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:	***2016.012aS***	(to be completed by ICTV officers)

Short title: 2 new species (*Mischivirus B*, *Mischivirus C*) in the genus *Mischivirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐ **11** ☒

Author(s):

Roland Zell on behalf of the *Picornaviridae* Study Group

Corresponding author with e-mail address:

Roland Zell (roland.zell@med.uni-jena.de)

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 Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:	15/06/2016
Date of this revision (if different to above):	02/08/2016

ICTV-EC comments and response of the proposer:

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	***2016.012aS***

(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Mischivirus***
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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Mischivirus B	Bat picornavirus BatPV/V1/13 Hun	KP054273
Mischivirus C	African bat icavirus PREDICT-06105	KP100644

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 11

Novel bat picornaviruses were detected in faecal samples of clinically healthy Schreibers' bats (*Miniopterus schreibersii*) in Hungary and in oral swabs of giant roundleaf bats (*Hipposideros gigas*) in the Democratic Republic of the Congo. The novel picornaviruses share significant similarities to *Mischivirus A*, i.e.

(i) the *Microchiroptera* (microbats) host,

(ii) similar genome layout (compare Figure 1, Appendix):

VPg+5'UTR$^{\text{IRES-II}}$[L/1AB-1C-1D-2A$^{\text{NPG}\downarrow\text{P}}$/2B-2C$^{\text{Hel}}$/3A-3B$^{\text{VPg}}$-3C$^{\text{Pro}}$-3D$^{\text{Pol}}$]3'UTR-poly(A);

(iii) significant amino acid identities of capsid proteins (>43%) and 3CD (>54%) protein (compare Tables 1, 2; Appendix)

(iv) clustering with *Mischivirus A* in phylogenetic trees (compare Figures 2,3; Appendix).

It was shown that *Mischivirus A* und *B* have a type II IRES. Two types of *Mischivirus B* are known. *Mischivirus C* differs from *Mischivirus A* and *B* in having divergent L and 3A proteins and a shorter 2A protein (32 aa vs. 55 aa).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Mischivirus B:

Kemenesi G, Zhang D, Marton S, Dallos B, Görföl T, Estok P, Boldogh S, Kurucz K, Oldal M, Kutas A, Banyai K, Jakab F. 2015. Genetic characterization of novel picornavirus detected in *Minoopterus schreibersii* bats. J. Gen. Virol. 96:815-821.

Mischivirus C:

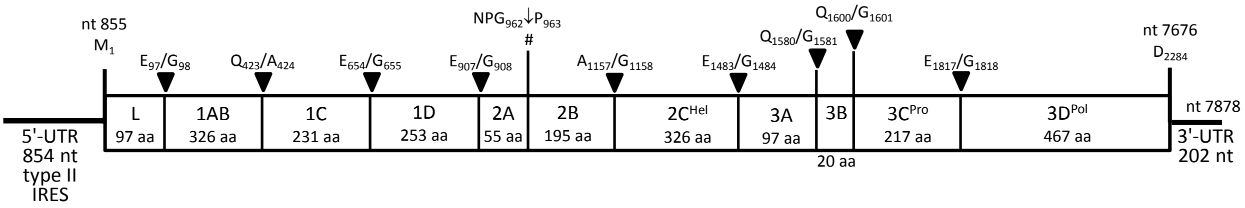
unpublished

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.

Genome organization:

Proposed: *Mischivirus B,* bat picornavirus, GenBank acc. nos. KP054273-KP054278



Proposed: *Mischivirus C,* African bat icavirus, GenBank acc. no. KP100644

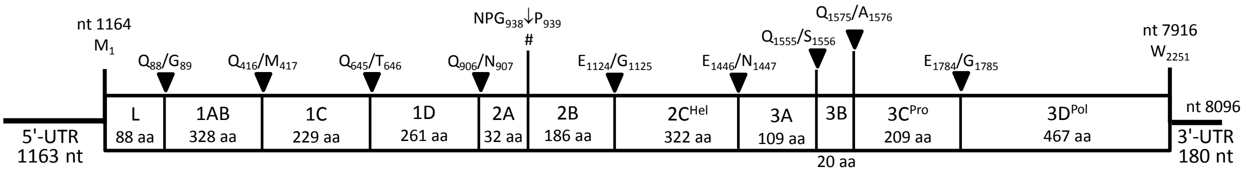
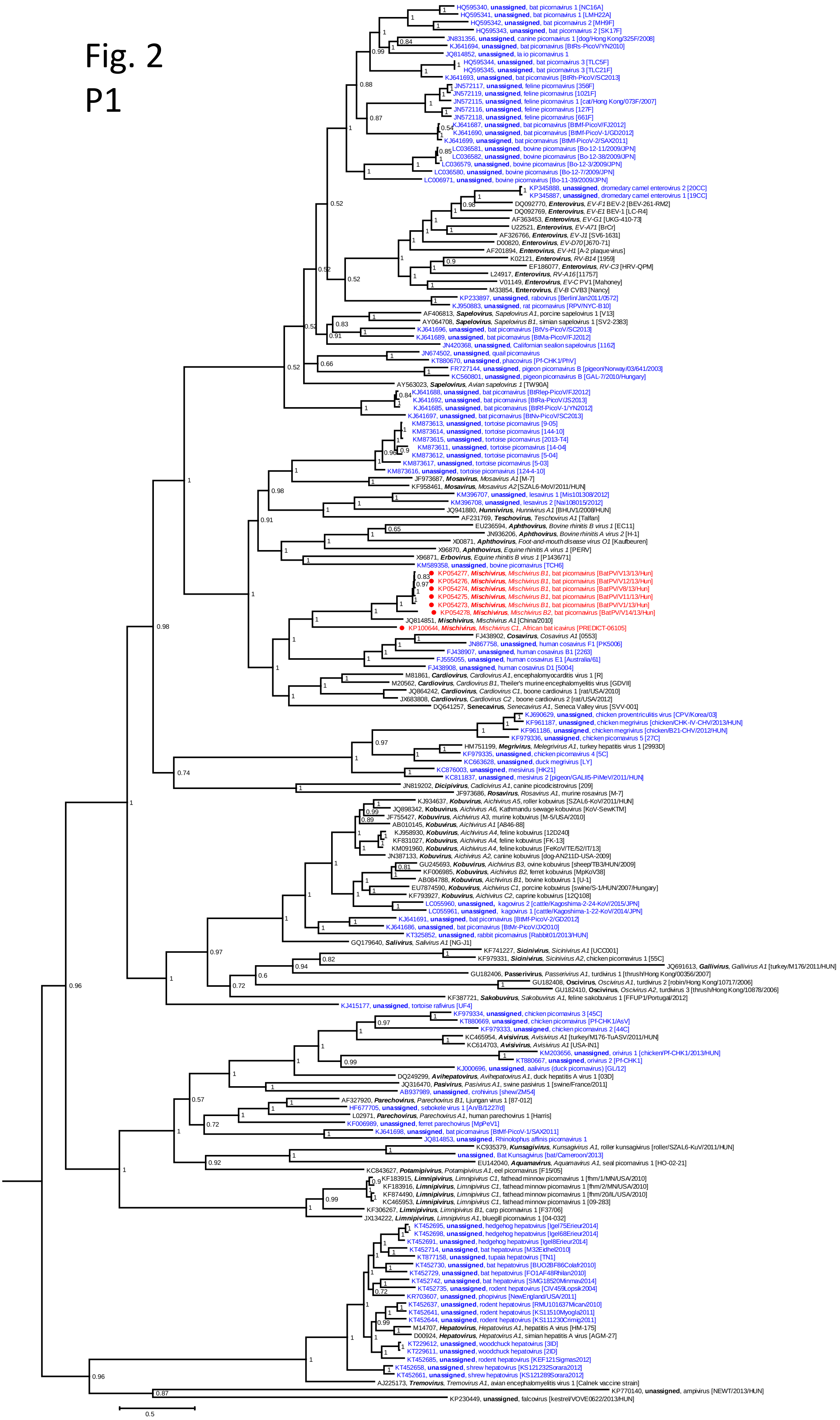


