



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:	2016.015a-dS	(to be completed by ICTV officers)
Short title: Create 1 new species (<i>Rabovirus A</i>) in a new genus (<i>Rabovirus</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	2016.015aS	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Rabovirus</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>Rabovirus A</i>	Rabovirus [Berlin/Jan2011/0572]	KP233897

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 picornaviruses were detected in faecal samples from Norway rats (*Rattus norvegicus*) in USA and Germany. Sequences of two raboviruses are known (KP233897, KJ950883); the amino acid identity of the P1 genome region of these two viruses is ~86.2%; distinction of 2 types when applying the 25% nt divergence/12% aa divergence rule (compare Table 1; Appendix).

Typical L-4-3-4 picornavirus genome layout (compare Figure 1, Appendix):

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

Amino acid identities from raboviruses (compare Tables 1, 2; Appendix):

	<i>Enterovirus</i>	<i>Sapelovirus</i>
P1	34-40%	39-41%
3CD	46-54%	51-53%

MODULE 3: NEW GENUS

creating a new genus

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

Code	2016.015bS	(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	2016.015cS	(assigned by ICTV officers)
To name the new genus: <i>Rabovirus</i>		

Assigning the type species and other species to a new genus

Code	2016.015dS	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Rabovirus 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

Although raboviruses are closely related to *Enterovirus* and *Sapelovirus* (compare Figures 2, 3; Appendix), they exhibit significant distinctive features:

- (i) a type II IRES which is uncommon in *Enterovirus* (type I IRES) and *Sapelovirus* (type IV IRES),
- (ii) a unique L protein,

Origin of the new genus name:

Rabovirus: from rat-borne picornavirus

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:

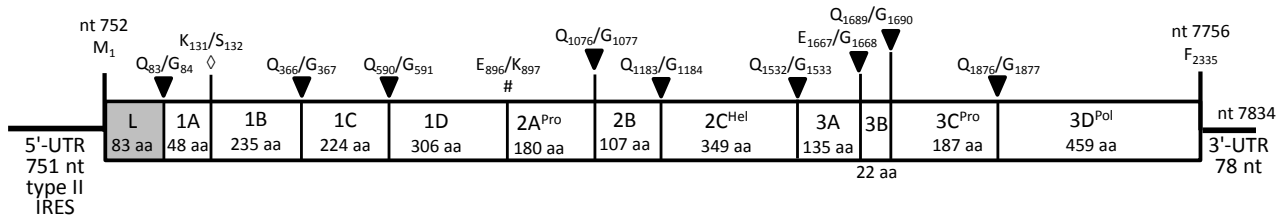
- Ng TF, Sachsenröder J, Reuter G, Knowles NJ, Delwart E, Johne R. 2015. *Rabovirus*: a proposed new picornavirus genus that is phylogenetically basal to enteroviruses and sapeloviruses. Arch. Virol. 160:2569-2575.
- Firth C, Bhat M, Firth MA, Williams SH, Frye MJ, Simmonds P, Conte JM, Ng J, Garcia J, Bhuvu NP, Lee B, Che X, Quan PL, Lipkin WI. 2014. Detection of zoonotic pathogens and characterization of novel viruses carried by commensal *Rattus norvegicus* in New York City. mBio 5(5):e01933-14.

Annex:

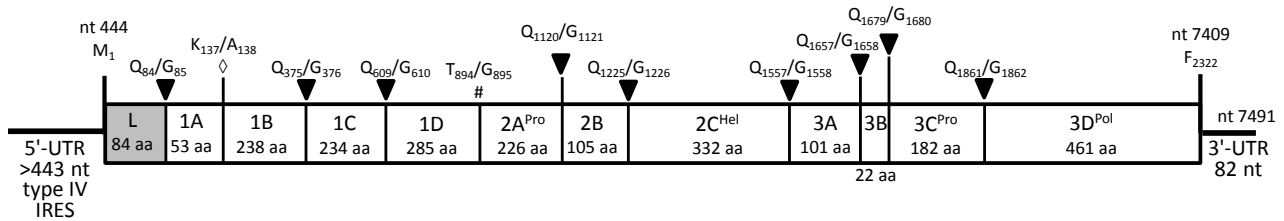
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate 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: *Rabovirus A1* [Berlin/Jan2010/0572], GenBank acc. no. KP233897



