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:	***2011.001a-dF***	(to be completed by ICTV officers)

Short title: create the genus Cafeteriavirus in the family Mimiviridae for the new species Cafeteria roenbergensis virus
(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:

Matthias G. Fischer (mfischer@mpimf-heidelberg.mpg.de), Curtis A. Suttle (csuttle@eos.ubc.ca)

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

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**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2011.001aF***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Cafeteriavirus* (new)**
Subfamily:	**unassigned**
Family:	***Mimiviridae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Cafeteria roenbergensis virus	GU244497

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Cafeteria roenbergensis virus (CroV) is a novel nucleocytoplasmic large DNA virus (NCLDV, Fig.1) that infects the marine phagotrophic flagellate *Cafeteria roenbergensis* and was isolated in 1991 from Gulf of Mexico coastal waters[1]. The virion consists of a 300 nm icosahedral capsid with internal lipid membranes (Fig.2). Within the host cell, CroV replicates in the cytoplasm via large virion factories. The CroV genome is a 730 kb linear, double-stranded DNA chromosome (Fig.3) with 20-90 kb long repeat regions at the genome termini[2]. The G+C content of the genome is 23%. The diverse coding potential comprises 544 predicted protein-coding genes and 22 tRNA genes. About one-third of the genes have detectable homologues in *Acanthamoeba polyphaga* mimivirus. CroV encodes its own transcription machinery, multiple DNA repair enzymes including two DNA photolyases, translation proteins including isoleucyl-tRNA synthetase, and enzymes for the biosynthesis of KDO, a bacterial lipopolysaccharide component[2]. The genome is rich in FNIP-like repeats (>400 copies) and two promoter motifs, associated with early and late genes, have been identified[2]. Four genes contain an intein: DNA polymerase B, RNA polymerase II subunit Rpb2, DNA topoisomerase IIA, and ribonucleotide reductase large subunit.

Because of these unique features, we propose to establish the new species *Cafeteria roenbergensis virus* (CroV) within the new genus *Cafeteriavirus* within the family *Mimiviridae*.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2011.001bF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***unassigned***
Family:	***Mimiviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2011.001cF***	(assigned by ICTV officers)

To name the new genus: *Cafeteriavirus*

Assigning the type species and other species to a new genus

Code	***2011.001dF***	(assigned by ICTV officers)

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

Cafeteria roenbergensis virus

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

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

As outlined in module 2, *Cafeteria roenbergensis* virus has many unique features and is clearly distinct from *Acanthamoeba polyphaga* mimivirus, the only current member of the *Mimiviridae*. Although both viruses have very large genomes (730 kb and 1.181 kb) and share the same early promoter motif as well as many predicted proteins that are exclusive to this family, there are substantial differences in coding potential (544 vs. 981 protein-coding genes), late promoter motifs, genome organization, particle size (300 vs. 500 nm), and host range (marine flagellate vs. freshwater amoeba). Furthermore, there is no detectable sequence conservation at the DNA level. All these observations argue strongly in favor of establishing the new genus *Cafeteriavirus* within the family *Mimiviridae*.

Origin of the new genus name:

Cafeteria is the genus name of the eukaryotic host of *Cafeteria roenbergensis* virus. The host belongs to the phylum Heterokontophyta, subkingdom Stramenopila.

Reasons to justify the choice of type species:

CroV is the only characterized species in the proposed genus

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.

Not applicable (only one species)

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Garza D.R. & Suttle C.A. (1995) Large double-stranded DNA viruses which cause the lysis of a marine heterotrophic nanoflagellate (Bodo sp) occur in natural marine viral communities. Aquat Microb Ecol 9:203-210.
2. Fischer M.G., Allen M.A., Wilson W.H. and Suttle C.A. (2010). A giant virus with a remarkable complement of genes infects marine zooplankton. PNAS 107:19508-19513.