Figure 1: Schematic depiction of the mischivirus B and C genomes (*top*: bat picornaviruses, *below*: African bat virus [PREDICT-06105]). The open reading frames are indicated by boxes. Positions of putative nt and aa cleavage sites and the lengths of the deduced proteins are shown. Triangles (▼) indicate the putative $3C^{pro}$ cleavage sites; the hash (#) indicates ribosomal skipping sites at the NPG↓P motif.

Fig. 2

P1


HQ595340, unassigned, bat picornavirus 1 [NC16A]
HQ595341, unassigned, bat picornavirus 1 [LMH22A]
HQ595342, unassigned, bat picornavirus 2 [MH9F]
HQ595343, unassigned, bat picornavirus 2 [SK17F]
JN831356, unassigned, canine picornavirus 1 [dog/Hong Kong/325F/2008]
KJ641694, unassigned, bat picornavirus [BtRs-PicoV/YN2010]
JQ814852, unassigned, la io picornavirus 1
HQ595344, unassigned, bat picornavirus 3 [TLC5F]
HQ595345, unassigned, bat picornavirus 3 [TLC21F]
KJ641693, unassigned, bat picornavirus [BtRh-PicoV/SC2013]
JN572117, unassigned, feline picornavirus [356F]
JN572119, unassigned, feline picornavirus [1021F]
JN572115, unassigned, feline picornavirus 1 [cat/Hong Kong/073F/2007]
JN572116, unassigned, feline picornavirus [127F]
JN572118, unassigned, feline picornavirus [661F]
KJ641687, unassigned, bat picornavirus [BtMf-PicoV/FJ2012]
KJ641690, unassigned, bat picornavirus [BtMf-PicoV-1/GD2012]
KJ641699, unassigned, bat picornavirus [BtMf-PicoV-2/SAX2011]
LC036581, unassigned, bovine picornavirus [Bo-12-11/2009/JPN]
LC036582, unassigned, bovine picornavirus [Bo-12-38/2009/JPN]
LC036579, unassigned, bovine picornavirus [Bo-12-3/2009/JPN]
LC036580, unassigned, bovine picornavirus [Bo-12-7/2009/JPN]
LC006971, unassigned, bovine picornavirus [Bo-11-39/2009/JPN]
KP345888, unassigned, dromedary camel enterovirus 2 [20CC]
KP345887, unassigned, dromedary camel enterovirus 1 [19CC]
DQ092770, Enterovirus, EV-F1 BEV-2 [BEV-261-RM2]
DQ092769, Enterovirus, EV-E1 BEV-1 [LC-R4]
AF363453, Enterovirus, EV-G1 [UKG-410-73]
U22521, Enterovirus, EV-A71 [BrCr]
AF326766, Enterovirus, EV-J1 [SV6-1631]
D00820, Enterovirus, EV-D70 [J670-71]
AF201894, Enterovirus, EV-H1 [A-2 plaque virus]
K02121, Enterovirus, RV-B14 [1959]
EF186077, Enterovirus, RV-C3 [HRV-QPM]
L24917, Enterovirus, RV-A16 [11757]
V01149, Enterovirus, EV-C PV1 [Mahoney]
M33854, Enterovirus, EV-B CVB3 [Nancy]
KP233897, unassigned, rabovirus [Berlin/Jan2011/0572]
KJ950883, unassigned, rat picornavirus [RPV/NYC-B10]
AF406813, Sapelovirus, Sapelovirus A1, porcine sapelovirus 1 [V13]
AY064708, Sapelovirus, Sapelovirus B1, simian sapelovirus 1 [SV2-2383]
KJ641696, unassigned, bat picornavirus [BtVs-PicoV/SC2013]
KJ641689, unassigned, bat picornavirus [BtMa-PicoV/FJ2012]
JN420368, unassigned, Californian sealion sapelovirus [1162]
JN674502, unassigned, quail picornavirus
KT880670, unassigned, phacovirus [Pf-CHK1/PhV]
FR727144, unassigned, pigeon picornavirus B [pigeon/Norway/03/641/2003]
KC560801, unassigned, pigeon picornavirus B [GAL-7/2010/Hungary]
AY563023, Sapelovirus, Avian sapelovirus 1 [TW90A]
KJ641688, unassigned, bat picornavirus [BtRlep-PicoV/FJ2012]
KJ641692, unassigned, bat picornavirus [BtRa-PicoV/JS2013]
KJ641685, unassigned, bat picornavirus [BtRf-PicoV-1/YN2012]
KJ641697, unassigned, bat picornavirus [BtNv-PicoV/SC2013]
KM873613, unassigned, tortoise picornavirus [9-05]
KM873614, unassigned, tortoise picornavirus [144-10]
KM873615, unassigned, tortoise picornavirus [2013-T4]
KM873611, unassigned, tortoise picornavirus [14-04]
KM873612, unassigned, tortoise picornavirus [5-04]
KM873617, unassigned, tortoise picornavirus [5-03]
KM873616, unassigned, tortoise picornavirus [124-4-10]
JF973687, Mosavirus, Mosavirus A1 [M-7]
KF958461, Mosavirus, Mosavirus A2 [SZAL6-MoV/2011/HUN]
KM396707, unassigned, lesavirus 1 [Mis101308/2012]
KM396708, unassigned, lesavirus 2 [Nai108015/2012]
JQ941880, Hunnivirus, Hunnivirus A1 [BHUV1/2008/HUN]
AF231769, Teschovirus, Teschovirus A1 [Talfan]
EU236594, Aphthovirus, Bovine rhinitis B virus 1 [EC11]
JN936206, Aphthovirus, Bovine rhinitis A virus 2 [H-1]
X00871, Aphthovirus, Foot-and-mouth disease virus O1 [Kaufbeuren]
X96870, Aphthovirus, Equine rhinitis A virus 1 [PERV]
X96871, Erbovirus, Equine rhinitis B virus 1 [P1436/71]
KM589358, unassigned, bovine picornavirus [TCH6]
● KP054277, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]
● KP054276, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]
● KP054274, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]
● KP054275, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]
● KP054273, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]
● KP054278, Mischivirus, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun]
JQ814851, Mischivirus, Mischivirus A1 [China/2010]
● KP100644, Mischivirus, Mischivirus C1, African bat icavirus [PREDICT-06105]
FJ438902, Cosavirus, Cosavirus A1 [0553]
JN867758, unassigned, human cosavirus F1 [PK5006]
FJ438907, unassigned, human cosavirus B1 [2263]
FJ555055, unassigned, human cosavirus E1 [Australia/61]
FJ438908, unassigned, human cosavirus D1 [5004]
M81861, Cardiovirus, Cardiovirus A1, encephalomyocarditis virus 1 [R]
M20562, Cardiovirus, Cardiovirus B1, Theiler's murine encephalomyelitis virus [GDVII]
JQ864242, Cardiovirus, Cardiovirus C1, boone cardiovirus 1 [rat/USA/2010]
JX683808, Cardiovirus, Cardiovirus C2 , boone cardiovirus 2 [rat/USA/2012]
DQ641257, Senecavirus, Senecavirus A1, Seneca Valley virus [SVV-001]
KJ690629, unassigned, chicken proventriculitis virus [CPV/Korea/03]