Sapelovirus A1, porcine sapelovirus [V13], GenBank acc. no. AF406813



Enterovirus C, poliovirus 1 [Mahoney], GenBank acc. no. V01149

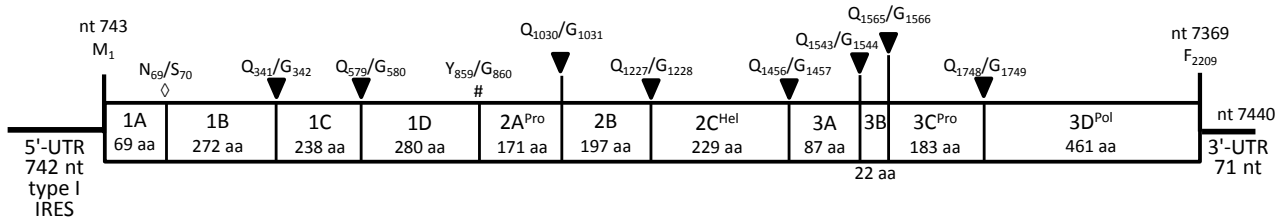


Figure 1: Comparison of the *Rabovirus* (top), *Sapelovirus* (middle) and *Enterovirus* (below) genome organization (schematic depiction). The open reading frames are indicated by boxes. Positions of putative amino acid cleavage sites and the lengths of the deduced proteins are shown as proposed by Ng et al. (2015). Triangles (▼) indicate the putative 3C^{Pro} cleavage sites, hash tags (#) the 2C^{Pro} processing sites and diamonds (◇) the 1AB processing sites. The L-encoding genome regions of rabovirus and sapelovirus which lack significant sequence homology are shaded.

