This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: TITLE, AUTHORS, etc

Code assigned:	***2009.002a-fF***	(to be completed by ICTV officers)

Short title: Create unassigned genus, Bacilladnavirus, infecting marine diatoms (Bacillariophytes)
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Yuji Tomaru (tomaruy@affrc.go.jp), Keizo Nagasaki (nagasaki@affrc.go.jp)

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.002aF***	(assigned by ICTV officers)

To create 1 new species with the name(s):

Chaetoceros salsugineum DNA virus 01

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.002bF***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Bacilladnavirus*** **(new)**
Subfamily:	***unassigned***
Family:	***unassigned***
Order:	***unassigned***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

CsalDNAV01 (*Chaetoceros salsugineum DNA virus 01*) is an ssDNA virus infecting a colony-forming marine diatom *C. salsugineum*. As the virions were found to be accumulating in the nucleus, it was first reported as "CsNIV (*C. salsugineum* nuclear inclusion virus)" by Nagasaki et al. (2005). Due to the increase in number of algal viruses made into culture, here we propose to change the virus abbreviation name (into *CsalDNAV01*) to avoid nomenclatural confusion. The genome structure is very strange, which consists of a single molecule of covalently closed circular single-stranded DNA (ssDNA; 6,000 nt), as well as a segment of linear ssDNA (997 nt); the linear segment is complementary to a portion of the closed circle creating a partially double-stranded region. Integrating the above information, it is rational to propose *CsalDNAV01* as a new virus species. Full nucleotide sequence of *CsalDNAV01* genome is registered with GenBank accession number AB193315.

In "Virus Taxonomy: the 8th Report of the International Committee on Taxonomy of Viruses", there are currently no reports of diatom-infecting ssDNA viruses. Since its publication, the full genome sequence of *CsalDNAV01* has been elucidated and the virus has been intensively characterized. Based on these reason, proposing *CsalDNAV01* as new species, and in addition, creating a new genus for this virus species are considered to be rational.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.002cF***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Chaetoceros salsugineum DNA virus 01

Code	***2009.002dF***	(assigned by ICTV officers)

To name the new genus: *Bacilladnavirus*

assigning a new genus to higher taxa

Code	***2009.002eF***	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	***unassigned***
Family:	***unassigned***
Order:	***unassigned***

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	***2009.002fF***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Chaetoceros salsugineum DNA virus 01 (CsalDNAV01)

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Code		(assigned by ICTV officers)

To assign the following as additional species of the new genus:

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

In "Virus Taxonomy: the 8th Report of the International Committee on Taxonomy of Viruses", there are currently no reports of diatom-infecting ssDNA viruses. Since then, the full genome sequence of a diatom-infecting ssDNA virus (*CsalDNAV01*) has been elucidated and the virus has been intensively characterized. Based on the results, here we propose a new diatom-infecting ssDNA genus "*Bacilladnavirus*". *CsalDNAV01* is proposed as the type species of the genus *Bacilladnavirus*.

Origin of the new genus name:

ss*DNA* *virus* infecting *Bacilla*riophytes → *Bacilladnavirus*

Reasons to justify the choice of type species:

CsalDNAV01 is the first-isolated diatom-infecting ssDNA virus and the only intensively-studied virus species within the genus *Bacilladnavirus*.

Species demarcation criteria in the new genus:

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Nagasaki, K., Tomaru, Y., Takao, Y., Nishida, K., Shirai, Y., Suzuki, H., Nagumo. T. (2005) Previously unknown virus infects marine diatom. Appl. Environ. Microbiol., 71(7): 3528-3535.
2. Park, Y., Jung, S.-E., Tomaru, Y., Choi, W.-B., Mizumoto, H., Nagasaki, K., Choi, T.-J. (2009) Characterization of the Chaetoceros salsugineum nuclear inclusion virus coat protein gene. Virus Res. in press.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.
The use of Figures and Tables is strongly recommended.

