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:	***2015.008aP***	(to be completed by ICTV officers)

Short title: A new species in the genus *Aureusvirus*

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

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Corresponding author with e-mail address:

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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)	*Tombusviridae* SG

ICTV Study Group comments (if any) and response of the proposer:

The study group supports the inclusion of YSV in the aureusvirus genus.

Date first submitted to ICTV:	June 5, 2015
Date of this revision (if different to above):	

ICTV-EC comments and response of the proposer:

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	***2015.008aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Aureusvirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

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.

Name of new species:	**Representative isolate:** (only 1 per species please)	**GenBank sequence accession number(s)**
Yam spherical virus	**Nigerian isolate**	KF482072

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

Yam spherical virus (YSV) was recently isolated from yam in Nigeria. YSV is mechanically transmissible and causes systemic infection in *Nicotiana benthamiana* and four other *Nicotiana* species [Menzel et al., 2014]. The genome has been completely sequenced, and the sequence and its genome structure (Fig. 1) were shown to be most closely related to aureusviruses [Menzel et al. 2014].

The following species demarcation criteria are listed in the 9th Report of the International Committee on Taxonomy of Viruses [Rochon et al., 2011].

- Serological specificity (known species are serologically unrelated)
- Extent of sequence identity between relevant gene products
- Less than 40% aa sequence identity of the CP
- Less than 80% aa sequence identity of the polymerase
- Differential cytopathological features
- Transmission by a vector
- Natural host range
- Artificial host range reactions

Phylogenetic analyses of three of the four encoded proteins (Figs. 2, 4, 5) and amino acid (aa) sequence identity for RNA dependent RNA polymerase (RdRp) and coat protein (CP) further indicate that YSV is most closely related to aureusviruses compared to viruses with related genome organizations: tombusviruses and maize necrotic streak virus. Due to recombination, tombusvirid CPs are not always monophyletic (Fig. 3). Among the aureusviruses, the RdRp of YSV shares 86% (aa) sequence identity to cucumber leaf spot virus (CLSV) (Table 1) which is above the species demarcation threshold of 80% [Rochon et al., 2011]. However, the YSV CP aa sequence differs significantly from that of CLSV (33%) and from other recognized aureusviruses (32% to 46%) (Table 2). The partial genome sequence (DQ367845.1) of sesame necrotic mosaic virus (SNMV), which has characteristics consistent with tombusviridae suggests it is an aureusvirus, and its CP sequence has 56% identity to YSV (Table 2). Immunological analyses of YSV polyclonal antiserum (DAS-ELISA) against YSV, CLSV, pothos latent virus (PoLV) and johnsongrass chlorotic stripe mosaic virus (JCSMV) showed no cross reactivity [Menzel et al., 2014]. Thus, another species criterium, serological specificity, is met for distinction from CLSV, PoLV and JCSMV. These data indicate that YSV should be considered a separate species within genus *Aureusvirus* since the sum of its known characteristics distinguishes it from other recognized aureusviruses (Rochon et al., 2011).

The CP % identity analysis along with serological data and the dispersion of aureusvirus CPs among other CPs with protruding domains in phylogenetic trees (Fig. 3 and data not shown) indicate that a higher cut-off for CP identities would still provide discrimination of species, so the committee has modified the demarcation criteria for CP to less than 60% identity. The revised criteria are shown below.

Revised species demarcation criteria in genus *Aureusvirus*:

- Serological specificity (known species are serologically unrelated)
- Extent of sequence identity between relevant gene products
- Less than 60% aa sequence identity of the CP
- Less than 80% aa sequence identity of the polymerase
- Differential cytopathological features
- Transmission by a vector
- Natural host range
- Artificial host range reactions

MODULE 10: **APPENDIX**: supporting material
References:

Menzel, W, Thottapilly, G, Winter, S (2014) Characterization of an isometric virus isolated from yam (*Dioscorea rotundata*) in Nigeria suggests that it belongs to a new species in the genus *Aureusvirus*. Arch Virol 159: 603-606

Rochon D, Lommel S, Martelli GP, Rubino L, Russo M (2011) Tombusviridae. In: King A, Adams MJ, Carstens EB, Lefkowitz E (eds) Virus Taxonomy. Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, New York, pp 1111-1138

