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:	***2011.021a-dV***	(to be completed by ICTV officers)

Short title: create genus named *Salivirus* in the family *Picornaviridae*, order *Picornavirales*
(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:

Eric Delwart (delwarte@medicine.ucsf.edu), Linlin Li (linlinli99013@gmail.com), Nick Knowles (nick.knowles@iah.ac.uk)

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:
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		(assigned by ICTV officers)

To create one new species within:

Genus:	***Salivirus*** (new)
Subfamily:	n/a
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:**
Salivirus A	GQ179640, GQ507022, GQ184145, GQ253930, GU245894

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

The salivirus genome (NG-J1) has an organization typical of picornaviruses. It is 7,124 bp in length with a GC content of 57%, excluding the poly(A) tail. Variant NG-J1 contained a large open reading frame of 7,125 bp encoding a putative polyprotein precursor of 2,374 amino acids (aa), a 5´ untranslated region (UTR) of 709 bp, and a 3´ UTR of 148 bp.

Comparison of NG-J1 with all known picornaviruses showed it was most closely related to Aichi virus (genus *Kobuvirus*), with average amino acid similarities of 42.6%, 35.2%, and 44.6% for the P1, P2, and P3 regions, respectively (Table S1).

Phylogenetic analysis based on the P1 and 3CD products using the maximum likelihood method with the amino acid Tamura-Nei model and 1,000 bootstrap replications also showed that salivirus NG-J1 was most closely related to the kobuviruses as a deep-rooted lineage (Figs. 1 and 2).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code		(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***n/a***
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		(assigned by ICTV officers)

To name the new genus: *Salivirus*

Assigning the type species and other species to a new genus

Code		(assigned by ICTV officers)

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

Salivirus 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

Comparison of salivirus NG-J1 with the kobuviruses showed it was most closely related to Aichi virus, with amino acid identities of 42.6%, 35.2%, and 44.6% for the P1, P2, and P3 regions, respectively (Table S1).

According to the *Picornaviridae* Study Group (http://www.picornastudygroup.com/definitions/genus_definition.htm), the members of a picornavirus genus should share>40%, >40%, and >50% amino acid similarities in their P1, P2, and P3 regions, respectively. Salivirus is therefore at the borderline between a new genus and a highly divergent species in the kobuvirus family.

We believe new genus is warranted based on genetic distance criteria as well as difference in the 2A protein which unlike all the kobuviruses (including Aichi virus) does not contain the HBoX/NC domain. The salivirus 2A protein also shows no related protein in Genbank using BLASTx. Based on the detection of H, C, and D catalytic triad residues at approximately the same 2A location as in rhinoviruses and enteroviruses, we postulate that the salivirus 2A protein is a trypsin-like protease.

Origin of the new genus name:

Salivirus from Stool Aichi-like virus

Reasons to justify the choice of type species:

Salivirus NG-J1 was the first member of this group of virus whose sequence was released in GenBank (submitted May 20, 2009). Online version of manuscript describing virus was released Sept 16, 2009. Closely related viruses have also been reported as Klassevirus.

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 one species so far based on available sequence data based on enterovirus species criteria.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Li, L., Victoria, J., Kapoor, A., Blinkova, O., Wang, C., Babrzadeh, F., Mason, C., Pandey, P., Triki, H., Bahri, O., Oderinde, BS., Baba, M.M., Bukbuk, D.N., Besser, J.M., Bartkus, J.M., Delwart, E. A novel picornavirus associated with gastroenteritis. Journal of Virology 2009 doi:10.1128/JVI.01241-09

2. Greninger, A. L., C. Runckel, C. Y. Chiu, T. Haggerty, J. Parsonnet, D. Ganem, and J. L. Derisi. 2009. The complete genome of klassevirus—a novel picornavirus in pediatric stool. Virol. J. 6:82.

3. Holtz, L. R., S. R. Finkbeiner, G. Zhao, C. D. Kirkwood, R. Girones, J. M. Pipas, and D. Wang. 2009. Klassevirus 1, a previously undescribed member of the family Picornaviridae, is globally widespread. Virol. J. 6:86.

4. Shan, T., Wang, C., Cui, L., Yu, Y., Delwart, E., Zhao, W., Zhu, C., Lan, D., Dai, X. and Hua, X. (2010). Picornavirus salivirus/klassevirus in children with diarrhea, China. Emerg. Infect. Dis. 16: 1303-1305.

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.