KF961187, unassigned, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]
KF961186, unassigned, chicken megrivirus [chicken/B21-CHV/2012/HUN]
KF979336, unassigned, chicken picornavirus 5 [27C]
HM751199, Megrivirus, Melegrivirus A1, turkey hepatitis virus 1 [2993D]
KF979335, unassigned, chicken picornavirus 4 [5C]
KC663628, unassigned, duck megrivirus [LY]
KC876003, unassigned, mesivirus [HK21]
KC811837, unassigned, mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]
JN819202, Dicipivirus, Cadicivirus A1, canine picodicistrovirus [209]
JF973686, Rosavirus, Rosavirus A1, murine rosavirus [M-7]
KJ934637, Kobuvirus, Aichivirus A5, roller kobuvirus [SZAL6-KoV/2011/HUN]
JQ898342, Kobuvirus, Aichivirus A6, Kathmandu sewage kobuvirus [KoV-SewKTM]
JF755427, Kobuvirus, Aichivirus A3, murine kobuvirus [M-5/USA/2010]
AB010145, Kobuvirus, Aichivirus A1 [A846-88]
KJ958930, Kobuvirus, Aichivirus A4, feline kobuvirus [12D240]
KF831027, Kobuvirus, Aichivirus A4, feline kobuvirus [FK-13]
KM091960, Kobuvirus, Aichivirus A4, feline kobuvirus [FeKoV/TE/52/IT/13]
JN387133, Kobuvirus, Aichivirus A2, canine kobuvirus [dog-AN211D-USA-2009]
GU245693, Kobuvirus, Aichivirus B3, ovine kobuvirus [sheep/TB3/HUN/2009]
KF006985, Kobuvirus, Aichivirus B2, ferret kobuvirus [MpKoV38]
AB084788, Kobuvirus, Aichivirus B1, bovine kobuvirus 1 [U-1]
EU7874590, Kobuvirus, Aichivirus C1, porcine kobuvirus [swine/S-1/HUN/2007/Hungary]
KF793927, Kobuvirus, Aichivirus C2, caprine kobuvirus [12Q108]
LC055960, unassigned, kagovirus 2 [cattle/Kagoshima-2-24-KoV/2015/JPN]
LC055961, unassigned, kagovirus 1 [cattle/Kagoshima-1-22-KoV/2014/JPN]
KJ641691, unassigned, bat picornavirus [BtMf-PicoV-2/GD2012]
KJ641686, unassigned, bat picornavirus [BtMr-PicoV/JX2010]
KT325852, unassigned, rabbit picornavirus [Rabbit01/2013/HUN]
GQ179640, Salivirus, Salivirus A1 [NG-J1]
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KF979331, Sicinivirus, Sicinivirus A2, chicken picornavirus 1 [55C]
JQ691613, Gallivirus, Gallivirus A1 [turkey/M176/2011/HUN]
GU182406, Passerivirus, Passerivirus A1, turdivirus 1 [thrush/Hong Kong/00356/2007]
GU182408, Oscivirus, Oscivirus A1, turdivirus 2 [robin/Hong Kong/10717/2006]
GU182410, Oscivirus, Oscivirus A2, turdivirus 3 [thrush/Hong Kong/10878/2006]
KF387721, Sakobuvirus, Sakobuvirus A1, feline sakobuvirus 1 [FFUP1/Portugal/2012]
KJ415177, unassigned, tortoise rafivirus [UF4]
KF979334, unassigned, chicken picornavirus 3 [45C]
KT880669, unassigned, chicken picornavirus [Pf-CHK1/AsV]
KF979333, unassigned, chicken picornavirus 2 [44C]
KC465954, Avisivirus, Avisivirus A1 [turkey/M176-TuASV/2011/HUN]
KC614703, Avisivirus, Avisivirus A1 [USA-IN1]
KM203656, unassigned, orivirus 1 [chicken/Pf-CHK1/2013/HUN]
KT880667, unassigned, orivirus 2 [Pf-CHK1]
KJ000696, unassigned, aalivirus (duck picornavirus) [GL/12]
DQ249299, Avihepatovirus, Avihepatovirus A1, duck hepatitis A virus 1 [03D]
JQ316470, Pasivirus, Pasivirus A1, swine pasivirus 1 [swine/France/2011]
AB937989, unassigned, crohivirus [shew/ZM54]
AF327920, Parechovirus, Parechovirus B1, Ljungan virus 1 [87-012]
HF677705, unassigned, sebokele virus 1 [An/B/1227/d]
L02971, Parechovirus, Parechovirus A1, human parechovirus 1 [Harris]
KF006989, unassigned, ferret parechovirus [MpPeV1]
KJ641698, unassigned, bat picornavirus [BtMf-PicoV-1/SAX2011]
JQ814853, unassigned, Rhinolophus affinis picornavirus 1
KC935379, Kunsagivirus, Kunsagivirus A1, roller kunsagivirus [roller/SZAL6-KuV/2011/HUN]
unassigned, Bat Kunsagivirus [bat/Cameroon/2013]
EU142040, Aquamavirus, Aquamavirus A1, seal picornavirus 1 [HO-02-21]
KC843627, Potamipivirus, Potamipivirus A1, eel picornavirus [F15/05]
KF183915, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/1/MN/USA/2010]
KF183916, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/2/MN/USA/2010]
KF874490, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/20/IL/USA/2010]
KC465953, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [09-283]
KF306267, Limnipivirus, Limnipivirus B1, carp picornavirus 1 [F37/06]
JX134222, Limnipivirus, Limnipivirus A1, bluegill picornavirus 1 [04-032]
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KT452691, unassigned, hedgehog hepatovirus [Igel8Erieur2014]
KT452714, unassigned, bat hepatovirus [M32Eidhel2010]
KT877158, unassigned, tupaia hepatovirus [TN1]
KT452730, unassigned, bat hepatovirus [BUO2BF86Colafr2010]
KT452729, unassigned, bat hepatovirus [FO1AF48Rhilan2010]
KT452742, unassigned, bat hepatovirus [SMG18520Minmav2014]
KT452735, unassigned, rodent hepatovirus [CIV459Lopsik2004]
KR703607, unassigned, phopivirus [NewEngland/USA/2011]
KT452637, unassigned, rodent hepatovirus [RMU101637Micarv2010]
KT452641, unassigned, rodent hepatovirus [KS11510Myogla2011]
KT452644, unassigned, rodent hepatovirus [KS111230Crimig2011]
M14707, Hepatovirus, Hepatovirus A1, hepatitis A virus [HM-175]
D00924, Hepatovirus, Hepatovirus A1, simian hepatitis A virus [AGM-27]
KT229612, unassigned, woodchuck hepatovirus [3ID]
KT229611, unassigned, woodchuck hepatovirus [2ID]
KT452685, unassigned, rodent hepatovirus [KEF121Sigmas2012]
KT452658, unassigned, shrew hepatovirus [KS121232Sorara2012]
KT452661, unassigned, shrew hepatovirus [KS121289Sorara2012]
AJ225173, Tremovirus, Tremovirus A1, avian encephalomyelitis virus 1 [Calnek vaccine strain]
KP770140, unassigned, ampivirus [NEWT/2013/HUN]
KP230449, unassigned, falcovirus [kestrel/VOVE0622/2013/HUN]
0.5

