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

Code[†] 2005.225V.04 To create a new genus in the family* ***Reoviridae***

Code[†] 2005.226V.04 To name the new genus* ***Mimoreovirus***

Code[†] 2005.227V.04 To designate the species ***Micromonas pusilla reovirus***
As the type species of the new genus*

Code[†] 2005.228V.04 To designate the following as species of the new genus*:

Micromonas pusilla reovirus
Micromonas pusilla reovirus (MpRV) ???

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

[†] Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order

Order
Family *Reoviridae*
Genus
Type Species
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order

Order
Family *Reoviridae*
Genus *Mimoreovirus*
Type Species *Micromonas pusilla reovirus*
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

ICTV-EC comments and response of the SG

Argumentation to choose the type species in the genus

Micromonas pusilla reovirus (MpRV) was isolated from the marine photosynthetic protist Micromonas pusilla.
At present this virus is the only representative of genus Mimoreovirus.

Species demarcation criteria in the genus

The genome is composed of 11 segments of dsRNA. The longest genome segment is 5792 bp long which has no equivalent in the other members of the family in terms of length. This genome segment encodes a protein of 210 kDa which seems to be structural.

List of Species in the created genus

Micromonas pusilla reovirus

List of Tentative Species in the created genus

Argumentation to create a new genus:

Micromonas pusilla reovirus (MpRV) is an 11-segmented dsRNA virus. Its genome electrophoretic profile is distinct from the other members of family *Reoviridae* with 11 segmented genomes, namely the rotaviruses and aquareoviruses.

It is interesting to note that segment 1 of MpRV is 5792 bp long, the longest segment of any of the characterised reoviruses. Seg-1 from the other sequenced member-viruses of the family *Reoviridae,* are all shorter than 4350 bp (the length of Seg – 1 from Colorado tick fever virus).

A sequence analysis of MpRV Seg-1 showed that it contains a single ORF, spanning practically the whole length of the segment. It was found that the VP1 protein (encoded by Seg-1) is 1983 aa long. Amino acids 88 to 255 showed 24% identity with the minor capsid protein sigma-1 (hemagglutinin and cell attachment protein) of mammalian orthoreovirus (accession number AAA47276) and its equivalent sigma-c (22% identity to aa 172-321 of VP1) of the Pulau reovirus.

It is noteworthy that VP1 also showed matches with various other hemagglutinins including that of bacterial pathogen Bukholderia vietnamiensis (aa identity 20%, similarity 40% p value = 4e^{-06}), and Candida albicans (20% identity, 39% similarity p value = 3e^{-04}). It also matched some large DNA virus proteins, such as those of: (i) family *Phycodnaviridae* (including the paramecium bursaria chlorella virus (PBCV) Vp260, the surface antigen like protein of PBCV); (ii) family *Herspesviridae* (including the equine herpesvirus glycoprotein 2 (gp2)); (iii) bacteriophage (including the envelope protein of Acholeplasma phage L2 or the T4-like neck protein of cyanophage p-SSM4). All of these proteins are surface glycoproteins involved in envelopes or envelope-like structures.

The segment 2 of MpRV was found to encode the viral polymerase. RdRp core motifs were identified in the protein encoded by this segment, including the motif SG at position 801-802 and the motif GDD at position 835-837. Interestingly, a partial match (aa 647-962, identity 21%) within the enzyme core region of MpRV RdRp was found with the RdRp of human rotavirus C (accession number CAC44891), which is also an 11 segmented dsRNA virus belonging to family *Reoviridae.*

The terminal sequences of MpRV (**5′-GAAGA^{A}/$_{U}$---------^{A}/$_{G}$AAAGUC-3′**) are distinct from all those of sequenced members of family *Reoviridae*.

Phylogenetic analysis (annex 1) based on the polymerase sequences showed that MpRV does not cluster with any of the known genera and stands as a separate phylogenetic group.