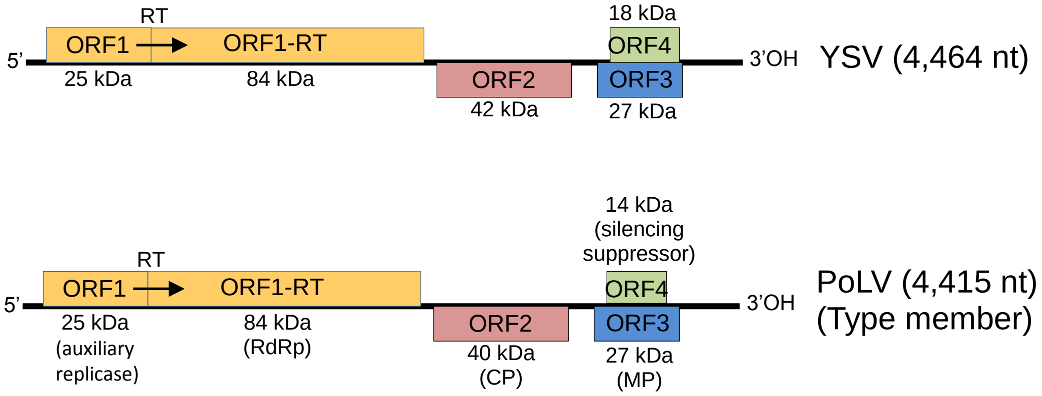

Figure 1. The genome structure of YSV in comparison to PoLV, the type member of the aureusvirus genus. Sizes of the indicated open reading frames (ORFs) are in kilodaltons (kDa). The putative functions of the proteins are indicated in brackets for PoLV. Similarly coloured boxes for ORFs indicate significant sequence similarity (See Tables 1-5). RT indicates readthrough of an amber stop codon. RdRp = RNA dependent RNA polymerase; CP= coat protein; MP = movement protein.