Figure 2: Phylogenetic analyses of picornavirus P1 using Bayesian tree inference (MEGA 5.2). 178 picornavirus sequences were retrieved from GenBank. Presented are GenBank accession numbers, ***genus names***, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 6,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

Fig. 3

3CD

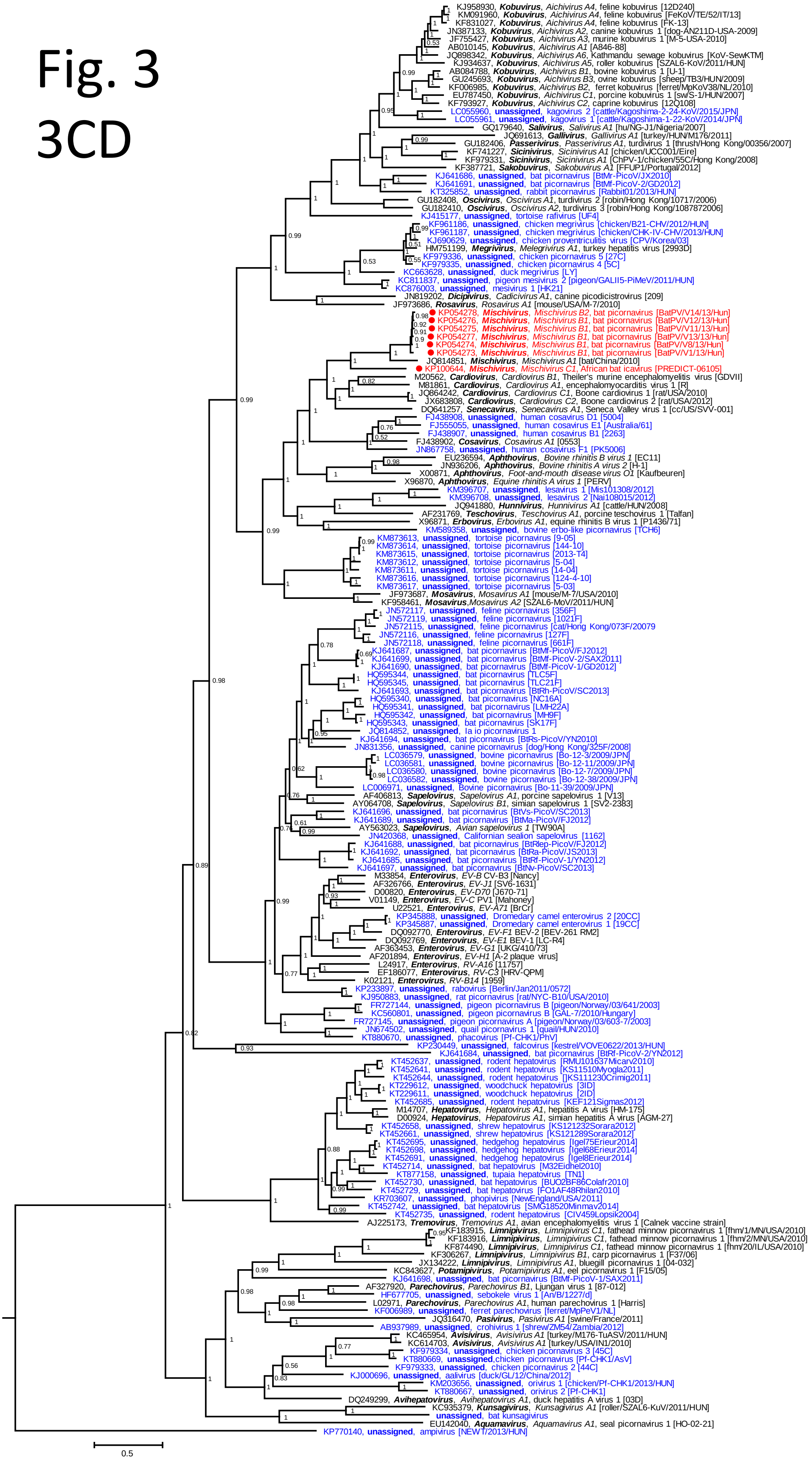
KJ958930, Kobuvirus, Aichivirus A4, feline kobuvirus [12D240]
KM091960, Kobuvirus, Aichivirus A4, feline kobuvirus [FeKoV/TE/52/IT/13]
KF831027, Kobuvirus, Aichivirus A4, feline kobuvirus [FK-13]
JN387133, Kobuvirus, Aichivirus A2, canine kobuvirus 1 [dog-AN211D-USA-2009]
JF755427, Kobuvirus, Aichivirus A3, murine kobuvirus 1 [M-5-USA-2010]
AB010145, Kobuvirus, Aichivirus A1 [A846-88]
JQ898342, Kobuvirus, Aichivirus A6, Kathmandu sewage kobuvirus [KoV-SewKTM]
KJ934637, Kobuvirus, Aichivirus A5, roller kobuvirus [SZAL6-KoV/2011/HUN]
AB084788, Kobuvirus, Aichivirus B1, bovine kobuvirus 1 [U-1]
GU245693, Kobuvirus, Aichivirus B3, ovine kobuvirus [sheep/TB3/HUN/2009]
KF006985, Kobuvirus, Aichivirus B2, ferret kobuvirus [ferret/MpKoV38/NL/2010]
EU787450, Kobuvirus, Aichivirus C1, porcine kobuvirus 1 [sw/S-1/HUN/2007]
KF793927, Kobuvirus, Aichivirus C2, caprine kobuvirus [12Q108]
LC055960, unassigned, kagovirus 2 [cattle/Kagoshima-2-24-KoV/2015/JPN]
LC055961, unassigned, kagovirus 1 [cattle/Kagoshima-1-22-KoV/2014/JPN]
GQ179640, Salivirus, Salivirus A1 [hu/NG-J1/Nigeria/2007]
JQ691613, Gallivirus, Gallivirus A1 [turkey/HUN/M176/2011]
GU182406, Passerivirus, Passerivirus A1, turdivirus 1 [thrush/Hong Kong/00356/2007]
KF741227, Sicinivirus, Sicinivirus A1 [chicken/UCC001/Eire]
KF979331, Sicinivirus, Sicinivirus A1 [ChPV-1/chicken/55C/Hong Kong/2008]
KF387721, Sakobuvirus, Sakobuvirus A1 [FFUP1/Portugal/2012]
KJ641686, unassigned, bat picornavirus [BtMr-PicoV/JX2010]
KJ641691, unassigned, bat picornavirus [BtMf-PicoV-2/GD2012]
KT325852, unassigned, rabbit picornavirus [Rabbit01/2013/HUN]
GU182408, Oscivirus, Oscivirus A1, turdivirus 2 [robin/Hong Kong/10717/2006)
GU182410, Oscivirus, Oscivirus A2, turdivirus 3 [robin/Hong Kong/1087872006]
KJ415177, unassigned, tortoise rafivirus [UF4]
KF961186, unassigned, chicken megrivirus [chicken/B21-CHV/2012/HUN]
KF961187, unassigned, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]
KJ690629, unassigned, chicken proventriculitis virus [CPV/Korea/03]
HM751199, Megrivirus, Melegrivirus A1, turkey hepatitis virus [2993D]
KF979336, unassigned, chicken picornavirus 5 [27C]
KF979335, unassigned, chicken picornavirus 4 [5C]
KC663628, unassigned, duck megrivirus [LY]
KC811837, unassigned, pigeon mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]
KC876003, unassigned, mesivirus 1 [HK21]
JN819202, Dicipivirus, Cadicivirus A1, canine picodicistrovirus [209]
JF973686, Rosavirus, Rosavirus A1 [mouse/USA/M-7/2010]
● KP054278, Mischivirus, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun]
● KP054276, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]
● KP054275, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]
● KP054277, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]
● KP054274, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]
● KP054273, Mischivirus, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]
JQ814851, Mischivirus, Mischivirus A1 [bat/China/2010]
● KP100644, Mischivirus, Mischivirus C1, African bat icavirus [PREDICT-06105]
M20562, Cardiovirus, Cardiovirus B1, Theiler's murine encephalomyelitis virus [GDVII]
M81861, Cardiovirus, Cardiovirus A1, encephalomyocarditis virus 1 [R]
JQ864242, Cardiovirus, Cardiovirus C1, Boone cardiovirus 1 [rat/USA/2010]
