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:	*2015.010a-tM*	(to be completed by ICTV officers)

Short title: Five (5) new unassigned genera in the order *Mononegavirales*
(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 ☒

Author(s):

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List the ICTV study group(s) that have seen this proposal:

ICTV *Bornaviridae*, *Filoviridae*, *Nyamiviridae*, *Paramyxoviridae*, and *Rhabdoviridae* Study Groups

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): | |

ICTV-EC comments and response of the proposer:

ICTV *Bornaviridae*, *Filoviridae*, *Nyamiviridae*, *Paramyxoviridae*, and *Rhabdoviridae* Study Groups

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	*2015.010aM*		(assigned by ICTV officers)

To create 1 new species within:

		Fill in all that apply.
Genus:	*Crustavirus*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:	*N/A*	
Family:	**unassigned**	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Mononegavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Wēnzhōu crustavirus[1]	Wēnzhōu crab virus 1 (WzCV-1)	Coding-complete genome: KM817644

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

Wēnzhōu crab virus 1 (WzCV-1) was first described in 2015 during a landmark next-generation sequencing study performed in China (Li *et al.*). WzCV-1 was found in crabs and barnacles (*Capitulum mitella, Charybdis japonica, Charybdis lucifera*) in Wēnzhōu (温州). While the length and genome organization of WzCV-1 is consistent with that of classified mononegaviruses, whole genome pairwise similarity analyses, as well as phylogenetic analyses using the RNA-dependent RNA polymerase gene (L) (Figures 1 and 2), place WzCV-1 consistently outside of established mononegavirus clades. The ICTV *Mononegavirales* Study Group recognizes the fact that many newly discovered viruses not associated with any disease, such as WzCV-1, may not be further analyzed in the future but consider them important for taxonomic/evolutionary considerations regarding the order *Mononegavirales*. Pairwise genome comparisons, overall genome organization, L-based phylogeny, geographic and host association are therefore considered sufficient for the classification of WzCV-1 into a new mononegaviral family [not yet proposed], genus, and species.

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[1] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics in taxon names. In case 2015.001aG.v1.Diacritics is ratified, the diacritical marks in this species name will simply be dropped (resulting in *Wenzhou crustavirus*). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

MODULE 3A: **<u>NEW GENUS</u>**

creating a new genus

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

Code	*2015.010bM*	(assigned by ICTV officers)

To create a new genus within:

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

Subfamily:	*N/A*
Family:	**unassigned**
Order:	*Mononegavirales*

naming a new genus

Code	*2015.010cM*	(assigned by ICTV officers)

To name the new genus: *Crustavirus*

Assigning the type species and other species to a new genus

Code	*2015.010dM*	(assigned by ICTV officers)

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

Wēnzhōu crustavirus[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

See Module 2A

Origin of the new genus name:

*Crustavirus***: sigil of <u>Crusta</u>cea and <u>virus</u>**

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

N/A

MODULE 2B: **<u>NEW SPECIES</u>**

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	*2015.010eM*		(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Anphevirus*	Fill in all that apply.
Subfamily:	*N/A*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	**unassigned**	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Mononegavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Xīnchéng anphevirus[2]	Xīnchéng mosquito virus (XcMV)	Coding-complete genome: KM817661

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

Xīnchéng mosquito virus (XcMV) was first described in 2015 during a landmark next-generation sequencing study performed in China (Li *et al*.). XcMV was found in mosquitoes (*Anopheles sinensis*) in Xīnchéng (新城). While the length and genome organization of XcMV is consistent with that of classified mononegaviruses, whole genome pairwise similarity analyses, as well as phylogenetic analyses using the RNA-dependent RNA polymerase gene (L) (Figures 1 and 2), place XcMV consistently outside of established mononegavirus clades. The ICTV *Mononegavirales* Study Group recognizes the fact that many newly discovered viruses not associated with any disease, such as XcMV, may not be further analyzed in the future but consider them important for taxonomic/evolutionary considerations regarding the order *Mononegavirales*. Pairwise genome comparisons, overall genome organization, L-based phylogeny, geographic and host association are therefore considered sufficient for the classification of XcMV into a new mononegaviral family [not yet proposed], genus, and species.

