

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

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| **Code assigned:** | **2021.031B** |  |
| **Short title:** Create one new genus (*Foxunavirus*) including four new species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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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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| 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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| 2021.031B.R.Foxunavirus |

**Abstract**

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| NCBI has identified several orphan phages which belong to the Class *Caudoviricetes* . Our multidimensional analyses places Xanthomonas phage FoX1, FoX2, FoX3 and FoX5 in a new genus, *Foxunavirus*. The average properties of the genomes of these phages are: 44.22 kb (59.5 mol%G+C) encoding for 80 proteins and 0-1 tRNA. Among each other, the phages share less than 95% sequence identity, but more than 70%. The closest phages according to a VipTree analysis share less than 20% similarity. According to phylogenetic analyses of the major capsid protein and large terminase sequence, the phages cluster together. This evidence suggests that these phages belong to a new phage genus. |

**Text of proposal**

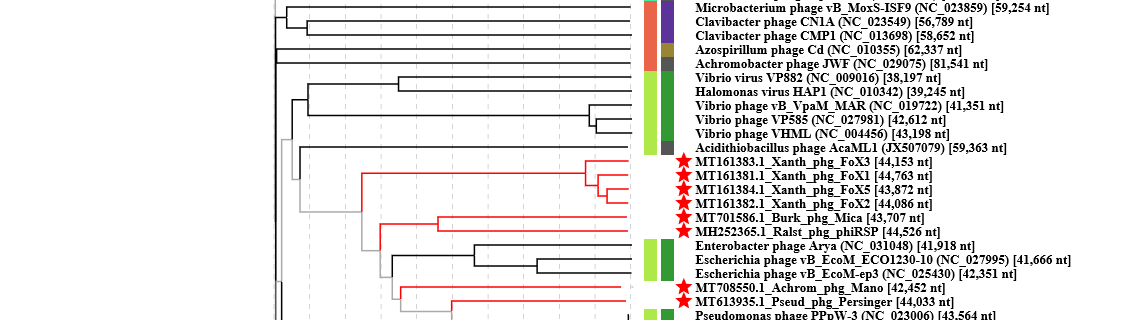
|  |  |
| --- | --- |
| |  | | --- | | **History:** Fields containing brassica crops (white cabbage, red cabbage, kale, brussels sprouts, cauliflower) with typical V-shaped necrotic lesions were sampled for *Xanthomonas campestris* pv. *campestris* bacteriophage isolation. As such, four lytic phages, *Myoviridae*, were isolated and referred to as FoX1, FoX2, FoX3 and FoX5.  **Species demarcation criteria:** The four phages belong to different species as the genomes share less than 95% BLASTn identity over their genome length as calculated according the intergenomic distance calculator VIRIDIC [1].  **Genus demarcation criteria:** Among each other, the four phages share over 70% of sequence identity. Other phages related phages (VipTree [2]), such as *Burkholderia* phage Mica and *Ralstonia* phage phiRSP, share less than 20% identity. According to the amino acid sequence of the major capsid protein, FoX1, FoX2, FoX3 and FoX5, cluster together. | |

**Supporting evidence**

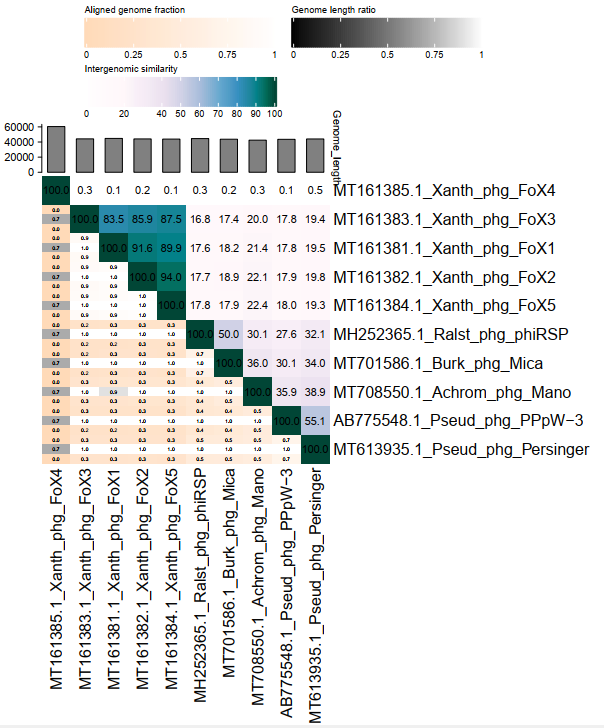
**Source of the name of this taxon:** This genus is named after the first representative of this taxon, *Xanthomonas* phage FoX1

**Molecular Characteristics -**

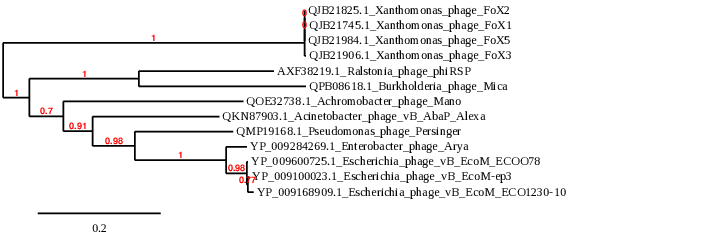
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [2])

**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.



**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein of FoX1 and related phages with phylogeny.fr in “one click” mode [3]. "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 [4] for details."

**MCP**

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) |
| *Xanthomonas* phage FoX1 |  | [MT161381.1](https://www.ncbi.nlm.nih.gov/nuccore/MT161381.1) | 44.76 | 59.4 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/100267/1598845%7CXanthomonas%20phage%20FoX1/viral%20segment/) | 1 | 100 |
| *Xanthomonas* phage FoX2 |  | MT161382.1 | 44.09 | 59.5 | 81 | 1 | 91.6 |
| *Xanthomonas* phage FoX3 |  | MT161383.1 | 44.15 | 59.3 | 78 | 0 | 83.5 |
| *Xanthomonas* phage FoX5 |  | MT161384.1 | 43.87 | 59.8 | 80 | 1 | 89.9 |

**(\*) Determined using VIRIDIC** [1]

**Electron micrograph:** Negatively stained (aqueous 0.5% uranyl acetate) preparation of Xanthomonas phage FoX3

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**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. 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.

4 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.