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:	***2013.012a-dV***	(to be completed by ICTV officers)

Short title: Create two new species, *Oscivirus A*, in a new genus, *Oscivirus*, 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	***2013.012aV***	(assigned by ICTV officers)

To create two new species within:

Genus:	***Oscivirus* (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:**
Oscivirus A	GU182408, GU182409 GU182410, GU182411

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 picornaviruses, which they named turdivirus (TV) 2 and 3, in wild birds; TV-2 from thrushes (family Turdidae) and TV-2 from Oriental Magpie Robins (family Muscicapidae; formerly classified in the family Turdidae). The *Picornaviridae* Study Group (PSG) has decided that turdivirus was not a suitable name and we now propose the species name *Oscivirus A*.

Growth in cell cultures

None of these viruses has been cultivated in cell cultures.

Untranslated regions

The 5′ UTR has been predicted to contain a type V internal ribosome entry site (IRES) in common with *Aichivirus A*, *Aichivirus B* (genus *Kobuvirus*) and *Salivirus A* (genus *Salivirus*) (Sweeney et al., 2012).

Genome organization/proteins

VPg+5'UTR$^{IRES\text{-}V}$[L/1AB-1C-1D/2A-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.

Genetic relationships

The complete genome sequence share the following nucleotide identities:

TV-2 vs TV-2, 96%
TV-3 vs TV-3, 94%
TV-2 vs TV-3, 64-65%

It is proposed that these two viruses should be classified as different (geno)types within a single species.

Analyses of the predicted polypeptide sequences showed that TV-2/TV-3 are distantly related to all other picornaviruses (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	***2013.012bV***	(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	***2013.012cV***	(assigned by ICTV officers)

To name the new genus: *Oscivirus*

Assigning the type species and other species to a new genus

Code	***2013.012dV***	(assigned by ICTV officers)

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

Oscivirus 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 sequence for the P1, P2 and P3 polypeptides of TV-2/TV-3 are *Salivirus A* (26.9%), gallivirus (34.3%) and *Aichivirus A* (47.2%), 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.

Woo et al. (2010) suggested that TV-2/TV-3 be classified in a new picornavirus genus and suggested the name "Paraturdivirus". However, the PSG has decided that "Paraturdivirus" is not a suitable name and we now propose the genus name *Oscivirus*.

Origin of the new genus name:

Oscivirus, from **Osci**nes (Latin oscen, "a songbird").

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:

Sweeney, T.R., Dhote, V., Yu, Y. and Hellen, C.U. (2012). A distinct class of internal ribosomal entry site in members of the *Kobuvirus* and proposed *Salivirus* and *Paraturdivirus* genera of the *Picornaviridae*. J. Virol. 86: 1468-1486. Epub 2011 Nov 23.

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.

