MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2014.014aV*	(to be completed by ICTV officers)

Short title: Creation of a new species (*Cardiovirus C*) within the genus *Cardiovirus*.
(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	*2014.014aV*	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Cardiovirus*	Fill in all that apply.
Subfamily:	*-*	• If the higher taxon has yet to be created (in a later module, below) write
Family:	*Picornaviridae*	"**(new)**" after its proposed name.
Order:	*Picornavirales*	• If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	Representative isolates:	GenBank sequence accession number(s)
Cardiovirus C	Boone cardiovirus 1 Boone cardiovirus 2	JQ864242 JX683808

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 cardio-like virus, named Boone cardiovirus (BCV), has been isolated from the faeces of laboratory brown rats (*Rattus norvegicus*) at the University of Missouri (Gohndrone and Riley, unpublished). Interestingly, its 2A/2B junction lacks an NPG↓P motif and possesses a putative 3C cleavage site (Q/G). Two strains/genotypes of BCV have been identified: BCV-1 and BCV-2.

Its genome layout is typical of cardioviruses and is approximately equidistantly related to the two existing cardiovirus species (Appendix Table 1), *Encephalomyocarditis virus* and *Theilovirus* (which are proposed to be renamed *Cardiovirus A* and *Cardiovirus* B, respectively).

The SG definitions for cardiovirus species determination state that a member of a species must share greater than 70% amino acid (aa) identity in the polyprotein (actual ~43%), greater than 60% aa identity in the P1 region (actual ~50%), greater than 70% aa identity in the 2C+3CD region (actual ~50%), share a natural host range, and a common genome organization. BCV, when compared to either EMCV or theiloviruses, satisfies only the latter two requirements and as a result should be considered a novel species within the cardiovirus genus. Phylogenetic relationships with other picornaviruses are shown in Appendix Figs. 1 and 2.

Genome layout:

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

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

http://www.google.com/patents/US20140024015

http://www.idexxbioresearch.com/radil/inside/News_and_Events/IDEXX_RADIL_Discovers_Novel_Picorn
    _Boone_Cardiovirus/index.html

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. P-distances between cardioviruses.

P1^{cap}	M81861	M20562	JQ864242	JX683808
M81861 Encephalomyocarditis virus	0.0	42.0	50.4	48.5
M20562 Theilovirus	42.0	0.0	48.9	47.5
JQ864242 Boone cardiovirus 1	50.4	48.9	0.0	13.8
JX683808 Boone cardiovirus 2	48.5	47.5	13.8	0.0

3D^{pol}	M81861	M20562	JQ864242
M81861 Encephalomyocarditis virus	0.0	35.0	38.6
M20562 Theilovirus	35.0	0.0	39.1
JQ864242 Boone cardiovirus 1	38.6	39.1	0.0

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 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 (♦).