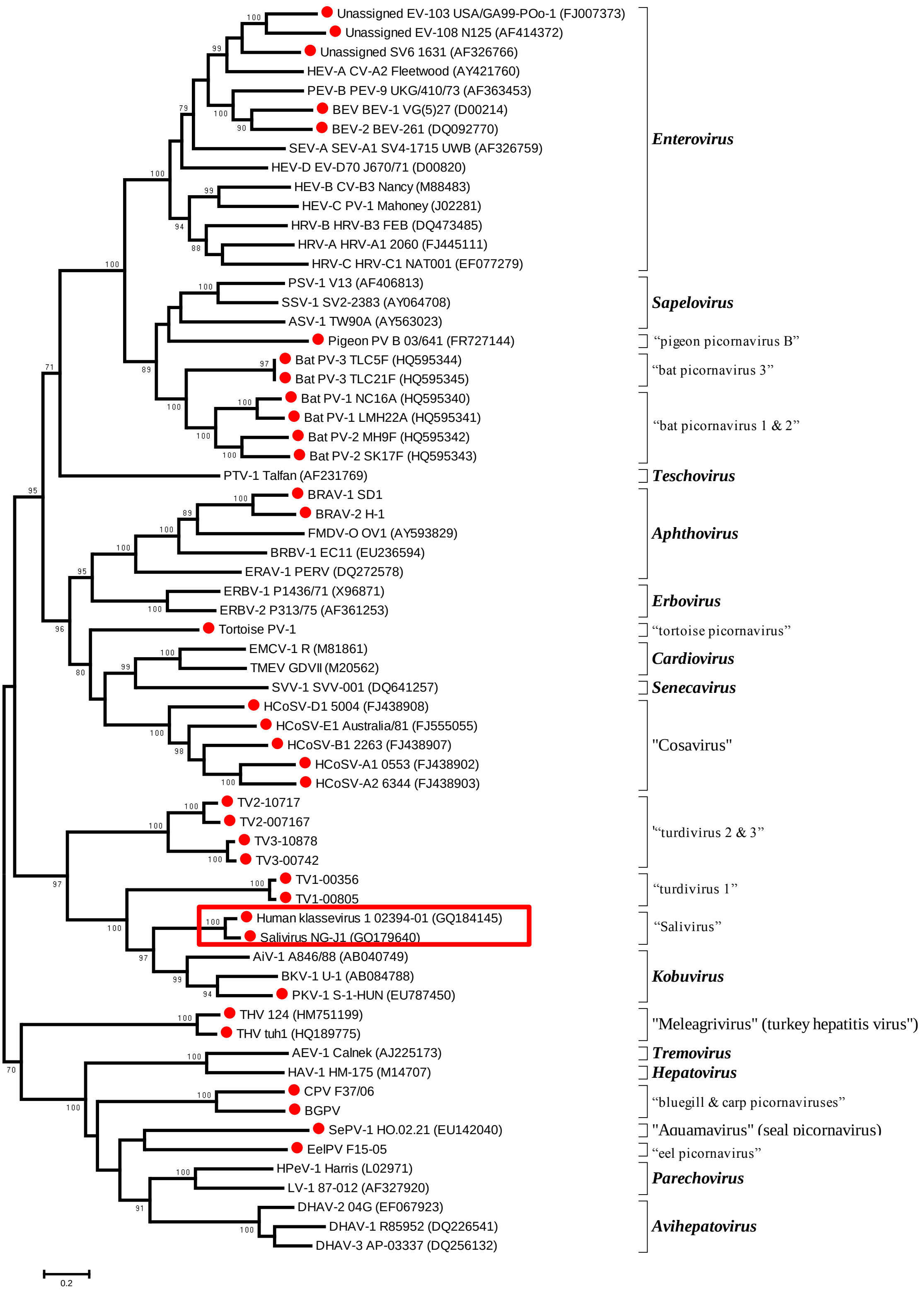

Fig. 1. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

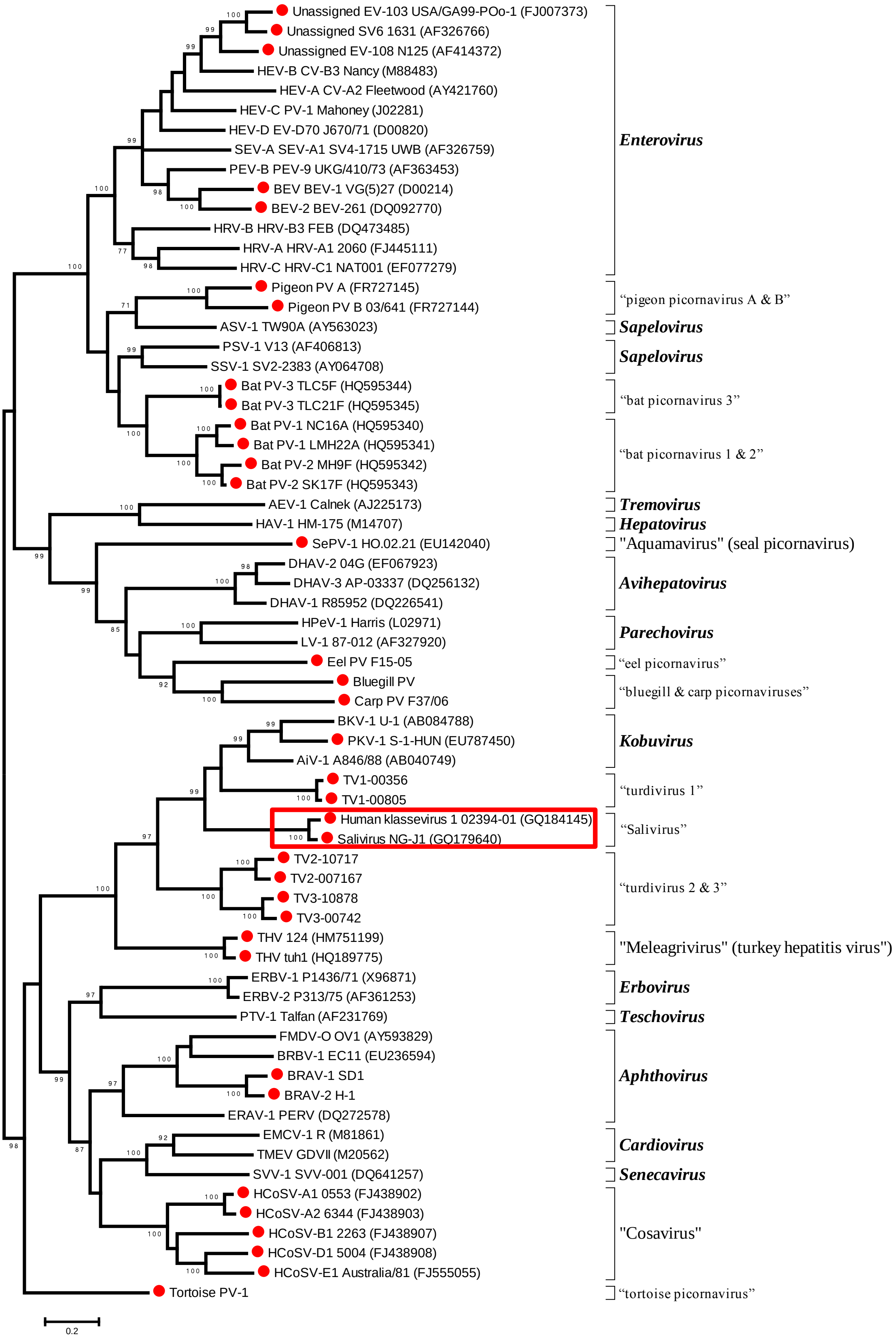

Fig. 2. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

Table S1. Amino acid identity of P1, P2 and P3 region for Salivirus with Klassevirus and kobuviruses

P1 similarity (%)	Salivirus GQ179640	Klassevirus GQ184145	Aichi virus AB010145	Aichi virus DQ028632	Aichi virus AY747174	Aichi virus AB040749	Bovine kobuvirus AB084788	Porcine Kobuvirus EU787450
Salivirus GQ179640								
Klassevirus GQ184145	95.4							
Aichi virus AB010145	41.9	41.4						
Aichi virus DQ028632	42.8	42.6	92.9					
Aichi virus AY747174	43.1	42.6	93.8	95.8				
Aichi virus AB040749	42.6	42.2	97.1	95.8	96.7			
Bovine kobuvirus AB084788	40.9	41.1	50.1	51.4	51.0	50.9		
Porcine Kobuvirus EU787450	39.5	41.0	53.4	55.2	54.5	54.8	62.9	

P2 similarity (%)	Salivirus GQ179640	Klassevirus GQ184145	Aichi virus AB010145	Aichi virus DQ028632	Aichi virus AY747174	Aichi virus AB040749	Bovine kobuvirus AB084788	Porcine Kobuvirus EU787450
