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:	***2013.010a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Mischivirus A*, in a new genus, *Mischivirus*, within the family *Picornaviridae* (order *Picornavirales*)
(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 J. 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: 25/06/2013
Date of this revision (if different to above):

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	***2013.010aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Mischivirus* (new)**
Subfamily:	**n/a**
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Mischivirus A	JQ814851

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

Virus discovery

Miniopterus schreibersii picornavirus 1 (MsPV-1) was found in the common bent-wing bat (aka Schreiber's long-fingered bat or Schreiber's bat; *Miniopterus schreibersii*) (Wu et al. 2012).

Growth in cell cultures

The virus has not been cultivated in cell cultures.

Untranslated regions

MsPV-1 has a very long 5′ UTR of 1407 nt which is related to the same region in cardioviruses (~64% nt identity over ~800 nt) suggesting the presence of a type II internal ribosome entry site (IRES). The 204 nt 3′ UTR is longer than that in cardioviruses (~127 nt). A part of the 3′ UTR (~40-50 nt) has a high level of nt identity (70-80%) with cardioviruses.

Genome organization/proteins

VPg+5′UTR[L/1A-1B-1C-1D-2A^{npgp}/2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3′UTR-poly(A)

[ ], defines the long ORF encoding the polyprotein.
/, Indicates primary polyprotein cleavages.
-, indicates secondary cleavages mainly performed by the 3C^{pro} polypeptide.

A 92 aa leader (L) polypeptide precedes the capsid. The 2A polypeptide is 45 to 54 aa long and ends in NPG↓P. Neither L or 2A shares any amino acid identity with any other picornavirus protein. VP0 is predicted to be cleaved into VP4/VP2 and contains a myristoylation signal at it is amino-terminus (GxxxT/S as GGNSS).

Genetic relationships

The P1, P2 and P3 polypeptides of MsPV-1 are most closely related to *Encephalomyocarditis virus* (42%), *Theilovirus* (40.3%) and *Seneca Valley virus* (46.6%), respectively.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.010bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	**n/a**
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	***2013.010cV***	(assigned by ICTV officers)

To name the new genus: *Mischivirus*

Assigning the type species and other species to a new genus

Code	***2013.010dV***	(assigned by ICTV officers)

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

Mischivirus 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:**

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

The closest relationships between MsPV-1 and other picornavirus genera in the P1, P2 and P3 polypeptides are 42% (*Cardiovirus*), 40.3% (*Cardiovirus*) and 46.6% (*Senecavirus*), respectively. The *Picornaviridae* Study Group (PSG) guidelines state that members of different genera share less that 40%, 40% and 50% amino acid difference in P1, P2 and P3, respectively. We therefore suggest that the proposed species *Mischivirus A* is placed in a new genus named *Mischivirus*.

Origin of the new genus name:

Mischivirus, from the host in which the virus was discovered, ***Mi****niopterus* ***sch****reibersii* (common bent-wing bat).

Reasons to justify the choice of type species:

The genus is proposed to contain 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.

None, since there is only a single species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Wu, Z., Ren, X., Yang, L., Hu, Y., Yang, J., He, G., Zhang, J., Dong, J., Sun, L., Du, J., Liu, L., Xue, Y., Wang, J., Yang, F., Zhang, S. and Jin, Q. (2012). Virome analysis for identification of novel mammalian viruses in bat species from Chinese provinces. J. Virol. 86: 10999-11012. Epub: 2012 Aug 1.

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.

