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:	***2014.015a-dV***	(to be completed by ICTV officers)

Short title: Creation of a new species (*Kunsagivirus A*) in a new genus (*Kunsagivirus*)
(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:	07/07/2014
Date of this revision (if different to above):	06/11/2014

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	***2014.015aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Kunsagivirus*** (new)
Subfamily:	-
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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Kunsagivirus A	SZAL6-KuV/2011/HUN	KC935379

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

A picornavirus has been found in the European Roller (*Coracias garrulus*), an Afro-Palearctic migrant bird (Boros et al., 2013). Sequence comparisons suggest that this virus is a novel species most closely related to the aquamaviruses, but distant enough to be regarded as belonging to a new genus (Boros et al., 2013). The authors have suggested the genus name "Kunsagivirus" (Boros et al., 2013). "Kunsagi" is derived from from the name of part of the Great Hungarian Plain – "Kunság" – where the samples were collected.

Genome organisation:

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

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2014.015bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	-
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	***2014.015cV***	(assigned by ICTV officers)

To name the new genus: *Kunsagivirus*

Assigning the type species and other species to a new genus

Code	***2014.015dV***	(assigned by ICTV officers)

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

Kunsagivirus 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:**

one

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 mostly closely related picornavirus species, *Aquamavirus A* (EU142040), has the following amino acid identities with the proposed *Kunsagivirus A* species: P1 (26.3%), P2 (25.8%), P3 (28.4%), 2C (34.7) and 3D (34.9%). Phylogenetic relationships with other picornaviruses are shown in Appendix Figures 1 and 2. Kunsagiviruses have a similar genome organization to aquamaviruses, except for differing in the number of VPg's encloded (one for kunsagivirus and two for aquamavirus). The Internal Ribosome Entry Site (IRES) type is IV-B, which is also found in viruses belonging to the *Aquamavirus*, *Sapelovirus* and *Teschovirus* genera. The G+C content of the complete genome sequence of kunsagivirus is 53.0% which is very different to that of the aquamaviruses (43.1%). The size of the most variable polypeptides of kunsagiviruses and aquamaviruses usually differ in length, i.e. VP0, VP1, 2A1, 2A2 and 3A (Table 1).

Despite similarities with *Aquamavirus A*, the low amino acid identities shared with "Kungsagivirus A" (as shown above) are far below those which we use for the designation of new genera (i.e. P1 <40%, P2 <40% and P3 <50%).

Origin of the new genus name:

"Kunsagi" is derived from the name of part of the Great Hungarian Plain – "Kunság" – where the samples were collected.

Reasons to justify the choice of type species:

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.

Only a single species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Boros, Á., Kiss, T., Kiss, O., Pankovics, P., Kapusinszky, B., Delwart, E. and Reuter, G. (2013). Genetic characterization of a novel picornavirus distantly related to the marine mammal-infecting aquamaviruses in a long-distance migrant bird species, European Roller (*Coracias garrulus*). J. Gen. Virol. 94: 2029–2035 [Epub 2013 Jun 26]

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.

Table 1. Comparison of the lengths of the kunsagivirus and aquamavirus polypeptides.

Polypeptide	**Kunsagivirus**	**Aquamavirus**
VP0	315	267
VP3	228	232
VP1	240	182
2A1	55	23
2A2	165	100
2B	111	110
2C	296	297
3A	132	108
3B1	not present	22
3B2	24	24
3C	206	202
3D	476	478

