

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

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| **Code assigned:** | **2022.002F** |  |
| **Short title:** Establishment of 4 new genera, 13 new species and renaming 9 species in the family *Bacilladnaviridae* | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Chair Fungal and Protist Viruses Subcommittee |

**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** |
|  |  |  |  |
|  |  |  |  |

**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)** |  |

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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 | 20 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\_Bacilladnaviridae\_4neg\_13\_nsp\_9\_rensp\_final.xlsx |

**Abstract**

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| Bacilladnaviruses are single-stranded (ss) DNA viruses and infect diatoms and so far, they have primarily been identified from marine environments. In the last 5 years, sixteen new genomes of viruses in the family *Bacilladnaviridae* have been sequenced. To classify these, we propose creating four new genera and thirteen new species. Also, we rename nine existing species to binomial format with a freeform epithet. |

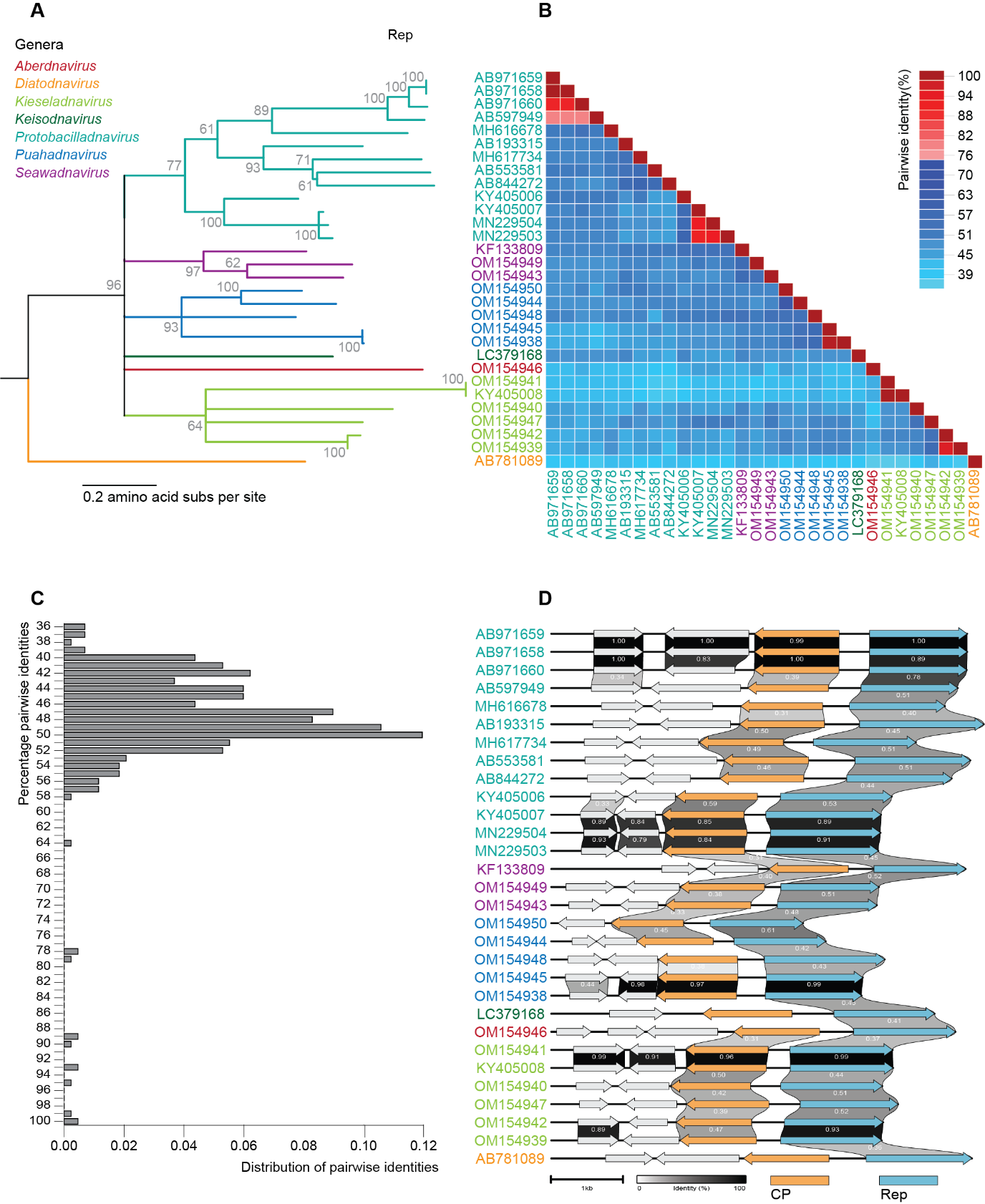
**Text of proposal**

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| |  | | --- | | Bacilladnaviruses are single-stranded DNA viruses in the Phylum *Cressdnaviricota* (class *Arfiviricetes* and order *Baphyvirales*) [1]. The Rep sequences of bacilladnaviruses have conserved motifs distinct from those typical of Reps of other cressdnaviruses, primarily in Motif I and Motif III [2]. The capsid protein of bacilladnaviruses is most closely related to the CP of positive-sense RNA viruses of the *Nodaviridae* family based on structural homology [2,3].  