

Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Genus in an existing Family

Code[†] To create a new genus in the family*

Code[†] To name the new genus*

Code[†] To designate the species
As the type species of the new genus*

Code[†] To designate the following viruses as species of the new genus*:

Heterosigma akashiwo virus 01 (HaV01)

Code[†] To designate the following viruses as tentative species in the new genus*:

~~Heterosigma akashiwo virus 01 (HaV01)~~
Heterosigma akashiwo virus 02 (HaV02)
Heterosigma akashiwo virus 03 (HaV03)
Heterosigma akashiwo virus 04 (HaV04)
Heterosigma akashiwo virus 05 (HaV05)
Heterosigma akashiwo virus 06 (HaV06)
Heterosigma akashiwo virus 07 (HaV07)
Heterosigma akashiwo virus 08 (HaV08)
Heterosigma akashiwo virus 09 (HaV09)
Heterosigma akashiwo virus 10 (HaV10)
Heterosigma akashiwo virus 11 (HaV11)
Heterosigma akashiwo virus 12 (HaV12)
Heterosigma akashiwo virus 13 (HaV13)
Heterosigma akashiwo virus 14 (HaV14)
Heterosigma akashiwo virus 15 (HaV15)

[†] Assigned by ICTV officers

* repeat these lines and the corresponding arguments for each genus created in the family

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New Taxonomic Order

Order	<i>Caudovirales</i>
Family	<i>Phycodnaviridae</i>
Genus	<i>Raphidovirus</i>

Type Species

List of Species in the genus

List of Tentative Species in the Genus

Heterosigma akashiwo virus 01 (HaV01)

Heterosigma akashiwo virus 01 (HaV01)

~~*Heterosigma akashiwo virus 01 (HaV01)*~~

Heterosigma akashiwo virus 02 (HaV02)

Heterosigma akashiwo virus 03 (HaV03)

Heterosigma akashiwo virus 04 (HaV04)

Heterosigma akashiwo virus 05 (HaV05)

Heterosigma akashiwo virus 06 (HaV06)

Heterosigma akashiwo virus 07 (HaV07)

Heterosigma akashiwo virus 08 (HaV08)

Heterosigma akashiwo virus 09 (HaV09)

Heterosigma akashiwo virus 10 (HaV10)

Heterosigma akashiwo virus 11 (HaV11)

Heterosigma akashiwo virus 12 (HaV12)

Heterosigma akashiwo virus 13 (HaV13)

Heterosigma akashiwo virus 14 (HaV14)

Heterosigma akashiwo virus 15 (HaV15)

Argumentation to choose the type species in the genus

Original isolate which has been most comprehensively characterised compared to the other isolates. The 294 kbp genome of the *Heterosigma akashiwo virus 01 (HaV01)* type species has been partially (ca. 80%) sequenced.

Species demarcation criteria in the genus

Not applicable

List of Species in the created genus

Official virus species names are in italics. Tentative virus names, alternative names (), strains, or serotypes are not italicised. Virus names and assigned abbreviations () are:

Heterosigma akashiwo virus 01 (HaV01)

List of Tentative Species in the created genus

~~**Heterosigma akashiwo virus 01 (HaV01)**~~

Heterosigma akashiwo virus 02 (HaV02)

Heterosigma akashiwo virus 03 (HaV03)

Heterosigma akashiwo virus 04 (HaV04)

Heterosigma akashiwo virus 05 (HaV05)

Heterosigma akashiwo virus 06 (HaV06)

Heterosigma akashiwo virus 07 (HaV07)

Heterosigma akashiwo virus 08 (HaV08)

Heterosigma akashiwo virus 09 (HaV09)

Heterosigma akashiwo virus 10 (HaV10)

Heterosigma akashiwo virus 11 (HaV11)

