



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:	2016.008a-dS	(to be completed by ICTV officers)
Short title: Create 1 new species (<i>Harkavirus A</i>) in a new genus (<i>Harkavirus</i>) (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	2 <input checked="" type="checkbox"/> 3 <input checked="" type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/> 11 <input checked="" type="checkbox"/>	

Author(s):

Roland Zell, Eric Delwart, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, Mark A. Pallansch, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Glyn Stanway and Teruo Yamashita

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):

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	2016.008aS	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Harkavirus</i> (new)	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.
Subfamily:		
Family:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Harkavirus A</i>	Falcovirus [kestrel/VOVE0622/2013/HUN]	KP230449

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

A novel picornavirus was detected in a faecal sample from a 5-week-old common kestrel (*Falco tinnunculus*) in Hungary. This virus has a 4-3-4 genome layout (compare Appendix Figure 1):

VPg+5'UTR^{IRES-I}[1A-1B-1C-1D/2A-2B-2C^{Hel}/3A-3B^{VPg}-3C^{Pro}-3D^{Pol}]3'UTR-poly(A)

Comparison of P1 and 3CD alignments reveals a highly divergent virus (compare Table 1, below).

Table 1: *Harkavirus* divergence in picornavirus sequence alignments

	p-Distance (mean±std.dev.)	mean % aai
P1	0.8721±0.013	12.79
3CD	0.7808±0.018	21.92
Proteins 2A, 2B, 3A, 3B exhibit no similarity to known picornavirus proteins.		

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2016.008bS	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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
Family:	Picornaviridae	
Order:	Picornavirales	

naming a new genus

Code	2016.008cS	(assigned by ICTV officers)
To name the new genus: <i>Harkavirus</i>		

Assigning the type species and other species to a new genus

Code	2016.008dS	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Harkavirus A</i>		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 11

<p><i>Harkavirus</i> is a highly divergent picornavirus with very low amino acid identities to the remaining picornaviruses. Its 1C protein has greatest similarity to the VP3 capsid protein of dicistroviruses! 1B, 1D and 2C have similarity to the respective hepatovirus proteins and 3C^{Pro} shows similarity to the kobuvirus proteinase. Part of the <i>Harkavirus</i> 3D^{Pol} exhibits similarity with the enterovirus polymerase. In addition, 3D^{Pol} has an unusual insertion of ~120 amino acids. The other proteins (1A, 2A, 2B, 3A, 3B) have no significant similarity to picornavirus proteins. <i>Harkavirus</i> has a variant type I IRES which is typical of <i>Enterovirus</i>. No virus isolate is available.</p>

Origin of the new genus name:

Harkavirus: from Harkakötöny (a village in Hungary where the first sample was collected)
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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 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Boros A, Pankovics P, Simmonds P, Pollak E, Matics R, Phan TG, Delwart E, Reuter G.
2015. Genome analysis of a novel, highly divergent picornavirus from common kestrel
(*Falco tinnunculus*): The first non-enteroviral picornavirus with type-I-like IRES. Inf.
Genet. Evol. 32:425-431.

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 *Harkavirus A* [kestrel/VOVE0622/2013/HUN], GenBank acc. no. KP230449

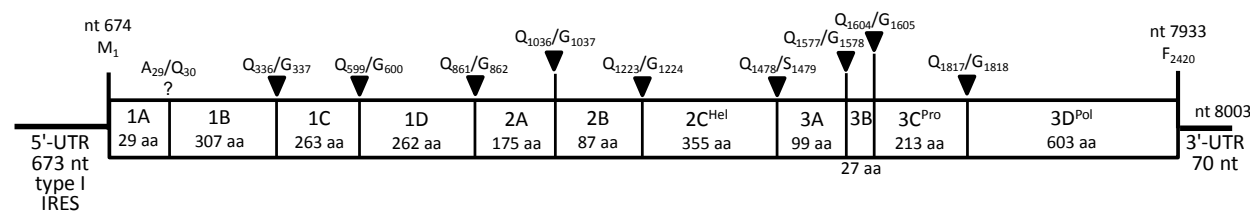


Figure 1: Schematic depiction of the harkavirus genome organization. The open reading frame is indicated by a box. Positions of putative amino acid cleavage sites and the lengths of the deduced proteins are shown as proposed by Boros et al. (2015). Triangles (▼) indicate the putative 3C^{Pro} cleavage sites, and a question mark (?) points to the unknown 1AB processing site.

