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:	***2013.014a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Rosavirus A*, in a new genus, *Rosavirus*, 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 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	***2013.014aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Rosavirus* (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:**
Rosavirus A	JF973686

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

A novel picornavirus (designation M-7) was identified in the faeces of a canyon mouse (*Peromyscus crinitus*) in the USA in 2010 (JF973686; Phan *et al*., 2011).

Growth in cell cultures

The virus has not been cultivated in cell cultures.

Untranslated regions

The 5′ UTR is at least 516 nt long and has a high level of nt identity (~60%) with viruses (e.g. EMCV) possessing a type II internal ribosome entry site (IRES). The 3′ UTR is extremely long (795 nt) and not related to any other picornaviruses. The 3′ UTRs of megriviruses also appear to be very long at 641-654 nt.

Genome organization/proteins

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

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

There is no leader polypeptide. VP0 is predicted to be cleaved to VP4/VP2, but VP0 does not possess a myristoylation signal at its amino-terminus. In this respect it resembles *Cadicivirus A* to which it is most closely related; however, *Cadicivirus A* is the only known dicistronic picornavirus having its P1 and P2P3 polypeptides located on two different ORFs which are separated by an intergenic region containing an IRES. Rosavirus has only a single ORF. The rosavirus 2A polypeptide has an H-box/NC motif.

Genetic relationships

The P1, P2 and P3 polypeptides of rosavirus are most closely related to *Cadicivirus A* (37.2%), *Melegrivirus A* (31.1%) and *Cadicivirus A* (43.6%), respectively.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.014bV***	(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	***2013.014cV***	(assigned by ICTV officers)

To name the new genus: *Rosavirus*

Assigning the type species and other species to a new genus

Code	***2013.014dV***	(assigned by ICTV officers)

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

Rosavirus 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 P1, P2 and P3 polypeptides of rosavirus are most closely related to members of the genera *Dicipivirus* (37.2%), *Megrivirus* (31.1%) and *Dicipivirus* (43.6%), 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. Additionally, rosavirus has a significantly different genome organization to its closest relative, *Cadicivirus A* (one versus two ORFs). We therefore suggest that the proposed species *Rosavirus A* is placed in a new genus named *Rosavirus*.

Origin of the new genus name:

Rosavirus, from **ro**dent **s**tool-**a**ssociated picornavirus

Reasons to justify the choice of type species:

Only a single species has been described.

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 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Phan, T.G., Kapusinszky, B., Wang, C., Rose, R.K., Lipton, H.L. and Delwart, E.L. (2011). The fecal viral flora of wild rodents. PLoS Pathog 7(9): e1002218.

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.