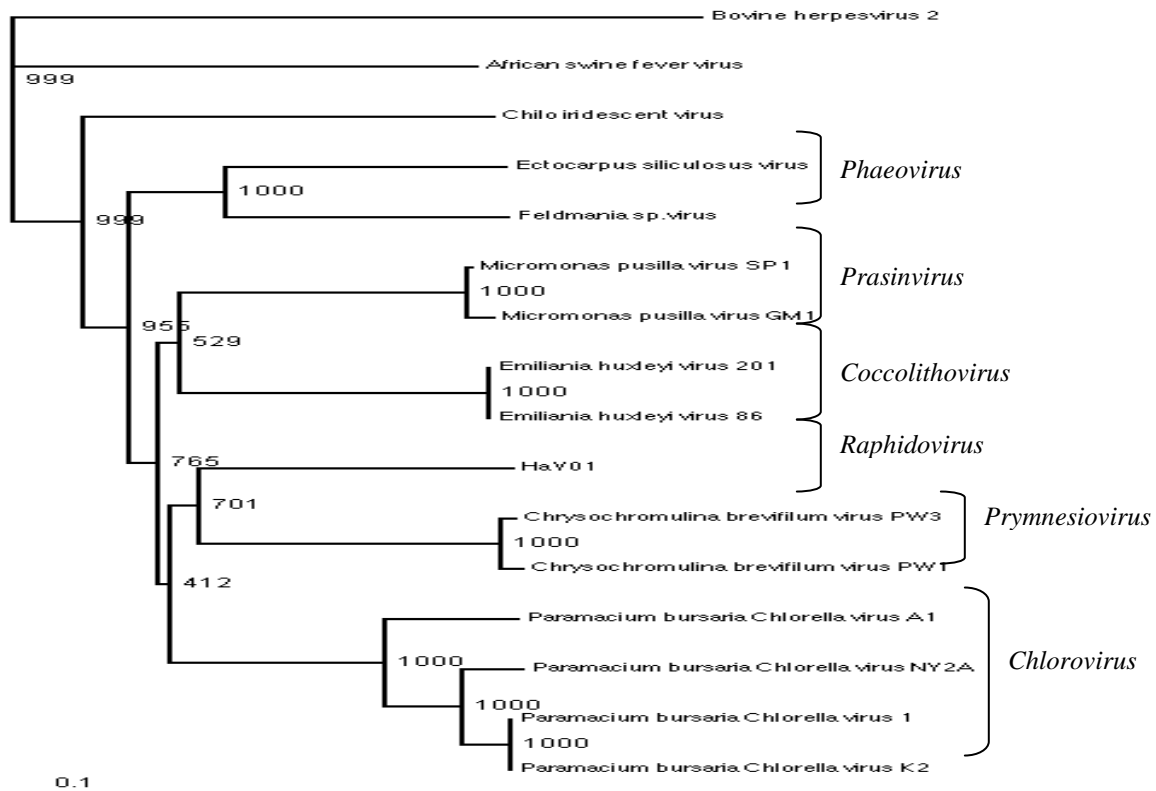
Heterosigma akashiwo virus 12 (HaV12)

Heterosigma akashiwo virus 13 (HaV13)

Heterosigma akashiwo virus 14 (HaV14)

Argumentation to create a new genus:

Phylogenetic analysis of DNA polymerase gene fragments of HaV01 suggests that *Heterosigma akashiwo* viruses belong to a new genus within the family of algal viruses, *Phycodnaviridae* (see figure below). These viruses infect a marine alga. The typical HaV strain HaV01 contains a large dsDNA genome approx. 294 kbp (~~in preparation for submission~~), it has icosohedral symmetry and is 202 +/- 6 nm (~~average +/- standard deviation~~); characteristics that collectively suggest they belong to the family *Phycodnaviridae*. Considering that the host *H. akashiwo* belongs to the class Raphidophyceae, a new genus “Raphidovirus” should be proposed according to the previous examples of Phycodnaviruses. Phylogenetic analysis in conjunction with the host range of the virus isolates suggest they do not belong to any of the current four genera within the *Phycodnaviridae*.



A neighbour-joining tree showing the phylogenetic relationships of *Heterosigma akashiwo* virus 01 (HaV01) and the other algal viruses based on sequence analysis of DNA polymerase gene fragments. The Bovine herpesvirus was used as an out-group. The numbers at the nodes indicate bootstrap values ($n = 1000$). The scale bar represents 0.1 fixed mutation per nucleotide position.

Raphidoviruses infect the harmful bloom causing raphidophyte, *Heterosigma akashiwo* (Raphidophyceae), a marine alga which has a world-wide distribution. *H. akashiwo* is well known for forming dense blooms in the coastal areas, and often causes serious damage to fish aquacultures. The *Raphidoviruses* outlined in this report were isolated from *H. akashiwo* blooms in Unoshima Port, Fukuoka Prefecture, Japan in June 1996 and in Nomi Bay, Kochi Prefecture, Japan in July 1996. These viruses are relatively easy to isolate and susceptible host strains usually lyse between 2 and 7 days after the addition of filtered seawater. Viral replication occurs in the host cytoplasm. The latent period and the burst size of HaV01 is 30-33 h and ca. 770 at 20 °C, respectively. HaV infection is considered one of the important factors causing the disintegration of *H. akashiwo* blooms. Although these viruses rapidly degrade to lose infectivity even when kept at 4 °C in the dark, they can be easily cryopreserved.

Origin of the proposed genus name

These viruses infect the harmful bloom-forming microalga *Heterosigma akashiwo* that belongs to the class Raphidophyceae. The genus name is derived from the class name of the host organism.

References

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- Tarutani K., Nagasaki K. & Yamaguchi M. (2000) Viral Impacts on Total Abundance and Clonal Composition of the Harmful Bloom-Forming Phytoplankton *Heterosigma akashiwo*. *Appl. Environ. Microbiol.* **66(11)**: 4916-4920
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Annexes:

Not applicable.