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:	***2013.007a-dV***	(to be completed by ICTV officers)

Short title: Create a new species, *Gallivirus A*, in a new genus, *Gallivirus*, 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	***2013.007aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Gallivirus* (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:**
Gallivirus A	JQ691613 to JQ691615 JF424824 to JF424830

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

Galliviruses have been detected in turkeys (*Meleagris gallopavo*) and chickens (*Gallus gallus*) by metagenomics (Boros et al., 2012) and picornavirus-specific RT-PCRs (Farkas et al., 2012). The complete genome of one virus was determined by conventional RT-PCR and DNA sequencing (Boros et al., 2012).

Growth in cell cultures

None of these viruses have been cultivated in cell cultures.

Untranslated regions

The lengths of the 5′ and 3′ untranslated regions (UTRs) are 761 and 310 nt, respectively. The internal ribosome entry site (IRES) is predicted to be type II, although this remains to be confirmed.

Genome organization/proteins

VPg+5′UTR$^{\text{IRES-II?}}$[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 3C$^{\text{pro}}$ polypeptide.

Gallivirus turkey/M176/2011/HUN encodes a 150 aa leader (L) protein upstream of the capsid-encoding genome region but it has no significant sequence similarity the equivalent polypeptide of other picornaviruses. The 2A polypeptide contains an H-Box/NC motif similar to that of some other picornaviruses, i.e. members of the genera *Avihepatovirus, Kobuvirus, Megrivirus, Parechovirus* and *Tremovirus* as well as members of the proposed genera "Avisivirus", "Rosavirus" and "Saapivirus".

Genetic relationships

The closest relationships to other picornaviruses in the P1, P2 and P3 polypeptides are 25.5% (*Aichivirus C*, genus *Kobuvirus*), 39.4% (turdivirus 1; proposed species "Saapivirus A", genus "Saapivirus") and 50.7% (turdivirus 1), respectively. Figures 1 and 2 show the phylogenetic relationship of avisiviruses to other picornaviruses for the P1 capsid and $3D^{pol}$ polypeptides.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.007bV***	(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	***2013.007cV***	(assigned by ICTV officers)

To name the new genus: *Gallivirus*

Assigning the type species and other species to a new genus

Code	***2013.007dV***	(assigned by ICTV officers)

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

Gallivirus 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 to other picornaviruses in the P1, P2 and P3 polypeptides are 25.5% (*Aichivirus C*, genus *Kobuvirus*), 39.4% (turdivirus 1; proposed species "Saapivirus A", genus "Saapivirus") and 50.7% (turdivirus 1), respectively. The *Picornaviridae* Study Group 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 gallivirus and turdivirus 1 in P3 is 50.7%, examination of the individual polypeptide identities show the relationship is not straightforward; for 3C the value is only 25% while in 3D it is 64%. It is the opinion of the PSG that "Gallivirus" and "Saapivirus" should be separate genera.

Origin of the new genus name:

Gallivirus, from the order **Galli**formes which contains turkeys and chickens.

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:

Boros, Á., Nemes, C., Pankovics, P., Kapusinszky, B., Delwart, E. and Reuter, G. (2012). Identification and complete genome characterization of a novel picornavirus in turkey (*Meleagris gallopavo*). J Gen Virol. 93: 2171-2182. Epub 2012 Aug 8.

Farkas, T., Fey, B., Hargitt E. 3rd, Parcells, M., Ladman, B., Murgia, M. and Saif, Y. (2012). Molecular detection of novel picornaviruses in chickens and turkeys. Virus Genes 44: 262-272.

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.