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[2] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics in taxon names. In case 2015.001aG.v1.Diacritics is ratified, the diacritical marks in this species name will simply be dropped (resulting in *Xincheng anphevirus*). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

MODULE 3B: **NEW GENUS**

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

Code	*2015.010fM*	(assigned by ICTV officers)

To create a new genus within:

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

Subfamily:	*N/A*
Family:	**unassigned**
Order:	*Mononegavirales*

Code	*2015.010gM*	(assigned by ICTV officers)

To name the new genus: *Anphevirus*

Code	*2015.010hM*	(assigned by ICTV officers)

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

Xīnchéng anphevirus[2]	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

See Module 2B

Origin of the new genus name:

*Anphevirus***: sigil of** *Anopheles* **and** **virus**

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

N/A

MODULE 2C-1: **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	*2015.010iM*	(assigned by ICTV officers)

To create 1 new species within:

Fill in all that apply.

Genus:	*Arlivirus*
Subfamily:	*N/A*
Family:	**unassigned**
Order:	*Mononegavirales*

- 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)
Lǐshì arlivirus[3]	Lǐshì spider virus 2 (LsSV-2)	Coding-complete genome: KM817632

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

Lǐshì spider virus 2 (LsSV-2) was first described in 2015 during a landmark next-generation sequencing study performed in China (Li *et al.*). LsSV-2 was found in spiders in Lǐshì (李市). While the length and genome organization of LsSV-2 is consistent with that of classified mononegaviruses, whole genome pairwise similarity analyses, as well as phylogenetic analyses using the RNA-dependent RNA polymerase gene (L) (Figures 1 and 2), place LsSV-2 consistently outside of established mononegavirus clades. The ICTV *Mononegavirales* Study Group recognizes the fact that many newly discovered viruses not associated with any disease, such as LsSV-2, may not be further analyzed in the future but consider them important for taxonomic/evolutionary considerations regarding the order *Mononegavirales*. Pairwise genome comparisons, overall genome organization, L-based phylogeny, geographic and host association are therefore considered sufficient for the classification of LsSV-2 into a new mononegaviral family [not yet proposed], genus, and species.

---

[3] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics in taxon names. In case 2015.001aG.v1.Diacritics is ratified, the diacritical marks in this species name will simply be dropped (resulting in *Lishi arlivirus*). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

MODULE 3C-1: **<u>NEW GENUS</u>**

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

Code	*2015.010jM*	(assigned by ICTV officers)

To create a new genus within:

Fill in all that apply.

Subfamily:	*N/A*
Family:	**unassigned**
Order:	*Mononegavirales*

- 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	*2015.010kM*	(assigned by ICTV officers)

To name the new genus: *Arlivirus*

Assigning the type species and other species to a new genus

Code	*2015.010lM*	(assigned by ICTV officers)

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

Lǐshì arlivirus[3]

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

See Module 2C-1

Origin of the new genus name:

Arlivirus: sigil of <u>Ar</u>achnida, <u>Lí</u>shí, and <u>virus</u>

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

N/A

MODULE 2C-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	*2015.010mM*	(assigned by ICTV officers)

To create 1 new species within:

		Fill in all that apply.
Genus:	*Wastrivirus*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:	*N/A*	
Family:	**unassigned**	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Mononegavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Sānxiá wastrivirus[4]	Sānxiá water strider virus 4 (SxWSV-4)	Coding-complete genome: KM817633.1

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

Sānxiá water strider virus 4 (SxWSV-4) was first described in 2015 during a landmark next-generation sequencing study performed in China (Li *et al.*). SxWSV-4was found in spiders in Sānxiá (三峡). While the length and genome organization of SxWSV-4 is consistent with that of classified mononegaviruses, whole genome pairwise similarity analyses, as well as phylogenetic analyses using the RNA-dependent RNA polymerase gene (L) (Figures 1 and 2), place SxWSV-4 consistently outside of established mononegavirus clades, in a branch together with LsSV-2. The ICTV *Mononegavirales* Study Group recognizes the fact that many newly discovered viruses not associated with any disease, such as SxWSV-4, may not be further analyzed in the future but consider them important for taxonomic/evolutionary considerations regarding the order *Mononegavirales*. Pairwise genome comparisons, overall genome organization, L-based phylogeny, geographic and host association are therefore considered sufficient for the classification of SxWSV-4 into a new mononegaviral family [not yet proposed], genus, and species.