Fig. 2
P1

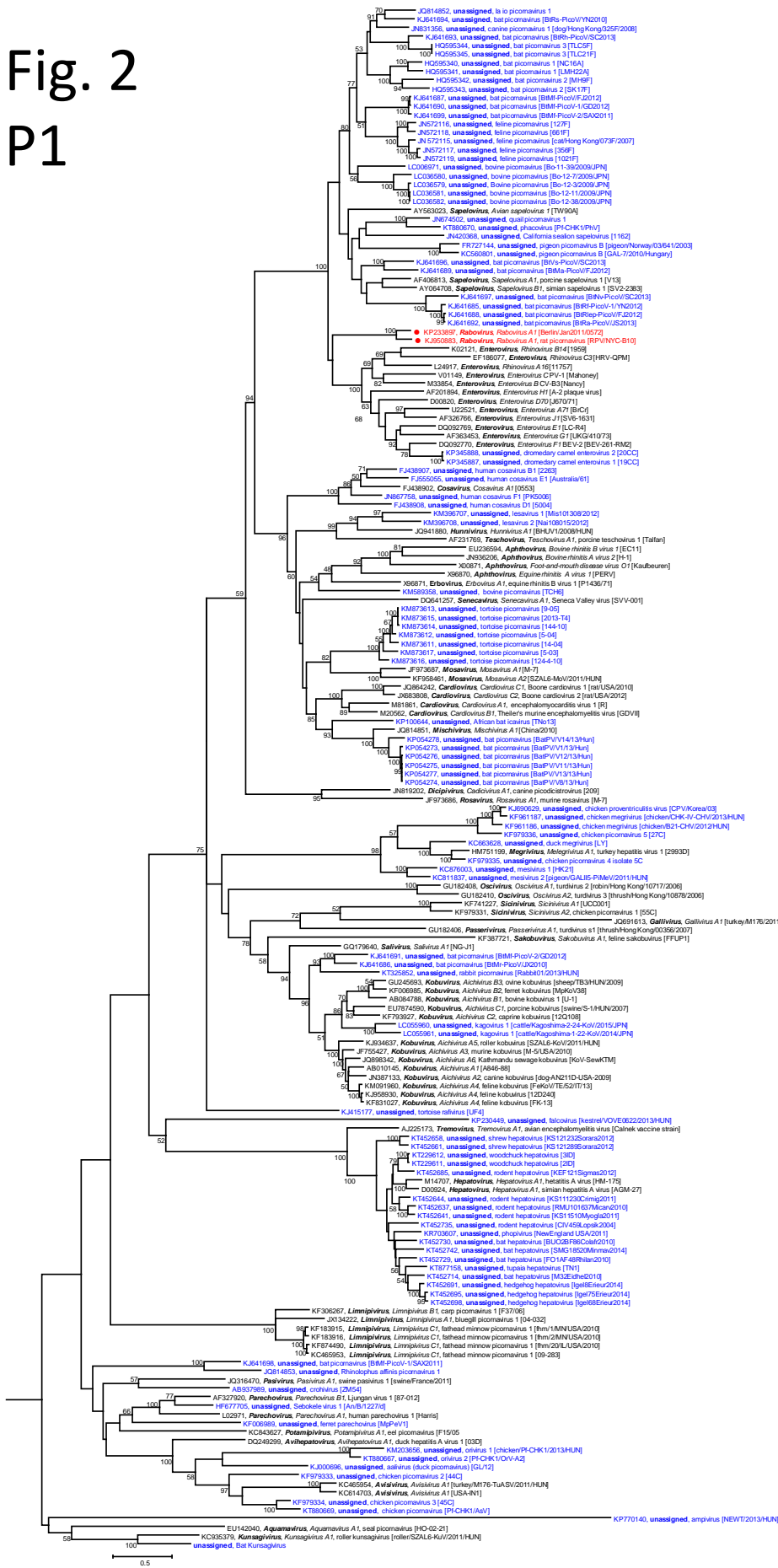


Figure 2 (previous page): Phylogenetic analyses of picornavirus P1 using maximum likelihood tree inference (MEGA5.2). 178 picornavirus sequences were retrieved from GenBank. Presented are GenBank accession numbers, ***genus names***, *species names* and *types*. If available, common names and designations 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