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

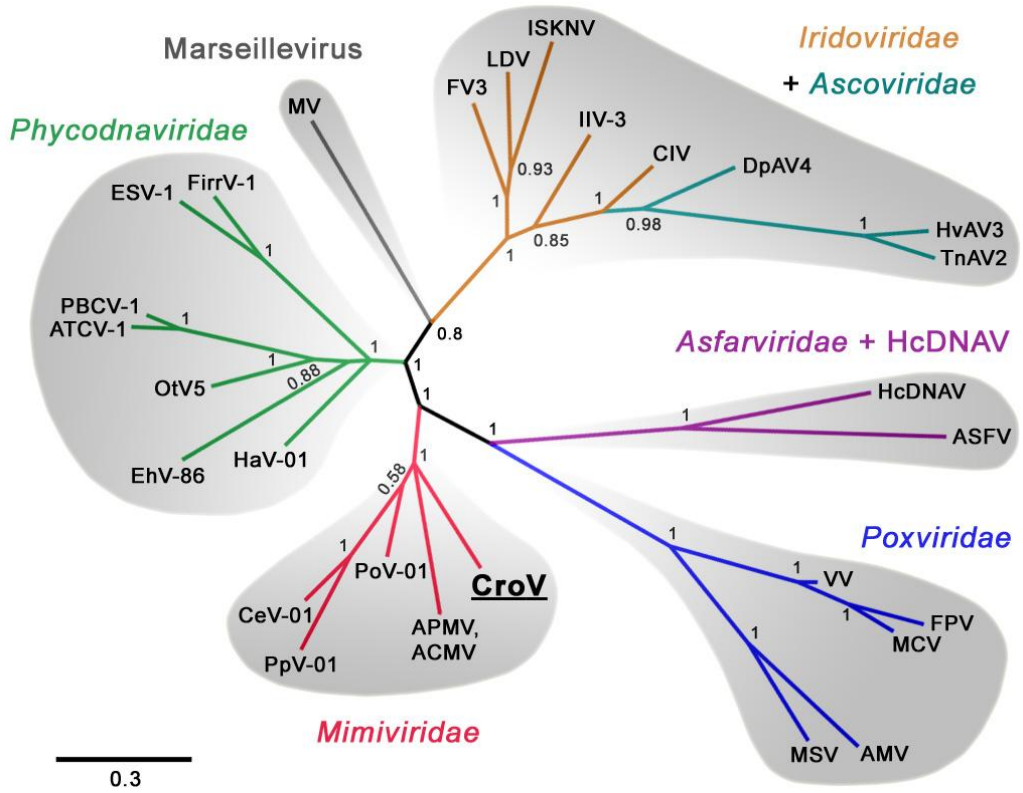

Fig.1. Phylogenetic tree of nucleocytoplasmic large DNA viruses. This Bayesian Inference tree was generated from an alignment of conserved regions of DNA-dependent DNA polymerase B. Abbreviations are as follows: ACMV, *Acanthamoeba castellanii* mamavirus; AMV, *Amsacta moorei* entomopoxvirus; APMV, *Acanthamoeba polyphaga* mimivirus; ASFV, African swine fever virus; ATCV-1, *Acanthocystis turfacea* virus 1; CeV-01, *Chrysochromulina ericina* virus 01; CIV, Chilo iridiscent virus; CroV, *Cafeteria roenbergensis* virus; DpAV4, *Diadromus pulchellus* ascovirus 4a; EhV-86, *Emiliania huxleyi* virus 86; ESV-1, *Ectocarpus siliculosus* virus 1; FirrV-1, *Feldmannia irregularis* virus 1; FPV, Fowlpox virus; FV3, Frog virus 3; HaV-01, *Heterosigma akashiwo* virus 01; HcDNAV, *Heterocapsa circularisquama* DNA virus; HvAV3, *Heliothis virescens* ascovirus 3e; IIV-3, Invertebrate iridiscent virus 3; ISNKV, Infectious

spleen and kidney necrosis virus; LDV, Lymphocystis disease virus; MCV, *Molluscum contagiosum* virus; MSV, *Melanoplus sanguinipes* entomopoxvirus; MV, Marseillevirus; OtV5, *Ostreococcus tauri* virus 5; PBCV-1, *Paramecium bursarium* chlorella virus 1; PoV-01, *Pyramimonas orientalis* virus 01; PpV-01, *Phaeocystis pouchetti* virus 01; TnAV2, *Trichoplusia ni* ascovirus 2C; VV, Vaccinia virus.