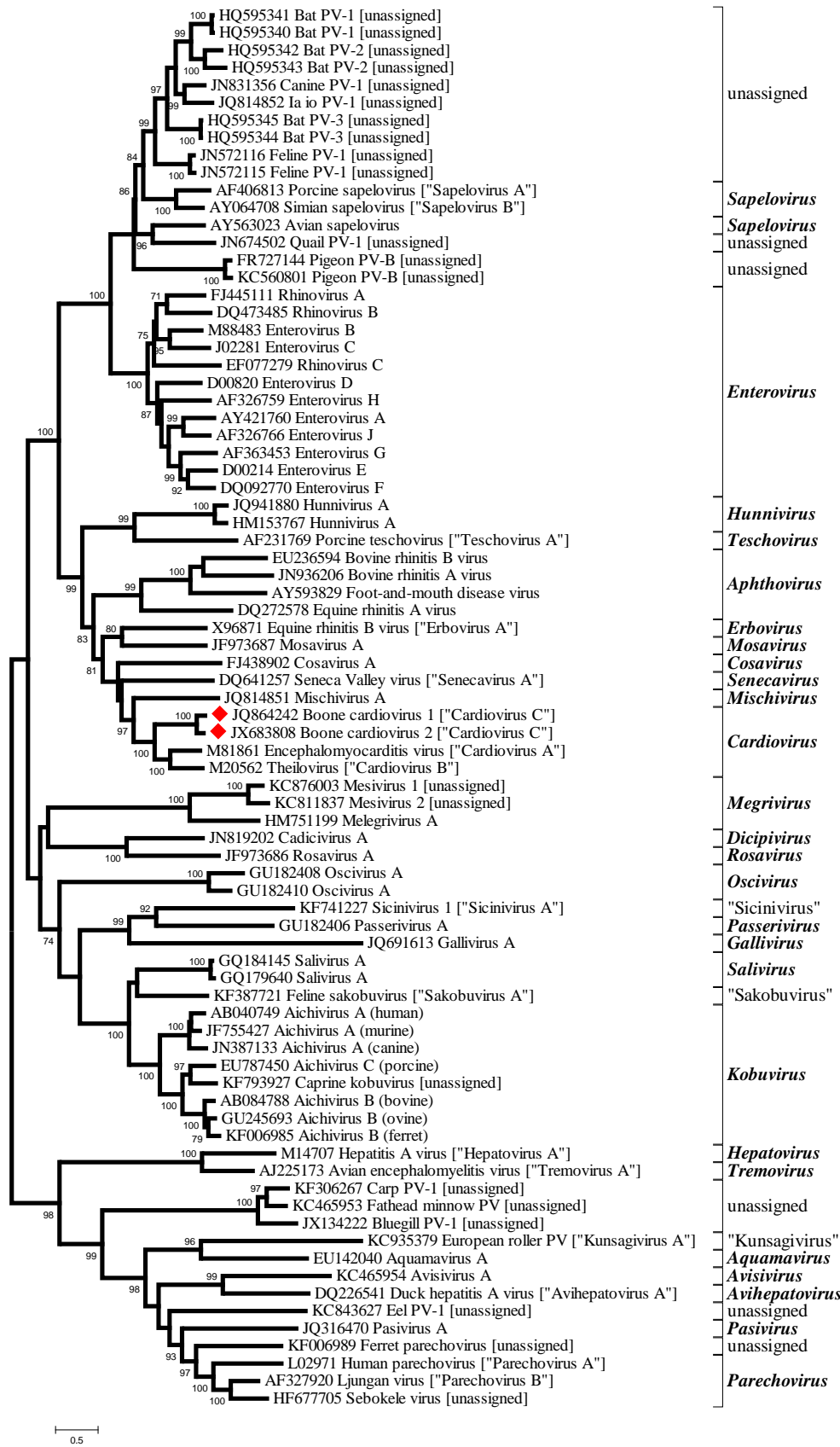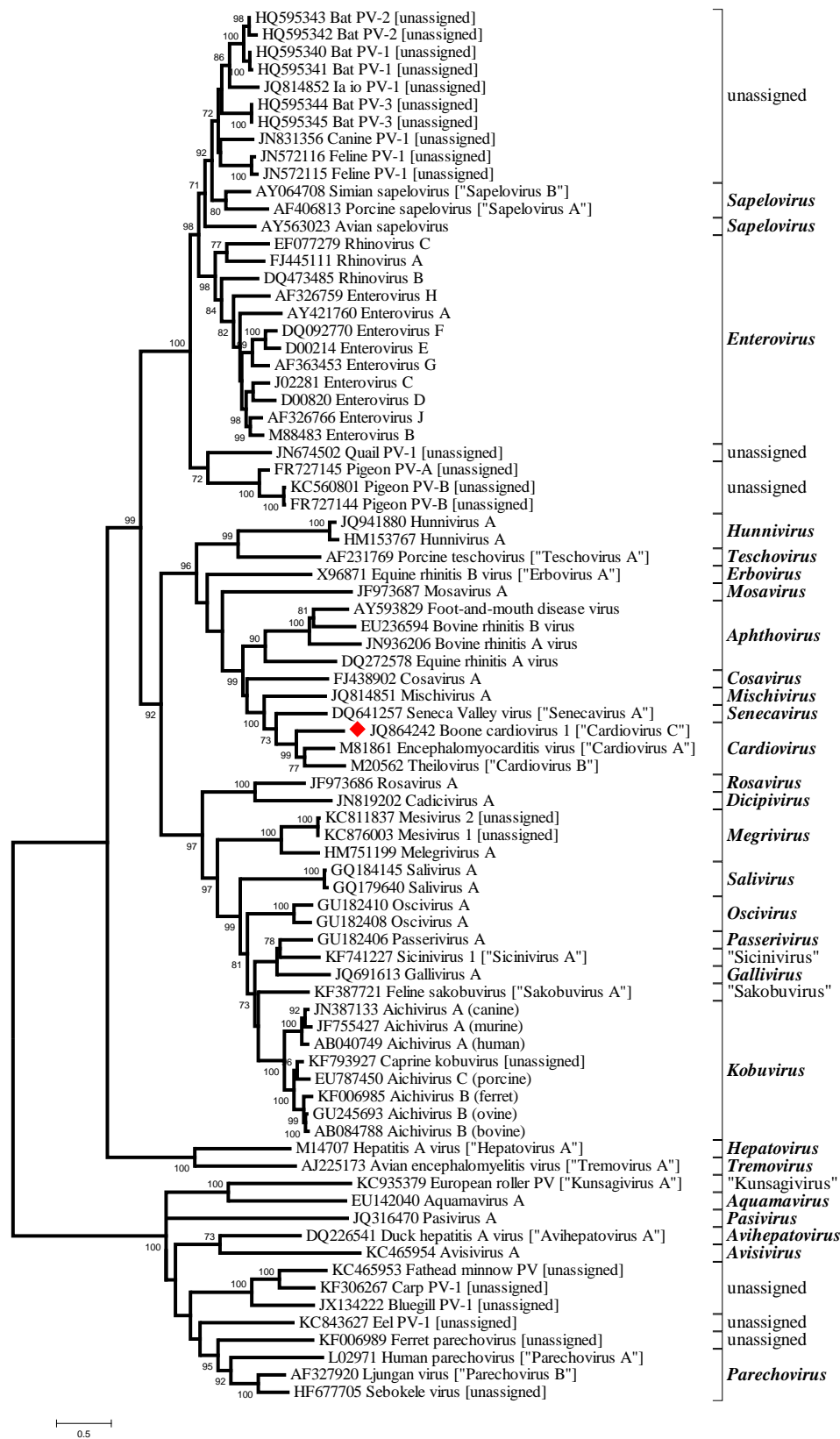| Accession / Virus	Genus
98 — HQ595343 Bat PV-2 [unassigned]	
100 — HQ595342 Bat PV-2 [unassigned]	
86 — HQ595340 Bat PV-1 [unassigned]	
100 — HQ595341 Bat PV-1 [unassigned]	
JQ814852 Ia io PV-1 [unassigned]	
72 — HQ595344 Bat PV-3 [unassigned]	unassigned
100 — HQ595345 Bat PV-3 [unassigned]	
JN831356 Canine PV-1 [unassigned]	
92 — JN572116 Feline PV-1 [unassigned]	
100 — JN572115 Feline PV-1 [unassigned]	
71 — AY064708 Simian sapelovirus ["Sapelovirus B"]	*Sapelovirus*
80 — AF406813 Porcine sapelovirus ["Sapelovirus A"]	
98 — AY563023 Avian sapelovirus	*Sapelovirus*
77 — EF077279 Rhinovirus C	
FJ445111 Rhinovirus A	
98 — DQ473485 Rhinovirus B	
AF326759 Enterovirus H	
84 — AY421760 Enterovirus A	
82 — 100 — DQ092770 Enterovirus F	
9 — D00214 Enterovirus E	*Enterovirus*
AF363453 Enterovirus G	
J02281 Enterovirus C	
D00820 Enterovirus D	
98 — AF326766 Enterovirus J	
99 — M88483 Enterovirus B	
JN674502 Quail PV-1 [unassigned]	unassigned
72 — FR727145 Pigeon PV-A [unassigned]	unassigned
100 — KC560801 Pigeon PV-B [unassigned]	
100 — FR727144 Pigeon PV-B [unassigned]	
100 — JQ941880 Hunnivirus A	*Hunnivirus*