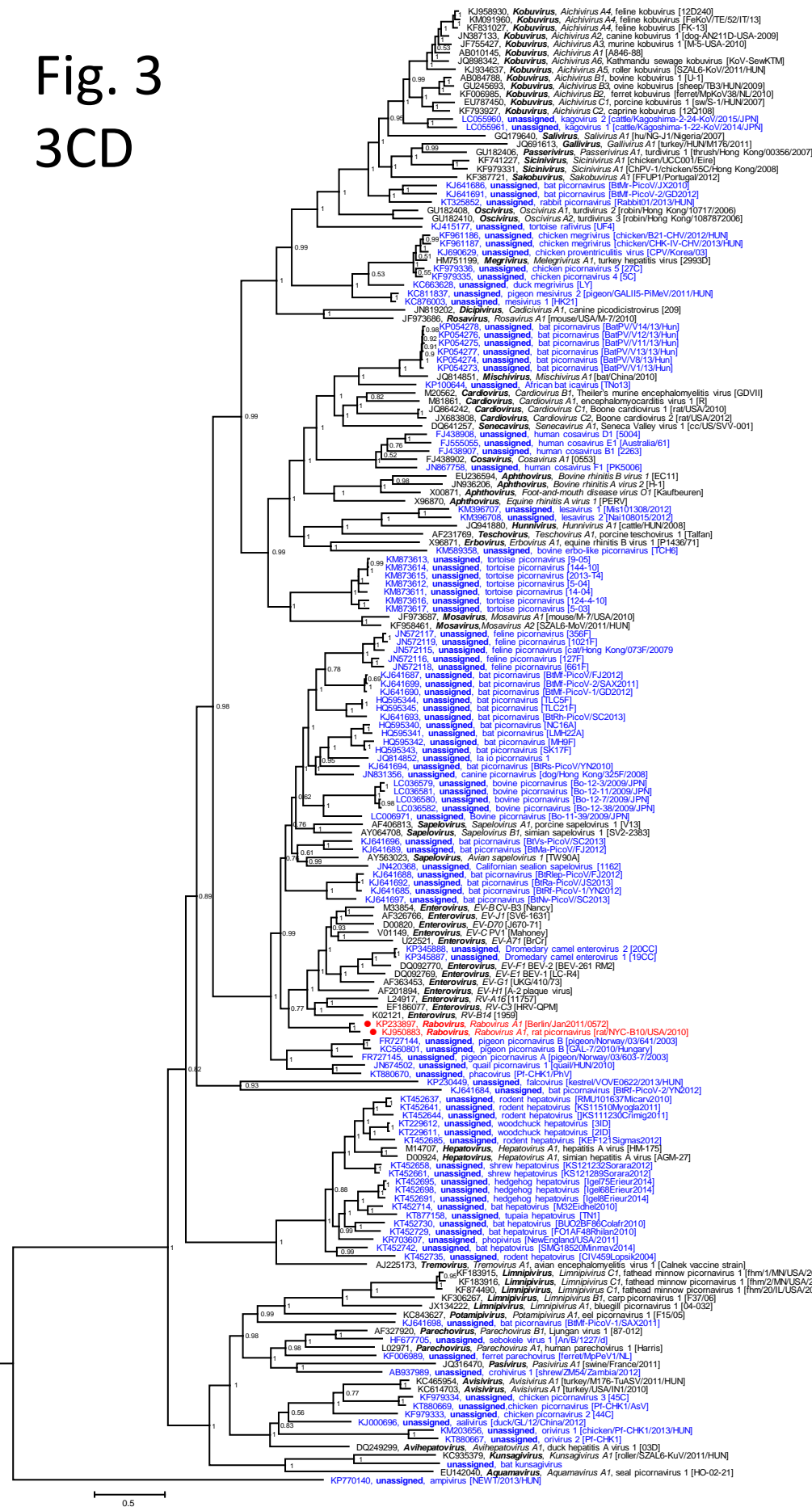


Figure 3 (previous page): Phylogenetic analyses of picornavirus 3CD gene regions using Bayesian tree inference (MrBayes 3.2). 178 sequences were retrieved from GenBank. Presented are GenBank accession numbers, *genus names*, *species names* and *types*. If available, common names and designations of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

