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:	***2013.015a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Saapivirus A*, in a new genus, *Saapivirus*, 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	***2013.015aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Saapivirus* (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:**
Saapivirus A	GU182406 & GU182407

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

Woo et al. (2010) detected and sequenced the genomes of two picornaviruses, which they named turdivirus (TV) 1, in wild birds of the family Turdidae (thrushes). The *Picornaviridae* Study Group (PSG) has decided that turdivirus is not a suitable name and we propose the species name *Saapivirus A.*

Growth in cell cultures

None of these viruses have been cultivated in cell cultures.

Untranslated regions

The 5′ and 3′ untranslated regions (UTRs) of TV-1 are 415 and 317 nt, respectively. The internal ribosome entry site (IRES) type is unknown.

Genome organization/proteins

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

[], defines the long ORF encoding the polyprotein.
/, Indicates primary polyprotein cleavages.
-, indicates secondary cleavages mainly performed by the 3Cpro polypeptide.

A leader polypeptide of unknown function precedes the capsid. It has no significant sequence identity to any other picornavirus leader polypeptide. A single 2A is present containing an H-

box/NC motif similar to a number of other picornaviruses, e.g. kobuviruses, to which it is most closely related having ~50% aa identity.

Genetic relationships
The two TV-1 viruses share 96% nt identity across their complete genomes. Analyses of the genome sequences showed that TV-1 is distinct from all other picornavirus species (see Figures 1 and 2 and also arguments for creation of a new genus).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.015bV***	(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	***2013.015cV***	(assigned by ICTV officers)

To name the new genus: *Saapivirus*

Assigning the type species and other species to a new genus

Code	***2013.015dV***	(assigned by ICTV officers)

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

Saapivirus 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 picornavirus sequences to the P1, P2 and P3 polypeptides of *Saapivirus A* (TV-1) are *Aichivirus A* (30.6%), gallivirus (39.4%) and gallivirus (50.9%), respectively. The PSG guidelines state that members of different genera share less that 40%, 40% and 50% amino acid difference in P1, P2 and P3, respectively. Although the relationship between TV-1 and gallivirus in P3 is 50.9%, examination of the individual polypeptide relationships is not straightforward; for 3C the value is only 25% while in 3D it is 64%. The PSG consider the suggested genus name "Orthoturdivirus" to be unsuitable and proposes the genus name *Saapivirus*. It is the opinion of the majority of the PSG that *Saapivirus* and *Gallivirus* (see separate proposal) should be separate genera.

Origin of the new genus name:

Saapivirus, from **s**tool-**a**ssociated **a**vian **pi**cornavirus

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

References:

Woo, P.C., Lau, S.K., Huang, Y., Lam, C.S., Poon, R.W., Tsoi, H.W., Lee, P., Tse, H., Chan, A.S., Luk, G., Chan, K.H. and Yuen, K.Y. (2010). Comparative analysis of six genome sequences of three novel picornaviruses, turdiviruses 1, 2 and 3, in dead wild birds and proposal of two novel genera, *Orthoturdivirus* and *Paraturdivirus*, in *Picornaviridae*. J. Gen. Virol. 91: 2433-2448.

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.

