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:	***2012.013a-dV***	(to be completed by ICTV officers)

Short title: 1. Create a new species (*Cadicivirus A*) in a new genus (*Dicipivirus*) within the *Picornaviridae*.
(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@iah.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: 01/07/2012
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	***2012.013aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Dicipivirus* (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Cadicivirus A	JN819202, JN819203 & JN819204

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 novel small RNA virus has recently been found in dogs (Woo et al., 2012). The authors named the virus "canine picodicistrovirus" (CPDV). The sequences of the most highly conserved genome regions (P1, 2C, 3C, 3D) are most closely related to the picornaviruses. The virus has a similar genome organization to picornaviruses, except that the P1 and P2/P3 regions are encoded in two separate ORFs separated by an intergenic region (of 588 nt) containing a second internal ribosome entry site (IRES). Woo et al. (2012) have demonstrated that both IRESs are functional using a dual-luciferase activity assay. The virus sequences were detected in 47 faecal and urine samples from dogs over a 22 month period in Hong Kong. Four samples, positive for CPDV, were cultured in MDCK (Madin-Darby canine kidney), DH82 (canine macrophagemonocyte), RD (human rhadomyosarcoma), Vero E6 (monkey kidney), and HEL (human embryonic lung fibroblast) cells, but no growth was detected in any of the cell cultures. Likewise no virus replication was detected when inoculated, by a variety of routes, into in suckling mice. Quantitative RT-PCR showed that numbers of viral RNAs ranged from 7.55 x 10^6 to 1.26 x 10^9 copies/ml of urine and 1.82 x 10^6 to 4.97 x 10^{10} copies/ml of faecal sample suggesting the likely replication of this virus in dogs. However, the use of nucleotide composition analysis (NCA) to infer hosts (Kapoor et al., 2010) suggests a possible invertebrate origin for the virus (Fig. 1).

Despite have two ORFs, phylogenetically (using distance or maximum likelihood algorithms) the virus falls within the *Picornaviridae* when homologous conserved proteins are compared; P1 capsid (Fig. 2), 2C (Woo et al., 2012), $3C^{pro}$ (data not shown) and $3D^{pol}$ (Fig. 3; Woo et al., 2012).

The genome organization of the proposed species *Cadicivirus A* is:

VPg+5'UTR^{IRES}[1A-1B-1C-1D]IGR^{IRES}[2A-2B-2C/3A-3B^{VPg}-3C^{pro}-3D^{pol}]3'UTR-poly(A)

[ ] open reading frame
/, primary cleavages
-, secondary/tertiary cleavages
IGR, intergenic region
IRES, internal ribosome entry site

The name of the species is derived from **ca**nine **dici**stronic **virus** (canine only indicating that this was the species in which this virus was first recognized and not implying that dogs are the actual host).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.013bV***	(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	***2012.013cV***	(assigned by ICTV officers)

To name the new genus: *Dicipivirus*

Assigning the type species and other species to a new genus

Code	***2012.013dV***	(assigned by ICTV officers)

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

Cadicivirus 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 "canine picodicistrovirus" is clearly phylogenetically distinct from other presently-classified picornaviruses and has a novel genome organization (two ORFs under the translational control of two IRESs).

Origin of the new genus name:

The genus name *Dicipivirus* is derived from **dici**stronic **pi**corna**virus**.

Reasons to justify the choice of type species:

There is only a single known species in the proposed genus.

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.

There is only a single known species in the proposed genus.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Kapoor, A., Simmonds, P,, Lipkin, W.I., Zaidi, S. and Delwart, E. (2010). Use of nucleotide composition analysis to infer hosts for three novel picorna-like viruses. J Virol. 84: 10322-10328.

Woo, P.C., Lau, S.K., Choi, G.K., Huang, Y., Teng, J.L., Tsoi, H.W., Tse, H., Yeung, M.L., Chan, K.H., Jin, D.Y. and Yuen, K.Y. (2012). Natural occurrence and characterization of two internal ribosome entry site elements in a novel virus, canine picodicistrovirus, in the picornavirus-like superfamily. J. Virol. 86: 2797-2808. Epub 2011 Dec 28.

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.