Table 1: Estimates of Evolutionary Divergence between P1 Sequences

```
[ 1] #KP233897_Rabovirus_A_isolate_Berlin/Jan2011/0572
[ 2] #KJ950883_Rat_picornavirus_isolate_RPV/NYC-B10
[ 3] #U22521_Enterovirus_A_EV-71-BrCr
[ 4] #M33854_Enterovirus_B_CVB3-Nancy
[ 5] #V01149_Enterovirus_C_PV1-Mahoney
[ 6] #D00820_Enterovirus_D_EV-70-J670-7
[ 7] #DQ092769_EV-E_BEV-1_LC-R4
[ 8] #DQ092770_EV-F_BEV-2_BEV-261_RM2
[ 9] #AF363453_EV-G_PEV-9_UKG-410-73
[10] #AF201894_EV-H_A-2_plaque
[11] #AF326766_EV-J_SV6-1631
[12] #KP345888_"EV-K"_Dromedary_camel_enterovirus_20CC
[13] #KP345887_"EV-K"_Dromedary_camel_enterovirus_19CC
[14] #L24917_Enterovirus_A_HRV-16-11757
[15] #K02121_Enterovirus_B_HRV-14-1959
[16] #EF186077_Enterovirus_C_HRV-QPM
[17] #AF406813_Sapelovirus_A_PSV-1_V13
[18] #AY064708_Sapelovirus_B_SSV-1_SV2-2383
[19] #AY563023_Avian_Sapelovirus_ASV-1_TW90A
```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19]
[1]	0.0000																		
[2]	0.1421	0.0000																	
[3]	0.6399	0.6532	0.0000																
[4]	0.6343	0.6415	0.5508	0.0000															
[5]	0.6345	0.6540	0.5689	0.4762	0.0000														
[6]	0.6359	0.6425	0.5089	0.5387	0.5602	0.0000													
[7]	0.6201	0.6295	0.4958	0.5453	0.5614	0.4940	0.0000												
[8]	0.6116	0.6078	0.4921	0.5121	0.5280	0.4742	0.3409	0.0000											
[9]	0.6470	0.6511	0.4892	0.5453	0.5783	0.5168	0.3986	0.3973	0.0000										
[10]	0.6008	0.6245	0.5178	0.5234	0.5221	0.5287	0.5181	0.4837	0.5060	0.0000									
[11]	0.6213	0.6375	0.4463	0.5319	0.5624	0.4785	0.4562	0.4401	0.4820	0.4827	0.0000								
[12]	0.5992	0.6167	0.4722	0.5223	0.5401	0.4754	0.3574	0.2857	0.4046	0.4976	0.4274	0.0000							
[13]	0.6005	0.6167	0.4734	0.5235	0.5401	0.4766	0.3574	0.2869	0.4022	0.4988	0.4286	0.0096	0.0000						
[14]	0.6479	0.6572	0.5759	0.5239	0.5292	0.5585	0.5425	0.5366	0.5605	0.5447	0.5749	0.5341	0.5366	0.0000					
[15]	0.6441	0.6611	0.5695	0.5339	0.5343	0.5626	0.5605	0.5371	0.5569	0.5778	0.5680	0.5445	0.5445	0.4929	0.0000				
[16]	0.6371	0.6509	0.5864	0.5497	0.5662	0.5809	0.5866	0.5673	0.5896	0.5741	0.5886	0.5680	0.5680	0.5030	0.5345	0.0000			
[17]	0.5863	0.5954	0.6430	0.6381	0.6663	0.6431	0.6502	0.6373	0.6523	0.6540	0.6491	0.6450	0.6450	0.6612	0.6662	0.6532	0.0000		
[18]	0.5961	0.5946	0.6401	0.6237	0.6584	0.6477	0.6434	0.6407	0.6418	0.6472	0.6461	0.6343	0.6355	0.6562	0.6671	0.6632	0.3870	0.0000	
[19]	0.6024	0.6098	0.6593	0.6629	0.6575	0.6550	0.6360	0.6349	0.6583	0.6344	0.6450	0.6382	0.6382	0.6667	0.6771	0.7045	0.5670	0.5551	0.0000

P1: intra-typic -
inter-typic (within species) observed rabovirus aa divergence: <15% ⇒ aa identity: >85%
between species only 1 rabovirus species
between genera observed aa divergence from rabovirus: >58% ⇒ aa identity: <42%

