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:	***2016.017a-kS***	(to be completed by ICTV officers)

Short title: Create a new family of positive-sense RNA viruses, *Solinviviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☒ **4** ☐ **5** ☒ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Andrew E. Firth and Steven M. Valles

Corresponding author with e-mail address:

Andrew E. Firth, email: aef24@cam.ac.uk

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/Iflaviridae

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

Date first submitted to ICTV: 1 June 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2a: **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	***2016.017aS***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Invictavirus* (new)
Subfamily:	-
Family:	*Solinviviridae* (new)
Order:	Unassigned

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)**
Solenopsis invicta virus 3	Solenopsis invicta virus 3 DM/USA/2007	FJ528584 (NC_012531)

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 11

The RNA genome of SINV-3 has been completely sequenced and the polyprotein exhibits only 26% amino acid identity over 67% coverage to its closest relative (NfV-1) among sequenced virus genomes. SINV-3 has been isolated as virus particles and the host species, *Solenopsis invicta*, has been confirmed (Valles et al., 2009; 2010; 2014; Porter et al., 2013; 2015). To our knowledge, no other similar virus species infecting *Solenopsis invicta* have been previously described.

MODULE 2b: **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	***2016.017bS***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Nyfulvavirus* (new)
Subfamily:	-
Family:	*Solinviviridae* (new)
Order:	Unassigned

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)**
Nylanderia fulva virus 1	Nylanderia fulva virus 1 Florida/USA/2011	KX024775 (NC_030651)

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 11

The RNA genome of NfV-1 has been completely sequenced and the polyprotein exhibits only 26% amino acid identity over 67% coverage to its closest relative (SINV-3) among sequenced virus genomes. NfV-1 has been isolated as virus particles and the host species, *Nylanderia fulva*, has been confirmed (Valles et al., 2016). To our knowledge, no other similar virus species infecting *Nylanderia fulva* have been previously described.

MODULE 3a: **NEW GENUS**

creating a new genus

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

Code	***2016.017cS***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	*Solinviviridae* (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	***2016.017dS***	(assigned by ICTV officers)

To name the new genus: *Invictavirus*

Assigning the type species and other species to a new genus

Code	***2016.017eS***	(assigned by ICTV officers)

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

***Solenopsis invicta virus 3* (new)**	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 11

The three species assigned to the new family *Solinviviridae*, viz. *Solenopsis invicta virus 3* (SINV-3), *Nylanderia fulva virus 1* (NfV-1) and *Kelp fly virus*, are highly divergent (NfV1/SINV3 26% aa identity over 67% coverage; SINV3/KFV 31% aa identity over 47% coverage; KFV/NfV1 34% aa identity over 26% coverage) justifying their assignment to separate genera. Furthermore, notwithstanding the similarities that justify their grouping at family level, they have differences in genome structure (Valles et al., 2014, 2016). In NfV-1, Hel-Pro-RdRp-dsRBP-JR-CPextn domains are encoded in a single ORF, whereas in SINV-3 there is a programmed ribosomal frameshift between the JR and CPextn domains. NfV-1 also has an OTU domain upstream of Hel that has not been found in SINV-3. The currently available KFV sequence has a major genome rearrangement relative to SINV-3 and NfV-1, but it is possible that the available sequence is defective, so that KFV should remain unassigned pending clarification.

Origin of the new genus name:

Invictavirus, from the type species Solenopsis ***invicta*** virus 3.

Reasons to justify the choice of type species:

Solenopsis invicta virus 3 (SINV-3) is the only characterized virus in the new genus and the best

characterized virus of the three comprising the new family. Studies have established the tissue and stage tropism of SINV-3 (Valles et al. 2009), its phenology (Valles et al. 2010), its host specificity (Porter et al. 2013, 2015), its use as a biopesticide (Valles et al. 2013) and classical biological control agent (Valles and Oi 2014), its pathogenesis (Valles et al. 2014), and its capsid proteins and gene expression (Valles et al. 2014).

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.