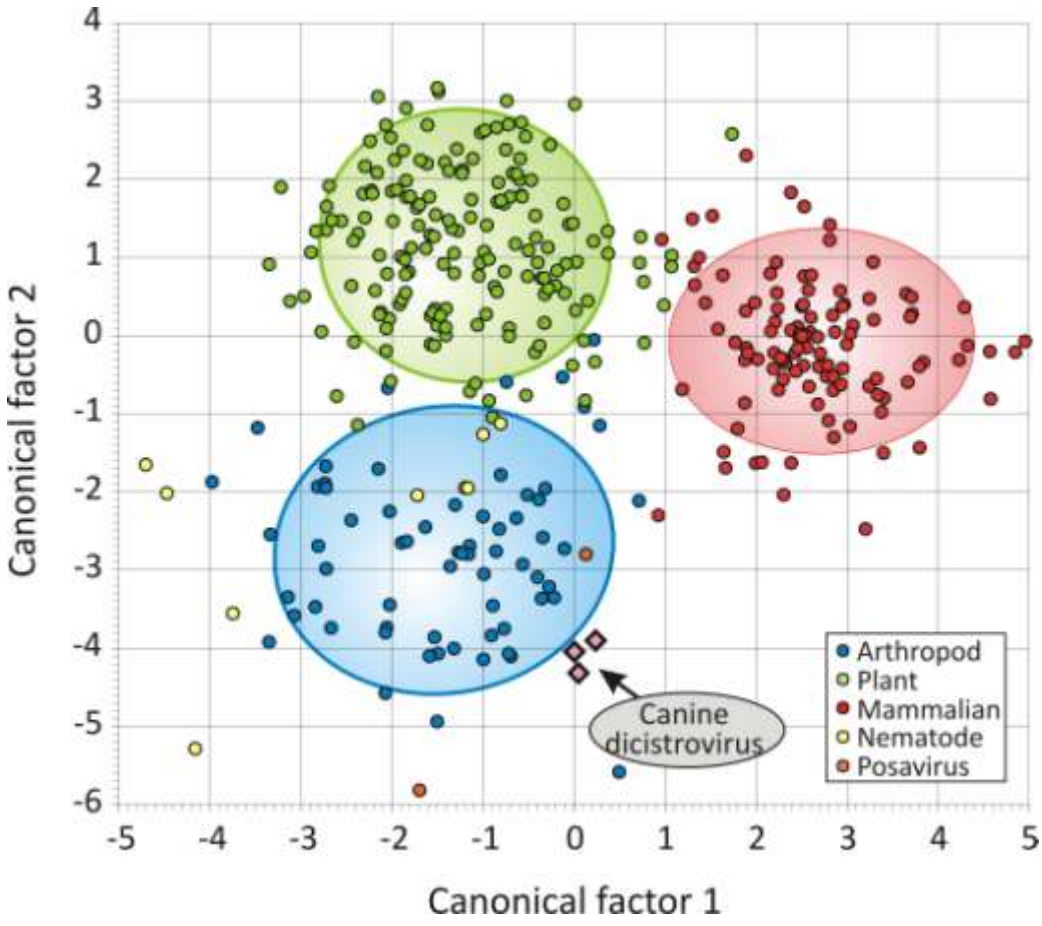

Fig. 1. Nucleotide composition analysis (NCA) to infer hosts (Kapoor et al., 2010).

