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:	***2015.006a-eS***	(to be completed by ICTV officers)

Short title: *Triatovirus:* A new genus in the family *Dicistroviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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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)	Dicistroviridae Study Group, Steven Valles, chair (steven.valles@ars.usda.gov).

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

Date first submitted to ICTV:	18/06/2015
Date of this revision (if different to above):	31/10/2015

ICTV-EC comments and response of the proposer:

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.006aS***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	-
Family:	***Dicistroviridae***
Order:	***Picornavirales***

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

naming a new genus

Code	***2015.006bS***	(assigned by ICTV officers)

To name the new genus: *Triatovirus*

Assigning the type species and other species to a new genus

Code	***2015.006cS***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Triatoma virus

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:**

5

Reasons to justify the creation of a new genus:

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

Triatoma virus (TrV) differs substantially in surface features from Cricket paralysis virus (CrPV), in the absence of an ordered VP4 molecule in the capsid interior and in the presence in VP3 of a structurally conserved catalytic motif involving the same DDF sequence as in VP1.

The two main differences between the TrV and CrPV capsids are the projections at the TrV surface, which are absent in CrPV. These projections are made from an inserted sequence element, and the presence of the same insertion in other members of the proposed genus (Plautia stali intestine virus –PSIV-, Himetobi P virus –HiPV-, and Black queen cell virus -BQCV-) suggest that they are also likely to have the same structural features **(Agirre et al., 2011, Squirres et al., 2013)**. The structure suggests that the exposed residues in these projections are likely to play a role in the interactions with the host; for instance, an entry receptor.

The second difference is the presence of a DDF motif in the homologous location in VP3, where it is also exposed to the capsid interior, whereas in CrPV, Aphid lethal paralysis virus –ALPV-, Drosophila C virus -DCV- and Rhopalosiphum padi virus –RhPV-, this motif is only found in VP1, where it is believed to account for cleavage of the VP0 precursor. This difference may account for additional proteolysis in VP1 during RNA release. Intriguingly, a second DDF motif (3254–3256) is present in VP3 at the same location in the structure at the corner between the BIDG sheet and the $\beta_{x1}\beta_{x2}$ sheet, which is equivalent to the $\beta_{x3}\beta_{x4}$ sheet in VP1. This motif is also conserved in BQCV, HiPV, PSIV and TrV but is not found in CrPV or in DCV, APLV or RhPV, which is the closest neighbour to CrPV in the current Dicistroviridae phylogenetic tree. Finally, the most striking difference is the absence of ordered VP4. The fact that this protein is not part of the ordered capsid in fully infectious TrV virions is in sharp contrast to what occurs with the same protein in CrPV, where it is found to be well structured around the fivefold axis. Such differences preclude assignment of a general function to VP4 in the Dicistroviridae family, and this also remains to be further elucidated **(Squires et al, 2013)**.

Sequence alignment

Taking into account that in the phylogenetic tree of the dicistrovirus family TrV belongs to a different branch from that of ABPV and CrPV **(Bonning and Miller, 2010),** as well as the biological, genetic, and structural knowledge regarding this virus, it is reasonable to propose TrV as the reference for a third Dicistroviridae family genus named *Triatovirus* (**Agirre et al., 2011).**

Phylogenetic analysis of deduced amino-acid sequences of the three major coat proteins (ORF 2) from the following dicistroviruses were done. The criterion employed for the selection of the viruses was based on the availability of seqeuences in GenBank. The alignment was performed using the Clustal2 phylogeny.

Homalodisca coagulata virus (HocV-1) do not have any DDF motif, but in the phylogenetic tree is nearest the *Triatovirus* genus proposed. Please see (Figure 1).

Origin of the new genus name:

Triatovirus from the type member ***Triato**ma virus*

Reasons to justify the choice of type species:

Triatoma virus is study extensively since 20 years. Together with Cricket paralysis virus is one of the most studied around the world concerning, protein, structure and sequences and its potential value as a biocide for the control of pestiferous insects (**Muscio et al., 2000),** or in others biotechnological applications (**Sánchez-Eugenia et al., 2015).**

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.

