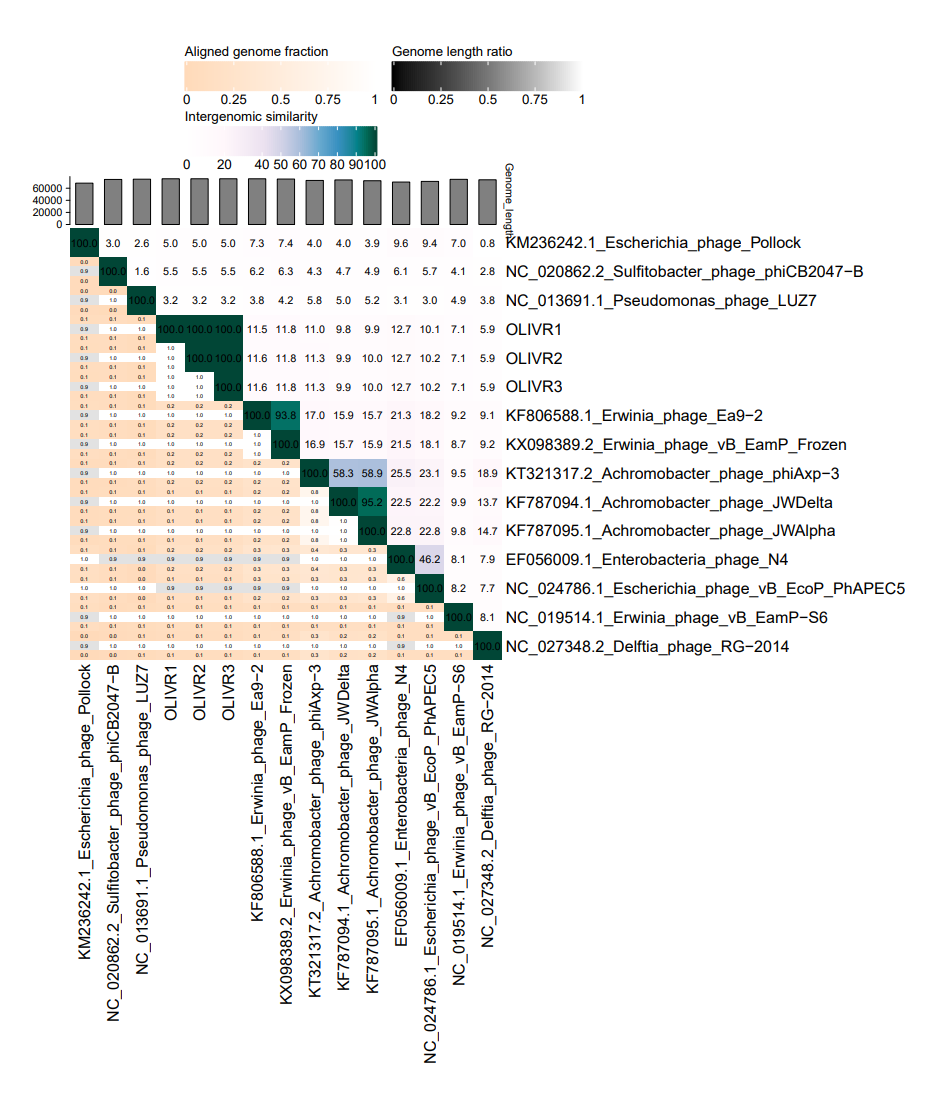
|  |  |
| --- | --- |
| |  | | --- | | History: Tomato greenhouses showing symptoms of crazy roots were sampled for rhizogenic *Agrobacterium* biovar 1 phage isolations. As such three lytic phages, belonging to the *Schitoviridae*, were isolated and referred to as OLIVR1, OLIVR2 and OLIVR3.  Species demarcation criteria: The three phages in collection belong to the same species as they share over 95% BLASTn identity over their genome length as calculated by the distance calculator VIRIDIC [1].  Genus demarcation criteria: A VipTree analysis shows that the phages are quite distant from the other members of the *Schitoviridae* as they share less than 15% intergenomic similarity with the closest phages being *Erwinia* phage Ea9-2 and *Erwinia* phage Frozen. This observation is further supported by phylogenetic analyses based on the virion-associated RNA polymerase and the major capsid protein. | |

