



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:	2012.001a-gF	(to be completed by ICTV officers)				
Short title: create a new mycovirus species in a new genus, Quadrivirus, in a new family, Quadriviridae (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 checked="" type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input checked="" 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)

The proposal was submitted to Dr Said A Ghabrial, the chair of the Fungal Virus Subcommittee, for consideration by members of the subcommittee.

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

Said Ghabrial, FVS chair, made comments regarding the supporting material in Module 9, Table 1, and forwarded the changes to the proposer. A member of the FVS expressed concern that there is only one characterized member in the proposed new family.

Response to FVS Chair: Table 1 has been modified accordingly.

Response to FVS member: There is an example of a mycovirus family, i.e., Barnaviridae with only a single member. Moreover, another strain (W1118) of RnQV1 is being characterized that shows approximately 70% RdRp sequence identity to RnQV1-W1075.

Date first submitted to ICTV:

January 20, 2012

Date of this revision (if different to above):

June 4, 2012

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.

Code	2012.001aF	(assigned by ICTV officers)
To create a new species within:		
Genus:	<i>Quadrivirus</i> (new)	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>Quadriviridae</i> (new)	
Order:		
And name the new species:		
<i>Rosellinia necatrix quadrivirus</i>		

Reasons to justify the creation and assignment of the new species:

The virus, termed *Rosellinia necatrix quadrivirus* 1 (RnQV1/W1075), isolated from strain W1075 of the phytopathogenic fungus *Rosellinia necatrix*, forms rigid spherical particles of approximately ~48 nm in diameter in infected mycelia. The particles encompass 4 dsRNA segments, dsRNA1 to dsRNA4 ranging in size from 3.7 to 4.9 kbp (Fig. 1). Each segment possesses a single large open reading frame potentially encoding a polypeptide (P1 to P4), and a terminal sequence of seven 5’- and fourteen 3’-nucleotides strictly conserved in all segments. Sequence heterogeneity at the extreme terminal ends of each segment (5’-C/U-----G/A-3’) is noteworthy. DsRNA3-encoded P3 has sequence motifs characteristic of RNA dependent RNA polymerase (RdRP) and shares sequence identities of 20-41% with RdRPs from other mycoviruses and dsRNA elements (Table 1). Its closest relation is to RdRPs from large (L) dsRNA elements (L-dsRNA3 and L-dsRNA4) associated with Amasya cherry disease (ACD) and cherry chlorotic rusty spot (CCRS), while RnQV1 dsRNA1-encoded protein (P1) shows low levels of sequence similarities to uncharacterized protein encoded by ACD L-dsRNA1 and L-dsRNA2. DsRNA2 and dsRNA4 encode structural proteins (P2 and P4), with no sequence similarity to known proteins. P2 and P4 appear to be processed or degraded within cells or during particle purification. Phylogenetic analysis with RdRP sequences revealed that RnQV1 is more distantly related to chrysovirus with quadripartite genomes than to monopartite totiviruses (victoriviruses), and is placed in a distinct group from other mycoviruses (Fig. 2).

All these properties distinguish RnQV1 from any other reported mycoviruses.

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.
- Provide accession numbers for genomic sequences

EMBL/GenBank/DBJ Accession Nos: AB620061 to AB620064.

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

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2012.001bF	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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
Family:	<i>Quadriviridae</i>	
Order:		

naming a new genus

Code	2012.001cF	(assigned by ICTV officers)
To name the new genus: <i>Quadrivirus</i>		

Assigning the type species and other species to a new genus

Code	2012.001dF	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Rosellinia necatrix quadrivirus</i>		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

Only one family member is well characterized. See “Reasons to justify the creation of a new family”.

Origin of the new genus name:

Like the name of the proposed family (see module 5), “Quadri” is from the quadripartite nature of the virus genome.

Reasons to justify the choice of type species:

RnQV1/W1075, the prototype of the species *Rosellinia necatrix quadrivirus*, is the only virus fully characterized at the molecular level (Lin et al., 2011). Phylogenetic analysis based on RdRP sequences (Fig. 2) indicates that RnQV1 is closely related to unassigned dsRNA elements ACD L-dsRNA3 and L-dsRNA4, and CCRS L-dsRNA3 and L-dsRNA4.

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.