Table 2: Estimates of Evolutionary Divergence between 3CD Sequences

```
[ 1] #KP233897_Rabovirus_A_isolate_Berlin/Jan2011/0572
[ 2] #KJ950883_Rat_picornavirus_isolate_RV-A_rat/NYC-B10/USA/2010
[ 3] #U22521_EV-A71_BrCr
[ 4] #M33854_EV-B_CV-B3_Nancy
[ 5] #V01149_EV-C_PV1_Mahoney
[ 6] #D00820_EV-D70_J670-71
[ 7] #DQ092769_EV-E1_BEV-1_LC-R4
[ 8] #DQ092770_EV-F1_BEV-2_BEV-261_RM2
[ 9] #AF363453_EV-G1_PEV-9_UKG/410/73
[10] #AF201894_EV-H1_SEV-A1_A-2_plaque
[11] #AF326766_EV-J1_SV6-1631
[12] #KP345887_Dromedary_camel_enterovirus_strain_19CC
[13] #KP345888_Dromedary_camel_enterovirus_strain_20CC
[14] #L24917_RV-A_HRV-16_strain_11757
[15] #K02121_RV-B_HRV-14_strain_1959
[16] #EF186077_RV-C_strain_HRV-QPM
[17] #AF406813_Sapelovirus_A_PSV-1_PEV8-V13
[18] #AY064708_Sapelovirus_B_SSV-1_SV2-2383
[19] #AY563023_Sapelovirus_ASV-1_TW90A
```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19]
[1]	0.0000																		
[2]	0.0217	0.0000																	
[3]	0.4969	0.4966	0.0000																
[4]	0.4859	0.4847	0.3798	0.0000															
[5]	0.4984	0.4983	0.3649	0.2950	0.0000														
[6]	0.4763	0.4846	0.3922	0.2703	0.2844	0.0000													
[7]	0.5078	0.5102	0.3975	0.3276	0.3463	0.3703	0.0000												
[8]	0.4953	0.4966	0.4006	0.3307	0.3354	0.3563	0.1894	0.0000											
[9]	0.4906	0.5017	0.3866	0.3276	0.3214	0.3531	0.2748	0.2702	0.0000										
[10]	0.5173	0.5204	0.4299	0.3567	0.3583	0.3699	0.3847	0.3692	0.3816	0.0000									
[11]	0.4592	0.4644	0.3457	0.1984	0.2826	0.2891	0.3323	0.3168	0.3292	0.3411	0.0000								
[12]	0.4906	0.4949	0.4053	0.3214	0.3385	0.3531	0.1910	0.1025	0.2640	0.3676	0.3106	0.0000							
[13]	0.4897	0.4940	0.4069	0.3239	0.3365	0.3528	0.1972	0.1049	0.2645	0.3689	0.3099	0.0125	0.0000						
[14]	0.5071	0.4992	0.4798	0.4486	0.4735	0.4514	0.4564	0.4579	0.4564	0.4625	0.4315	0.4626	0.4631	0.0000					
[15]	0.5118	0.5195	0.4252	0.3816	0.4065	0.4060	0.4346	0.4174	0.4003	0.4313	0.3879	0.4206	0.4239	0.4602	0.0000				
[16]	0.5338	0.5331	0.4766	0.4486	0.4424	0.4404	0.4455	0.4611	0.4408	0.4625	0.4393	0.4502	0.4490	0.4346	0.4321	0.0000			
[17]	0.4858	0.4915	0.4945	0.4679	0.4796	0.4637	0.4969	0.4765	0.4734	0.4858	0.4413	0.4765	0.4724	0.4906	0.4733	0.5079	0.0000		
[18]	0.4703	0.4747	0.4938	0.4674	0.4837	0.4648	0.4930	0.4666	0.4603	0.4977	0.4581	0.4728	0.4702	0.4961	0.5008	0.5039	0.3484	0.0000	
[19]	0.4725	0.4737	0.5102	0.5023	0.5047	0.5079	0.4953	0.5016	0.5016	0.5063	0.4883	0.4984	0.5008	0.5063	0.5142	0.5299	0.4649	0.4090	0.0000

3CD: intra-typic -
inter-typic (within species) observed rabovirus aa divergence: <3% ⇒ aa identity: >97%
between species only 1 rabovirus species
between genera observed aa divergence from rabovirus: 47-54% ⇒ aa identity: 46-53%