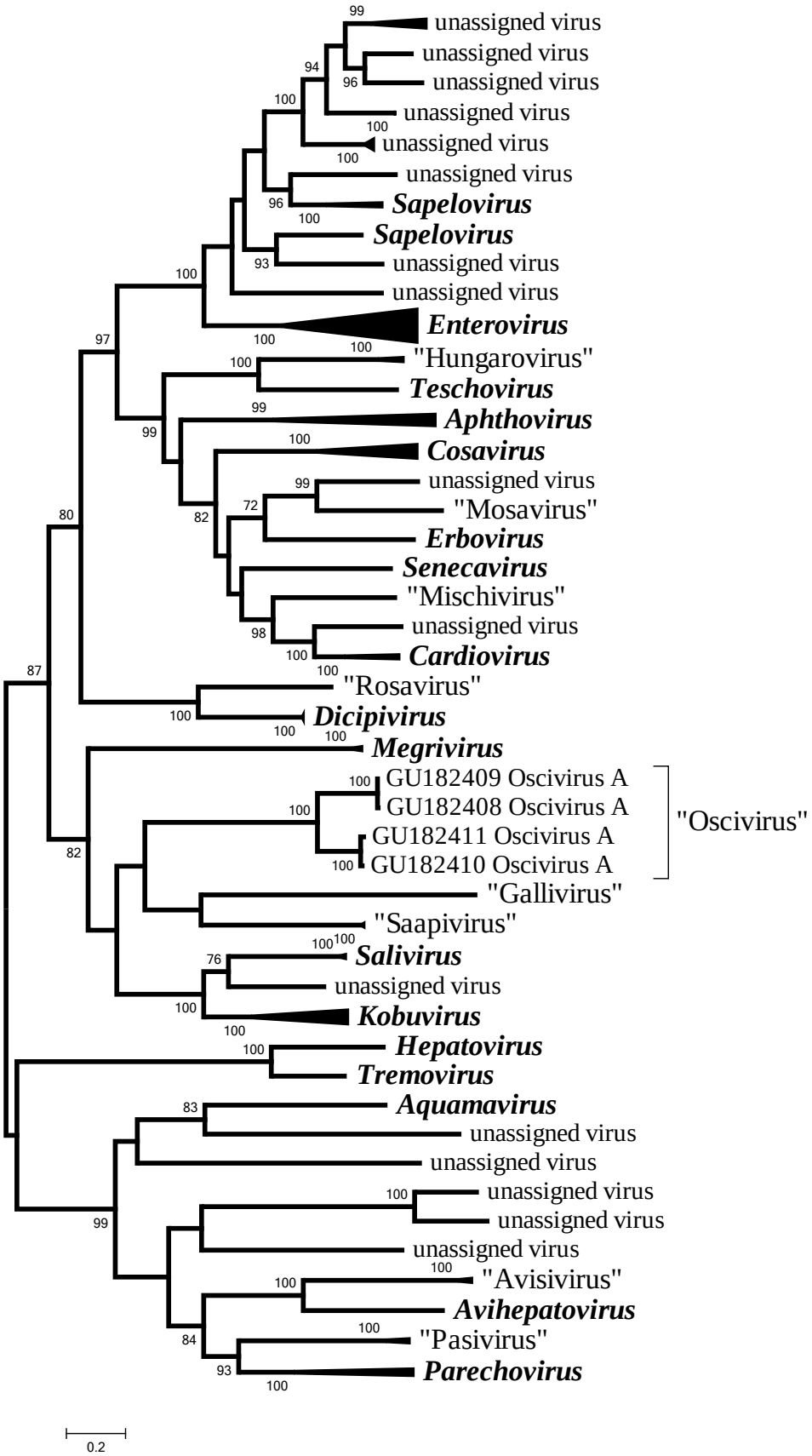

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

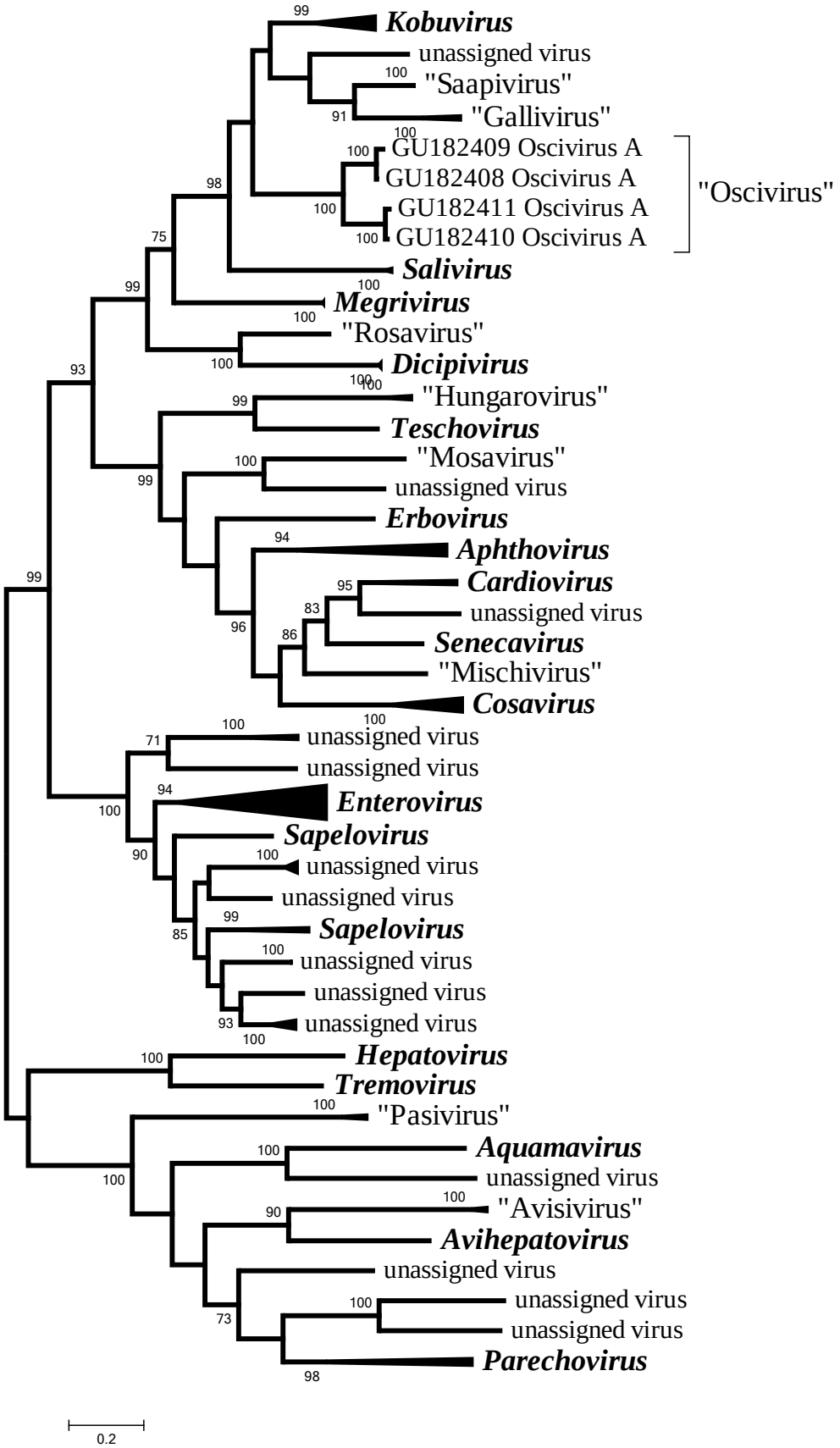

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.