NA

MODULE 3b: **NEW GENUS**

creating a new genus

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

Code	***2016.017fS***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	-
Family:	*Solinviviridae* (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	***2016.017gS***	(assigned by ICTV officers)

To name the new genus: *Nyfulvavirus*

Assigning the type species and other species to a new genus

Code	***2016.017hS***	(assigned by ICTV officers)

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

***Nylanderia fulva virus 1* (new)**

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 11

The three viruses assigned to the new family *Solinviviridae*, viz. Solenopsis invicta virus 3 (SINV-3), Nylanderia fulva virus 1 (NfV-1) and Kelp fly virus, are highly divergent (NfV1/SINV3 26% aa identity over 67% coverage; SINV3/KFV 31% aa identity over 47% coverage; KFV/NfV1 34% aa identity over 26% coverage) justifying their assignment to separate genera. Furthermore, notwithstanding the similarities that justify their grouping at family level, they have differences in genome structure (Valles et al., 2014, 2016). In NfV-1, Hel-Pro-RdRp-dsRBP-JR-CPextn domains are encoded in a single ORF, whereas in SINV-3 there is a programmed ribosomal frameshift between the JR and CPextn domains. NfV-1 also has an OTU domain upstream of Hel that has not been found in SINV-3. The currently available KFV sequence has a major genome rearrangement relative to SINV-3 and NfV-1, but it is possible that the available sequence is defective, so that KFV should remain unassigned pending clarification.

Origin of the new genus name:

Nyfulvavirus, from the type species ***Ny***landeria ***fulva*** virus 1.

Reasons to justify the choice of type species:

Nylanderia fulva virus 1 (NfV-1) is the only characterized virus in the new genus (Valles et al.,

2016).

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.

NA

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2016.017iS***	(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	***2016.017jS***	(assigned by ICTV officers)

To name the new family: *Solinviviridae*

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 'MOVE' it from its existing family

NA

Code	***2016.017kS***	(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 'MOVE' it from that family

Invictavirus (new), *Nyfulvavirus* (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 7). **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:

Overview

Solenopsis invicta virus 3 (SINV-3) (Valles et al., 2009) and Kelp fly virus (KFV) (Hartley et al., 2005) are currently unassigned "picorna-like" viruses. The recent discovery and characterization of Nylanderia fulva virus 1 (NfV-1) (Valles et al., 2016) clearly indicates a distinct phylogenetic group comprising these 3 viruses. Although SINV-3 and KFV have previously been associated with the order *Picornavirales*, Valles et al. (2014) shows this to be incorrect due to the presence of a single jelly-roll capsid domain encoded in the genome (instead of three) and the production of a subgenomic RNA for capsid protein expression. All three viruses infect insects and several related sequences have been identified from transcriptome shotgun assembly (TSA) sequences of (only) insect-derived RNA (Valles et al.,

2016).

Morphology

Virions are roughly spherical with a particle diameter ranging from 27 to 33 nm in diameter. Projections on the surface of the virion have been observed by electron microscopy for SINV-3 (Valles et al., 2009) and NfV-1 (Valles et al., 2016), and by cryoelectron microscopy and image reconstruction for KFV (Hartley et al. 2005).

Genome

SINV-3, KFV, and NfV-1 all possess a monopartite, single-stranded positive-sense RNA genome (10.4-11 kb). All exhibit Hel-Pro-RdRp arrangement and likely also encode a VPg protein between Hel and Pro.

SINV-3 is the best characterized of the three viruses (Valles et al., 2014). It encodes a single jelly-roll capsid protein domain (VP1) downstream of RdRp. Ribosomal frameshifting into a 3' ORF appends a frameshift extension domain (FSD) onto a proportion of VP1. The resulting VP1 and VP1-FSD proteins are both present in the virion and the FSD domain is thought to form the projections observed by electron microscopy. A second protein (VP2), also present in the virion, is encoded downstream of FSD in the 3' ORF. A predicted dsRNA binding protein (dsRBP) is encoded between RdRp and VP1. While all viral proteins are translatable from the genomic RNA, a subgenomic RNA corresponding to the regions encoding dsRBP, VP1, FSD and VP2 is also produced in infected cells. Similarities with the *Caliciviridae* genome organization have been noted (Valles et al. 2014).

