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:	***2015.002a-gS***	(to be completed by ICTV officers)

Short title: Create a new genus for classification of extra small virus, a satellite virus of *Macrobrachium rosenbergii* nodavirus.
(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)	

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

Date first submitted to ICTV: June 15, 2015
Date of this revision (if different to above): July 30, 2015

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	***2015.002aS***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Macronovirus*** **(new)**
Subfamily:	
Family:	***Sarthroviridae*** **(new)**
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)**
Macrobrachium satellite virus 1	extra small virus (XSV)	AY247793

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

Extra small virus (XSV) is a satellite virus of Macrobrachium rosenbergii nodavirus (MrNV). Both viruses have isometric, spherical virions (Figure 1), infect giant fresh water prawn, and cause white tail disease, which is responsible for mass mortalities and important economic losses in hatcheries and farms [2]. MrNV is currently unclassified but sequence analyses clearly show that it is a genuine member of the family *Nodaviridae* [1]. XSV replication is dependent on that of MrNV and the two viruses are always found together [2, 10]. XSV and MrNV have been detected in aquatic insects of several species, which were collected from nursery ponds containing freshwater prawn (*Macrobrachium rosenbergii*) infected with MrNV and XSV [6]. Both viruses could also replicate in mosquito cell lines, suggesting that aquatic insects serve as vectors for XSV and MrNV transfer [6].

The XSV genome is linear positive-sense RNA molecule of 796 nucleotides which, unlike in other satellite viruses, contains a short poly(A) tail of 15-20 nucleotides at the 3'-end [9]. XSV virions are spherical, ≈15 nm in diameter and serologically unrelated to those of MrNV [4, 5]. The virion is constructed from two CPs, CP-17 (17 kDa) and CP-16 (16 kDa), which are present in nearly equimolar ratios and are independently translated initiating from different start codons within the same gene [8, 9]. It has been reported that 3' UTR plays an important role in selective encapsidation of the XSV genome [3]. The capsid protein is not recognizably similar to proteins in the public sequence databases [9].

Several XSV isolates from geographically remote locations, including French West Indies, Thailand, Taiwan, China and India, have been reported [2]. The isolates display 96-99% sequence identity in their capsid protein genes [7].

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.002bS***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Sarthroviridae* (new)**
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.002cS***	(assigned by ICTV officers)

Macronovirus

Assigning the type species and other species to a new genus

Code	***2015.002dS***	(assigned by ICTV officers)

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

Macrobrachium satellite virus 1

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

XSV does not display considerable genome or capsid protein sequence similarity to other known viruses. Therefore, classification of this virus calls for creation of a new genus.

Origin of the new genus name:

Macro- for *Macrobrachium rosenbergii*, *no-* for nodavirus (helper virus).

Reasons to justify the choice of type species:

This representative was the first to be sequenced.

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.

Not applicable; the proposed genus includes a single species.

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2015.002eS***	(assigned by ICTV officers)

To create a new family containing the subfamilies and/or genera listed below within the Order: *unassigned*

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.

Code	***2015.002fS***	(assigned by ICTV officers)

To name the new family: *Sarthroviridae*

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)

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.

- 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	***2015.002gS***	(assigned by ICTV officers)

To assign the following genera to the new family:
You may list several genera here. For each genus, please state whether it is new or existing.

- 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

***Macronovirus* (new)**

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):**

0

Reasons to justify the creation of the new family:
Additional material in support of this proposal may be presented in the Appendix, Module 9

XSV does not display considerable genome or capsid protein sequence similarity to any other known virus. Therefore, classification of this virus calls for creation of a new family.

Origin of the new family name:

S- for small, *arthro-* for arthropod.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Bonami JR, Shi Z, Qian D, Sri Widada J (2005) White tail disease of the giant freshwater prawn, Macrobrachium rosenbergii: separation of the associated virions and characterization of MrNV as a new type of nodavirus. J Fish Dis 28:23-31
2. Bonami JR, Sri Widada J (2011) Viral diseases of the giant fresh water prawn Macrobrachium rosenbergii: a review. J Invertebr Pathol 106:131-142
3. Liang Y, Zhang W, Zhang H, Shi Z (2014) 3'-UTR sequence of Macrobrachium rosenbergii extra small virus (XSV) is important for viral RNA packaging. Virol Sin 29:133-135
4. Longyant S, Senapin S, Sanont S, Wangman P, Chaivisuthangkura P, Rukpratanporn S, Sithigorngul P (2012) Monoclonal antibodies against extra small virus show that it co-localizes with Macrobrachium rosenbergii nodavirus. Dis Aquat Organ 99:197-205
5. Qian D, Shi Z, Zhang S, Cao Z, Liu W, Li L, Xie Y, Cambournac I, Bonami JR (2003) Extra small virus-like particles (XSV) and nodavirus associated with whitish muscle disease in the giant freshwater prawn, Macrobrachium rosenbergii. J Fish Dis 26:521-527
6. Sudhakaran R, Haribabu P, Kumar SR, Sarathi M, Ahmed VP, Babu VS, Venkatesan C, Hameedl AS (2008) Natural aquatic insect carriers of Macrobrachium rosenbergii nodavirus (MrNV) and extra small virus (XSV). Dis Aquat Organ 79:141-145
7. Sudhakaran R, Syed Musthaq S, Rajesh Kumar S, Sarathi M, Sahul Hameed AS (2008) Cloning and sequencing of capsid protein of Indian isolate of extra small virus from Macrobrachium rosenbergii. Virus Res 131:283-287
8. Wang J, Zhang H, Shi Z (2008) Expression and assembly mechanism of the capsid proteins of a satellite virus (XSV) associated with Macrobrachium rosenbergii nodavirus. Virol Sin 23:73-77
9. Widada JS, Bonami JR (2004) Characteristics of the monocistronic genome of extra small virus, a virus-like particle associated with Macrobrachium rosenbergii nodavirus: possible candidate for a new species of satellite virus. J Gen Virol 85:643-646
10. Zhang H, Wang J, Yuan J, Li L, Zhang J, Bonami JR, Shi Z (2006) Quantitative relationship of two viruses (MrNV and XSV) in white-tail disease of Macrobrachium rosenbergii. Dis Aquat Organ 71:11-17

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.

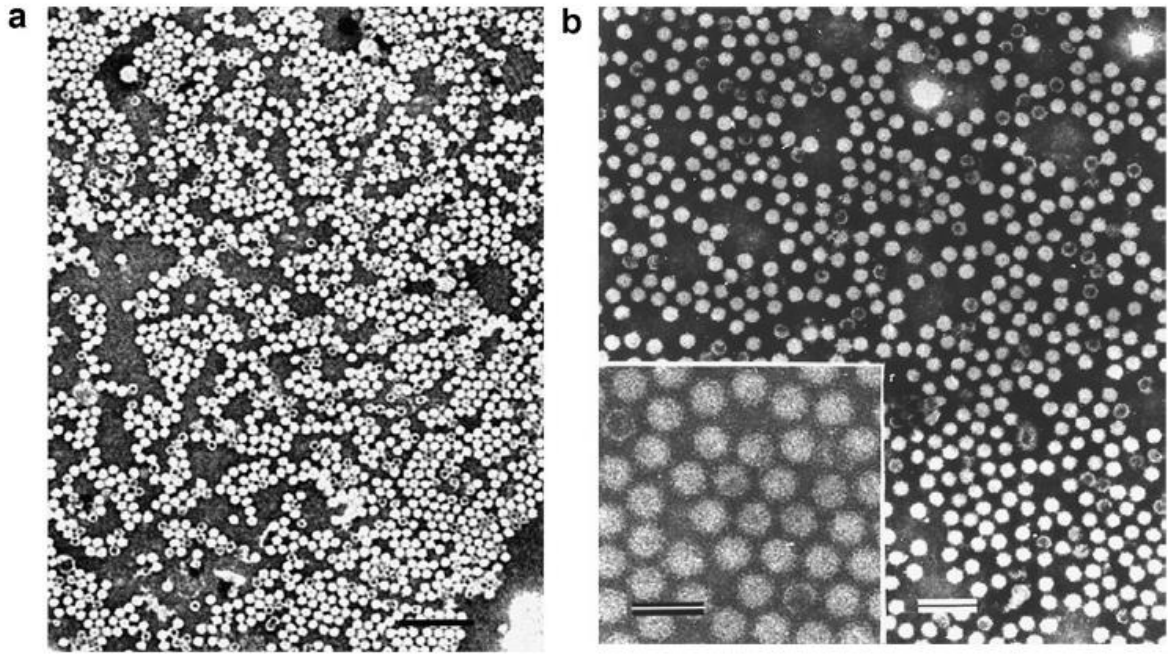

Figure 1. Transmission electron micrographs of XSV (a) and MrNV (b) virions purified on the CsCl gradient. Bars = 100 nm. Inset in b: higher magnification of MrNV; bar = 50 nm. Reproduced from [2] with permission from Elsevier.