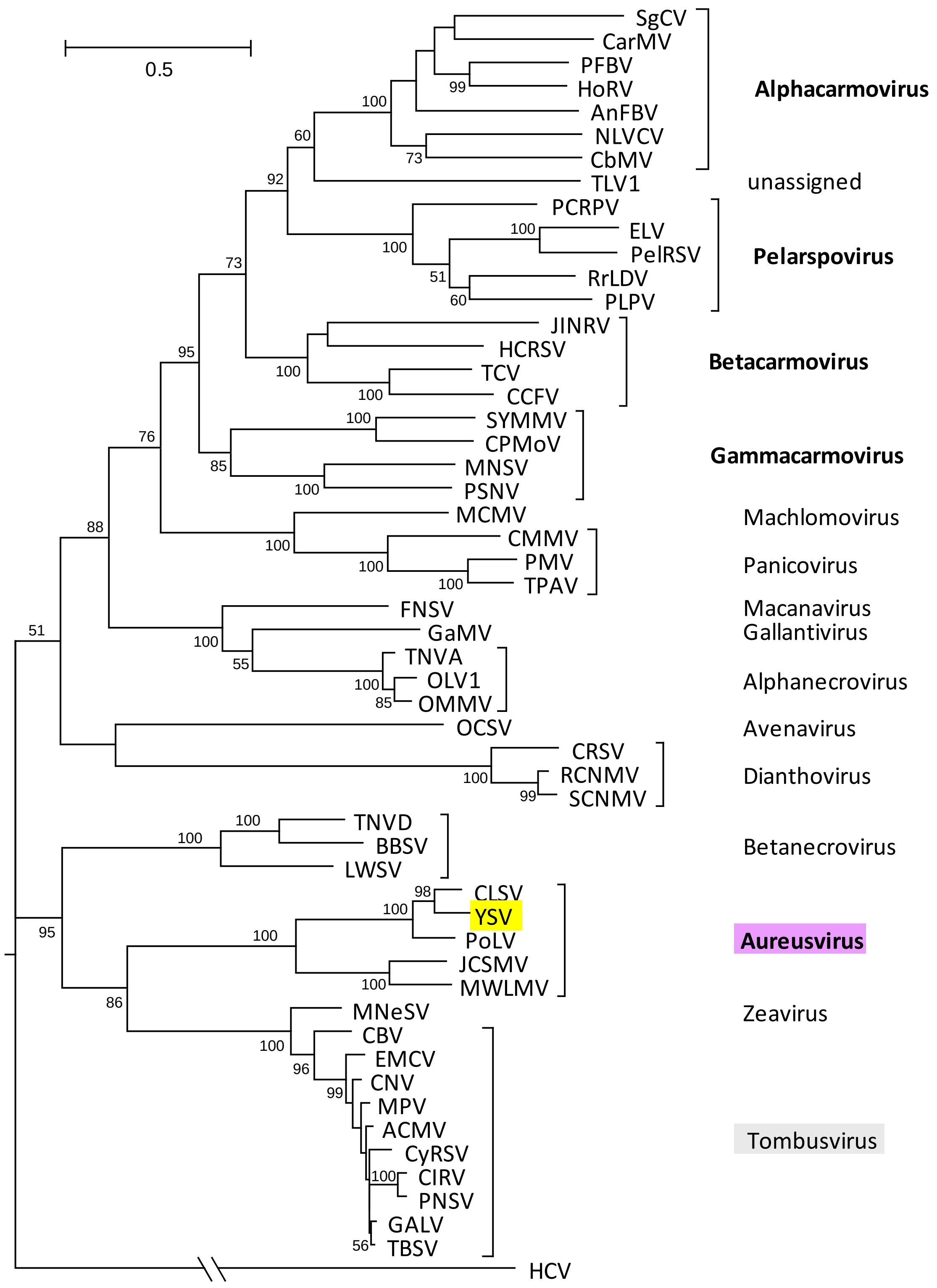

Figure 2. Phylogenetic (distance) analysis of the RdRp of several members of the tombusviridae showing the relationship of YSV (highlighted in yellow) to the aureusvirus lineage. Alignments were made using MUSCLE while trees were generated with the Maximum Likelihood (ML) algorithm using 1000 bootstrap replicates (showing values >50%). Positions with < 50% site coverage were eliminated. Monophyletic proposed genera are also shown (bold) and include alphacarmovirus, betacarmovirus, gammacarmovirus and pelarspovirus. Brackets mark monophyletic lineages. Hepatitis C virus was used as the outgroup. See Table 3 for abbreviations.