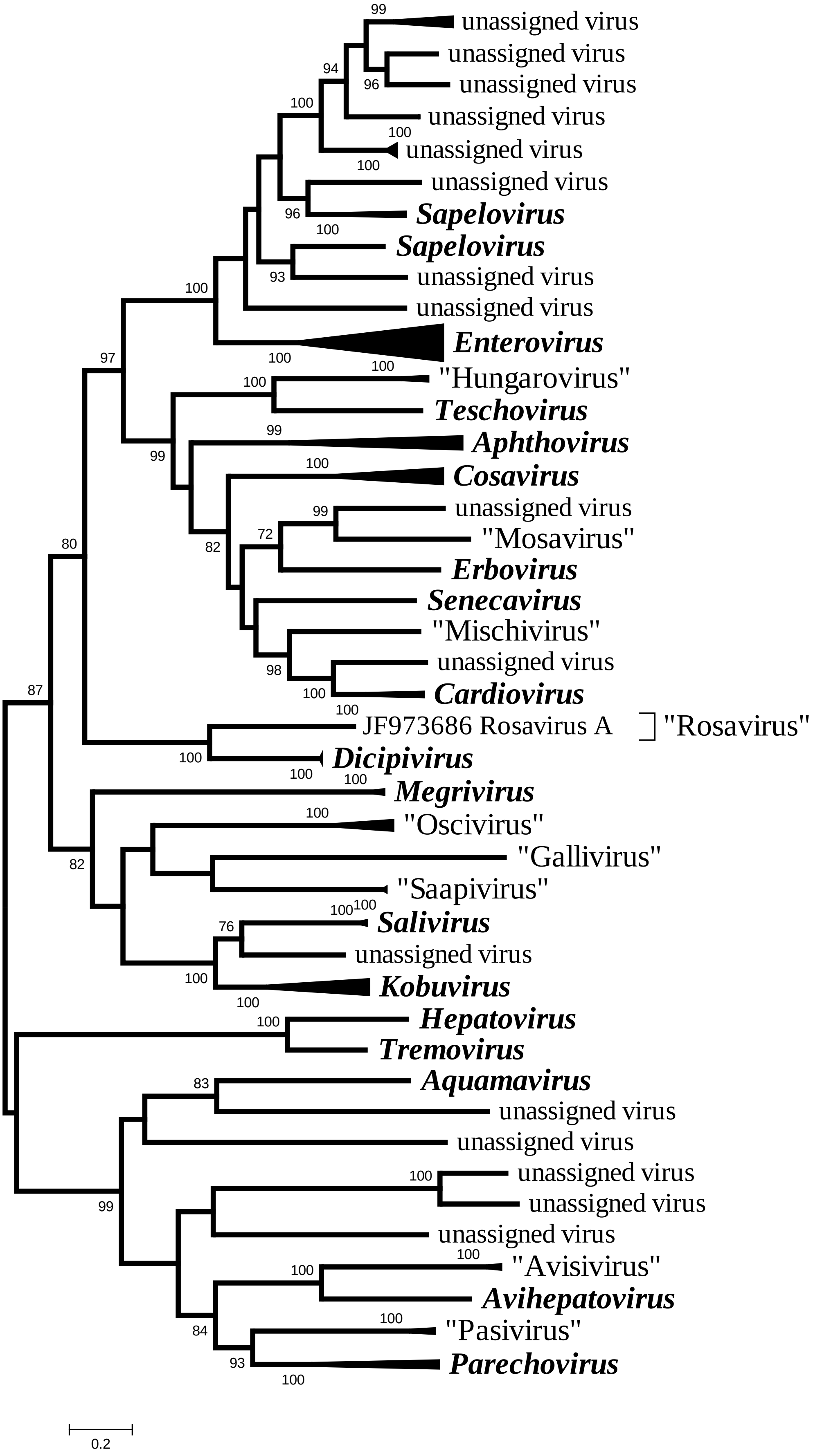

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

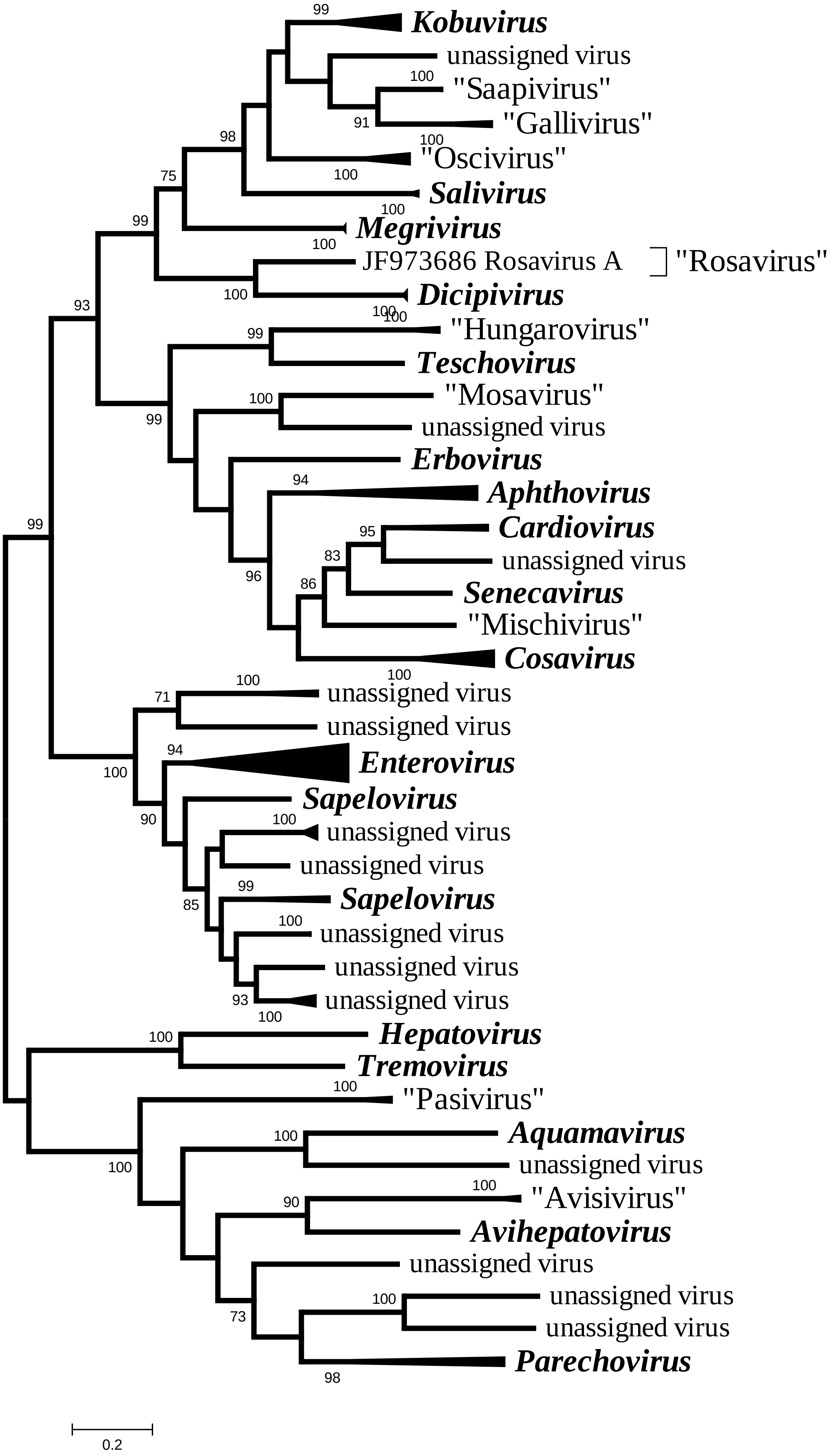

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.