Taken together these arguments indicate that MpRV should be recognised as a member of a new and distinct genus that we designated *Mimoreovirus*.

Origin of the proposed genus name

Mimoreovirus (sigla from : Micromonas pusilla reovirus).

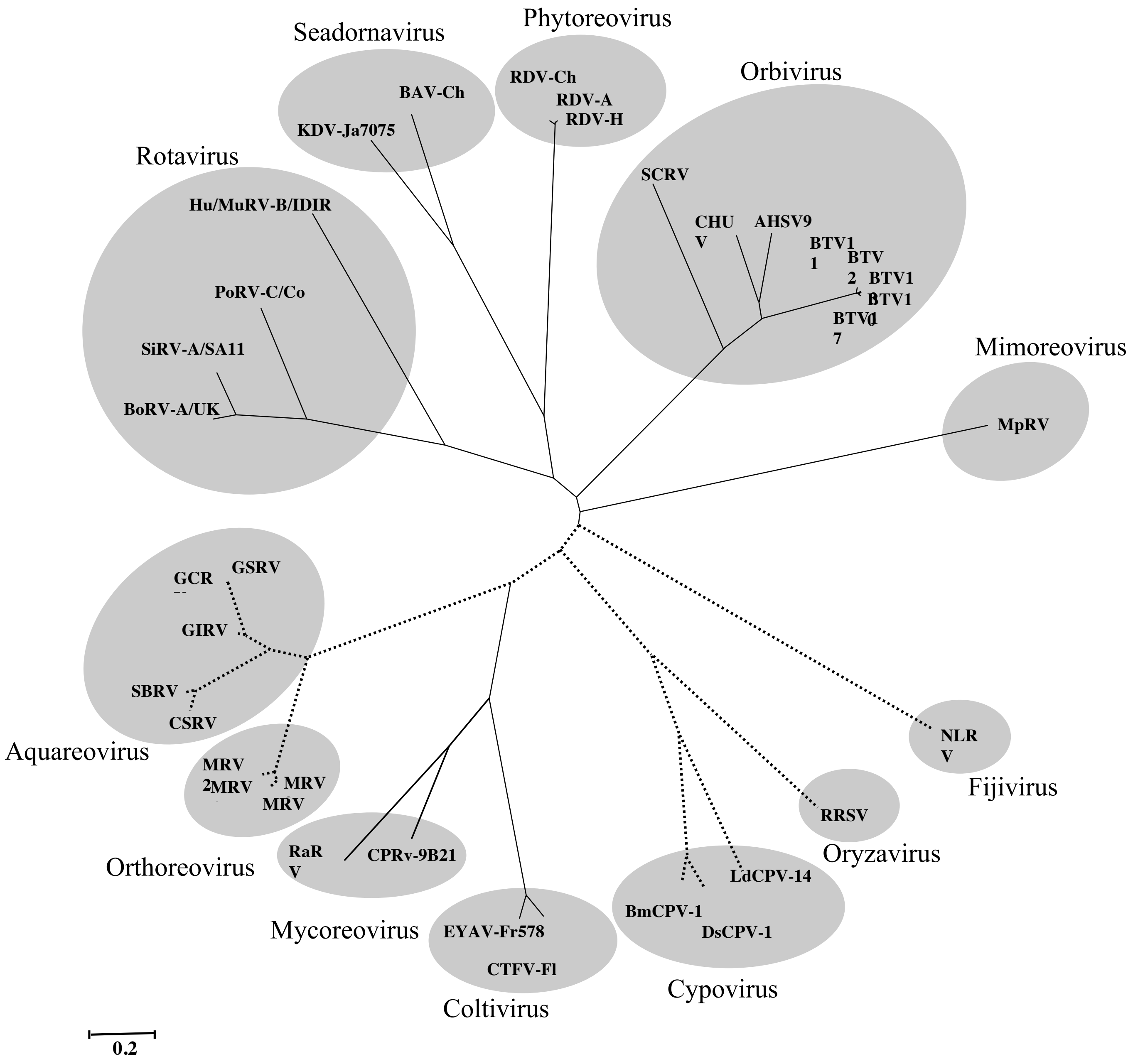
References

Brussaard, C.P., Noordeloos, A.A., Sandaa, R.A., Heldal, M., Bratbak, G. (2004).Discovery of a dsRNA virus infecting the marine photosynthetic protist Micromonas pusilla. Virology. 319, 280-291.