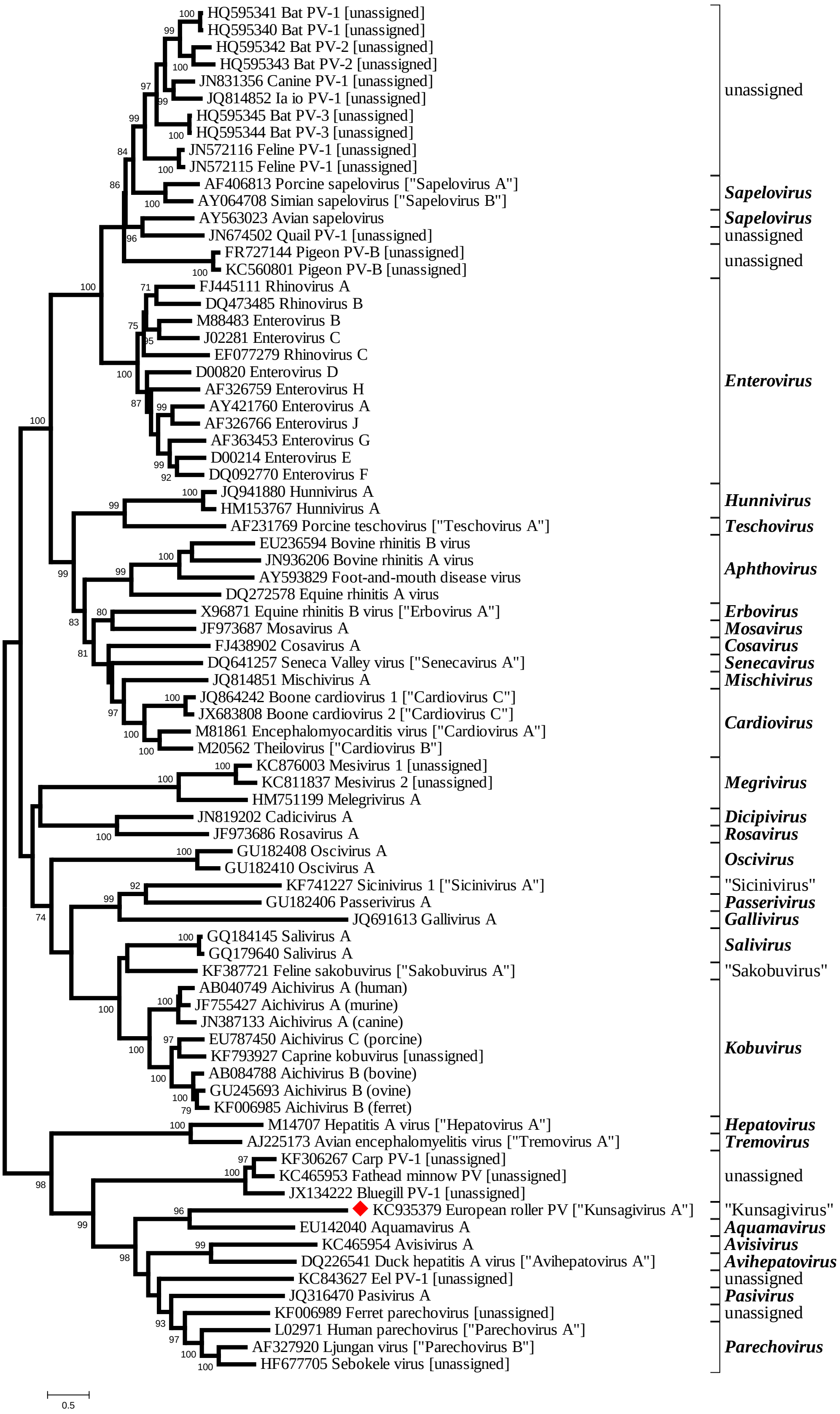

Fig. 1. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the P1 capsid. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstrap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []). The subject(s) of this proposal are indicated by a red diamond (♦).

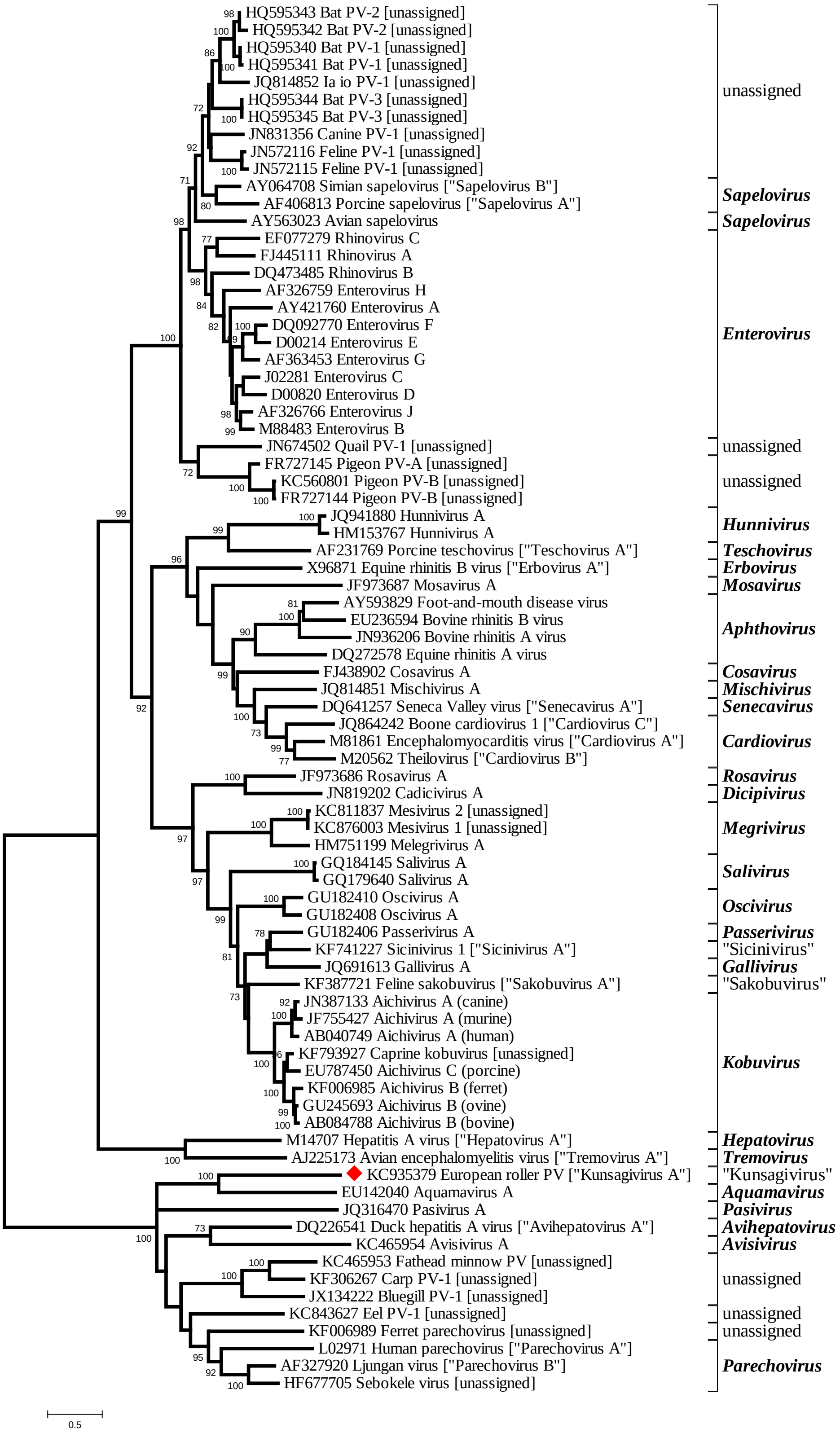

Fig. 2. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the 3D polymerase. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []).The subject(s) of this proposal are indicated by a red diamond (♦).