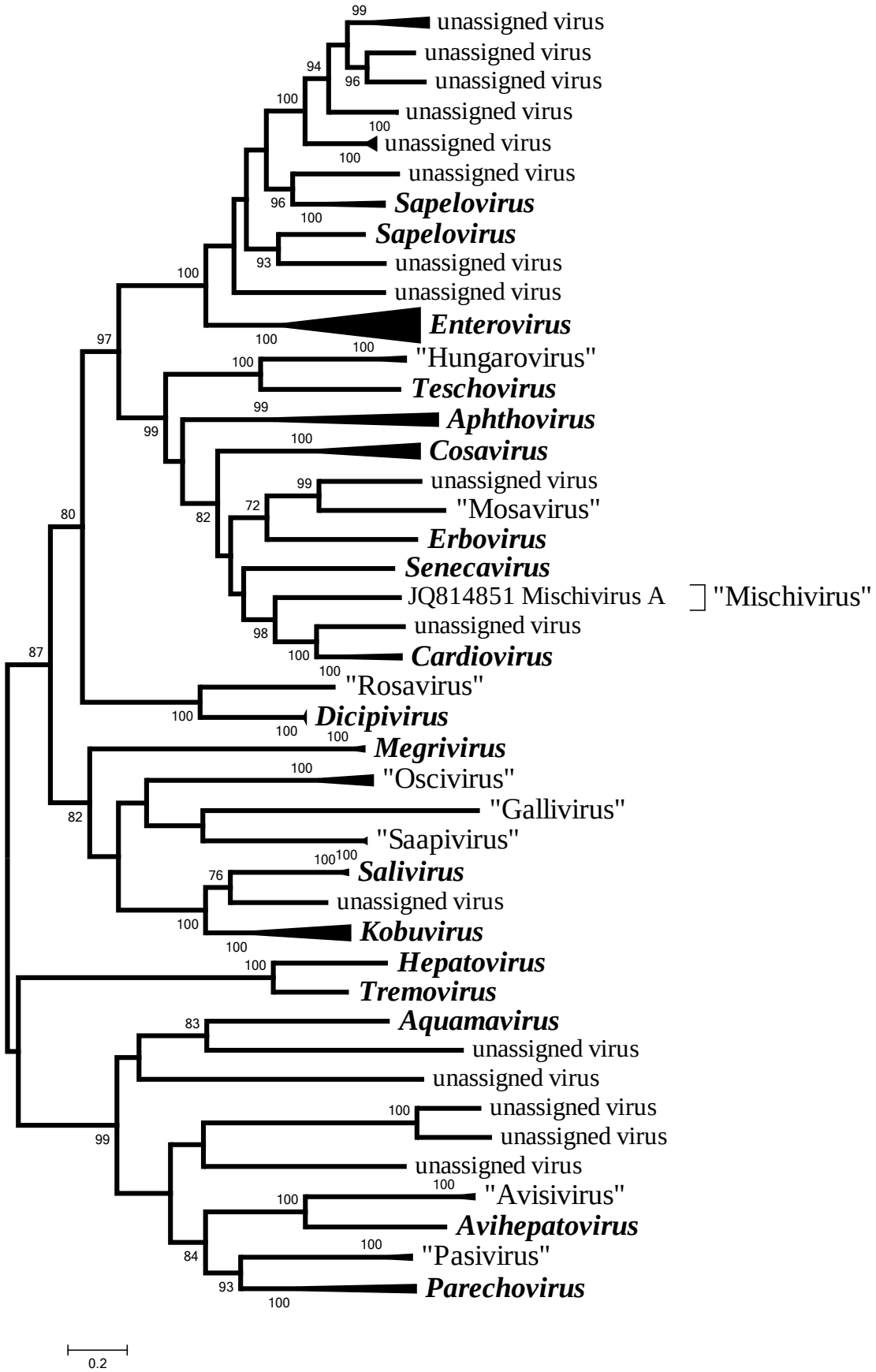

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

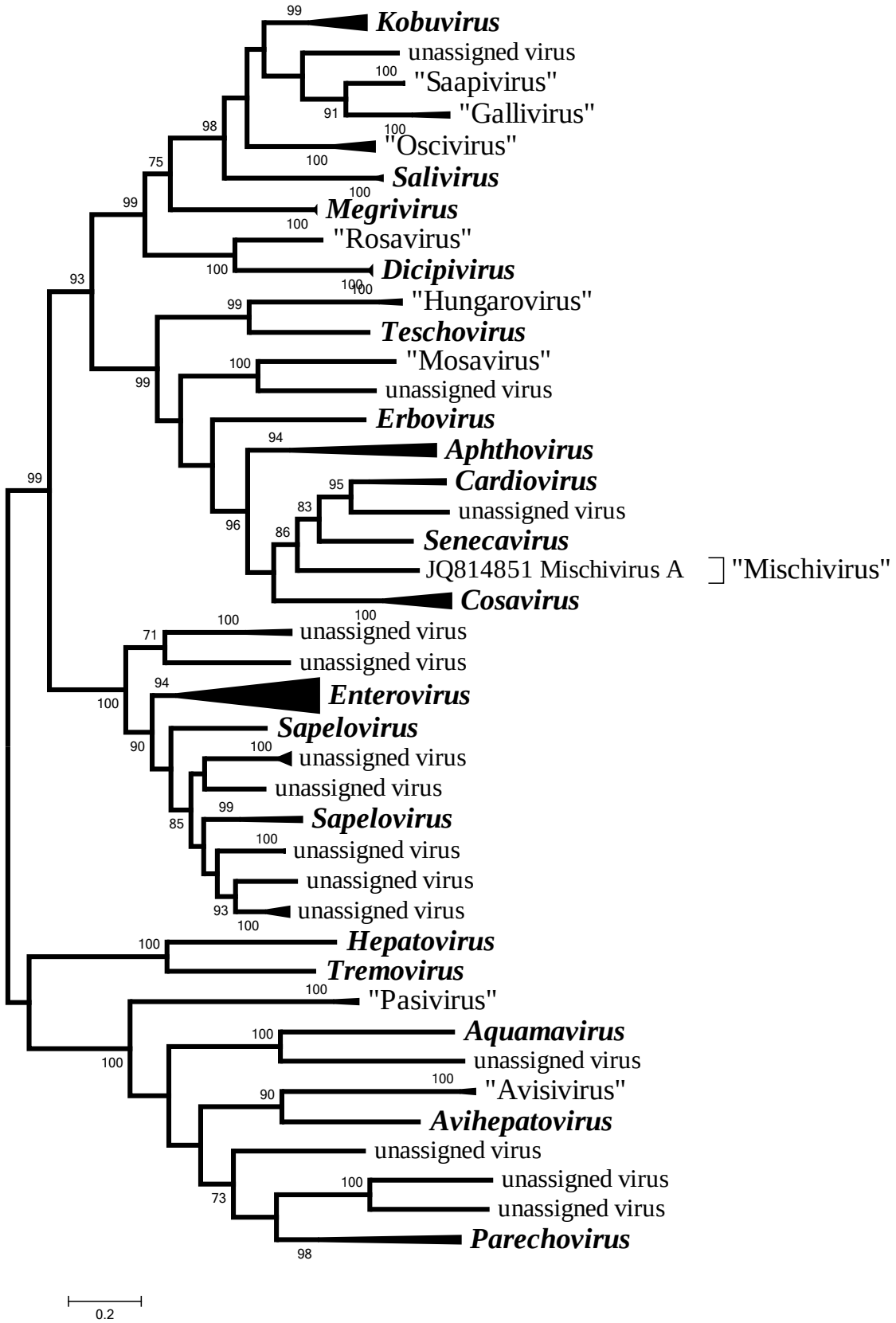

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.