Houssam ATTOUI, Fauziah MOHD JAAFAR, Mourad BELHOUCHET, Philippe de MICCO, Xavier de LAMBALLERIE, and Corina BRUSSAARD. The complete sequence characterisation of the genome of the *Micromonas pusilla* reovirus: proposal for the assignment to a new genus (Mimoreovirus) within family *Reoviridae*. Manuscript in preparation.

Annexes:

Annexe 1: neighbour-joining tree built with the available sequences of RdRps of representative members of family *Reoviridae*.



The sequences used in RdRps phylogenetic analysis of MpRV: the abbreviations listed are those used in the figure above.

Species	Isolate	Abbreviation	Accession number
Genus *Seadornavirus* (12 segments)			
Banna virus	Ch	BAV-Ch	AF168005
Kadipiro virus	Java-7075	KDV-Ja7075	AF133429
Genus *Coltivirus* (12 segments)			
Colorado tick fever virus	Florio	CTFV-Fl	AF134529
Eyach virus	Fr578	EYAV-Fr578	AF282467
Genus *Orthoreovirus* (10 segments)			
Mammalian orthoreovirus	Lang strain	MRV-1	M24734
	Jones strain	MRV-2	M31057
	Dearing strain	MRV-3	M31058
Genus *Orbivirus* (10 segments)			
African horse sickness virus	serotype 9	AHSV-9	U94887
Bluetongue virus	serotype 2	BTV-2	L20508
	serotype 10	BTV-10	X12819
	serotype 11	BTV-11	L20445
	serotype 13	BTV-13	L20446
	serotype 17	BTV-17	L20447
Palyam virus	Chuzan	CHUV	Baa76549
St Croix river virus	SCRV	SCRV	AF133431
Genus *Rotavirus* (11 segments)			
Rotavirus A	bovine strain UK	BoRV-A/UK	X55444
	simian strain SA11	SiRV-A/SA11	AF015955
Rotavirus B	human/murine strain IDIR	Hu/MuRV-B/IDIR	M97203
Rotavirus C	porcine Cowden strain	PoRV-C/Co	M74216
Genus *Aquareovirus* (11 segments)			
Golden shiner reovirus	GSRV	GSRV	AF403399
Grass Carp reovirus	GCRV-873	GCRV	AF260511
Chum salmon reovirus	CSRV	CSRV	AF418295
Striped bass reovirus	SBRV	SBRV	AF450318
Genus *Fijivirus* (10 segments)			
Nilaparvata lugens reovirus	Izumo strain	NLRV-Iz	D49693
Genus *Phytoreovirus* (10 segments)			
Rice dwarf virus	isolate China	RDV-Ch	U73201
	isolate H	RDV-H	D10222
	isolate A	RDV-A	D90198
Genus *Oryzavirus* (10 segments)			
Rice ragged stunt virus	Thai strain	RRSV-Th	U66714
Genus *Cypovirus* (10 segments)			
Bombyx mori cytoplasmic polyhedrosis virus 1	Strain I	BmCPV-1	AF323782
Dendrlymus punctatus cytoplasmic polyhedrosis 1	DsCPV-1	DsCPV-1	AAN46860
Lymantria dispar cytoplasmic polyhedrosis 14	LdCPV-14	LdCPV-114	AAK73087
Genus *Mycoreovirus* (11 or 12 segments)			
Rosellinia anti-rot virus	W370	RaRV	AB102674
Cryphonectria parasitica reovirus	9B21	CPRV	AY277888