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MODULE 5: NEW FAMILY

creating and naming a new family

Code	2012.001eF	(assigned by ICTV officers)
<p>To create a new family containing the subfamilies and/or genera listed below within the Order: unassigned</p> <p>If there is no Order, write “unassigned” here. If the Order has yet to be created (in Module 6) please write “(new)” after the proposed name.</p>		

Code	2012.001fF	(assigned by ICTV officers)
<p>To name the new family: <i>Quadriviridae</i></p>		

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)
<p>To assign the following subfamilies (if any) to the new family: You may list several subfamilies here. For each subfamily, please state whether it is new or existing.</p> <ul style="list-style-type: none"> • If the subfamily is new, it must be created in Module 4 • If the subfamily already exists, please complete Module 7 to ‘REMOVE’ it from its existing family 		

Code	2012.001gF	(assigned by ICTV officers)
<p>To assign the following genera to the new family: <i>Quadriviridae</i> You may list several genera here. For each genus, please state whether it is new or existing.</p> <ul style="list-style-type: none"> • If the genus is new, it must be created in Module 3 • If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to ‘REMOVE’ it from that family 		

<p>The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):</p>		
<p> </p>		

Reasons to justify the creation of the new family:

The proposed family can be readily differentiated from other known mycovirus families based on the size of its quadripartite genome (4.9~3.7 kbp, totally 17 kbp), and particle size (~48 nm in diameter). Of the four proteins encoded by the only known member of the family, the RdRP sequence (P3) and dsRNA1-encoded polypeptide (P1) show low levels of identities (approximately 20-41% for P3; approximately 19-27% for P1) (see Table 1) to those from other mycoviruses and unassigned dsRNA elements, while the remaining two proteins (P2 and P4) do not show any significant sequence similarities to other mycovirus proteins.

A phylogenetic tree (Fig. 2) generated by the maximum-likelihood method based on an RdRP sequence alignment is attached in Module 9 that places the prototype (RnQV1/W1075) of the proposed family into a distinct clade from other known dsRNA mycovirus families. RnQV1 and quadripartite chrysovirus or *Alternaria alternata* virus-1 (AaV-1) are more distantly related than are RnQV1 and dsRNAs associated with ACD and CCRS or *Totiviridae* (with monopartite genomes). A tree created by the neighbor-joining method shows a very similar topology to that shown in the ML tree.

[Additional material in support of this proposal may be presented in the Appendix, Module 9](#)

Origin of the new family name:

“Quadri” is from the quadripartite nature of the virus genome.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Lin, Y.-H., Chiba, S., Tani, A., Kondo, H., Sasaki, A., Kanematsu, S and Suzuki N. A novel quadripartite dsRNA virus isolated from a phytopathogenic filamentous fungus, *Rosellinia necatrix*. *Virology* 462: 42-50.

Ghabrial, S. A., and N. Suzuki. 2009. Viruses of plant pathogenic fungi. *Annu. Rev. Phytopathol.* 47: 353-384.

Ikeda, K., H. Nakamura, and N. Matsumoto. 2005. Comparison between *Rosellinia necatrix* isolates from soil and diseased roots in terms of hypovirulence. *FEMS Microbiol. Ecol.* 54: 307-315.

Covelli, L., Coutts, R. H., Di Serio, F., Citir, A., Acikgoz, S., Hernandez, C., Ragozzino, A., and Flores, R. (2004). Cherry chlorotic rusty spot and Amasya cherry diseases are associated with a complex pattern of mycoviral-like double-stranded RNAs. I. Characterization of a new species in the genus *Chrysovirus*. *J Gen Virol* 85, 3389-3397.

Kozlakidis, Z., Covelli, L., Di Serio, F., Citir, A., Acikgoz, S., Hernandez, C., Ragozzino, A., Flores, R., and Coutts, R. H. (2006). Molecular characterization of the largest mycoviral-like double-stranded RNAs associated with Amasya cherry disease, a disease of presumed fungal aetiology. *J Gen Virol* 87, 3113-3117.

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.

Table 1 Summary of the results of a BLASTP search with RnQV1dsRNA3-encoded P3.