Fig. 2
P1

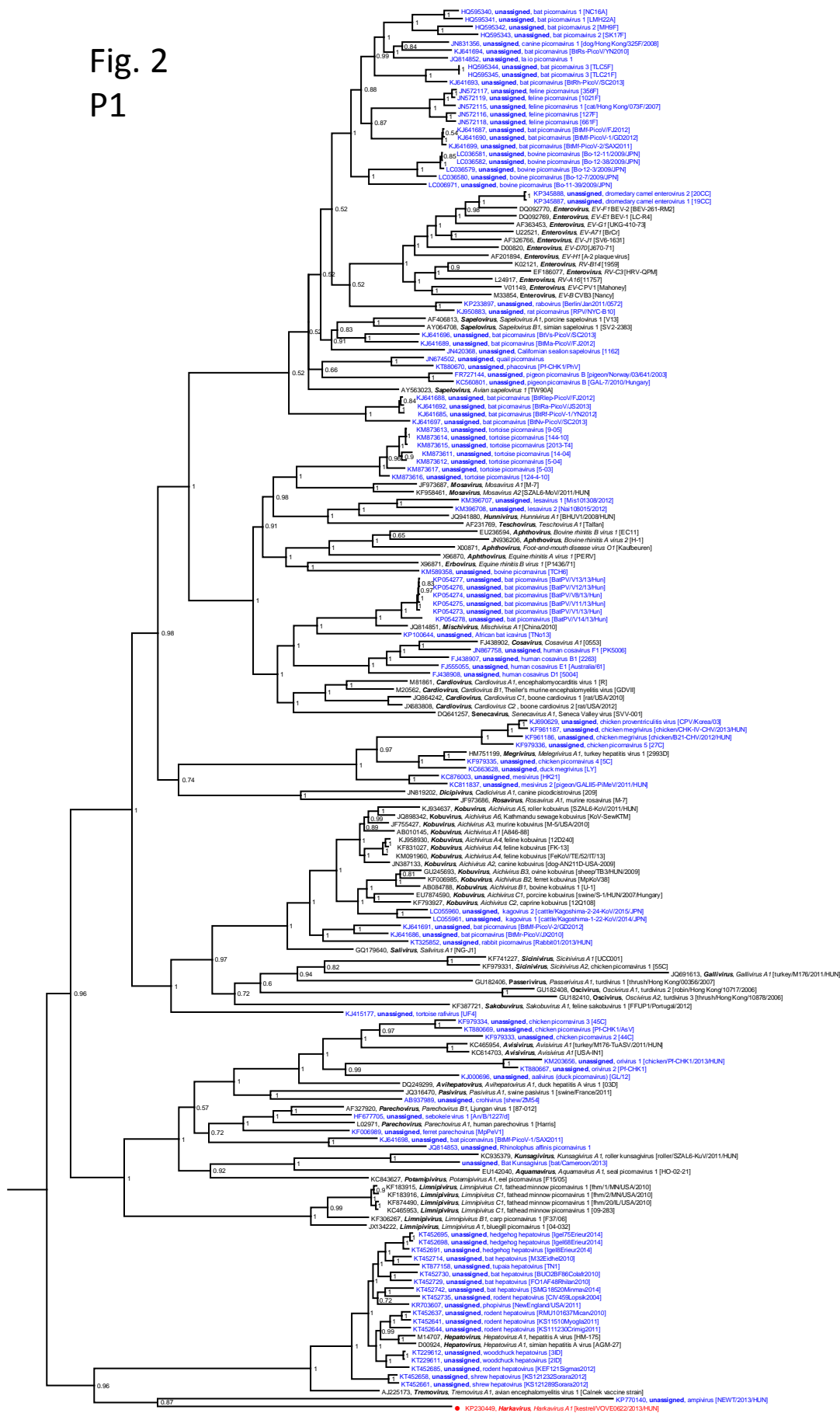


Figure 2 (previous page): Phylogenetic analyses of picornavirus P1 using maximum likelihood tree inference (MEGA5.2). 178 picornavirus sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations 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 bootstrap values obtained after 200 replications. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