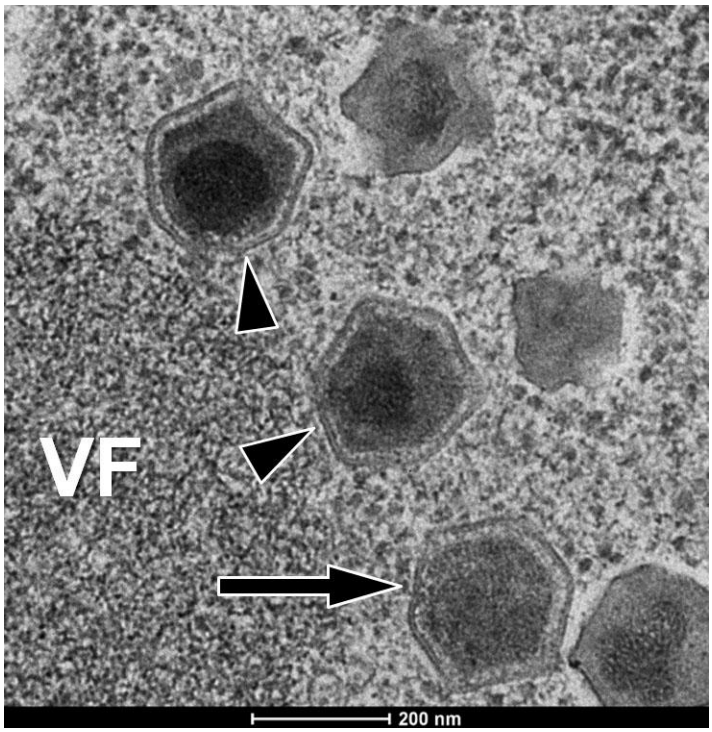

Fig.2. Transmission electron micrograph of CroV particles at the periphery of the cytoplasmic virion factory (VF). Immature particles still attached to the VF are marked by arrowheads, a mature particle is marked by an arrow.

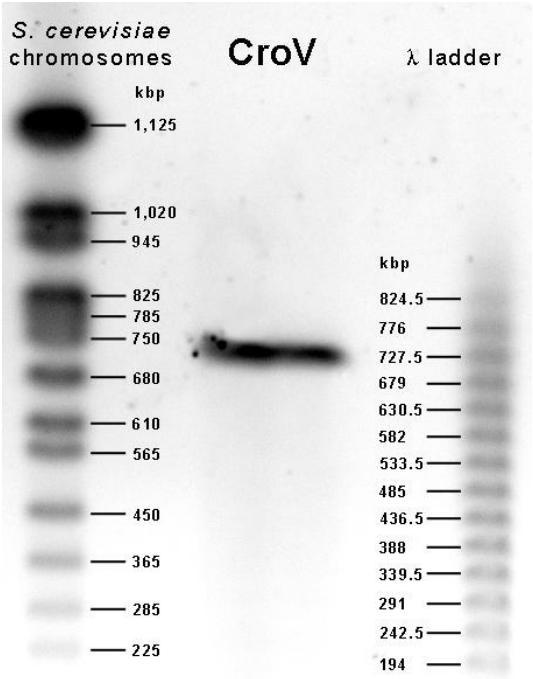

Fig.3. Pulsed-field gel electrophoresis of CroV genomic DNA.