NfV-1 is quite divergent (tblastn 26% aa identity over 67% query coverage) and its genome organization differs from SINV-3 in that it contains a single long ORF instead of two ORFs connected by ribosomal frameshifting. Hel-Pro-RdRp-dsRBP-VP1 domains are present in the same order as in SINV-3 while sequence presumed to correspond to the SINV-3 FSD-VP2 domains is present downstream. Since NfV-1 lacks a break in reading frame after VP1, NfV is expected to produce a single VP1-containing protein (equivalent to SINV-3 VP1-FSD) and equal amounts of this protein and VP2, in contrast to SINV-3 where VP1-FSD and VP2 are produced at sub-stoichiometric levels.

The third characterized virus, KFV, clearly falls within the clade defined by SINV-3 and NfV-1. However, KFV has a major genome rearrangement relative to SINV-3, NfV-1 and currently available TSA sequences, and a 638-nt sequence duplication coinciding with the site of rearrangement, suggesting that the sequence may not be representative of the natural virus (Valles et al., 2014). (For this reason, the currently available KFV sequence may be unsuitable for establishing KFV as a type species of a new genus, and therefore we suggest KFV remains unassigned within the *Solinviviridae* family pending clarification of its genome structure.)

Phylogeny

To establish an RdRp-based phylogeny, we extracted the picornavirus-like superorder RdRp sequences provided in the supplementary material of Koonin et al. (2008), appended the equivalent region from SINV-3 and related sequences, and rebuilt the alignment using MUSCLE (Edgar, 2004). We then used MrBayes (Ronquist et al., 2012) to generate a Bayesian Markov chain Monte Carlo based phylogenetic tree (see Appendix). The analysis revealed that

the SINV-3, KFV, and NfV-1 and related TSA sequences form a distinct cluster.
Origin of the new family name:
***Solinviviridae* from the type species, *Sol*enopsis *invic*ta virus 3**

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Edgar RC. 2004. MUSCLE: a multiple sequence alignment method with reduced time and space complexity. BMC Bioinformatics 5: 1-19.

Hartley CJ, Greenwood DR, Gilbert RJ, Masoumi A, Gordon KH, Hanzlik TN, Fry EE, Stuart DI, Scotti PD. Kelp fly virus: a novel group of insect picorna-like viruses as defined by genome sequence analysis and a distinctive virion structure. J Virol. 2005 Nov; 79(21):13385-98.

Koonin EV, Wolf YI, Nagasaki K, Dolja VV. 2008. The big bang of picorna-like virus evolution antedates the radiation of eukaryotic supergroups. Nature Reviews Microbiology 6: 925-39.

Porter SD, Valles SM, Oi DH. 2013. Host specificity and colony impacts of Solenopsis invicta virus 3. Journal of Invertebrate Pathology 114: 1-6.

Porter SD, Valles SM, Wild AL, Dieckmann R, Plowes NJR. 2015. *Solenopsis invicta virus 3*: further host-specificity tests with native *Solenopsis* ants (Hymenoptera: Formicidae). Florida Entomologist 98: 122-125.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539-542.

Valles SM, Hashimoto Y. Isolation and characterization of Solenopsis invicta virus 3, a new positive-strand RNA virus infecting the red imported fire ant, *Solenopsis invicta*. Virology. 2009 Jun 5; 388(2):354-61.

Valles SM, Oi DH, Porter SD. 2010. Seasonal variation and the co-occurrence of four pathogens and a group of parasites among monogyne and polygyne fire ant colonies. Biological Control 54: 342-348.

Valles SM, Porter SD, Choi MY, Oi DH. 2013. Successful transmission of Solenopsis invicta virus 3 to *Solenopsis invicta* fire ant colonies in oil, sugar, and cricket bait formulations. Journal of Invertebrate Pathology 113: 198-204.

Valles SM, Bell S, Firth AE. 2014. *Solenopsis invicta virus 3*: mapping of structural proteins, ribosomal frameshifting, and similarities to *Acyrthosiphon pisum virus* and *Kelp fly virus*. PLoS ONE 9: e93497.

Valles SM, Oi DH. 2014. Successful transmission of Solenopsis invicta virus 3 to field colonies of *Solenopsis invicta* (Hymenoptera: Formicidae). Florida Entomologist 97: 1244-1246.

Valles SM, Porter SD, Firth AE. 2014. Solenopsis invicta virus 3: pathogensis and stage specificity in red imported fire ants. Virology 461: 66-71.