99 — HM153767 Hunnivirus A	*Hunnivirus*
AF231769 Porcine teschovirus ["Teschovirus A"]	*Teschovirus*
96 — X96871 Equine rhinitis B virus ["Erbovirus A"]	*Erbovirus*
JF973687 Mosavirus A	*Mosavirus*
81 — AY593829 Foot-and-mouth disease virus	
100 — EU236594 Bovine rhinitis B virus	
90 — JN936206 Bovine rhinitis A virus	*Aphthovirus*
DQ272578 Equine rhinitis A virus	
99 — FJ438902 Cosavirus A	*Cosavirus*
JQ814851 Mischivirus A	*Mischivirus*
DQ641257 Seneca Valley virus ["Senecavirus A"]	*Senecavirus*
100 — ♦ JQ864242 Boone cardiovirus 1 ["Cardiovirus C"]	*Cardiovirus*
73 — M81861 Encephalomyocarditis virus ["Cardiovirus A"]	
99 — M20562 Theilovirus ["Cardiovirus B"]	
77	
100 — JF973686 Rosavirus A	*Rosavirus*
JN819202 Cadicivirus A	*Dicipivirus*
100 — KC811837 Mesivirus 2 [unassigned]	*Megrivirus*
100 — KC876003 Mesivirus 1 [unassigned]	
HM751199 Melegrivirus A	
97 — 100 — GQ184145 Salivirus A	*Salivirus*
GQ179640 Salivirus A	
97 — 100 — GU182410 Oscivirus A	*Oscivirus*
GU182408 Oscivirus A	
99 — GU182406 Passerivirus A	*Passerivirus*
78 — KF741227 Sicinivirus 1 ["Sicinivirus A"]	"Sicinivirus"
81 — JQ691613 Gallivirus A	*Gallivirus*