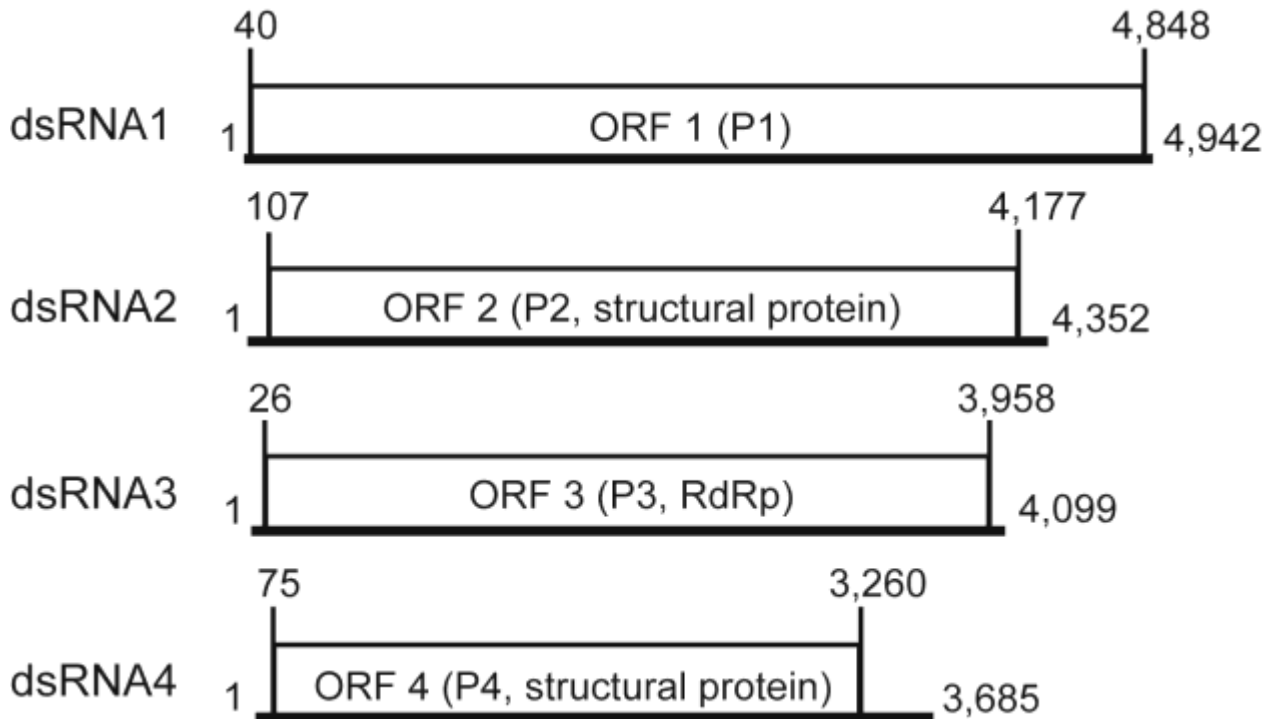
Virus name ^a	Accession no.	Sequence length (aa)	BLASTP				
			Overlap region	Coverage (%)	Expect	Score	Identity (%)
Unassigned							
ACD L dsRNA3	CAJ29958	1363	257-1318	78	0	631	35
ACD L dsRNA4	CAJ29959	1294	318-1294	72	0	619	36
CCRS L dsRNA4	CAJ57274	1162	318-1155	62	2e-167	537	36
CCRS L dsRNA3	CAJ57273	324	1-279	21	3e-58	211	41
Totivirus							
BRVF	YP_001497151	814	133-620	38	1e-40	170	26
UmV-H1 ^b	NP_620728	1820	1246-1532	21	1e-08	68.2	24
ScV-L-BC	NP_042581	863	204-679	38	2e-39	167	26
TaV1	ADQ54106	795	224-602	30	5e-39	165	31
ScV-L-A	NP_620495	731	159-549	32	3e-38	162	28
AsV 1816	ABX79996	1084	370-835	33	9e-08	65.5	22
PMCV (fish)	YP_004581250	726	340-507	13	1.4	41.6	23
Victorivirus							
HmTV1-17	NP_898833	845	215-596	31	1e-12	80.9	27
BfTV1	YP_001109580	838	355-641	24	5e-10	72.4	25
MoV1	YP_122352	832	202-603	32	6e-10	72	26
MoV2	YP_001649206	830	341-576	20	1e-09	71.6	27
GaRV-L2	YP_044807	825	338-571	19	9e-09	68.6	26
AMV178	ABX79995	775	288-521	19	1e-08	68.2	28
GaRV-L1	AAK11656	825	338-571	19	2e-08	67.4	26
SsRV2	NP_047560	825	344-592	20	8e-08	65.5	25
CmRV	YP_392467	829	182-575	32	4e-07	63.2	24
EfV1	CAK02788	827	345-573	19	3e-06	60.1	27
SsRV1	NP_047558	838	214-587	31	4e-05	56.6	24
HvV190S	NP_619670	835	357-607	20	6e-04	52.8	26
Megabirnavirus							
RnMBV1	YP_003288763	1111	486-748	19	7e-06	59.3	25
Chrysovirus							
HvV145S	YP_052858	1086	494-837	27	0.023	47.8	23
GaCV1	ADO60926	957	396-663	21	0.053	46.6	23
MoCV1	YP_003858286	1127	396-737	25	0.22	44.3	23
ACDCV	CAH03664	1087	426-807	29	2.7	40.8	20
CnCV1	ACT79255	962	650-859	17	4.4	40	25