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[4] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics in taxon names. In case 2015.001aG.v1.Diacritics is ratified, the diacritical marks in this species name will simply be dropped (resulting in *Sanxia wastrivirus*). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography

MODULE 3C-2: **NEW GENUS**

creating a new genus

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

Code	*2015.010nM*	(assigned by ICTV officers)

To create a new genus within:

Fill in all that apply.

Subfamily:	*N/A*
Family:	**unassigned**
Order:	*Mononegavirales*

- 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	*2015.010oM*	(assigned by ICTV officers)

To name the new genus: *Wastrivirus*

Assigning the type species and other species to a new genus

Code	*2015.010pM*	(assigned by ICTV officers)

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

Sānxiá wastrivirus[4]

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

See Module 2C-2

Origin of the new genus name:

Wastrivirus: sigil of <u>wa</u>ter <u>stri</u>der and <u>vir</u>us

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

N/A

MODULE 2C-3: **<u>NEW SPECIES</u>**

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	*2015.010qM*	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Chengtivirus*	Fill in all that apply.
Subfamily:	*N/A*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	**unassigned**	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Mononegavirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Tǎchéng chengtivirus[5]	Tǎchéng tick virus 6 (TcTV-6)	Coding-complete genome: KM817641

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

Tǎchéng tick virus 6 (TcTV-6) was first described in 2015 during a landmark next-generation sequencing study performed in China (Li *et al.*). TcTV-6 was found in ticks (*Argas miniatus*) in Tǎchéng (塔城). While the length and genome organization of TcTV-6 is consistent with that of classified mononegaviruses, whole genome pairwise similarity analyses, as well as phylogenetic analyses using the RNA-dependent RNA polymerase gene (L) (Figures 1 and 2), place TcTV-6 consistently outside of established mononegavirus clades, in a branch together with LsSV-2 and SxWSV-4. The ICTV *Mononegavirales* Study Group recognizes the fact that many newly discovered viruses not associated with any disease, such as TcTV-6, may not be further analyzed in the future but consider them important for taxonomic/evolutionary considerations regarding the order *Mononegavirales*. Pairwise genome comparisons, overall genome organization, L-based phylogeny, geographic and host association are therefore considered sufficient for the classification of TcTV-6 into a new mononegaviral family [not yet proposed], genus, and species.

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[5] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics in taxon names. In case 2015.001aG.v1.Diacritics is ratified, the diacritical marks in this species name will simply be dropped (resulting in ***Tacheng chengtivirus***). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

MODULE 3C-3: **NEW GENUS**

creating a new genus

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

Code	*2015.010rM*	(assigned by ICTV officers)

To create a new genus within:

Fill in all that apply.

Subfamily:	*N/A*	
Family:	**unassigned**	
Order:	*Mononegavirales*	

- 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	*2015.010sM*	(assigned by ICTV officers)

To name the new genus: *Chengtivirus*

Assigning the type species and other species to a new genus

Code	*2015.010tM*	(assigned by ICTV officers)

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

Tǎchéng chengtivirus[5]	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

See Module 2C-3

Origin of the new genus name:

Chengtivirus: sigil of Tǎchéng, tick, and virus

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

N/A

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Li CX, Shi M, Tian JH, Lin XD, Kang YJ, Chen LJ, Qin XC, Xu J, Holmes EC, Zhang YZ. 2015. Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. Elife **4:**e05378.