KF387721 Feline sakobuvirus ["Sakobuvirus A"]	"Sakobuvirus"
73 — 92 — JN387133 Aichivirus A (canine)	
100 — JF755427 Aichivirus A (murine)	
AB040749 Aichivirus A (human)	
6 — KF793927 Caprine kobuvirus [unassigned]	
100 — EU787450 Aichivirus C (porcine)	*Kobuvirus*
100 — KF006985 Aichivirus B (ferret)	
99 — GU245693 Aichivirus B (ovine)	
100 — AB084788 Aichivirus B (bovine)	
M14707 Hepatitis A virus ["Hepatovirus A"]	*Hepatovirus*
100 — AJ225173 Avian encephalomyelitis virus ["Tremovirus A"]	*Tremovirus*
100 — KC935379 European roller PV ["Kunsagivirus A"]	"Kunsagivirus"
EU142040 Aquamavirus A	*Aquamavirus*
JQ316470 Pasivirus A	*Pasivirus*
73 — DQ226541 Duck hepatitis A virus ["Avihepatovirus A"]	*Avihepatovirus*
KC465954 Avisivirus A	*Avisivirus*
100 — KC465953 Fathead minnow PV [unassigned]	
100 — KF306267 Carp PV-1 [unassigned]	unassigned
JX134222 Bluegill PV-1 [unassigned]	
KC843627 Eel PV-1 [unassigned]	unassigned
KF006989 Ferret parechovirus [unassigned]	unassigned
95 — L02971 Human parechovirus ["Parechovirus A"]	
92 — AF327920 Ljungan virus ["Parechovirus B"]	*Parechovirus*
100 — HF677705 Sebokele virus [unassigned]	

0.5

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 (♦).