^aAbbreviated names of dsRNA elements and viruses (listed as members or proposed members of the genera *Totivirus*, *Victorivirus*, *Megabirnavirus* and *Chrysovirus*) are: ACD-L3 and -L4, Amasya cherry disease associated L-dsRNA3 and L-dsRNA4; CCRS-L4, cherry chlorotic rusty spot associated L dsRNA4; BRVF, Black raspberry virus F; UmV-H1, Ustilago maydis virus H1; ScV-L-BC, Saccharomyces cerevisiae virus L-BC; TaV1, Tuber aestivum virus 1; ScV-L-A, Saccharomyces cerevisiae virus L-A; AsV1816, Aspergillus mycovirus 1816; PMCV, Piscine myocarditis virus; HmTV1-17, Helicobasidium mompa totivirus 1-17; BfTV1, Botryotinia fuckeliana totivirus 1; MoV1 and MoV2, Magnaporthe oryzae virus 1 and 2; GaRV-L1 and -L2, Gremmeniella abetina RNA virus L1 and L2; AMV178, Aspergillus mycovirus 178; SsRV1 and SsRV2, Sphaeropsis sapinea RNA virus 1 and 2; CmRV, Coniothyrium minitans RNA virus; EfV1, Epichloe festucae virus 1; HvV190S, Helminthosporium victoriae virus 190S; RnMBV1, Rosellinia necatrix megabirnavirus 1/W779; HvV145S, Helminthosporium victoriae virus 145S;

GaCV1, Grapevine associated chrysovirus-1; MoCV1, Magnaporthe oryzae chrysovirus 1; ACDCV, Amasya cherry disease associated chrysovirus; CnCV1, Cryphonectria nitschkei chrysovirus 1.