Valles SM, Porter SD. 2015. Dose response of red imported fire ant colonies to Solenopsis invicta virus 3. Archives of Virology 160: 2407-2413.

Valles SM, Oi D, Becnel JJ, Wetterer JK, Lapolla JS, Firth AE. 2016. Isolation and characterization of Nylanderia fulva virus 1, a positive-sense, single-stranded RNA virus infecting the tawny crazy ant, *Nylanderia fulva*. Virology 496: 244-254.

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.

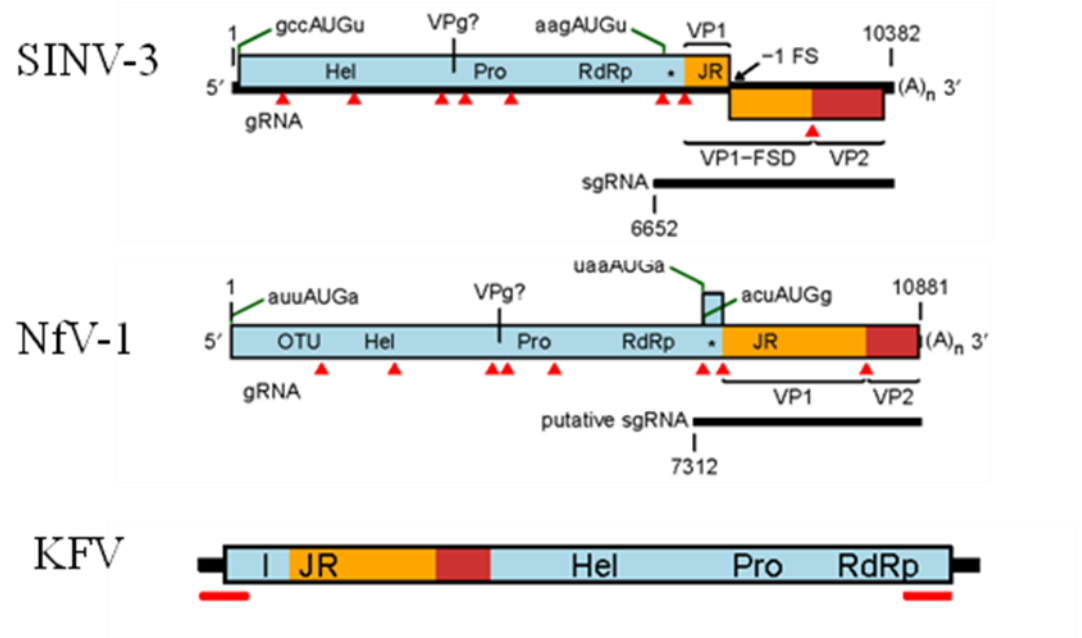

Figure 1. Adapted from Valles et al. (2016). Genome organization of viruses comprising the proposed family *Solinviviridae* (SINV-3, the type species, NfV-1, and KFV). Positions of picorna-like helicase (Hel), protease (Pro) and RNA-dependent RNA polymerase (RdRp) protein domains are shown within the polyprotein ORF. Predicted ovarian tumor (OTU), picorna/calici-like jelly-roll fold capsid protein (JR) and dsRNA binding protein (*) domains are also indicated. Potential virus protease cleavage sites are indicated with red triangles. The sequence upstream of Pro is likely to correspond to VPg. The sgRNA (demonstrated for SINV-3, presumed for NfV-1) is indicated. VP1/VP1-FSD (orange) and VP2 (red) are annotated based on analogy with the mapped structural proteins of SINV-3. Red bars in the possibly defective KFV sequence indicate a 638-nt sequence duplication.