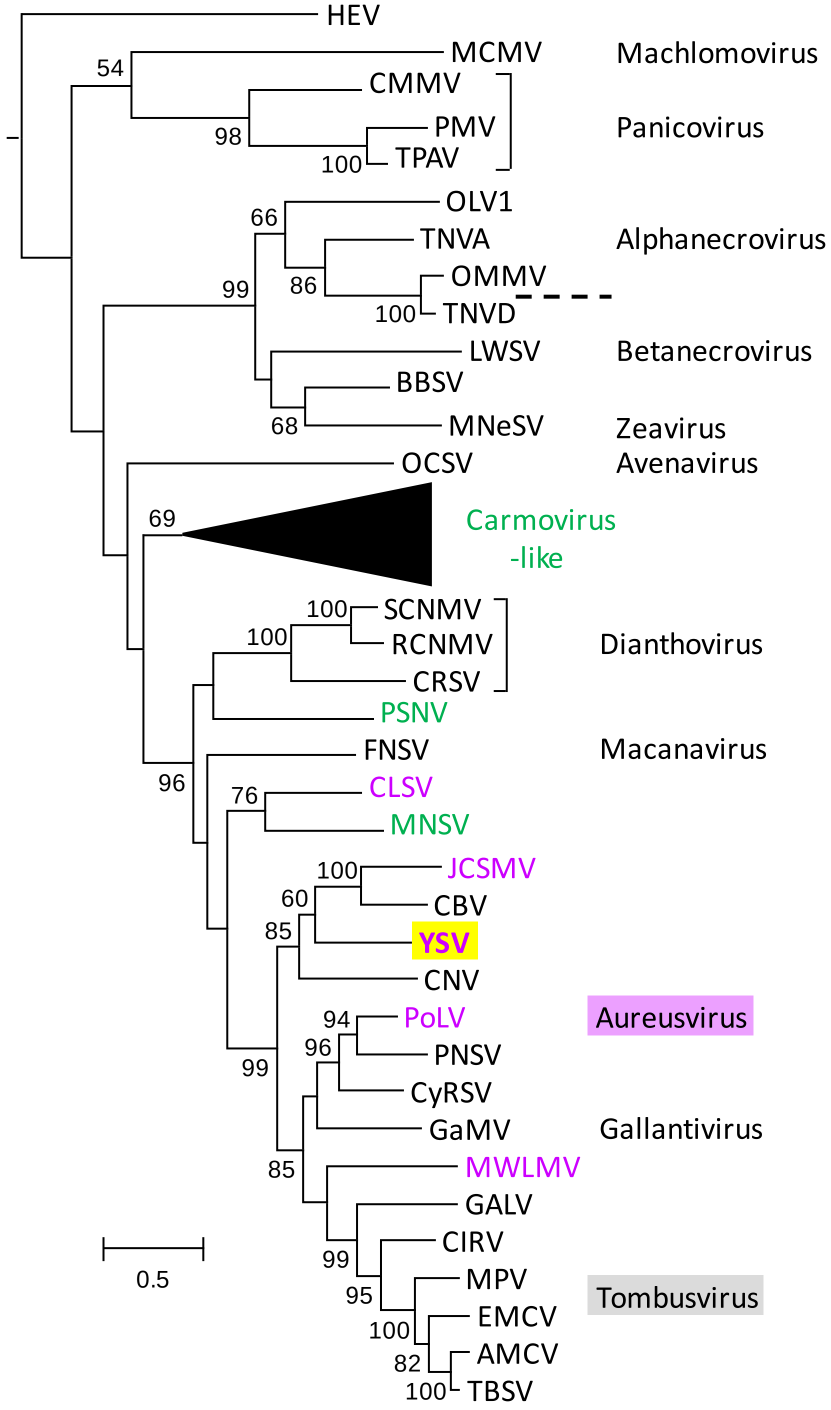

Figure 3. Phylogenetic (distance) analysis of the CPs of CP-encoding tombusvirids. Trees were generated using the same conditions as Fig. 2. There were 356 positions in the final dataset. Brackets mark monophyletic lineages. Hepatitis E virus was used as an outgroup. YSV is highlighted in yellow.

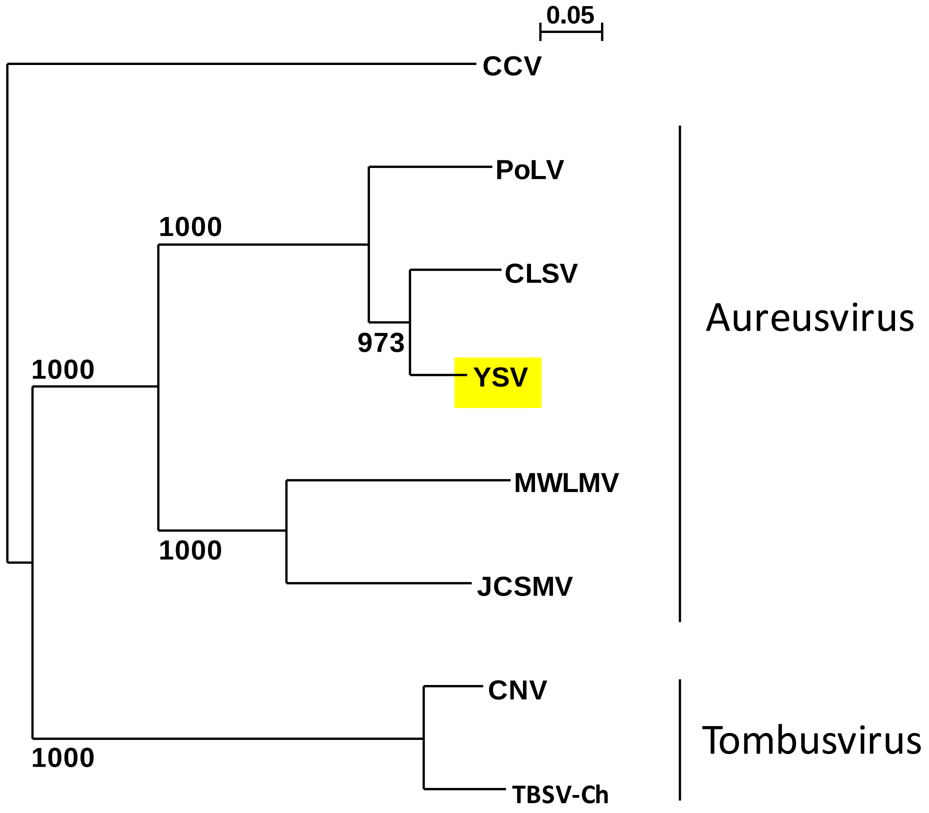

Figure 4. Phylogenetic (distance) analysis of the MP of YSV with those of aureusviruses and tombusviruses. Proteins were aligned using ClustalX 2.1 and the phylogenetic tree was generated using Nearest Neighbor Joining algorithm with 1000 bootstrap replicates. The outgroup is the movement protein of the ourmiavirus, cassava C virus (CCV). YSV is highlighted in yellow. The CNV and TBSV-Ch are shown to indicate that YSV does not fall within the tombusvirus lineage. See Table 3 for abbreviations.

