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:	***2014.018a-dV***	(to be completed by ICTV officers)

Short title: Creation of a new species (*Sicinivirus A*) in a new genus (*Sicinivirus*).
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

Nick Knowles (nick.knowles@pirbright.ac.uk) on behalf of the *Picornaviridae* Study Group

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)	*Picornaviridae* Study Group

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	07/07/2014
Date of this revision (if different to above):	06/11/2014

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	***2014.018aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Sicinivirus*** (new)
Subfamily:	-
Family:	***Picornaviridae***
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 genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Sicinivirus A	chicken/UCC001/Eire (sicinivirus 1)	KF741227

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

Sicinivirus 1 is a new picornavirus detected in chickens in the Republic of Ireland. Sicini is the Gaelic word for chicken. Sicinivirus 1 is most closely related to passerivirus A1 (formerly turdivirus 1) having amino acid identities of 30.5%, 38.1% and 46.8% in the P1, P2 and P3 polypeptides, respectively.

Genome organisation:

VPg+5'UTR$^{IRES\text{-}II}$[L/1AB-1C-1D/2A-2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3'UTR-poly(A)

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2014.018bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	-
Family:	***Picornaviridae***
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	***2014.018cV***	(assigned by ICTV officers)

To name the new genus: *Sicinivirus*

Assigning the type species and other species to a new genus

Code	***2014.018dV***	(assigned by ICTV officers)

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

Sicinivirus A

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:**

one

Reasons to justify the creation of a new genus:

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

Sicinivirus 1 is most closely related to the species *Passerivirus A* having amino acid identities of 30.5%, 38.1% and 46.8% in the P1, P2 and P3 polypeptides, respectively. Current SG criteria states that members of the same picornavirus genus share greater than 40%, 40%, and 50% amino acid identities for the P1–P3 regions, respectively. Phylogenetic relationships with other picornaviruses are shown in Appendix Figures 1 and 2.

In common with members of the *Passerivirus* and *Gallivirus* genera, Sicinivirus 1 has a genome layout of the L-3-3-4 type. In all three viruses the leader polypeptide has an unknown function and the capsid polypeptide VP0 remains uncleaved. The 2A of members of the *Passerivirus* and *Gallivirus* genera contain H-Box/NC motifs while sicinivirus 1 does not.

Origin of the new genus name:

Sicini is the Gaelic word for chicken.

Reasons to justify the choice of type species:

Only a single species.

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.

Only a single species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bullman, S., Kearney, K., O'Mahony, M., Kelly, L., Whyte, P., Fanning, S. and Morgan, J.G. (2014). Identification and genetic characterisation of a novel picornavirus from chickens. J. Gen. Virol. 95: 1094-1103.

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.

Table 1. Predicted lengths of the mature polypeptides of sicini-, passeri- and galliviruses.

Region	Sicinivirus 1	Passerivirus A	Gallivirus A
L	462	173	150
VP0	340	308	356
VP3	208	232	232
VP1	315	248	265
2A	151	129	137
2B	196	188	186
2C	340	349	385
3A	150	95	73
3B	19	42*	28
3C	175	189	185
3D	472	475	477

*, possibly two VPgs.