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
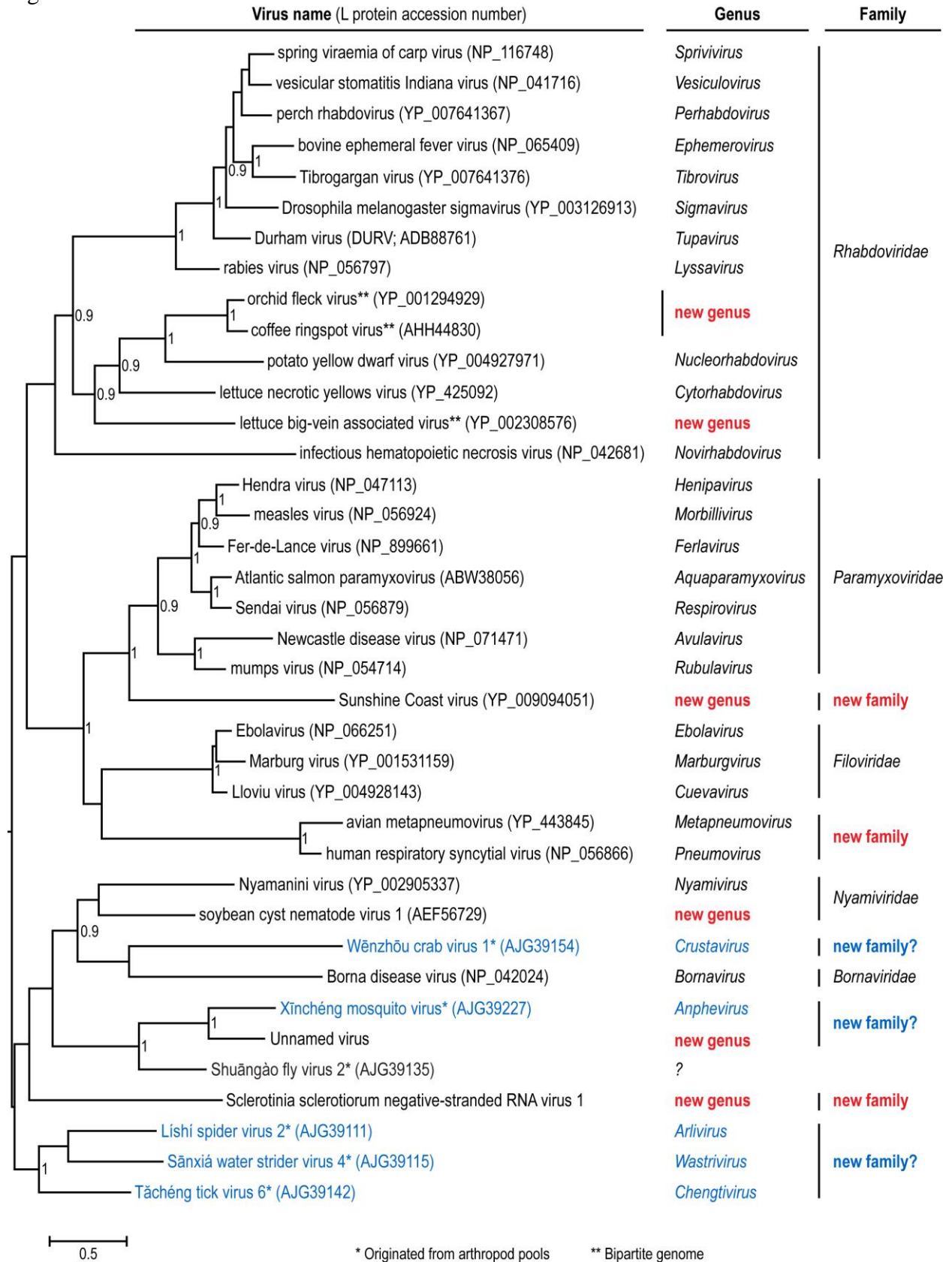
Phylogenetic relationships of selected mononegaviruses. A maximum-likelihood tree was constructed using PhyML 3.0 (http://www.atgc-montpellier.fr/phyml/) based on a multiple amino acid sequence alignment of the entire L polymerase. Ambiguously aligned regions were removed using Gblocks 0.91b (http://molevol.cmima.csic.es/castresana/Gblocks_server.html) with the all

options of less stringent selection. The best-fit model LG+I +G+F was selected using ProtTest ver. 2.4 (http://darwin.uvigo.es/software/prottest2_server.html). Virus names (the member of type species or others) and GenBank/Refseq accession numbers are shown. The names of proposed genera are highlighted in blue. Numbers at the nodes represent aLRT values derived using an SH like calculation (only values greater than 0.9 are shown).