JX683808, Cardiovirus, Cardiovirus C2, Boone cardiovirus 2 [rat/USA/2012]
DQ641257, Senecavirus, Senecavirus A1, Seneca Valley virus 1 [cc/US/SVV-001]
FJ438908, unassigned, human cosavirus D1 [5004]
FJ555055, unassigned, human cosavirus E1 [Australia/61]
FJ438907, unassigned, human cosavirus B1 [2263]
FJ438902, Cosavirus, Cosavirus A1 [0553]
JN867758, unassigned, human cosavirus F1 [PK5006]
EU236594, Aphthovirus, Bovine rhinitis B virus 1 [EC11]
JN936206, Aphthovirus, Bovine rhinitis A virus 2 [H-1]
X00871, Aphthovirus, Foot-and-mouth disease virus O1 [Kaufbeuren]
X96870, Aphthovirus, Equine rhinitis A virus 1 [PERV]
KM396707, unassigned, lesavirus 1 [Mis101308/2012]
KM396708, unassigned, lesavirus 2 [Nai108015/2012]
JQ941880, Hunnivirus, Hunnivirus A1 [cattle/HUN/2008]
AF231769, Teschovirus, Teschovirus A1, porcine teschovirus 1 [Talfan]
X96871, Erbovirus, Erbovirus A1, equine rhinitis B virus 1 [P1436/71]
KM589358, unassigned, bovine erbo-like picornavirus [TCH6]
KM873613, unassigned, tortoise picornavirus [9-05]
KM873614, unassigned, tortoise picornavirus [144-10]
KM873615, unassigned, tortoise picornavirus [2013-T4]
KM873612, unassigned, tortoise picornavirus [5-04]
KM873611, unassigned, tortoise picornavirus [14-04]
KM873616, unassigned, tortoise picornavirus [124-4-10]
KM873617, unassigned, tortoise picornavirus [5-03]
JF973687, Mosavirus, Mosavirus A1 [mouse/M-7/USA/2010]
KF958461, Mosavirus,Mosavirus A2 [SZAL6-MoV/2011/HUN]
JN572117, unassigned, feline picornavirus [356F]
JN572119, unassigned, feline picornavirus [1021F]
JN572115, unassigned, feline picornavirus [cat/Hong Kong/073F/20079
JN572116, unassigned, feline picornavirus [127F]
JN572118, unassigned, feline picornavirus [661F]
KJ641687, unassigned, bat picornavirus [BtMf-PicoV/FJ2012]
KJ641699, unassigned, bat picornavirus [BtMf-PicoV-2/SAX2011]
KJ641690, unassigned, bat picornavirus [BtMf-PicoV-1/GD2012]
HQ595344, unassigned, bat picornavirus [TLC5F]
HQ595345, unassigned, bat picornavirus [TLC21F]
KJ641693, unassigned, bat picornavirus [BtRh-PicoV/SC2013]
HQ595340, unassigned, bat picornavirus [NC16A]
HQ595341, unassigned, bat picornavirus [LMH22A]
HQ595342, unassigned, bat picornavirus [MH9F]
HQ595343, unassigned, bat picornavirus [SK17F]
JQ814852, unassigned, la io picornavirus 1
KJ641694, unassigned, bat picornavirus [BtRs-PicoV/YN2010]
JN831356, unassigned, canine picornavirus [dog/Hong Kong/325F/2008]
LC036579, unassigned, bovine picornavirus [Bo-12-3/2009/JPN]
LC036581, unassigned, bovine picornavirus [Bo-12-11/2009/JPN]
LC036580, unassigned, bovine picornavirus [Bo-12-7/2009/JPN]
LC036582, unassigned, bovine picornavirus [Bo-12-38/2009/JPN]
LC006971, unassigned, Bovine picornavirus [Bo-11-39/2009/JPN]
AF406813, Sapelovirus, Sapelovirus A1, porcine sapelovirus 1 [V13]
AY064708, Sapelovirus, Sapelovirus B1, simian sapelovirus 1 [SV2-2383]
KJ641696, unassigned, bat picornavirus [BtVs-PicoV/SC2013]
KJ641689, unassigned, bat picornavirus [BtMa-PicoV/FJ2012]
AY563023, Sapelovirus, Avian sapelovirus 1 [TW90A]
JN420368, unassigned, Californian sealion sapelovirus [1162]
KJ641688, unassigned, bat picornavirus [BtRlep-PicoV/FJ2012]
KJ641692, unassigned, bat picornavirus [BtRa-PicoV/JS2013]
KJ641685, unassigned, bat picornavirus [BtRf-PicoV-1/YN2012]
KJ641697, unassigned, bat picornavirus [BtNv-PicoV/SC2013]
M33854, Enterovirus, EV-B CV-B3 [Nancy]
AF326766, Enterovirus, EV-J1 [SV6-1631]
D00820, Enterovirus, EV-D70 [J670-71]
V01149, Enterovirus, EV-C PV1 [Mahoney]
U22521, Enterovirus, EV-A71 [BrCr]
KP345888, unassigned, Dromedary camel enterovirus 2 [20CC]
KP345887, unassigned, Dromedary camel enterovirus 1 [19CC]
DQ092770, Enterovirus, EV-F1 BEV-2 [BEV-261 RM2]