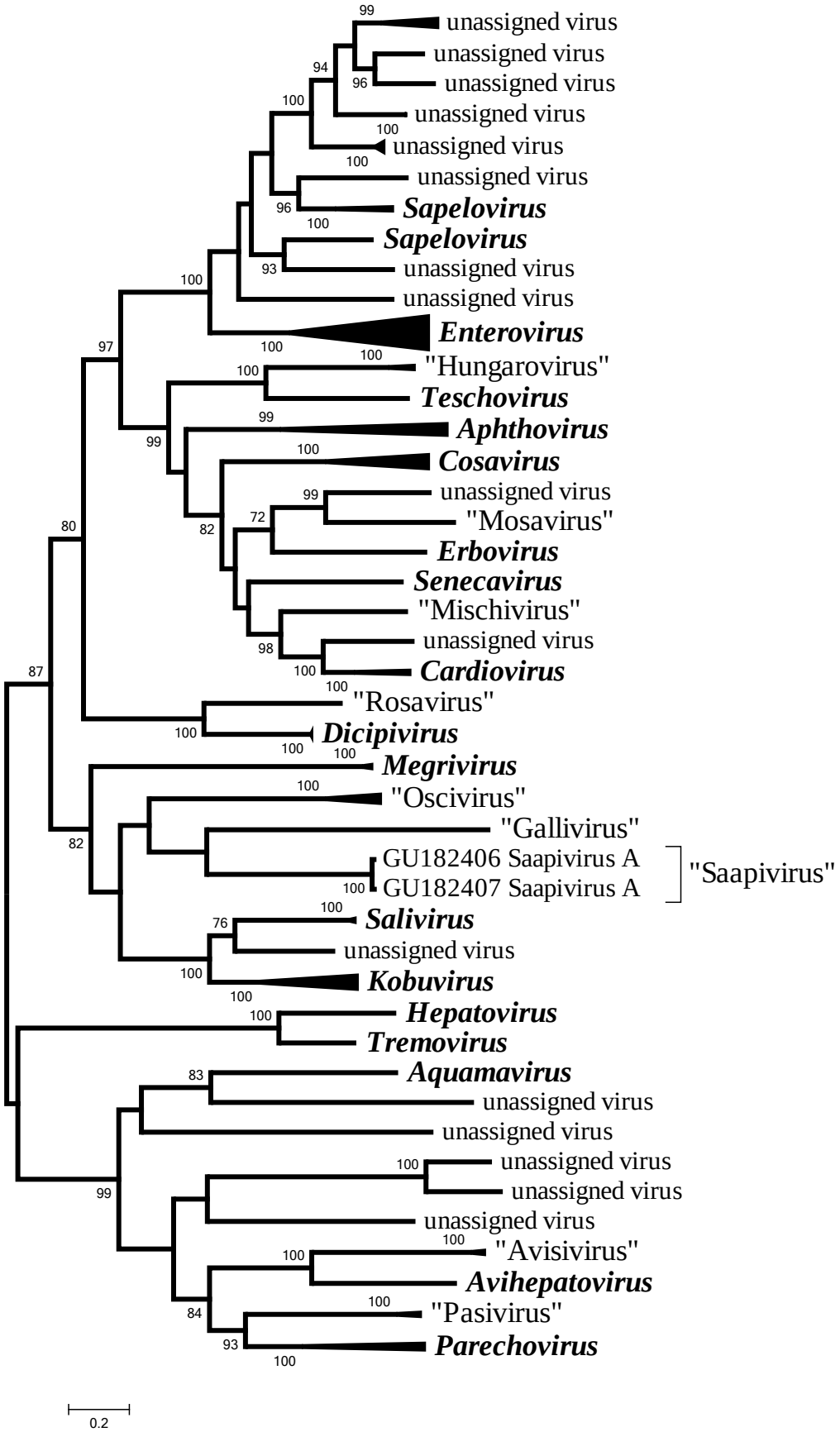

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

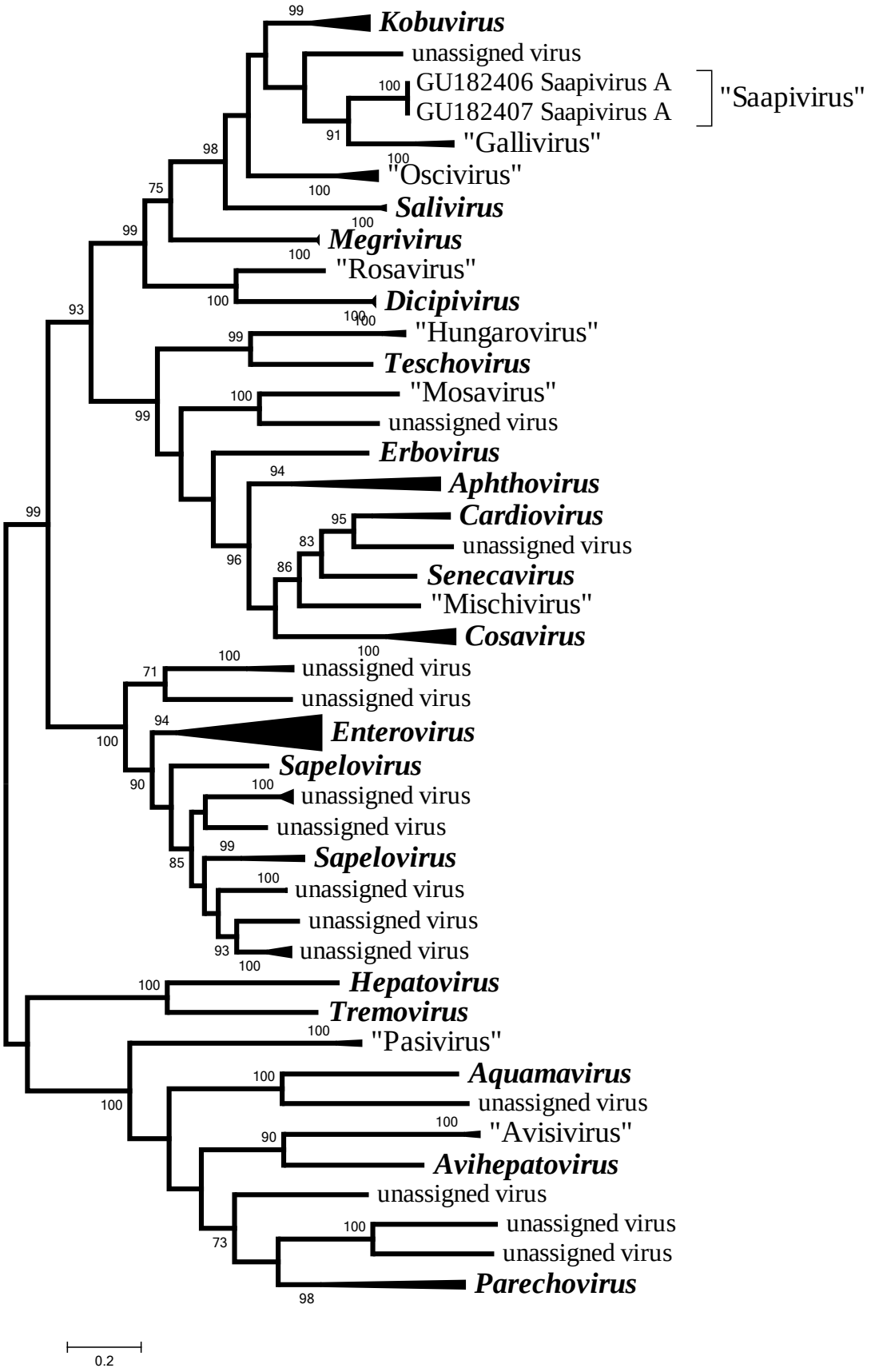

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.