**Supporting evidence**

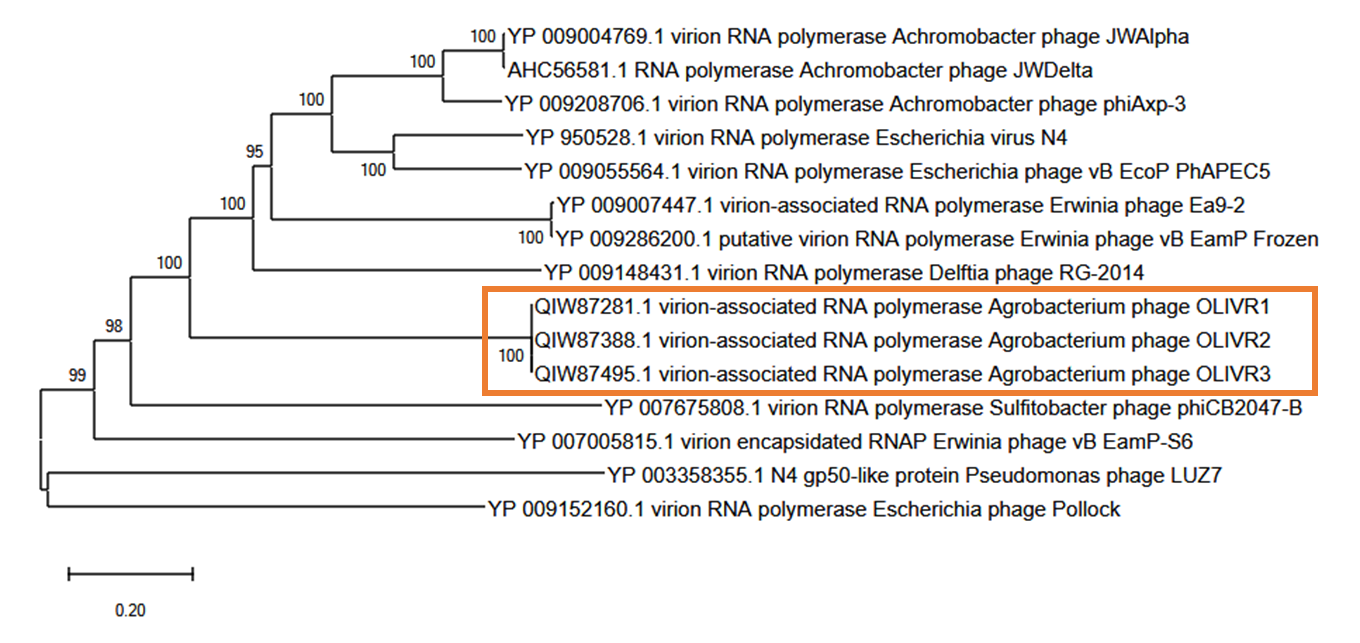
ViPTree analysis ([https://www.genome.jp/viptree/](about:blank)) of OLIVR1 as representative for the phage species [2].