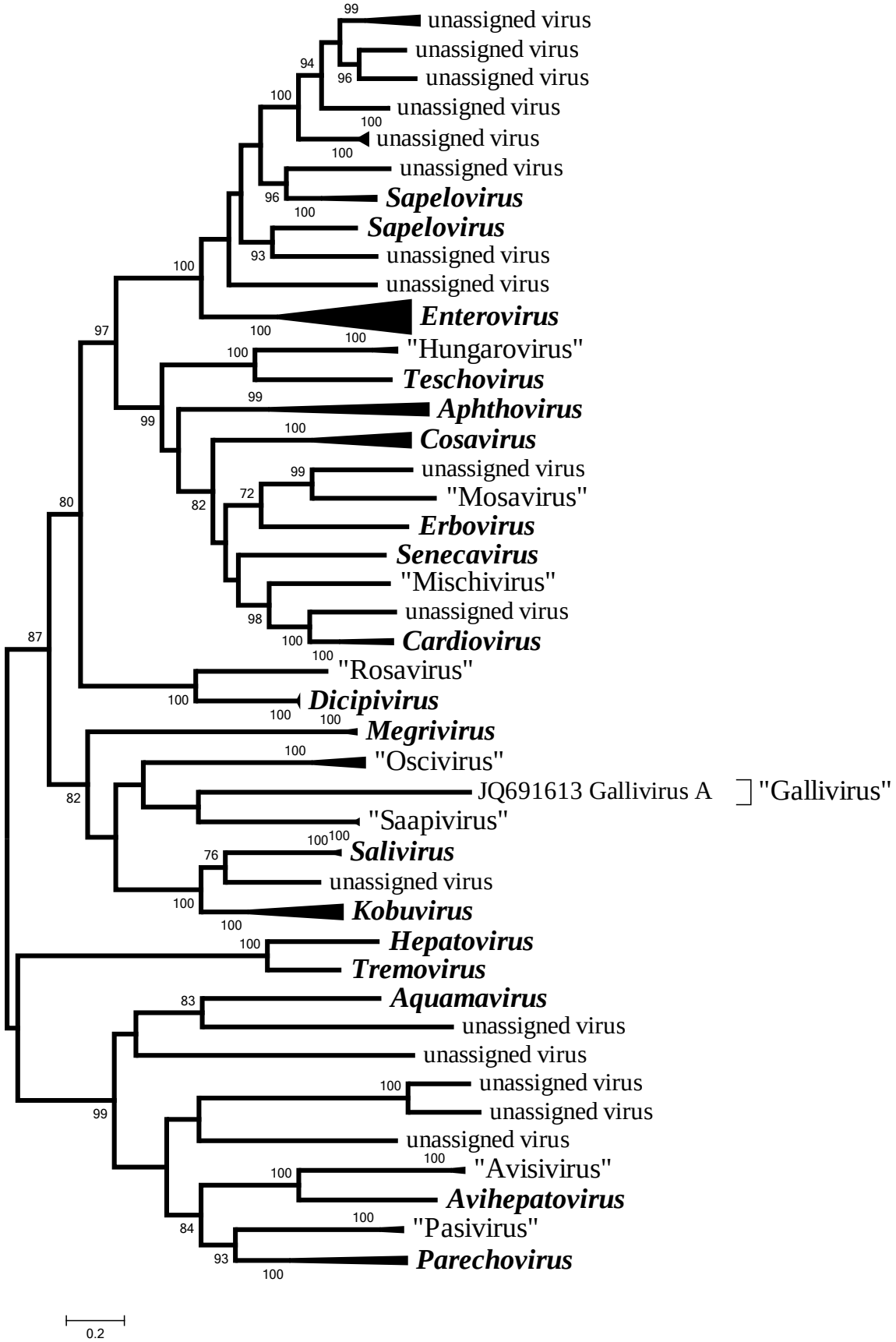

Figure 1. Maximum likelihood tree showing the relationship between picornaviruses in the P1 capsid. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.