The criteria are

Natural host range

Sequence identity between capsid proteins of strains is above 90%.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.006dS***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Triatoma virus, Plautia stali intestine virus, Himetobi P virus, Black queen cell virus, Homalodisca coagulata virus 1

The present taxonomic position of these taxon/taxa:

Genus:	***Cripavirus***	Fill in all that apply.
Subfamily:	-	
Family:	***Dicistroviridae***	
Order:	***Picornavirales***	

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

See Modules 3 & 10

Part (b) re-assign to a higher taxon

Code	***2015.006eS***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Triatovirus (new)***	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	-	
Family:	***Dicistroviridae***	
Order:	***Picornavirales***	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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
- Further material in support of this proposal may be presented in the Appendix, Module 9

See Modules 3 & 10

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bonning BC, Miller WA. (2010). Dicistroviruses. Annu Rev Entomol. 55:129-50

Agirre J, Aloria K, Arizmendi JM, Iloro I, Elortza F, Sánchez-Eugenia R, Marti GA, Neumann E, Rey FA, Guérin DM. (2011). Capsid protein identification and analysis of mature Triatoma virus (TrV) virions and naturally occurring empty particles. Virology 409:91-101

Squires G, Pous J, Agirre J, Rozas-Dennis GS, Costabel MD, Marti GA, Navaza J, Bressanelli S, Guérin DM, Rey FA. (2013). Structure of the Triatoma virus capsid. Acta Crystallogr D Biol Crystallogr. 69:1026-37.

Rubén Sánchez-Eugenia, Fernando Méndez, Jailson F. B. Querido, Marcelo Sousa Silva, Diego M. A. Guérin, and José F. Rodríguez (2015). Triatoma virus structural polyprotein expression, processing and assembly into virus-like particles. *J. Gen. Virol. 96*: 64-73

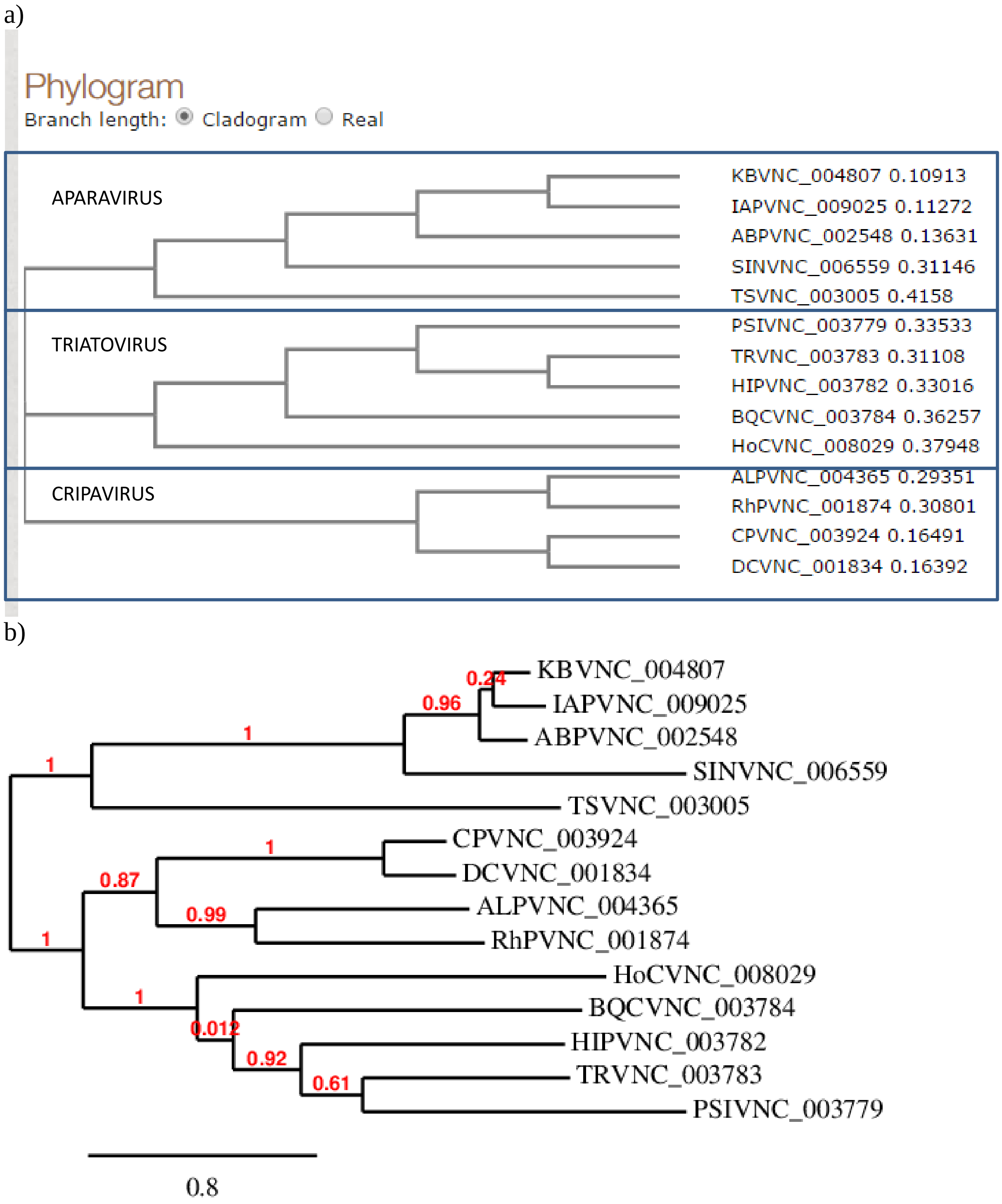
Muscio, O. A., Bonder, M., La Torre, J. L. & Scodeller, E. A. (2000) Horizontal Transmission of Triatoma Virus Through the Fecal-Oral Route in *Triatoma infestans* (Hemiptera: Triatomidae). J. Med. Entomol. 37(2): 271-275