DQ092769, Enterovirus, EV-E1 BEV-1 [LC-R4]
AF363453, Enterovirus, EV-G1 [UKG/410/73]
AF201894, Enterovirus, EV-H1 [A-2 plaque virus]
L24917, Enterovirus, RV-A16 [11757]
EF186077, Enterovirus, RV-C3 [HRV-QPM]
K02121, Enterovirus, RV-B14 [1959]
KP233897, unassigned, rabovirus [Berlin/Jan2011/0572]
KJ950883, unassigned, rat picornavirus [rat/NYC-B10/USA/2010]
FR727144, unassigned, pigeon picornavirus B [pigeon/Norway/03/641/2003]
KC560801, unassigned, pigeon picornavirus B [GAL-7/2010/Hungary]
FR727145, unassigned, pigeon picornavirus A [pigeon/Norway/03/603-7/2003]
JN674502, unassigned, quail picornavirus 1 [quail/HUN/2010]
KT880670, unassigned, phacovirus [Pf-CHK1/PhV]
KP230449, unassigned, falcovirus [kestrel/VOVE0622/2013/HUN]
KJ641684, unassigned, bat picornavirus [BtRf-PicoV-2/YN2012]
KT452637, unassigned, rodent hepatovirus [RMU101637Micarv2010]
KT452641, unassigned, rodent hepatovirus [KS11510Myogla2011]
KT452644, unassigned, rodent hepatovirus []KS111230Crimig2011]
KT229612, unassigned, woodchuck hepatovirus [3ID]
KT229611, unassigned, woodchuck hepatovirus [2ID]
KT452685, unassigned, rodent hepatovirus [KEF121Sigmas2012]
M14707, Hepatovirus, Hepatovirus A1, hepatitis A virus [HM-175]
D00924, Hepatovirus, Hepatovirus A1, simian hepatitis A virus [AGM-27]
KT452658, unassigned, shrew hepatovirus [KS121232Sorara2012]
KT452661, unassigned, shrew hepatovirus [KS121289Sorara2012]
KT452695, unassigned, hedgehog hepatovirus [Igel75Erieur2014]
KT452698, unassigned, hedgehog hepatovirus [Igel68Erieur2014]
KT452691, unassigned, hedgehog hepatovirus [Igel8Erieur2014]
KT452714, unassigned, bat hepatovirus [M32Eidhel2010]
KT877158, unassigned, tupaia hepatovirus [TN1]
KT452730, unassigned, bat hepatovirus [BUO2BF86Colafr2010]
KT452729, unassigned, bat hepatovirus [FO1AF48Rhilan2010]
KR703607, unassigned, phopivirus [NewEngland/USA/2011]
KT452742, unassigned, bat hepatovirus [SMG18520Minmav2014]
KT452735, unassigned, rodent hepatovirus [CIV459Lopsik2004]
AJ225173, Tremovirus, Tremovirus A1, avian encephalomyelitis virus 1 [Calnek vaccine strain]
KF183915, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/1/MN/USA/2010]
KF183916, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/2/MN/USA/2010]
KF874490, Limnipivirus, Limnipivirus C1, fathead minnow picornavirus 1 [fhm/20/IL/USA/2010]
KF306267, Limnipivirus, Limnipivirus B1, carp picornavirus 1 [F37/06]
JX134222, Limnipivirus, Limnipivirus A1, bluegill picornavirus 1 [04-032]
KC843627, Potamipivirus, Potamipivirus A1, eel picornavirus 1 [F15/05]
KJ641698, unassigned, bat picornavirus [BtMf-PicoV-1/SAX2011]
AF327920, Parechovirus, Parechovirus B1, Ljungan virus 1 [87-012]
HF677705, unassigned, sebokele virus 1 [An/B/1227/d]
L02971, Parechovirus, Parechovirus A1, human parechovirus 1 [Harris]
KF006989, unassigned, ferret parechovirus [ferret/MpPeV1/NL]
JQ316470, Pasivirus, Pasivirus A1 [swine/France/2011]
AB937989, unassigned, crohivirus 1 [shrew/ZM54/Zambia/2012]
KC465954, Avisivirus, Avisivirus A1 [turkey/M176-TuASV/2011/HUN]
KC614703, Avisivirus, Avisivirus A1 [turkey/USA/IN1/2010]
KF979334, unassigned, chicken picornavirus 3 [45C]
KT880669, unassigned,chicken picornavirus [Pf-CHK1/AsV]
KF979333, unassigned, chicken picornavirus 2 [44C]
KJ000696, unassigned, aalivirus [duck/GL/12/China/2012]
KM203656, unassigned, orivirus 1 [chicken/Pf-CHK1/2013/HUN]
KT880667, unassigned, orivirus 2 [Pf-CHK1]
DQ249299, Avihepatovirus, Avihepatovirus A1, duck hepatitis A virus 1 [03D]
KC935379, Kunsagivirus, Kunsagivirus A1 [roller/SZAL6-KuV/2011/HUN]
unassigned, bat kunsagivirus
EU142040, Aquamavirus, Aquamavirus A1, seal picornavirus 1 [HO-02-21]
KP770140, unassigned, ampivirus [NEWT/2013/HUN]
0.5