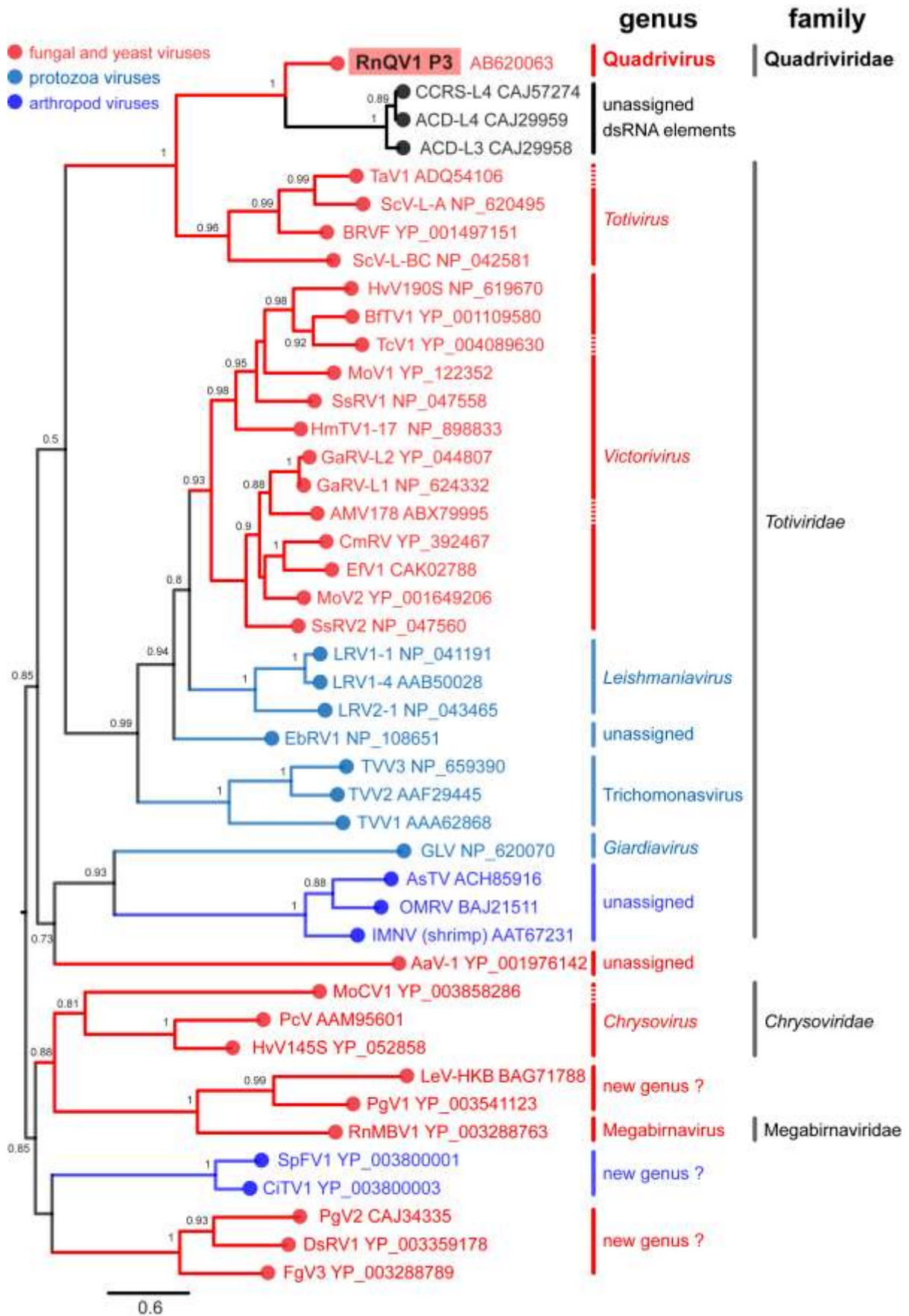
^b CP-RdRP fusion protein.

Fig. 1. Schematic representation of the RnQV1 genomic segments.



DsRNA1 to dsRNA4 are 4,942, 4,352, 4,099, and 3,685 bp in size. Each segment contains a relatively short 5' and 3' UTRs and a single large ORF shown by a box. The nucleotide positions of the initiation and termination codons are shown by numbers above the ORFs. Representative cDNA fragments indicated beneath the contigs by dashed line were used as probes in Northern analysis.

Fig 2. Phylogenetic analysis of RnQV1.



A phylogenetic tree was created based on the RdRP alignment that included representative members of fungal-, protozoa-, and arthropod-infecting dsRNA viruses and dsRNA elements. Definitive (in italics) and tentative (non-italics) virus genera and families are indicated by solid vertical lines. Dashed lines refer to dsRNA elements that are not recognized as virus species by the ICTV but closely associated with members of the virus families being proposed. Numbers at the nodes denote approximate likelihood ratio test (aLRT) values (~ 1) supporting reliability of branches. The scale bar represents the amino acid distances. Abbreviated names of viruses and dsRNA elements: TcV1, *Tolypocladium cylindrosporium* virus 1; LRV1-1, LRV1-4 and LRV2-1, *Leishmania* RNA virus 1-1, 1-4 and 2-1; EbRV1, *Eimeria brunetti* RNA virus 1; TVV1, TVV2 and TVV3, *Trichomonas vaginalis* virus 1, 2 and 3; GLV, *Giardia lamblia* virus; AsTV, *Armigeres subalbatus* virus SaX06-AK20; OMRV, Omono River virus AK4; IMNV, Penaeid shrimp infectious myonecrosis virus; AaV-1, *Alternaria alternata* virus-1; PcV, *Penicillium*; LeV-HKB, *Lentinula edodes* mycovirus; PgV1, *Phlebiopsis gigantea* mycovirus dsRNA 1; SpFV1, *Spissistilus festinus* virus 1; CiTV1, *Circulifer tenellus* virus 1; PgV2, *Phlebiopsis gigantea* mycovirus dsRNA 2; DsRV1, *Diplodia scrobiculata* RNA1; FgV3, *Fusarium graminearum* dsRNA mycovirus-3. See Table 1 footnote for other abbreviated virus names not listed here.