Figure 2 (taken from Li *et al.*)
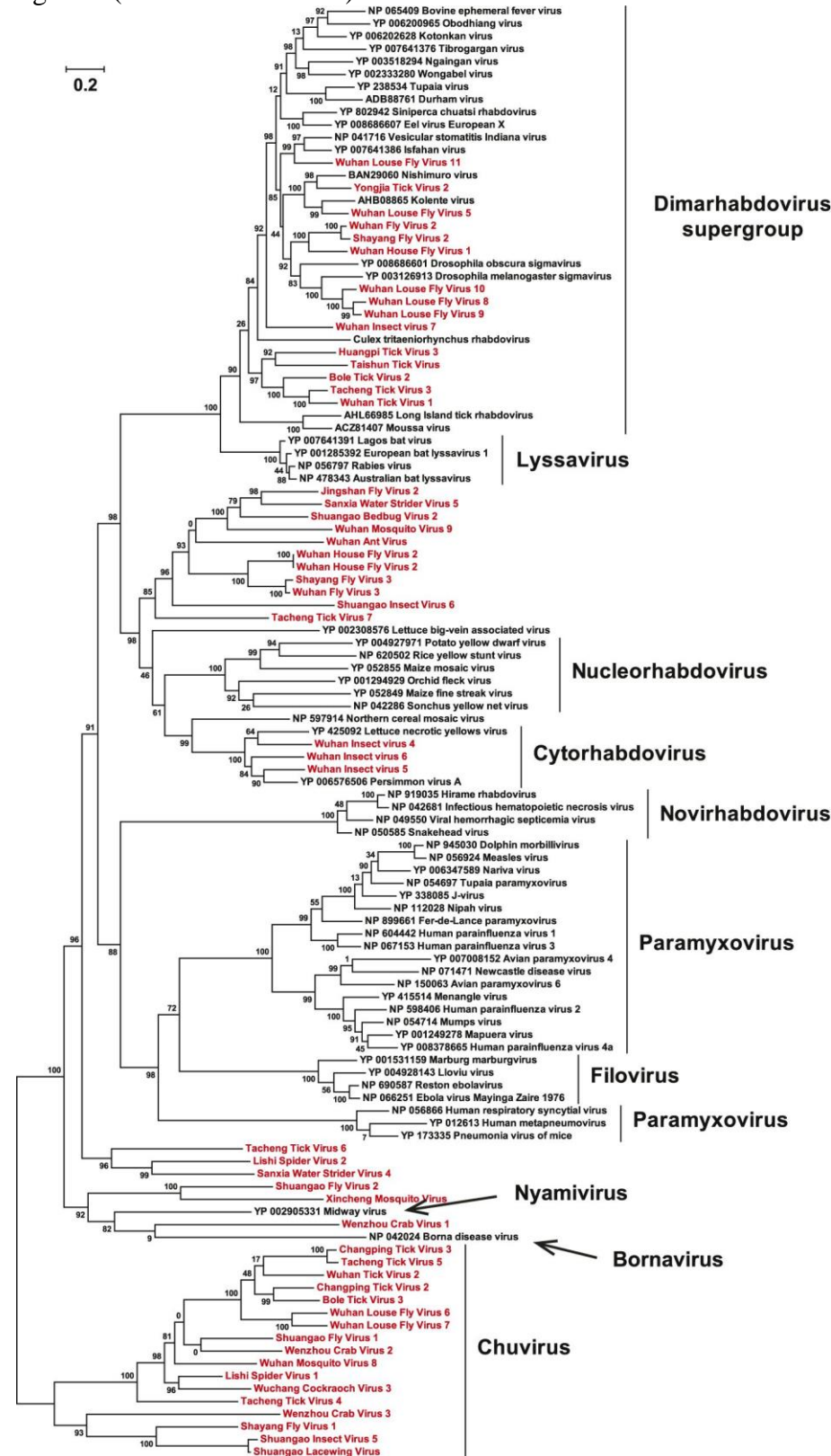
The phylogeny is reconstructed using RdRp alignments. Statistical support from the aLRT is shown on each node of the tree. The names of the viruses discovered in this study are shown in red. The names of reference sequences, which contain both the GenBank accession number and the virus species name, are shown in black.