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:	***2015.003a,bD***	(to be completed by ICTV officers)

Short title: New species in the Kappatorquevirus
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

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Corresponding author with e-mail address:

Tuija Kekarainen tuija.kekarainen@irta.cat

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)	Anelloviridae Study Group

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

ICTV SG agreed on this proposal

Date first submitted to ICTV: June 5, 2015
Date of this revision (if different to above): June 15, 2015

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	***2015.003aD***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Kappatorquevirus***
Subfamily:	
Family:	***Anelloviridae***
Order:	

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)**
Torque teno sus virus k2b	**38E23**	**JQ406846**

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 current criterion demarcating species in the genus is: ORF1 nucleotide sequence divergence >35%. The isolate listed above meets this criterion.

MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

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Renaming one or more taxa

Code	***2015.003bD***	(assigned by ICTV officers)

To rename the following taxon (or taxa):

Current name		**Proposed name**
Torque teno sus virus k2		***Torque teno sus virus k2a***

Reasons to justify the renaming:
Explain why the taxon (or taxa) should be renamed

Until now there was only one species in the genus *Kappatorquevirus* named *Torque teno sus virus k2*. When a second species was described, the ICTV SG recommended using similar naming as used in the genus *Iotatorquevirus*, where the species are referred to with alphabets (a, b). To follow this recommendation, we propose a new name (which is already used in the published works): *Torque teno sus virus k2a*. Also, see phylogenetic tree below.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Cornelissen-Keijsers Vivian, Jiménez-Melsió Alexandra, Sonnemans Denny, Cortey Martí, Segalés Joaquim, van den Born Erwin and Kekarainen Tuija "Discovery of a novel Torque teno sus virus species: genetic characterization, epidemiological assessment, and disease association" J Gen Virol. 2012; 93(Pt 12):2682-91.

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.

The study describes a novel Torque teno sus virus (TTSuV) species, provisionally named *Torque teno sus virus k2b* (TTSuVk2b), originally found in commercial pig sera by applying the rolling circle amplification technique. Full-length sequences of TTSuVk2b were obtained, annotated and used in the phylogenetic analyses, which revealed that TTSuVk2b is a novel anellovirus species within the genus *Kappatorquevirus* of the family *Anelloviridae*. Quantitative PCR techniques were developed to determine total TTSuV DNA quantities in pig blood as well as the prevalence and viral DNA quantities.

The phylogenetic analyses of the proposed TTSuVk2b nucleotide sequences [GenBank accession numbers: JQ406844 (TTSuVk2b-38E05), JQ406845 (TTSuVk2b-38E19) and JQ406846 (TTSuVk2b-38E23)] were performed using MEGA version 5 (Tamura et al., 2011), including TTSuV1 and TTSuVk2a sequences obtained from GenBank (Cortey et al., 2011; Huang et al., 2010b). The alignments were gained using a CLUSTAL W multiple alignment tool with a gap creation penalty of 10 and a gap extension penalty of 5. Phylogenies were inferred from p-distance matrices using the neighbour-joining method (Saitou & Nei, 1987). Statistical significance of the branching was estimated using bootstrap with 1000 replications and from this a consensus phylogenetic tree was built. Pairwise sequence comparison (PASC; http://www.ncbi.nlm.nih.gov/ sutils/pasc/) was performed using available anellovirus sequences from GenBank.

The isolate listed above meets the species demarcation criteria used in the family *Anelloviridae* (cutoff values for sequence divergence: species > 35%, genera > 56%).

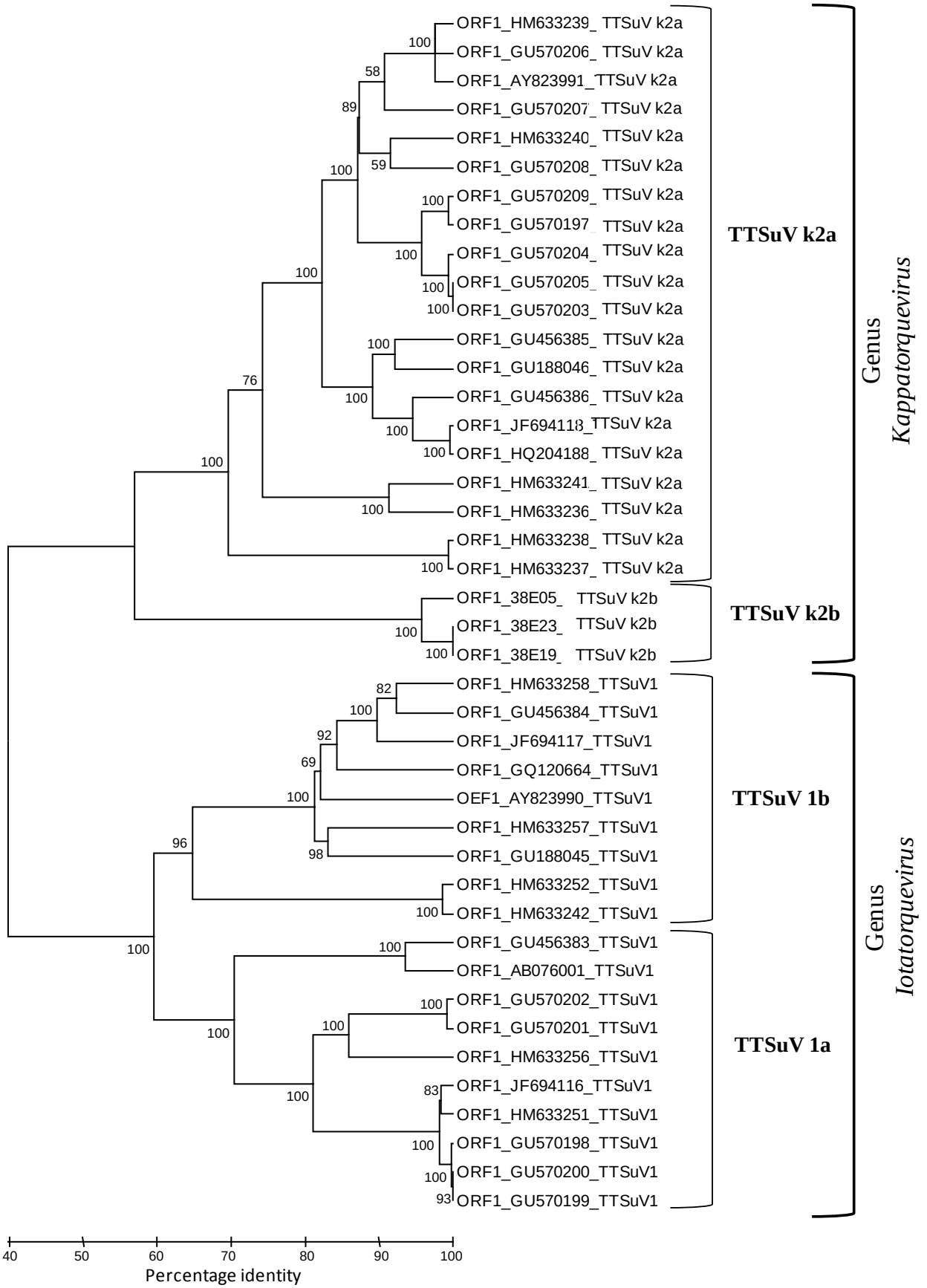

Figure 1. Neighbour-Joining phylogenetic tree based on the percentage identity of TTSuV ORF1

sequences available in GenBank. Confidence bootstrap values higher than 50% are shown in nodes.