Salivirus GQ179640								
Klassevirus GQ184145	95.1							
Aichi virus AB010145	35.4	34.9						
Aichi virus DQ028632	34.9	34.7	95.7					
Aichi virus AY747174	35.0	34.5	97.7	96.6				
Aichi virus AB040749	35.5	35.0	99.5	96.2	98.2			
Bovine kobuvirus AB084788	36.8	36.1	62.8	62.9	62.9	62.9		
Porcine Kobuvirus EU787450	36.1	35.7	63.3	63.8	63.8	63.6	72.2	

P3 similarity (%)	Salivirus GQ179640	Klassevirus GQ184145	Aichi virus AB010145	Aichi virus DQ028632	Aichi virus AY747174	Aichi virus AB040749	Bovine kobuvirus AB084788	Porcine Kobuvirus EU787450
Salivirus GQ179640								
Klassevirus GQ184145	97.3							
Aichi virus AB010145	44.6	44.3						
Aichi virus DQ028632	44.7	44.5	97.6					
Aichi virus AY747174	44.3	44.1	96.7	95.8				
Aichi virus AB040749	44.6	44.3	99.9	97.7	96.8			
Bovine kobuvirus AB084788	42.4	42.3	64.1	63.9	64.4	64.1		
Porcine Kobuvirus EU787450	43.0	42.9	64.2	64.5	64.1	64.3	72.7	