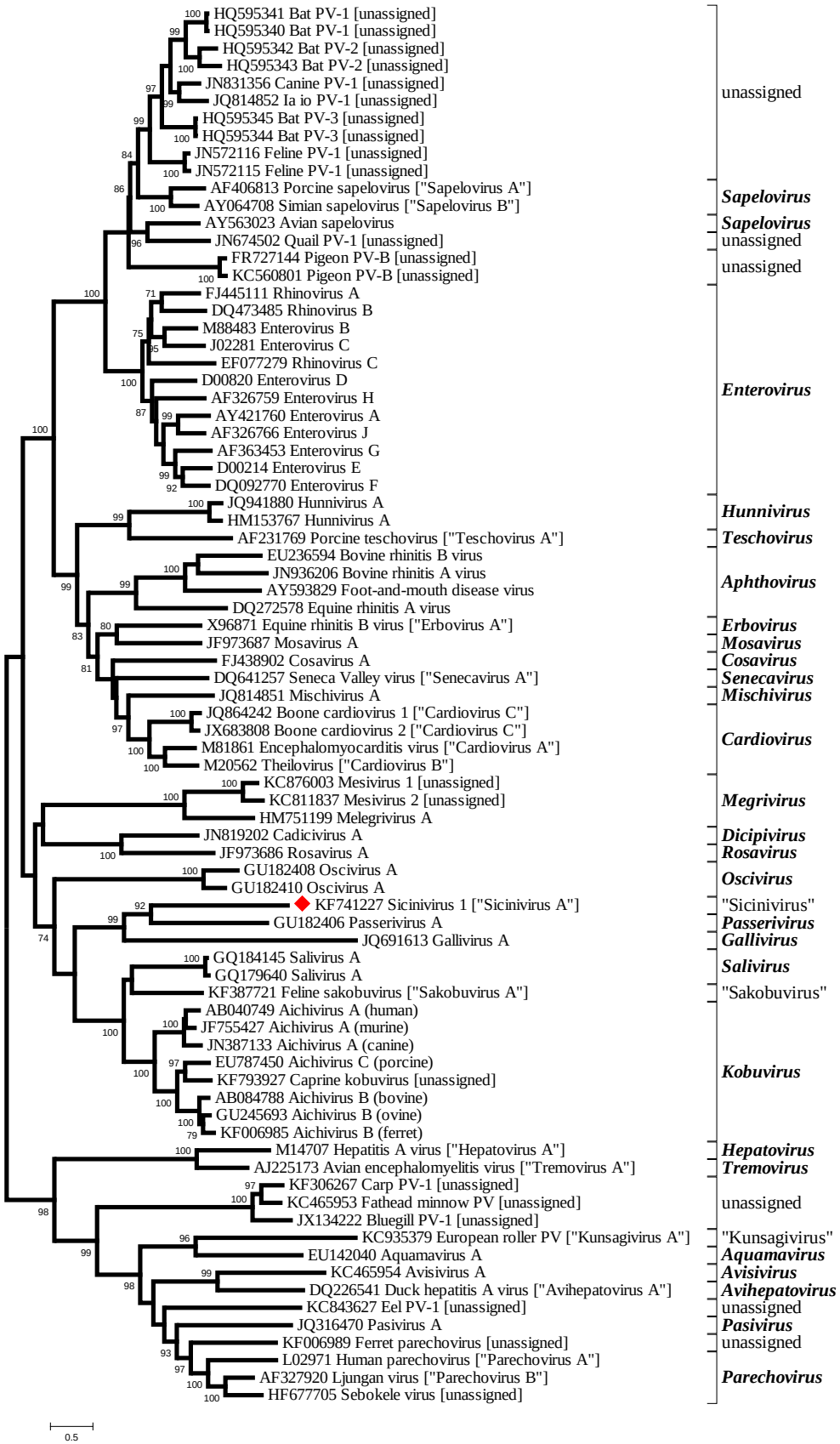

Fig. 1. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the P1 capsid. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstrap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []). The subject(s) of this proposal are indicated by a red diamond (♦).

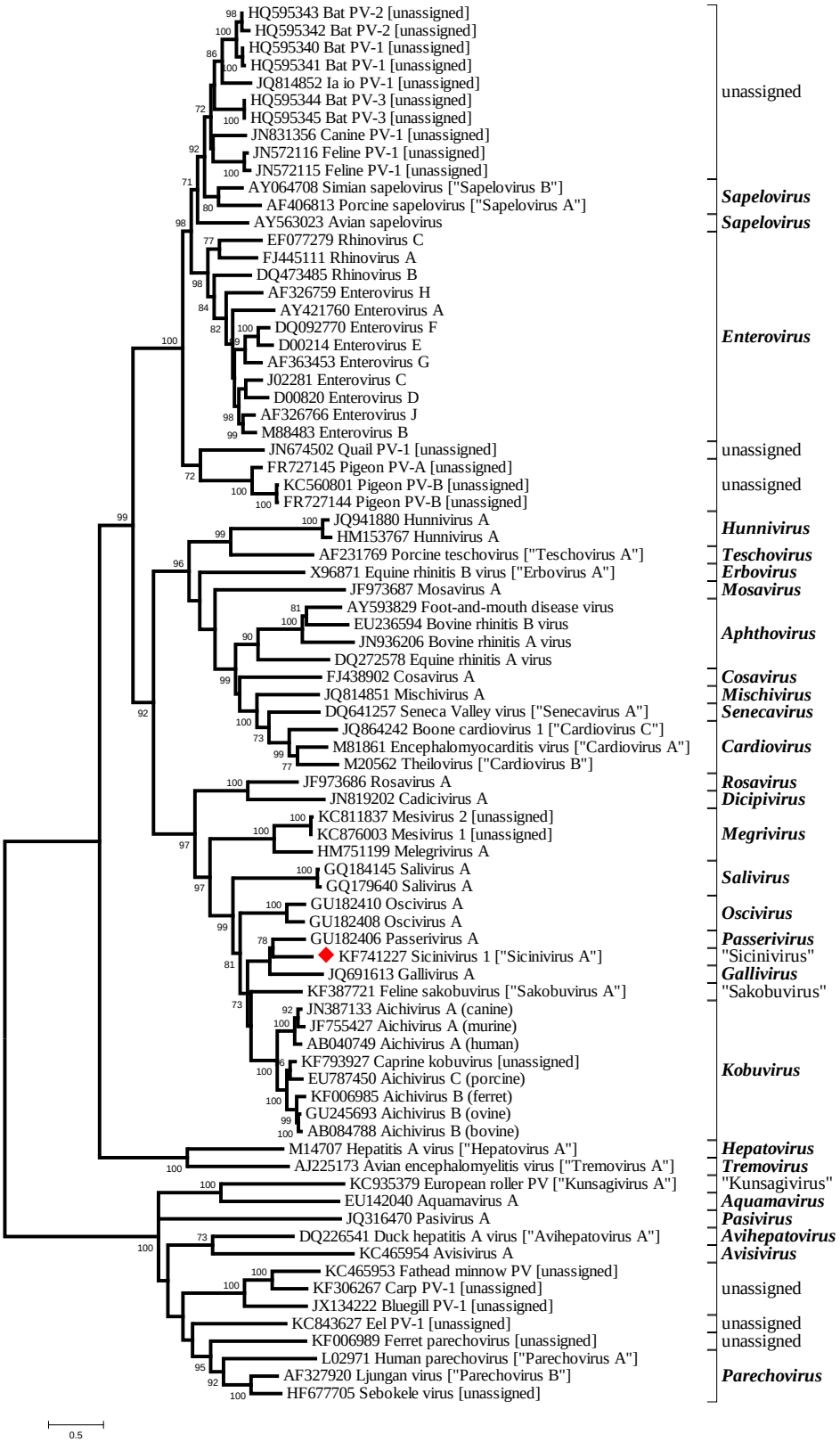

Fig. 2. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the 3D polymerase. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []).The subject(s) of this proposal are indicated by a red diamond (♦).