Fig. 3
3CD

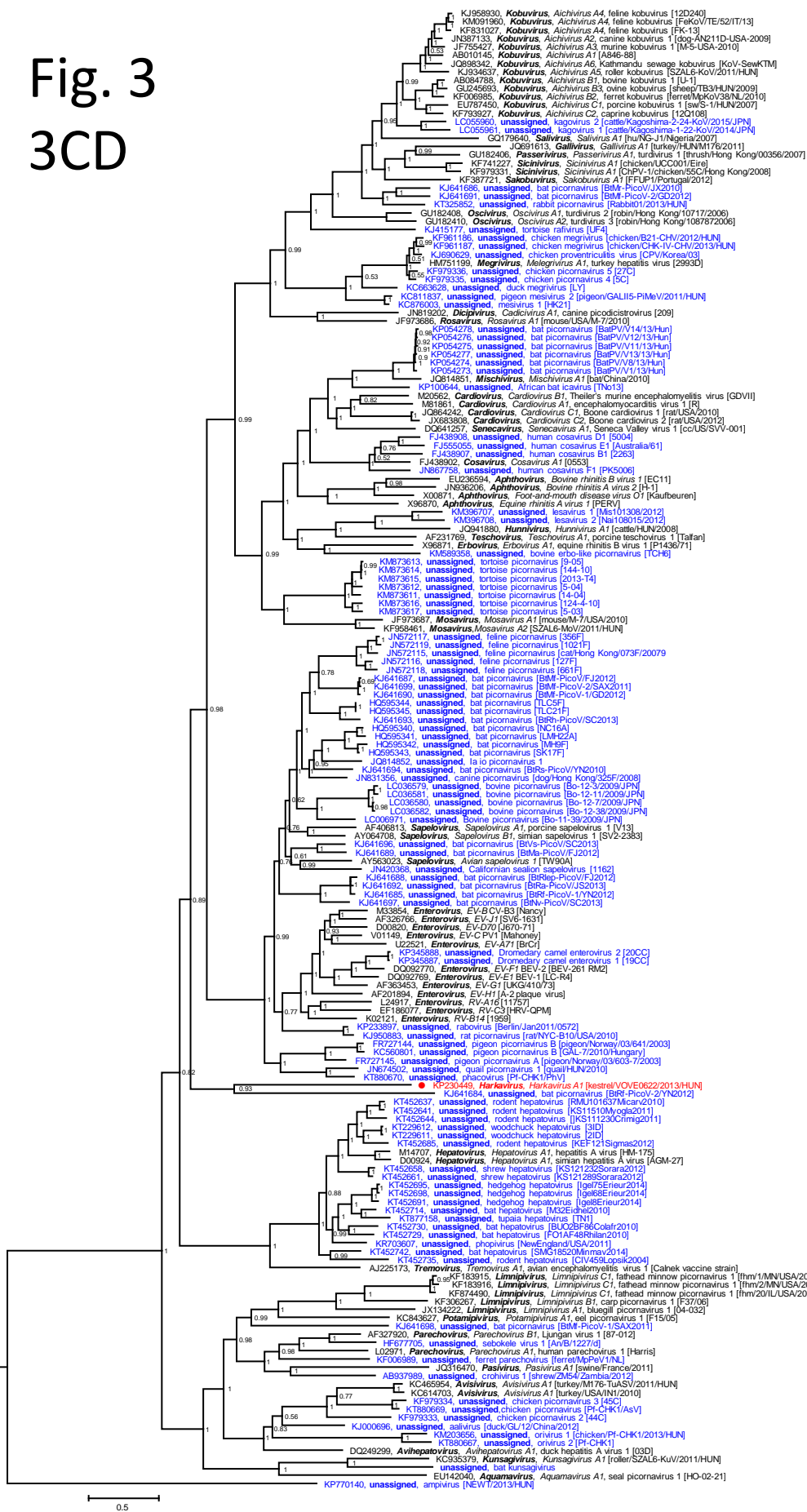


Figure 3 (previous page): Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of 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.