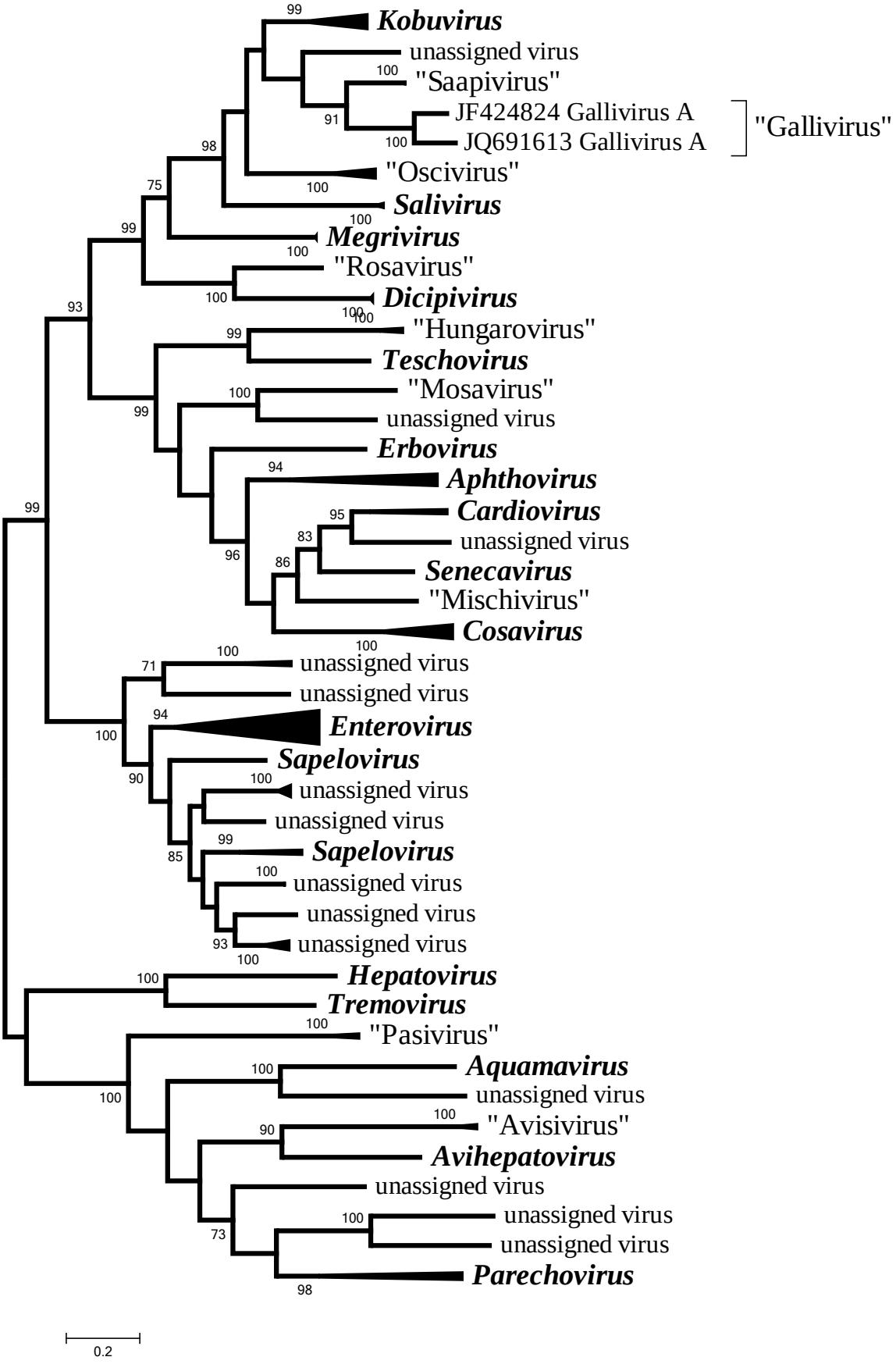

Figure 2. Maximum likelihood tree showing the relationship between picornaviruses in the 3D polymerase. Sequences were aligned using MUSCLE and the tree constructed using MEGA 5.2.