

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:	2010.003aF.N.v1	(to be completed by ICTV officers)				
Short title: Create species nam family <i>Phycodnaviridae</i> (e.g. 6 new species in the genus <i>A</i> Modules attached (modules 1 and 9 are required)	ned Ostreococcus tauri Zetavirus) 1 🔀 6 🗖	virus OtV5 2 🗌 7 🔲	5 in the ge 3 □ 8 □	nus <i>Prasin</i> 4 □ 9 ⊠	ovirus, 5 🗌	

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

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.

2010.003aF.N.v1 (assigned by ICTV officers) Code

To create 1 new species within:

		Fill	in all that apply.		
Genus: <i>Prasinovirus</i> Subfamily:		• If	If the higher taxon has yet to be		
		Cr "(created (In a later module, below) write "(new)" after its proposed name		
Family:	Phycodnaviridae	• If	If no genus is specified, enter		
Order:		"u	"unassigned" in the genus box.		
And name the new species:		GenBank sequence accession number(s) of reference isolate:			
Ostreococcus	tauri virus OtV5		<u>NC_010191</u>		

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 0 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

Host specificity: This virus infects a specific strain of Ostreococcus tauri. The genus Ostreococcus currently includes 4 "ecotypes," which we refer to as clades A, B, C and D, and that most likely represent 4 evolutionarily divergent species, 3 of which have not yet been officially described: O. lucimarinus (nomen nudem, clade A), clade B and clade D (O. tauri, the officially described species, being clade C). OtV5 infects only one of the 15 wild-type clonal lines of O. tauri in culture. O. tauri is a coastal marine species of the Order Mamiellales (Prasinophyceae) and the abundance of O. tauri viruses decreases offshore, in contrast to O. *lucimarinus*, an oceanic clade whose viruses are found worldwide, see Bellec at al., 2010 in the Appendix). The fully characterised dsDNA genome of OtV5 and its particle morphology (icosohedral, 110-130nm) clearly merit its inclusion in the Prasinovirus genus, as we described (relevant publications are given in the appendix, as requested). We suggest the nomenclature OtVn, where n is the strain number, for Ostreococcus tauri viruses, OlVn for Ostreococcus *lucimarinus* viruses, and OsVn for viruses of other unclassified species (clades) of hosts within the Ostreococcus genus. We suggest that a similar system is adopted for other members of the Order *Mamiellales*. *Bathycoccus prasinos* viruses should thus be called BpVn. The taxonomy for *Micromonas* viruses should also reflect the host species' name, and a similar situation exists to that in Ostreococcus, namely that there are several evolutionary divergent cryptic species in *Micromonas*, and indeed previous work on these viruses shows diverse particle characteristics, but historically viruses attacking *Micromonas spp.* were called *Micromonas pusilla* viruses before host clade/species distinctions became apparent. To avoid confusion, we suggest that the nomenclature MpVn should be retained, whatever the species specificity.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

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. A phylogenetic tree computed by Bayesian analysis (BI) and maximum likelihood (ML) analyses on the partial DNA polymerase gene DNA sequences of selected taxa of the family Phycodnaviridae and other large dsDNA viruses. Genbank accession numbers of reference taxa are given in parentheses. The position of OtV5 is indicated in large bold type. Numbers are posterior probabilities (BI) and bootstrap proportions (ML; values below 50 are indicated by "–") reflecting clade support. (Taken from Derelle et al., 2008)

References:

Concerning OtV5:

Derelle, E.; Ferraz, C.; Escande, M.-L.; Eychenie, S.; Cooke, R.; Piganeau, G.; Desdevises, Y.; Bellec, L.; Moreau, H. & Grimsley, N. Life-cycle and genome of OtV5, a large DNA virus of the pelagic marine unicellular green alga Ostreococcus tauri

PLoS ONE, 2008, 3, e2250, 1-13

Bellec, L.; Grimsley, N.; Moreau, H. & Desdevises, Y. Phylogenetic analysis of new Prasinoviruses (*Phycodnaviridae*) that infect the green unicellular algae *Ostreococcus*, *Bathycoccus* and *Micromonas*. *Environmental Microbiology Reports*, **2009**, *1*, 114-123

Bellec, L.; Grimsley, N. & Desdevises, Y. Isolation of Prasinoviruses of the Green Unicellular Algae Ostreococcus spp. on a Worldwide Geographical Scale. *Applied and Environmental Microbiology*, **2010**, *76*, 96-101

Bellec, L.; Grimsley, N.; Derelle, E.; Moreau, H. & Desdevises, Y. Abundance, spatial distribution and genetic diversity of *Ostreococcus tauri* viruses in two different environments. *Environmental Microbiology Reports*, **2010**, *2*, 313-321

Concerning cryptic host species in the Order Mamielalles:

Grimsley, N.; Pequin, B.; Bachy, C.; Moreau, H. & Piganeau, G. Cryptic Sex in the Smallest Eukaryotic Marine Green Alga. *Molecular Biology and Evolution*, **2010**, *27*, 47-54

Palenik, B.; Grimwood, J.; Aerts, A.; Rouze, P.; Salamov, A.; Putnam, N.; Dupont, C.; Jorgensen, R.; Derelle, E.; Rombauts, S.; Zhou, K. M.; Otillar, R.; Merchant, S. S.; Podell, S.; Gaasterland, T.; Napoli, C.; Gendler, K.; Manuell, A.; Tai, V.; Vallon, O.; Piganeau, G.; Jancek, S.; Heijde, M.; Jabbari, K.; Bowler, C.; Lohr, M.; Robbens, S.; Werner, G.; Dubchak, I.; Pazour, G. J.; Ren, Q. H.; Paulsen, I.; Delwiche, C.; Schmutz, J.; Rokhsar, D.; Van de Peer, Y.; Moreau, H. & Grigoriev, I. V. The tiny eukaryote *Ostreococcus* provides genomic insights into the paradox of plankton speciation. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, *104*, 7705-7710

Rodriguez, F.; Derelle, E.; Guillou, L.; Le Gall, F.; Vaulot, D. & Moreau, H. Ecotype diversity in the marine picoeukaryote Ostreococcus (Chlorophyta, Prasinophyceae) . *Environmental Microbiology*, **2005**, *7*, 853-859

Slapeta, J.; Lopez-Garcia, P. & Moreira, D. Global dispersal and ancient cryptic species in the smallest marine eukaryotes *Mol Biol Evol*, **2006**, *23*, 23-9