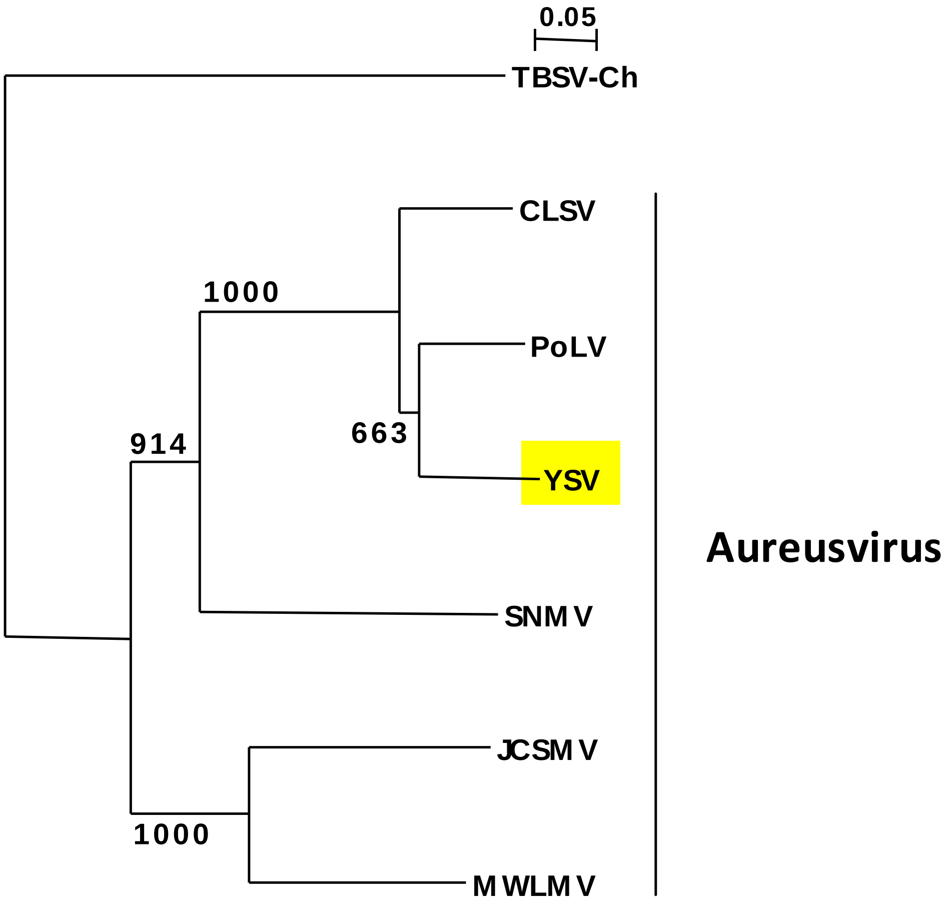

Figure 5. Phylogenetic (distance) analysis of the silencing suppressor protein of YSV with those of aureusviruses. Proteins were aligned using ClustalX 2.1 and the phylogenetic tree was generated using the Nearest Neighbor Joining algorithm with 1000 bootstrap replicates. The outgroup is the movement protein of the tombusvirus TBSV-Ch. YSV is highlighted in yellow. See Table 3 for abbreviations.

Table 1. Percent identity matrix of the RdRp of YSV with those of *Aureusviruses*. Yellow highlights the % identity observed between YSV and other *Aureusvirus* members.

	PoLV	**CLSV**	**JCSMV**	**MWLMV**
YSV	80	86	55	54
PoLV	-	80	55	54
CLSV		-	56	56
JCSMV			-	71
MWLMV				-

Table 2. Percent identity matrix of the CP of YSV with those of *Aureusviruses*. Yellow highlights the % identity observed between YSV and other *Aureusvirus* members.