Currently, the family *Bacilladnaviridae* comprises three genera, namely, *Diatodnavirus* (1 species), *Kieseladnavirus* (1 species) and *Protobacilladnavirus* (7 species) [4]. The genera were established based on the phylogeny of the HUH superfamily replication initiation protein (Rep), the most conserved protein encoded by bacilladnaviruses, whereas 75% amino acid identity threshold was chosen as a species demarcation criterion. Since the creation of the family *Bacilladnaviridae* in 2018 [4], the number of viral genomes within this family has doubled.  Based on the maximum likelihood phylogeny to the Rep sequences, we note four well supported clades (>64% bootstrap support) and three singletons (Figure 1A). Thus, we propose to establish four new genera to classify the new viruses and we move one species from *Protobacilladnavirus* (accession # KF133809) to a new genus, *Seawadnavirus*.  We propose the following four names for the new genera   1. *Aberdnavirus*: Derived from **aber** which is an estuary in Welsh 2. *Keisodnavirus*: Derived from **Keisō** (珪藻) which is diatom in Japanese 3. *Puahadnavirus*: Derived from **pūaha**tanga which is an estuary in Māori 4. *Seawadnavirus*: Derived from **seawa**ter   Analysis of the Rep amino acid sequences shows that most members display 36-58% pairwise identities, with only a small fraction showing >78% (Figure 1B, 1C).  The 75% pairwise identity as a species demarcation criterion was proposed for members of the genus *Protobacilladnavirus* [4] (because other genera were represented by singletons). Based on the distribution of the pairwise identities of all 30 bacilladnavirus Rep amino acid sequences, we propose to extend and apply the same demarcation criterion to all genera with more than one species.  Finally, to comply with the mandated binomial species naming format [5], we have renamed established species using binomial nomenclature with a freeform epithet. All epithets are either derivatives of host species or isolation source using names in local languages of people that inhabit that region or settlers (Table 1). | |