CsalDNAV01 is an icosahedral virus (~38 nm in diameter) accumulating in the nucleus of the bloom-forming diatom *Chaetoceros salsugineum* (Fig. 1). This virus was previously referred to under the abbreviation CsNIV (*Chaetoceros salsugineum* nuclear inclusion virus) in Nagasaki et al. (2005). The latent period and burst size are <24 h and ~300 infectious units per host cell, respectively (the burst size is most likely underestimated). *CsalDNAV01* genome structure is unique among those of previously reported viruses; it consists of a single molecule of covalently-closed circular single-stranded DNA (ssDNA; 6,000 nt), as well as a segment of linear ssDNA (997 nt). The linear segment is complementary to a portion of the closed circle creating a partially double-stranded region (only the dsDNA region is resistant to S1-nuclease). Six ORFs were found in the genome (Fig. 2). ORF2 and ORF3 respectively encode a replication-associated protein and a capsid protein; the former shows a relatively low similarity to the bird-infecting circoviruses having a circular ssDNA genome. Products of the other four ORFs are unknown.

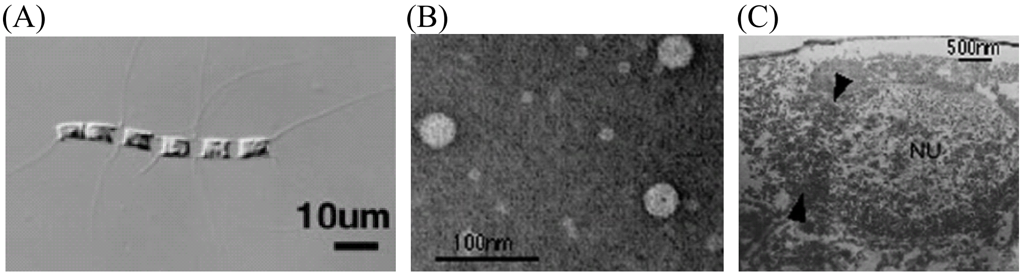

Fig. 1. (A) Colony of *Chaetoceros salsugineum* cells. (B) Negatively-stained CsalDNAV particles. (C) Thin section of a CsalDNAV-infected cell in which the nuclear envelope was partially ruptured (arrowhead). NU, a nucleus. (reprinted with copyright permission from the American Society for Microbiology: Nagasaki, K. et al. *Appl. Environ. Microbiol.* **71(7):** 3528-3535. [published in July 2005])

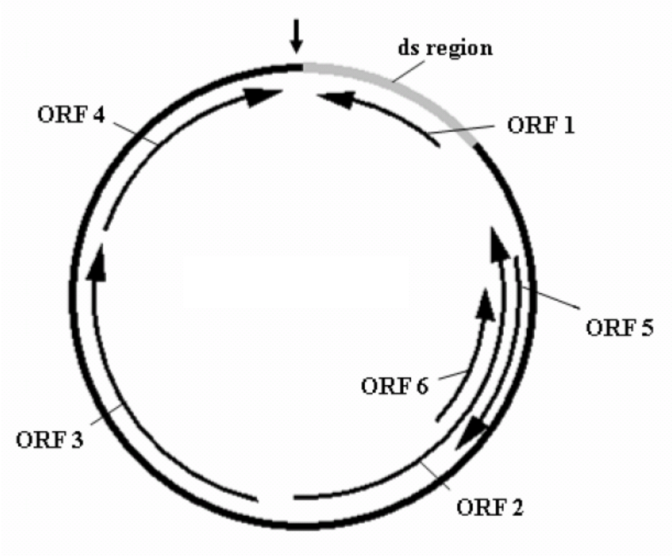

Fig. 2. Analysis of the complete nucleotide sequence of CsalDNAV which is 6,000 nt long. The presence of six putative ORFs is observed in CsalDNAV genome. The downward arrow indicates the beginning of the CsalDNAV nucleotide sequence. The position and orientation of each ORF is indicated by arc arrows. ds region = double-stranded DNA region which is 997 nt long. (reprinted with copyright permission from Elsevier B.V.: Choi, T-J. et al. *Virus Res.*, **142:** 127-133. [published in June 2009])