



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:	2010.001aF	(to be completed by ICTV officers)
Short title: Create species <i>Acanthocystis turfacea chlorella virus 1</i> in the genus <i>Chlorovirus</i>		
(e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>
	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>
		5 <input type="checkbox"/>

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

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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)

Fungal virus subcommittee

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

Date first submitted to ICTV:

April 30, 2010

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	2010.001aF	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Chlorovirus</i>	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.
Subfamily:		
Family:	<i>Phycodnaviridae</i>	
Order:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Acanthocystis turfacea chlorella virus 1</i>		NC_008724

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

Currently there are 3 species in the Chlorovirus genus. Each of these species infect different chlorella isolates; all of the chlorella isolates normally live as endosymbionts. Each of the species have multiple members, whose nucleotide sequences can differ by as much as 20-25% - even members in the same species. ATCV-1 infects a different chlorella isolate than the others - a chlorella that normally lives as a symbiont in the heliozoon *Acanthocystis turfacea*. The ~288 kb ATCV-1 genome has ~329 protein-encoding and 11 tRNA encoding genes. About 80% of these genes exist in all of the other Chlorovirus species and 20% differ. The amino acid identity between the prototype Chlorovirus PBCV-1 and ATCV-1 for DNA polymerase and DNA topoisomerase enzymes are 71% and 66%, respectively. ATCV-1 has some protein encoding genes that have not been detected in the other Chloroviruses, including ribonucleoside-triphosphate reductase, UDP-glucose 4,6 dehydratase, and mannose-6-phosphate isomerase.

A Bayesian Inference Tree of 15 DNA Polymerase protein sequences clearly indicates that ATCV-1 should be considered a new species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bubeck, J.A., and A.J.P. Pfitzner. (2005). Isolation and characterization of a new type of chlorovirus that infects an endosymbiotic chlorella strain of the heliozoon *Acanthocystis turfaceae*. *J. Gen. Virol.* 86, 2871-2877.

Fitzgerald, L.A., M.V. Graves, X. Li, J. Hartigan, A.J.P. Pfitzner, E. Hoffart, and J.L. Van Etten. (2007). Sequence and annotation of the 288-kb ATCV-1 virus that infects an endosymbiotic chlorella strain of the heliozoon *Acanthocystis turfacea*. *Virology* 362, 350-361.

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.

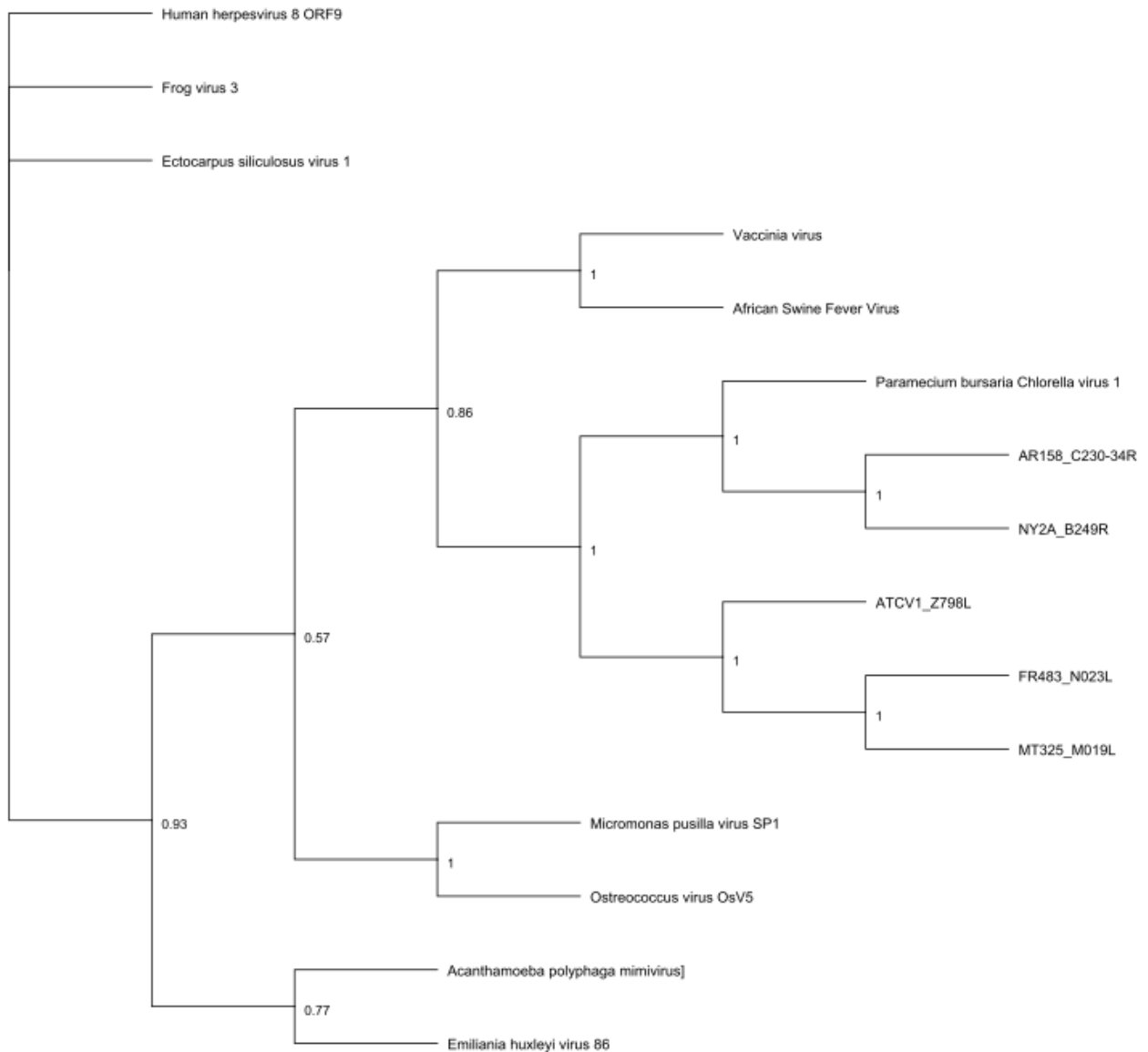


Figure 1. Bayesian Inference Tree of 15 DNA Polymerase protein sequences. The phylogenetic tree was generated using the MUSCLE alignment with a maximum number of iterations of 8 and MrBayes tree building programs within the Geneious Pro 4.8.5 software program. The Poisson amino acid rate matrix (gamma rate variation and an evaluation category of four) and the MCMC algorithm (chain length setting of 1,100,000; the number of chains was 4, the temperature of heated chains of 0.2, a subsampling frequency of 200, with a burn in length of 100,000 and a random seed number of 327) were utilized with the program having chosen NY2A B139R as the Outgroup (“Bootstrap” values are shown). [Tree made by Ms. Gentry Lewis]