Dereeper A., Guignon V., Blanc G., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. (2008). Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008 Jul 1;36 (Web Server issue):W465-9. Epub 2008 Apr 19.

Dereeper A., Audic S., Claverie J.M., Blanc G. (2010). BLAST-EXPLORER helps you building datasets for phylogenetic analysis. BMC Evol Biol. 10: 8.

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.



Phylogram
Branch length: ● Cladogram ○ Real

Figure 1. Phylogenetic analysis of deduced amino-acid sequences of the three major coat proteins (ORF 2) from the following dicistroviruses: KBV, Kashmir bee virus; IAPV, Israeli acute paralysis virus; ABPV, Acute bee paralysis virus; SINV, Solenopsis invicta virus-1; TSV, Taura syndrome virus; PSIV, Plautia stali intestine virus; TRV, Triatoma virus; HIPV, Himetobi P virus; BQCV, Black queen cell virus; HoCV, Homalodisca coagulata virus-1; ALPV, Aphid lethal paralysis virus; RhPV, Rhopalosiphum padi virus; CPV, Cricket paralysis virus; DCV, Drosophila C virus. The alignment was performed using the Clustal2 phylogeny. a) Cladogram; b) Maximum likelihood tree (Dereeper et al., 2008, 2010). See Table 1 for GenBank accession numbers.
http://www.phylogeny.fr/simple_phylogeny.cgi?workflow_id=9977873d62d85ee52aa0171b652e8229&tab_index=5&go_next=1

Table 1. Dicistrovirus species, abbreviations, RefSeq Nos. and Accession Nos.

Species	**Abbr.**	**RefSeq No.**	**Accession No.**
Kashmir bee virus	KBV	NC_004807	AY275710
Israeli acute paralysis virus	IAPV	NC_009025	EF219380
Acute bee paralysis virus	ABPV	NC_002548	AF150629
Solenopsis invicta virus-1	SINV	NC_006559	AY634314
Taura syndrome virus	TSV	NC_003005	AF277675
Cricket paralysis virus	CPV	NC_003924	AF218039
Drosophila C virus	DCV	NC_001834	AF014388
Aphid lethal paralysis virus	ALPV	NC_004365	AF536531
Rhopalosiphum padi virus	RhPV	NC_001874	AF022937
Homalodisca coagulata virus-1	HoCV	NC_008029	DQ288865
Black queen cell virus	BQCV	NC_003784	AF183905
Himetobi P virus	HIPV	NC_003782	AB017037
Triatoma virus	TRV	NC_003783	AF178440
Plautia stali intestine virus	PSIV	NC_003779	AB006531