**Supporting evidence**

**Table 1:** Summary of the taxonomy of bacilladnaviruses. New taxa names are provided in blue font.

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| **New genus** | **Accession** | **Virus name** | **species** | **Epithet notes** |
| *Keisodnavirus* | LC379168 | Chaetoceros tenuissimus DNA virus SS12-43V | *Keisodnavirus chaetenu* | ***Chae****toceros* ***tenu****issimus* |
| *Protobacilladnavirus* | AB193315 | Chaetoceros salsugineum DNA virus | *Protobacilladnavirus chasesal* | ***Chae****toceros* ***sal****sugineum* |
|  | MH617734 | Bacilladnaviridae sp. isolate ctia23 | *Protobacilladnavirus snap* | Red **snap**per |
|  | AB844272 | Chaetoceros sp. DNA virus 7 | *Protobacilladnavirus chaetoc* | ***Chaetoc****eros sp* |
|  | AB553581 | Chaetoceros lorenzianus DNA virus | *Protobacilladnavirus chaelor* | ***Chae****toceros* ***lor****enzianus* |
|  | MH616678 | Bacilladnaviridae sp. isolate ctdc18 | *Protobacilladnavirus redsnap* | **Red** **snap**per |
|  | AB971660 | Chaetoceros tenuissimus DNA virus type-II | *Protobacilladnavirus tenuis* | *Chaetoceros* ***tenuis****simus* |
|  | AB971659 | Chaetoceros tenuissimus DNA virus type-II | *Protobacilladnavirus tenuis* | *Chaetoceros* ***tenuis****simus* |
|  | AB971658 | Chaetoceros tenuissimus DNA virus type-II | *Protobacilladnavirus tenuis* | *Chaetoceros* ***tenuis****simus* |
|  | AB597949 | Chaetoceros tenuissimus DNA virus | *Protobacilladnavirus tenuis* | *Chaetoceros* ***tenuis****simus* |
|  | MN229504 | Haslea ostrearia associated bacilladnavirus | *Protobacilladnavirus hasleos* | ***Hasle****a* ***os****trearia* |
|  | KY405007 | Amphibola crenata associated bacilladnavirus 2 | *Protobacilladnavirus hasleos* | ***Hasle****a* ***os****trearia* |
|  | MN229503 | Haslea ostrearia associated bacilladnavirus | *Protobacilladnavirus hasleos* | ***Hasle****a* ***os****trearia* |
|  | KY405006 | Amphibola crenata associated bacilladnavirus 1 | *Protobacilladnavirus mudflat* | **mud**-**flat** snail common name for Amphibola crenata |
| *Puahadnavirus* | OM154950 | Avonheates virus SG\_479 | *Puahadnavirus kaisui* | seawater in Japanese |
|  | OM154944 | Avonheates virus SG\_19 | *Puahadnavirus aber* | estuary in Welsh |
|  | OM154948 | Avonheates virus SG\_146 | *Puahadnavirus inbhir* | estuary in Scotish |
|  | OM154945 | Avonheates virus SG\_28 | *Puahadnavirus takutai* | coast in Māori |
|  | OM154938 | Avonheates virus SG2\_28 | *Puahadnavirus takutai* | coast in Māori |
|  | OM154949 | Avonheates virus SG\_154 | *Puahadnavirus gataifale* | estuary / coast in Samoan |
| *Seawadnavirus* | KF133809 | Bacillariodnavirus LDMD-2013 | *Seawadnavirus kuhtahan* | seawater in Massaachusett |
|  | OM154943 | Avonheates virus SG\_924 | *Seawadnavirus avonheat* | **Avon**-**Heat**hcote estuary |
|  | OM154947 | Avonheates virus SG\_120 | *Seawadnavirus katao* | water in Māori |
| *Kieseladnavirus* | KY405008 | Avon-Heathcote estuary associated bacilladnavirus | *Kieseladnavirus ampcren* | ***Amp****hibola* ***Cren****ata* |
|  | OM154942 | Avonheates virus SG\_4\_10 | *Kieseladnavirus titiko* | Amphibola crenata in Māori |
|  | OM154939 | Avonheates virus Gas\_102 | *Kieseladnavirus titiko* | Amphibola crenata in Māori |
|  | OM154941 | Avonheates virus Gas\_1207 | *Kieseladnavirus ampcren* | ***Amp****hibola* ***Cren****ata* |
|  | OM154940 | Avonheates virus Gas\_1078 | *Kieseladnavirus karahue* | common name for Amphibola crenata in Māori |
| *Aberdnavirus* | OM154946 | Avonheates virus SG\_61 | *Aberdnavirus waitai* | Seawater in Māori |
| *Diatodnavirus* | AB781089 | Chaetoceros setoense DNA virus | *Diatodnavirus chaese* | ***Chaet****oceros* ***se****toense* |

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**Figure 1: A.** Maximum likelihood phylogenetic tree inferred from the aligned (MAFFT v7 [6]) Rep amino acid sequences of bacilladnaviruses using PhyML 3.0 [7] with rtREV+G+I as best substitution model determined using ProtTest [8]. Branches with <60% bootstrap support have been collapsed using TreeGraph2 [9]. **B**. Pairwise identity matrix of the Rep amino acid sequences of bacilladnaviruses determined using SDT v1.2 [10]. **C**. Distribution of pairwise identities of the Rep amino acid sequences of bacilladnaviruses determine using SDT v1.2 [10]. **D**. Genome organization and similarities between encoded proteins of the genomes of bacilladnaviruses determined using Clinker [11].

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