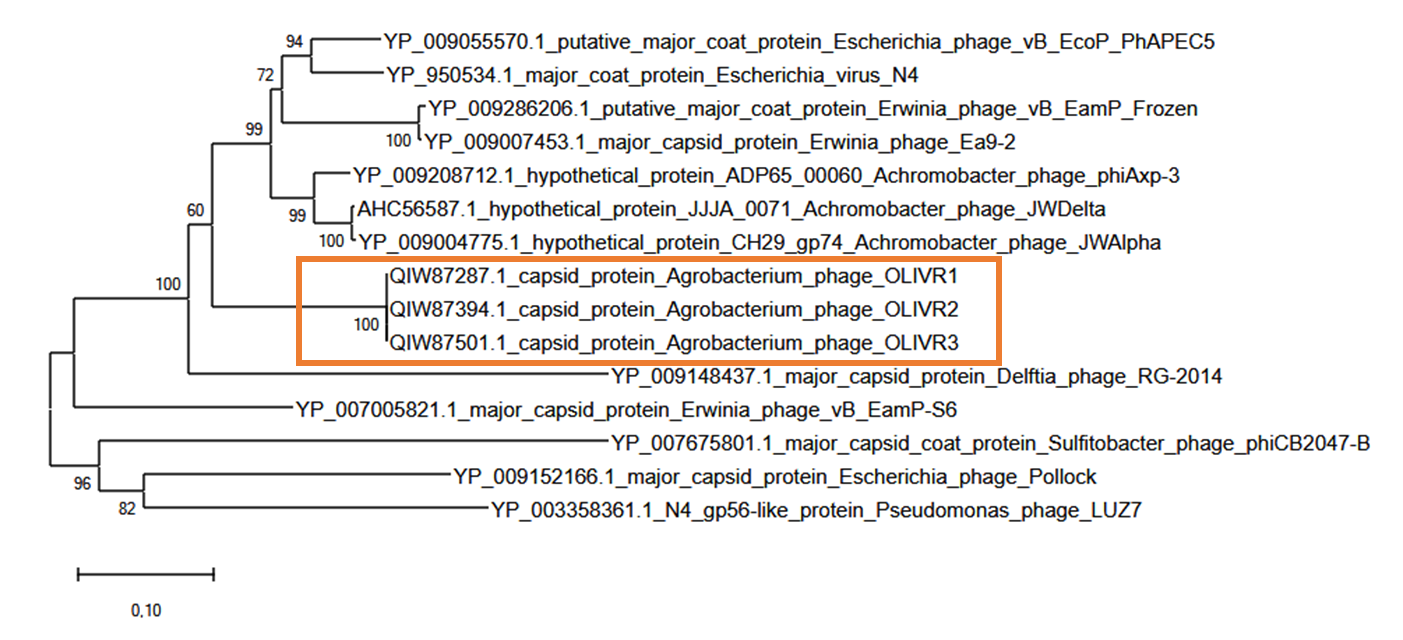


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

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The phylogenetic tree was constructed using the vRNAP (A) and major capsid protein (B) of OLIVR1 and related phages with MEGA X [3]. The amino acid sequence was aligned using MUSCLE and a neighbour joining tree with 1,000 bootstraps was constructed.

**A**

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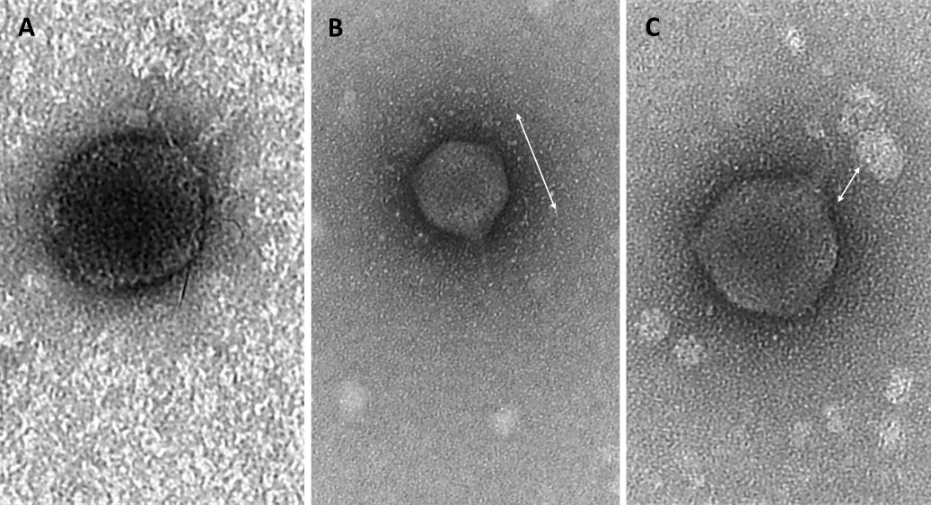
**B**

**Genbank summary**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) |
| *Agrobacterium* phage OLIVR1 |  | [MT234338](https://www.ncbi.nlm.nih.gov/nuccore/MT234338&doptcmdl=GenBank) | 75.57 | 45.4 | 108 | 4 | 100 |
| *Agrobacterium* phage OLIVR2 |  | [MT234339](https://www.ncbi.nlm.nih.gov/nuccore/MT234339&doptcmdl=GenBank) | 75.57 | 45.4 | 107 | 4 | 100 |
| *Agrobacterium* phage OLIVR3 |  | MT234340 | 75.57 | 45.4 | 107 | 4 | 100 |

**(\*) As identified using VIRIDIC; these phages isolates differ with a few SNPs.**

**Transmission electron microscopy:** Negatively stained (aqueous 0.5% uranyl acetate) preparation of Xanthomonas phage OLIVR1



**References**

1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12:1268. https://doi.org/10.3390/v12111268

2. Nishimura Y, Yoshida T, Kuronishi M, et al (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33:2379–2380. https://doi.org/10.1093/bioinformatics/btx157

3. Kumar S, Stecher G, Li M, et al (2018) MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Mol Biol Evol 35:1547–1549. https://doi.org/10.1093/molbev/msy096