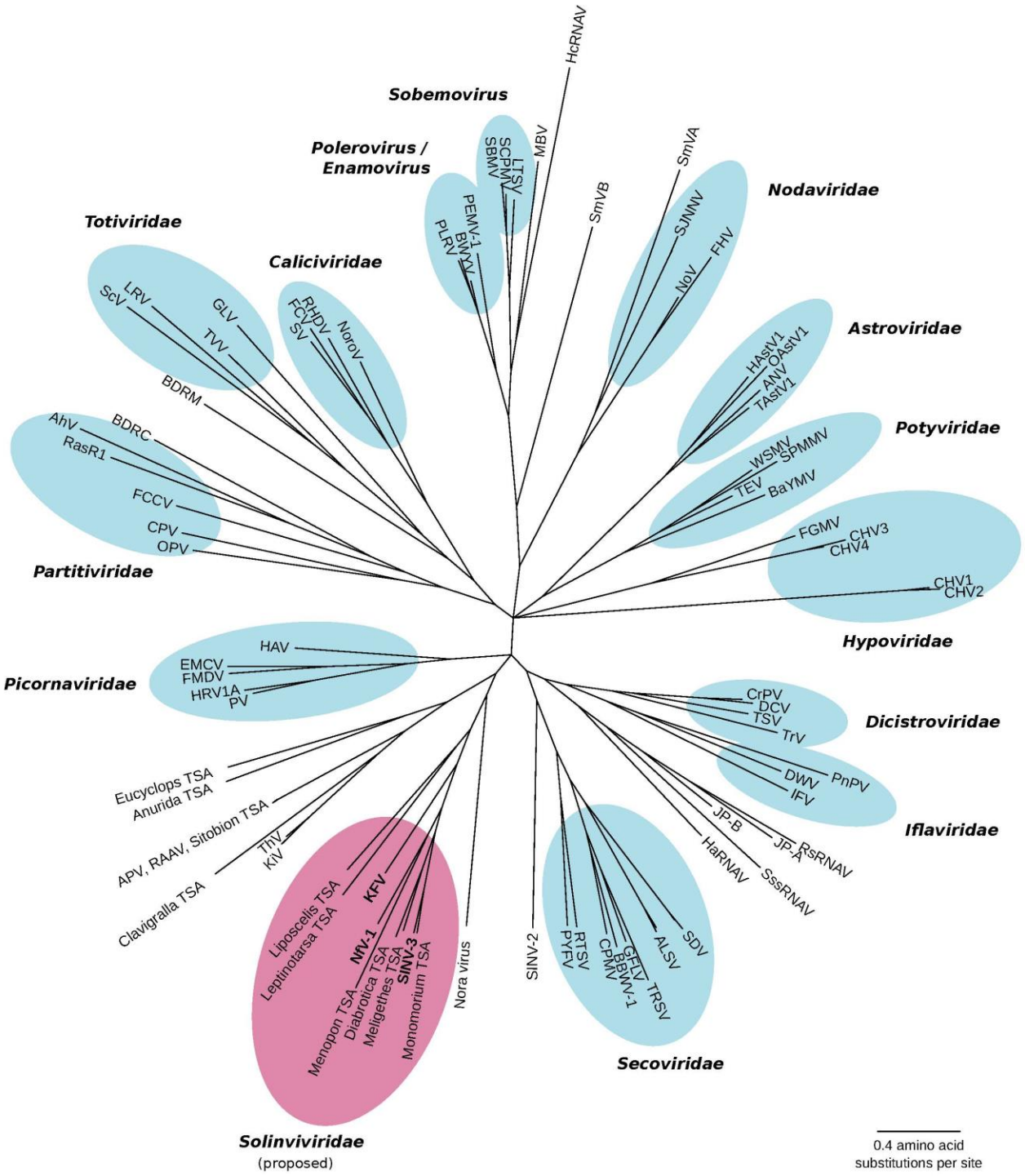

Figure 2. Adapted from Valles et al. (2016). Phylogenetic tree for picorna-like viruses. RdRp amino acid sequences from picorna-like viruses were obtained from Koonin et al. (2008), combined with the equivalent regions from SINV-3 and related sequences (including several TSA sequences from arthropod-derived RNA), realigned with MUSCLE, and a Bayesian Markov chain Monte Carlo based phylogenetic tree produced. The SINV-3/NfV-1-like clade is indicated with a red ellipse. Posterior probabilities were $\geq$0.9 except for the placement of Nora virus within the SINV-3-like/APV-like clades (p = 0.64), the placement of the *Liposcelis* and *Leptinotarsa* TSAs wthin the SINV-3-like clade (p = 0.68), and the placement of the *Eucyclops* and *Anurida* TSAs within the APV-like clade (p = 0.60). Abbreviations and accession numbers: AhV, Atkinsonella