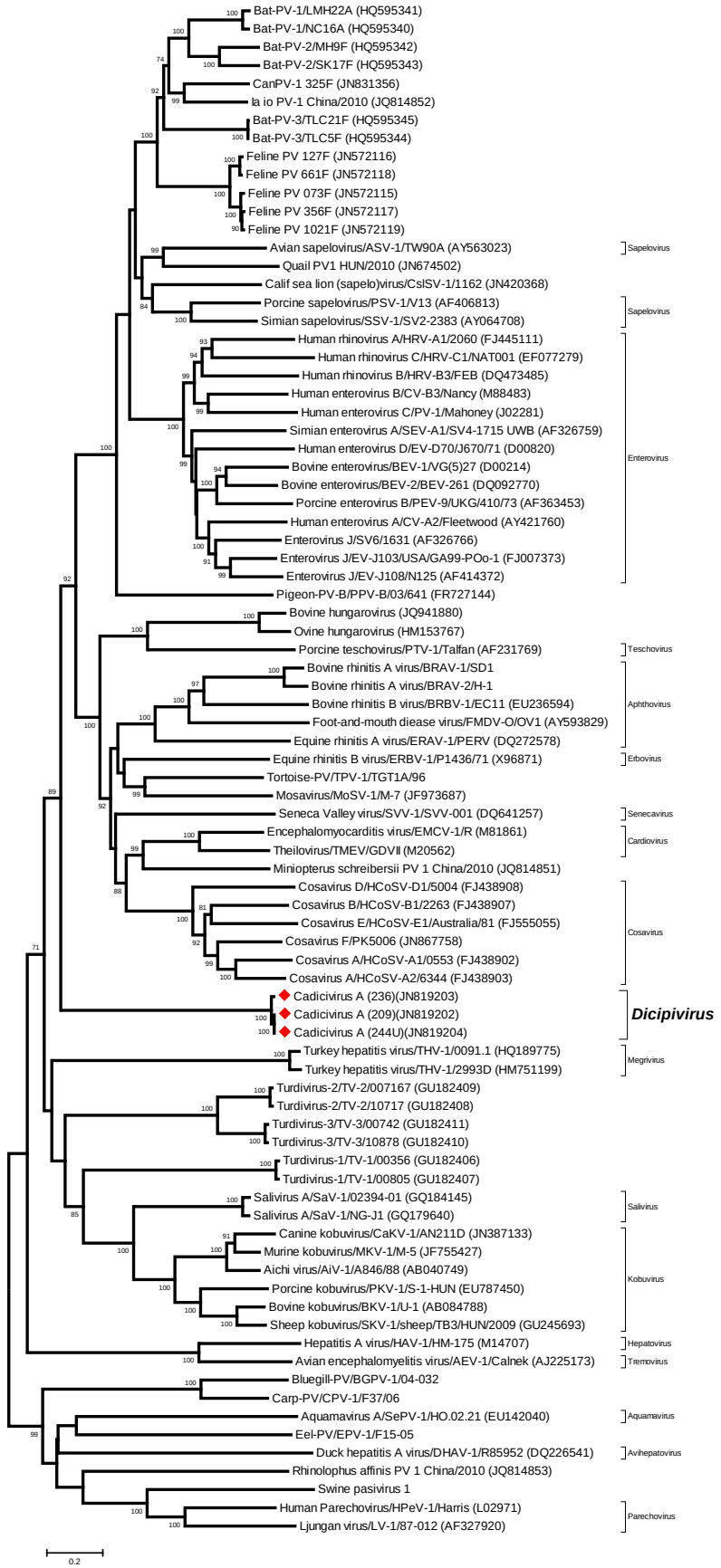

Fig. 2. Neighbor-joining tree comparing the P1 capsid of "canine picodicistrovirus" and other picornaviruses.

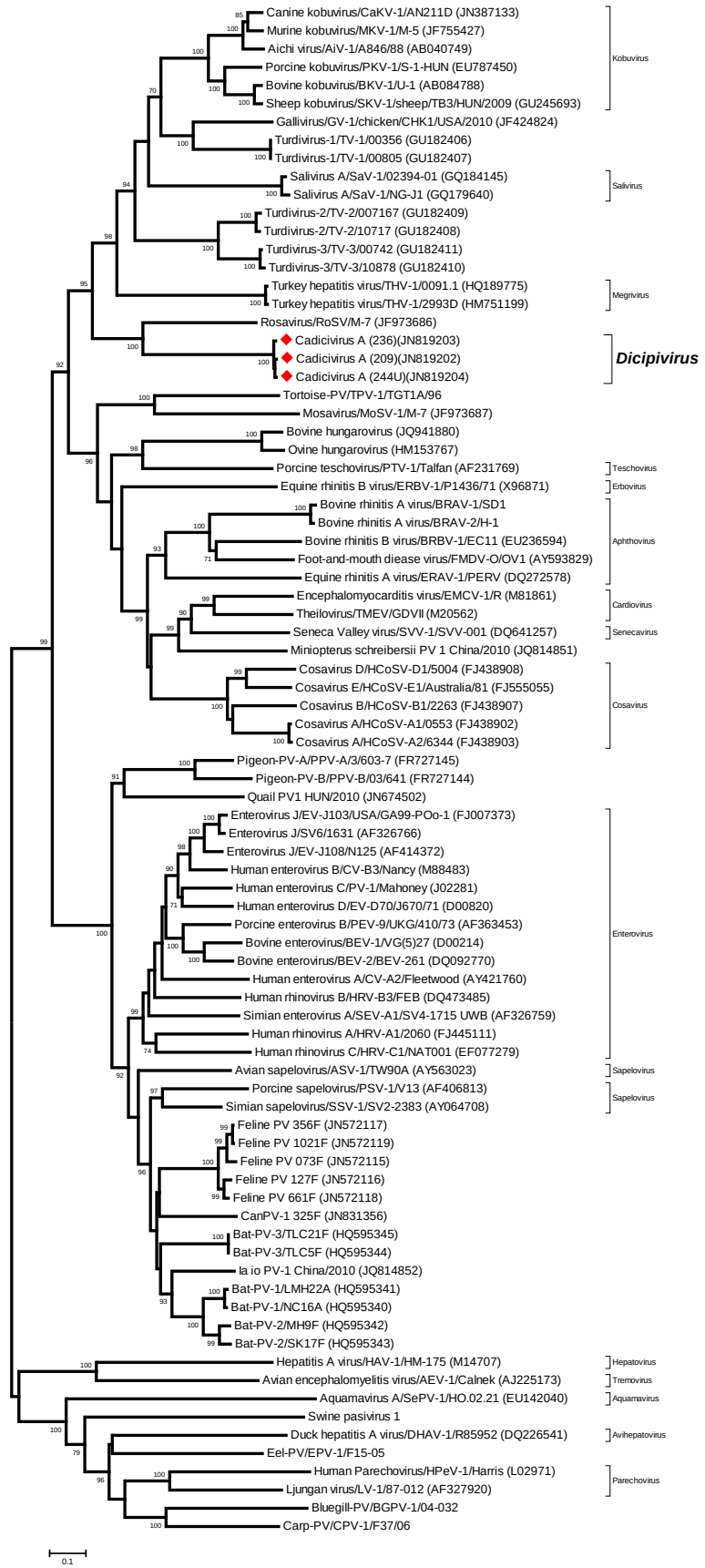

Fig. 3. Neighbor-joining tree comparing the $3D^{pol}$ capsid of "canine picodicistrovirus" and other picornaviruses.