	PoLV	**CLSV**	**SNMV**	**JCSMV**	**MWLMV**
YSV	44	33	56	46	32
PoLV		37	41	38	41
CLSV			37	37	34
SNMV				44	35
JCSMV					37
MWLMV					-

Table 3. Virus abbreviations and accession numbers for proposal

	Alphanecrovirus	
OLV1	Olive latent virus 1	X85989
OMMV	Olive mild mosaic virus	AY616760
TNVA	Tobacco necrosis virus A	M33002
	Aureusvirus	
CLSV	Cucumber leaf spot virus	EU127904
JCSMV	Johnsongrass chlorotic stripe mosaic virus	AJ557804
MWLMV	Maize white line mosaic virus	EF589670
PoLV	Pothos latent virus	X87115
YSV	Yam spherical virus (proposed)	KF482072
	Avenavirus	
OCSV	Oat chlorotic stunt virus	X83964
	Betanecrovirus	
BBSV	Beet black scorch virus	AF452884
LWSV	Leek white stripe virus	X94560
TNVD	Tobacco necrosis virus D	U62546

	Carmovirus (2014)		
	Alphacarmovirus (proposed)		
AnFBV	Angelonia flower break virus	DQ219415	
CbMV	Calibrachoa mottle virus	GQ244431	
CarMV	Carnation mottle virus	X02986	
HoRSV	Honeysuckle ringspot virus	HQ677625	
NLVCV	Nootka lupine vein clearing virus	EF207438	
PFBV	Pelargonium flower break virus	AJ514833	
SgCV	Saguaro cactus virus	U72332	
	Betacarmovirus (proposed)		
CCFV	Cardamine chlorotic fleck virus	L16015	
HCRSV	Hibiscus chlorotic ringspot virus	X86448	
JINRV	Japanese iris necrotic ring virus	D86123	
TCV	Turnip crinkle virus	M22445	
	Gammacarmovirus (proposed)		
CPMV	Cowpea mottle virus	U20976	
MNSV	Melon necrotic spot virus	M29671	
PSNV	Pea stem necrosis virus	AB086951	
SYMMV	Soybean yellow mottle mosaic virus	FJ457015	
	move to unassigned (proposed)		
AWV	Ahlum waterborne virus	na	
BMMV	Bean mild mottle virus	na	
CSBV	Cucumber soil-borne virus	na	
WWV	Weddel waterborne virus	na	
	Dianthovirus		
CRSV	Carnation ringspot virus	L18870, M88589	RCNMV
	Red clover necrotic mosaic virus	J04357, X08021	SCNMV
	Sweet clover necrotic mosaic virus	L07884, S46028	
	Gallantivirus		
GaMV	Galinsoga mosaic virus	Y13463	
	Macanavirus		
FNSV	Furcraea necrotic streak virus	FJ768020	
	Machlomovirus		
MCMV	Maize chlorotic mottle virus	X14736	
	Panicovirus		
CMMV	Cocksfoot mild mosaic virus	EU081018	
PMV	Panicum mosaic virus	U55002	
TPAV	Thin paspalum asymptomatic virus	JX848617	
	Tombusvirus		
AMCV	Artichoke mottled crinkle virus	X62493	
CIRV	Carnation Italian ringspot virus	X85215	
CBV	Cucumber Bulgarian virus	AY163842	
CNV	Cucumber necrosis virus	M25270	
CyRSV	Cymbidium ringspot virus	X15511	
EMCV	Eggplant mottled crinkle virus	JQ864181	
GALV	Grapevine Algerian latent virus	AY830918	
MPV	Moroccan pepper virus	**JX197071**	
PNSV	Pelargonium necrotic spot virus	AJ607402	
TBSV	Tomato bushy stunt virus	M21958	
	Zeavirus		
MNeSV	Maize necrotic streak virus	AF266518	

	unassigned Tombusviridae	
TLV1	Trailing lespedeza virus 1	HM640935
	Pelarspovirus (proposed)	
ELV	Elderberry latent virus	AY038066
PCRPV	Pelargonium chlorotic ring pattern virus	AY038069
PLPV	Pelargonium line pattern virus	AY613852
PelRSV	Pelargonium ringspot virus	AY038068
RrLDV	*Rosa rugosa* leaf distortion virus	KC166238
	other viral sequences	
HCV	Hepatitis C virus RdRp	ADC54804
HEV	Hepatitis E virus CP	AAA45727
CCV	Cassava C virus	ACI03054
SNMV	Sesame necrotic mosaic virus CP	ABD34313