

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

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| **Code assigned:** | **2021.030B** |  |
| **Short title:** Create one new genus (*Foxquatrovirus*) including one 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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| 2021.030B.R.Foxquatrovirus |

**Abstract**

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| NCBI has identified several orphan phages which belong to the Family *Siphoviridae*. Our multidimensional analyses places *Xanthomonas* phage FoX4 in a new genus, *Foxquatrovirus*. The representative phage has a genome size of 60.4 kb (61.8 mol%G+C) encoding 89 proteins. The phage is an orphan and shares no sequence identity with other phages in the current database. Based on a genome comparison (VipTree and VIRIDIC) along with a phylogenetic analysis of TerL, we propose a new phage genus. |

**Text of proposal**

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| |  | | --- | | **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. Lytic phage FoX4 is a member of the *Siphoviridae*. It is a genomic orphan.  **Species demarcation criteria:** Xanthomonas phage FoX4 is considered an orphan as it does not share homology with other phages currently present in the database. The two closest phages, Xylella phages Sano and Salvo, are quite distant as they share >9% sequence identity (BLASTn and VIRIDIC) [1].  **Genus demarcation criteria:** FoX4 does not share a substantial similarity to other phages currently in databases. According to a VipTree analysis, the closest phages, *Xylella* phages Sano and Salvo, share less than 70% sequence identity with FoX4, suggesting that this phage belongs to a new phage genus. This evidence is supported by a phylogenetic analysis of the TerL amino acid sequence. | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named after the first representative of this taxon, Xanthomonas phage FoX4

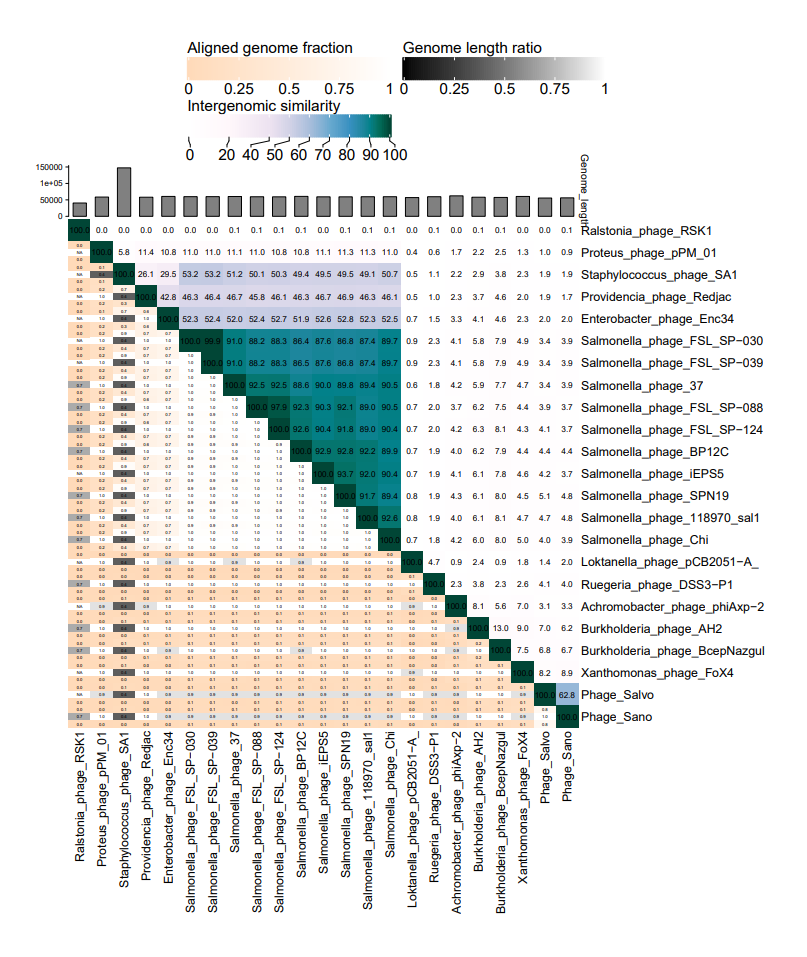
**Specific Reference: /**

**Molecular Characteristics:**

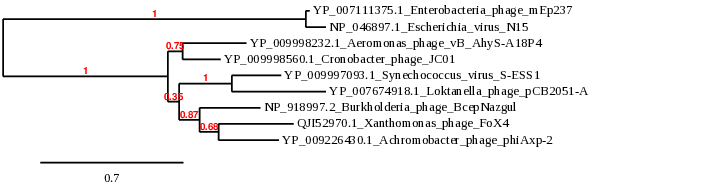
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [2])


**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 terminase large subunit protein of FoX4 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."

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**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Xanthomonas phage FoX4 |  | [MT161385.1](https://www.ncbi.nlm.nih.gov/nuccore/MT161385.1) | 60.42 | 61.8 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/100270/1598848%7CXanthomonas%20phage%20FoX4/viral%20segment/) | 0 |

**Electron micrograph:** Negatively stained (aqueous 0.5% uranyl acetate) preparation of *Xanthomonas* phage FoX4

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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.