Figure 3: Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, ***genus names***, *species names* and *types*. If available, common names and designations of isolates [in square brackets] are given. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,750,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

Table 1: Estimates of Evolutionary Divergence between P1 Sequences

```
Description
  Analysis
    Analysis ---------------------------- Distance Estimation
    Scope ------------------------------- Pairs of taxa
  Estimate Variance
    Variance Estimation Method ---------- None
  Substitution Model
    Substitutions Type ------------------ Amino acid
    Genetic Code Table ------------------ Standard
    Model/Method ------------------------ p-distance
    Substitutions to Include ------------ All
  Rates and Patterns
    Rates among Sites ------------------- Uniform rates
    Pattern among Lineages -------------- Same (Homogeneous)
  Data Subset to Use
    Gaps/Missing Data Treatment --------- Pairwise deletion
    Codons Included --------------------- 1st+2nd+3rd+Non-Coding
  No. of Sites : 1102
  d : Estimate

[ 1] JQ814851_MiV-A1 Mischivirus_A1
[ 2] KP054278_MiV-B2_Bat_picornavirus_strain_BatPV/V14/13/Hun
[ 3] KP054277_MiV-B1_Bat_picornavirus_strain_BatPV/V13/13/Hun
[ 4] KP054276_MiV-B1_Bat_picornavirus_strain_BatPV/V12/13/Hun
[ 5] KP054275_MiV-B1_Bat_picornavirus_strain_BatPV/V11/13/Hun
[ 6] KP054274_MiV-B1_Bat_picornavirus_strain_BatPV/V8/13/Hun
[ 7] KP054273_MiV-B1_Bat_picornavirus_strain_BatPV/V1/13/Hun
[ 8] KP100644_MiV-C1_African_bat_icavirus_A_isolate_TNo13

[ 9] DQ641257_SeV-A1_Senecavirus_SVV-001

[10] M81861_CaV-A1_EMCV-1_R
[11] M20562_CaV-B1_Cardio_TMEV_GDVII
[12] JQ864242_CaV-C1_Boone_cardiovirus_isolate_BCV-1
[13] JX683808_CaV-C2_Boone_cardiovirus_isolate_BCV-2

[14] FJ438902_CoSV-A1_0553
[15] FJ438907_CoSV-B1
[16] FJ438908_CoSV-D1
[17] FJ555055_CoSV-E1
[18] JN867758_CoSC_F1_PK5006

[19] X96870_ERAV_PERV
[20] X00871_FMDV_O1K
[21] EU236594_BRBV_EC11
[22] JN936206_BRAV_H-1
```

[	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22]
[1] MiV-A1	0.0000																					
[2] MiV-B2	0.2939	0.0000																				
[3] MiV-B1	0.2827	0.1481	0.0000																			
[4] MiV-B1	0.2802	0.1494	0.0037	0.0000																		
[5] MiV-B1	0.2814	0.1481	0.0025	0.0012	0.0000																	
[6] MiV-B1	0.2814	0.1481	0.0025	0.0012	0.0000	0.0000																
[7] MiV-B1	0.2814	0.1481	0.0037	0.0025	0.0012	0.0012	0.0000															
[8] MiV-C1	0.5643	0.5643	0.5554	0.5554	0.5554	0.5554	0.5554	0.0000														
[9] SeV-A1	0.6697	0.6654	0.6576	0.6589	0.6589	0.6589	0.6589	0.6594	0.0000													
[10] CaV-A1	0.6046	0.5951	0.5951	0.5939	0.5939	0.5939	0.5939	0.6269	0.6546	0.0000												
[11] CaV-B1	0.5952	0.6023	0.5934	0.5947	0.5947	0.5947	0.5947	0.6143	0.6489	0.3838	0.0000											
[12] CaV-C1	0.6256	0.6221	0.6221	0.6221	0.6221	0.6221	0.6221	0.6328	0.6641	0.5100	0.4919	0.0000										
[13] CaV-C2	0.6221	0.6145	0.6171	0.6171	0.6171	0.6171	0.6171	0.6252	0.6622	0.4928	0.4720	0.1383	0.0000									
[14] CoSV-A1	0.6568	0.6603	0.6538	0.6564	0.6564	0.6564	0.6564	0.6739	0.7059	0.6597	0.6491	0.6734	0.6658	0.0000								
[15] CoSV-B1	0.6505	0.6573	0.6586	0.6586	0.6586	0.6586	0.6586	0.6561	0.6970	0.6593	0.6537	0.6725	0.6570	0.4526	0.0000							
[16] CoSV-D1	0.6620	0.6531	0.6671	0.6645	0.6645	0.6645	0.6645	0.6772	0.7054	0.6630	0.6691	0.6705	0.6680	0.5331	0.5082	0.0000						
[17] CoSV-E1	0.6350	0.6500	0.6487	0.6487	0.6487	0.6487	0.6487	0.6586	0.7048	0.6605	0.6451	0.6734	0.6671	0.4728	0.4322	0.4895	0.0000					
[18] CoSV-F1	0.6628	0.6602	0.6576	0.6576	0.6576	0.6576	0.6576	0.6628	0.7003	0.6613	0.6561	0.6684	0.6547	0.4000	0.4212	0.5071	0.4776	0.0000				
[19] ERAV	0.6987	0.6960	0.6960	0.6946	0.6946	0.6946	0.6946	0.7074	0.7010	0.6871	0.6849	0.7141	0.7096	0.7305	0.7070	0.7318	0.7264	0.7236	0.0000			
[20] FMDV	0.7145	0.7006	0.7081	0.7111	0.7096	0.7096	0.7096	0.7263	0.7117	0.6984	0.6941	0.7143	0.7017	0.7325	0.7384	0.7434	0.7442	0.7314	0.6235	0.0000		
[21] BRBV	0.7260	0.7316	0.7161	0.7175	0.7175	0.7175	0.7175	0.7388	0.7346	0.7078	0.7000	0.7413	0.7336	0.7510	0.7500	0.7559	0.7358	0.7413	0.6198	0.5387	0.0000	
[22] BRAV	0.7446	0.7431	0.7302	0.7302	0.7302	0.7302	0.7302	0.7397	0.7413	0.7332	0.7279	0.7482	0.7423	0.7724	0.7555	0.7721	0.7734	0.7507	0.6556	0.5645	0.5471	0.0000

Table. Estimates of Evolutionary Divergence between Sequences
The number of amino acid differences per site from between sequences are shown. The analysis involved 22 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 1102 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

1. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739.