hypoxylon virus, L39125; ALSV, apple latent spherical virus, AB030940; ANV, avian nephritis virus, AB033998; APV, Acyrthosiphon pisum virus, AF024514; BaYMV, barley yellow mosaic virus, AJ132268; BBWV-1, broad bean wilt virus 1, AB084450; BDRC, Bryopsis cinicola chloroplast dsRNA replicon, AB070653; BDRM, Bryopsis mitochondria-associated dsRNA, D88669; BWYV, beet western yellows virus, AF473561; CHV, Cryphonectria parasitica hypovirus, DQ861913; CPMV, cowpea mosaic virus, X00206; CPV, Cryptosporidium parvum virus, U95995; CrPV, cricket paralysis virus, AF218039; DCV, Drosophila C virus, AF014388; DWV, deformed wing virus, AY292384; EMCV, encephalomyocarditis virus, M81861; FCCV, Fragaria chiloensis cryptic virus, DQ093961; FCV, feline calicivirus, L40021; FGMV, Fusarium graminearum mycovirus, AY533037; FHV, flock house virus, X77156; FMDV, foot-and-mouth disease virus, AY593850; GFLV, grapevine fanleaf virus, D00915; GLV, Giardia lamblia virus, L13218; HaRNAV, Heterosigma akashiwo RNA virus, AY337486; HAstV1, human astrovirus 1, Z25771; HAV, hepatitis A virus, M20273; HcRNAV, Heterocapsa circularisquama RNA virus, AB218609; HRV1A, human rhinovurus 1A, M16248; IFV, infectious flacherie virus, AB000906; JP-A, marine RNA virus JP-A, EF198241; JP-B, marine RNA virus JP-B, EF198242; KFV, kelp fly virus, DQ112227; KiV, Kilifi virus, KP714071; LRV, leishmania RNA virus 1-1, M92355; LTSV, lucerne transient streak virus, U31286; MBV, mushroom bacilliform virus, U07551; NfV-1, Nylanderia fulva virus 1, KX024775; Nora virus, DQ321720; NoroV, norovirus, M87661; NoV, Nodamura virus, AF174533; OAstV1, ovine astrovirus 1, Y15937; OPV, Ophiostoma partitivirus 1, AM087202; PEMV-1, pea enation mosaic virus 1, L04573; PLRV, potato leafroll virus, D00530; PnPV, Perina nuda picorna-like virus, AF323747; PV, poliovirus, AJ430385; PYFV, parsnip yellow fleck virus, D14066; RAAV, rosy apple aphid virus, DQ286292; RasR1, Raphanus sativus dsRNA 1, AY949985; RHDV, rabbit haemorrhagic disease virus, M67473; RsRNAV, Rhizosolenia setigera RNA virus, AB243297; RTSV, rice tungro spherical virus, M95497; SBMV, southern bean mosaic virus, AF055888; SCPMV, southern cowpea mosaic virus, M23021; ScV, Saccharomyces cerevisiae virus LA, M28353; SDV, satsuma dwarf virus, AB009958; SINV-2, Solenopsis invicta virus 2, EF428566; SINV-3, Solenopsis invicta virus 3, FJ528584; SJNNV, striped jack nervous necrosis virus, AB056571; SmVA, Sclerophtora macrospora virus A, AB083060; SmVB, Sclerophtora macrospora virus B, AB012756; SPMMV, sweet potato mild mottle virus, Z73124; SssRNAV, Schizochytrium single-stranded RNA virus, AB193726; SV, Sapporo virus, AY694184; TAstV1, turkey astrovirus 1, Y15936; TEV, tobacco etch virus, M15239; ThV, Thika virus, KP714072; TRSV, tobacco ringspot virus, U50869; TrV, Triatoma virus, AF178440; TSV, Taura syndrome virus, AF277675; TVV, Trichomonas vaginalis virus 1, U08999; WSMV, wheat streak mosaic virus, AF057533; Anurida TSA, GAUE01003473; Clavigralla TSA, GAJX01000318; Diabrotica TSA, GBSB01003728; Eucyclops TSA, GARW01000621; Meligethes TSA, GAPE01025462; Menopon TSA, GAWR01006667; Monomorium TSA, LA857567; Leptinotarsa TSA, GEEF01170301; Liposcelis TSA, GAYV02024882; Sitobion TSA, GAPL01023644.