

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

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| **Code assigned:** | ***2022.058B*** |  |
| **Short title:** Create three new genera of Ochrobactrum phages each with a single species (*Caudoviricetes*) | | |
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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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| 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**

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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 2022 |
| Date of this revision (if different to above) |  |

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

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**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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| 2022.058B.N.v1.Caudoviricetes\_3ng.xlsx |

**Abstract**

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| This represents the first proposal to officially characterize phages which infect *Ochrobactrum* sp. In each case the DNA sequence and phylogenetic analysis reveal that these phages are genomic orphans. We have created the following genera: *Abaiavirus*, *Namazuvirus* and *Wolominvirus*. |

**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] | |

**Supporting evidence – molecular data**

**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.

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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**.



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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Ochrobactrum phages and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of these genera are indicated with **blue rectangles**. In each case the closest BLASTP homolog is from a bacterium and probably represents a prophage sequence (Top panel). In the lower panel only viral homologs are considered.

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Proposal A. Create a new genus ***Abaiavirus* with a single species**Origin of the name of this taxon: This taxon is named after Abaia - a magical eel in Melanesian mythology.

Historical aspects: Ochrobactrum species are non-fermenting, aerobic, gram-negative  
bacilli that are widespread in the environment and have been isolated from various  
ecological niches, such as water, soil, plants, and animals [11]. Phage POA1180 was  
recovered by mitomycin treatment of strains O. anthropi O1180. This temperate myovirus  
can produce plaque on certain O. anthropic, O. intermedium and O. pseudogrignonense. Its  
head diameter is 66.2 nm; tail length 135.1 nm and tail width 18.3 nm.

Electron micrograph: N/A

Genome summary: genomic orphan

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Ochrobactrum phage POA1180 | KX669658.1 | 41.66 | 56.6 | 58 | 100 | 100 | 100 |

(\*) determined using BLASTn [1](\*\*) determined using CoreGenes 3.5 [5]

Proposal B. Create a new genus ***Namazuvirus***with a single species

Origin of the name of this taxon: This taxon is named after Namazu – a giant catfish which is known to cause earthquakes in Japanese mythology.

Historical aspects: Ochrobactrum species are non-fermenting, aerobic, gram-negative  
bacilli that are widespread in the environment and have been isolated from various  
ecological niches, such as water, soil, plants, and animals [11]. Phage POI1126 was  
recovered by mitomycin treatment of strains O. anthropi O1180. This temperate podovirus  
can produce plaque on certain O. anthropic, O. intermedium, O. oryzae and O. tritici. Its  
head diameter is 74.2 nm; tail length 19.2nm and tail width 15.1 nm.  
  
Electron micrograph: N/A

Genome summary: genomic orphan

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| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Ochrobactrum phage POI1126 | KY417925.1 | 59.78 | 56.2 | 78 | 100 | 100 |

(\*) determined using BLASTn [1](\*\*) determined using CoreGenes 3.5 [5]

Proposal C. Create a new genus *Wolominvirus*, with a single species

Origin of the name of this taxon: This taxon is named after the city in Poland where phage vB\_OspP\_OH was discovered.

Historical aspects: Ochrobactrum species are non-fermenting, aerobic, gram-negative  
bacilli that are widespread in the environment and have been isolated from various  
ecological niches, such as water, soil, plants, and animals [11]. Podophage vB\_OspP\_OH  
was isolated from Wolomin (Poland) sewage. It is the first lytic phage for this bacterium. Its  
genome possesses short (55 bp) terminal repeats.

Electron micrograph: N/A

Genome summary: genomic orphan

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| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Ochrobactrum phage vB\_OspP\_OH | MT028492.1 | 41.23 | 55.2 | 65 | 100 | 100 |

(\*) determined using BLASTn [1](\*\*) determined using CoreGenes 3.5 [5]

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