P1:				
	intra-typic	observed aa divergence: <1%	⇒	aa identity: >99%
	inter-typic (within species)	observed aa divergence: <15%	⇒	aa identity: >85%
	between species	observed aa divergence: 28-57%	⇒	aa identity: 43-72%
	between genera	observed aa divergence: >59%	⇒	aa identity: <41%

Table 2: Estimates of Evolutionary Divergence between 3CD Sequences

```
Description
  Analysis
    Analysis ---------------------------- Distance Estimation
    Scope ------------------------------- Pairs of taxa
  Estimate Variance
    Variance Estimation Method ---------- None
  Substitution Model
    Substitutions Type ------------------ Amino acid
    Genetic Code Table ------------------ Standard
    Model/Method ------------------------ p-distance
    Substitutions to Include ------------ All
  Rates and Patterns
    Rates among Sites ------------------- Uniform rates
    Pattern among Lineages -------------- Same (Homogeneous)
  Data Subset to Use
    Gaps/Missing Data Treatment --------- Pairwise deletion
    Codons Included --------------------- 1st+2nd+3rd+Non-Coding
  No. of Sites : 737
  d : Estimate

[ 1] JQ814851_MiV-A1_Mischivirus_A1_M._schreibersii_picornavirus_1_bat/China/2010
[ 2] KP054278_MiV-B2_Bat_picornavirus_strain_BatPV/V14/13/Hun
[ 3] KP054277_MiV-B1_Bat_picornavirus_strain_BatPV/V13/13/Hun
[ 4] KP054276_MiV-B1_Bat_picornavirus_strain_BatPV/V12/13/Hun
[ 5] KP054275_MiV-B1_Bat_picornavirus_strain_BatPV/V11/13/Hun
[ 6] KP054274_MiV-B1_Bat_picornavirus_strain_BatPV/V8/13/Hun
[ 7] KP054273_MiV-B1_Bat_picornavirus_strain_BatPV/V1/13/Hun
[ 8] KP100644_MiV-C1_African_bat_icavirus_A_isolate_TNo13

[ 9] DQ641257_SeV-A1_Senecavirus_A_SVV-1_cc/US/SVV-001

[10] M81861_CaV-A1_EMCV-R
[11] M20562_CaV-B1_TMEV_GDVII
[12] JQ864242_CaV-C1_Boone_cardiovirus_1_isolate_rat/USA/2010
[13] JX683808_CaV-C2_Boone_cardiovirus_2_isolate_rat/USA/2012

[14] FJ438908_CoSV-D1
[15] FJ555055_CoSV-E1
[16] FJ438907_CoSV-B1
[17] FJ438902_CoSV-A1
[18] JN867758_CoSV_F1_PK5006

[19] X96870_ERAV_PERV_P2P3
[20] X00871_FMDV_O1Kaufbeuren
[21] EU236594_BRBV_EC11
[22] JN936206_BRAV_H-1
```

[	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21]
[1] MiV-A1	0.0000																				
[2] MiV-B2	0.2018	0.0000																			
[3] MiV-B1	0.2018	0.0000	0.0000																		
[4] MiV-B1	0.2018	0.0015	0.0015	0.0000																	
[5] MiV-B1	0.2018	0.0029	0.0029	0.0044	0.0000																
[6] MiV-B1	0.2018	0.0000	0.0000	0.0015	0.0029	0.0000															
[7] MiV-B1	0.2047	0.0058	0.0058	0.0058	0.0088	0.0058	0.0000														
[8] MiV-C1	0.4527	0.4556	0.4556	0.4556	0.4556	0.4556	0.4571	0.0000													
[9] SeV-A1	0.5149	0.5134	0.5134	0.5134	0.5119	0.5134	0.5149	0.5419	0.0000												
[10] CaV-A1	0.5060	0.5227	0.5227	0.5227	0.5196	0.5227	0.5227	0.5121	0.4871	0.0000											
[11] CaV-B1	0.5382	0.5277	0.5277	0.5277	0.5277	0.5277	0.5262	0.5519	0.4910	0.4030	0.0000										
[12] CaV-C1	0.5388	0.5358	0.5358	0.5358	0.5388	0.5358	0.5358	0.5584	0.5150	0.4496	0.4687	0.0000									
[13] CoSV-D1	0.6006	0.6021	0.6021	0.6021	0.6021	0.6021	0.6021	0.6106	0.5927	0.5997	0.6088	0.6076	0.0000								
[14] CoSV-E1	0.6188	0.6233	0.6233	0.6233	0.6248	0.6233	0.6233	0.6288	0.6049	0.6074	0.6149	0.6121	0.2241	0.0000							
[15] CoSV-B1	0.6106	0.6242	0.6242	0.6242	0.6242	0.6242	0.6242	0.6191	0.6073	0.6037	0.6174	0.6191	0.3148	0.3343	0.0000						
[16] CoSV-A1	0.6067	0.6021	0.6021	0.6021	0.6036	0.6021	0.6021	0.6152	0.5866	0.5951	0.5921	0.5909	0.3368	0.3444	0.3042	0.0000					
[17] CoSV-F1	0.6036	0.6067	0.6067	0.6067	0.6082	0.6067	0.6067	0.6242	0.6064	0.6150	0.6088	0.6061	0.3614	0.3705	0.3605	0.3308	0.0000				
[18] ERAV	0.6261	0.6261	0.6261	0.6261	0.6246	0.6261	0.6246	0.6021	0.6073	0.6108	0.6031	0.5897	0.6235	0.6159	0.6290	0.6265	0.6260	0.0000			
[19] FMDV	0.6617	0.6662	0.6662	0.6662	0.6662	0.6662	0.6647	0.6547	0.6201	0.6313	0.6611	0.6357	0.6329	0.6360	0.6233	0.6284	0.6314	0.5314	0.0000		
[20] BRBV	0.6431	0.6566	0.6566	0.6566	0.6581	0.6566	0.6581	0.6375	0.6103	0.6143	0.6430	0.6265	0.6242	0.6242	0.6267	0.6273	0.6273	0.5452	0.3985	0.0000	
[21] BRAV	0.6447	0.6552	0.6552	0.6552	0.6567	0.6552	0.6537	0.6406	0.6346	0.6449	0.6506	0.6462	0.6375	0.6390	0.6445	0.6420	0.6526	0.5602	0.4174	0.4125	0.0000

Table. Estimates of Evolutionary Divergence between Sequences
The number of amino acid differences per site from between sequences are shown. The analysis involved 22 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 737 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

1. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739.

3CD:	intra-typic	observed aa divergence: <1%	⇒	aa identity: >99%
	inter-typic (within species)	observed aa divergence: <1%	⇒	aa identity: >99%
	between species	observed aa divergence: 20-46%	⇒	aa identity: >54%
	between genera	observed aa divergence: >51-66%	⇒	aa identity: <34%