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:	***2012.010aV***	(to be completed by ICTV officers)

Short title: create new species in the genus *Hantavirus*, family *Bunyaviridae*
(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:

Boris Klempa, boris.klempa@savba.sk

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)	*Bunyaviridae* 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	***2012.010aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Hantavirus***
Subfamily:	
Family:	***Bunyaviridae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Sangassou virus	Sequences are available for the three genomic segments of Sangassou virus, strain SA14 S segment: JQ082300 M segment: JQ082301 L segment: JQ082302

Reasons to justify the creation and assignment of the new species:

1. Sangassou virus (SANGV) shows sufficient amino acid sequence diversity to other known hantavirus species (current species demarcation criterion is 7% difference in the nucleocapsid protein (NP) and glycoprotein precursor GPC) amino acid sequences (Annex 1; Klempa et al., 2012). Currently the most closely related recognized hantavirus species is *Dobrava-Belgrade virus* (DOBV) with 11.5% (NP) and 19.6% (GPC) amino acid difference. Moreover, in phylogenetic analyses, SANGV sequences clearly form separate phylogenetic clade (Annex 2).
2. SANGV has been detected in African wood mouse (*Hylomyscus simus*), Murinae rodent species, which has not been recognized as a hantavirus reservoir yet. SANGV represents currently the only one indigenous Murinae-associated hantavirus from Africa (Klempa et al., 2006).
3. SANGV can be differentiated from other hantaviruses in focus reduction neutralization assay. In a very limited cross-neutralization study, mice were immunized with brain suspension of suckling mice infected intracerebrally with SANGV strain SA14 or DOBV strain SK/Aa. Although the observed titers were generally very low, sufficient difference in the neutralizing antibody titers was observed (Annex 3). Moreover, in the seroepidemiological study from Guinea, West Africa, human sera showing exclusive neutralizing titers to SANGV were observed (Klempa et al., 2010).

- 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

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Klempa, B., Fichet-Calvet, E., Lecompte, E., Auste, B., Aniskin, V., Meisel, H., Denys, C., Koivogui, L., ter Meulen, J., Krüger, D.H. (2006). Hantavirus in African Wood Mouse, Guinea. *Emerg Infect Dis*, 12, 838-840.
2. Klempa, B., Koivogui, L., Sylla, O., Koulemou, K., Auste, B., Krüger, D.H., ter Meulen, J. (2010). Serological evidence of human hantavirus infections in Guinea, West Africa. *J Infect Dis*, 201, 1031-4
3. Klempa, B., Witkowski, P.T., Popugaeva, E., Auste, B., Koivogui, L., Fichet-Calvet, E., Strecker, T., Ter Meulen, J., Krüger, D.H. (2012) Sangassou virus, the first hantavirus isolate from Africa, displays genetic and functional properties distinct from those of other murinae-associated hantaviruses. *Journal of Virology*, 86; 3819-27

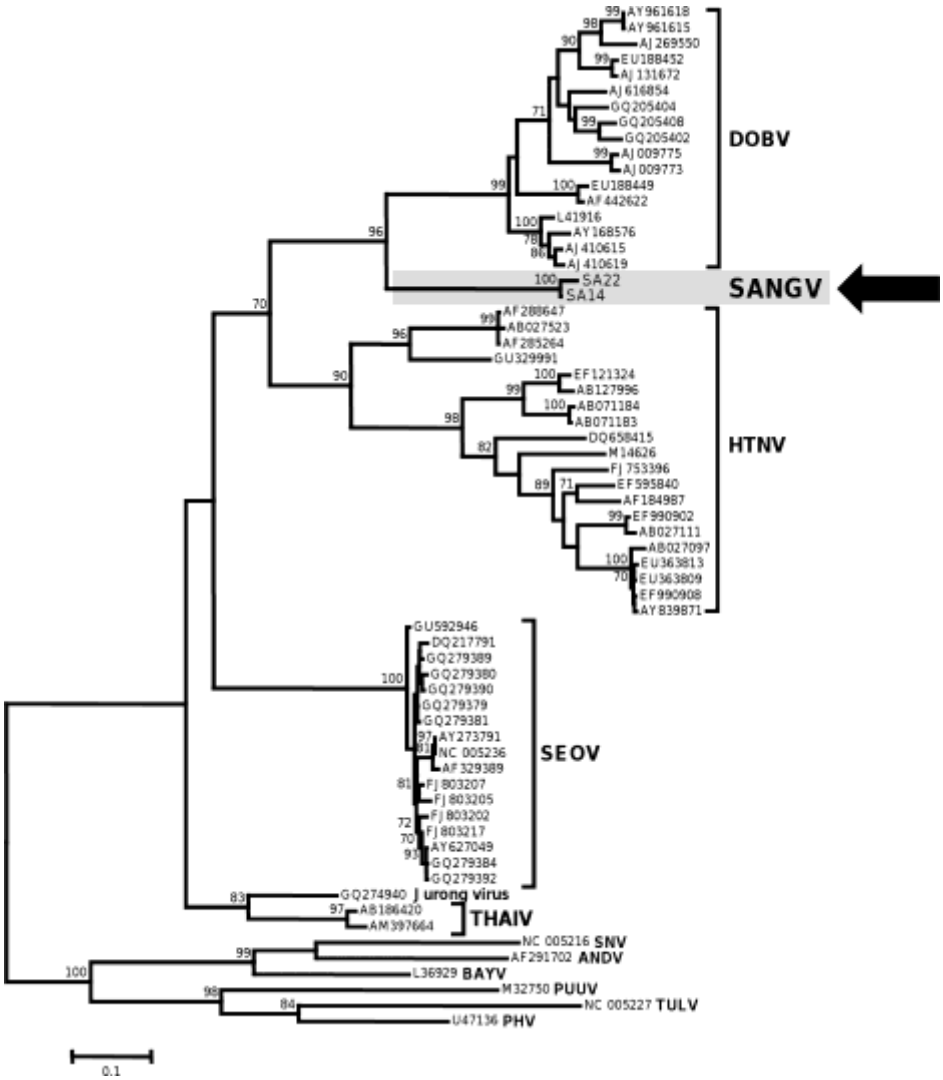
Annex:

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.

Annex 1. Complete nucleotide and amino acid sequence identities of the SANGV isolate SA14 compared with other rodent-borne hantavirus representatives[a]

	S segment		M segment		L segment	
	1,746 nt	429 aa	3,650 nt	1,135 aa	6,531 nt	2,151 aa
DOBV $_{SK/Aa}$	74.6	**88.5**	71.6	**80.4**	75.0	86.7
HTNV $_{76-118}$	67.8	81.8	68.7	76.2	73.9	84.3
SEOV $_{80-39}$	71.1	82.7	69.8	77.7	74.9	85.2
PUUV $_{CG1820}$	54.8	61.2	56.6	52.9	65.7	68.3
TULV $_{Moravia}$	54.1	61.7	56.7	53.7	65.2	68.5
SNV $_{NM\ H10}$	47.9	60.8	56.2	52.8	65.4	69.2
ANDV $_{Chile}$	51.0	62.2	56.3	53.3	65.1	68.2

[a]Values given in the table represent percent of identity. nt, nucleotides; aa, amino acids



Annex. 2. Maximum-Likelihood tree showing the phylogenetic placement of SANGV within the Murinae-associated hantaviruses constructed on the basis of complete S segment coding sequences. Evolutionary analysis was conducted in MEGA5. The evolutionary histories were inferred by using the Maximum-Likelihood method based on the Tamura-Nei model with using a discrete Gamma distribution (+G) with 5 rate categories and by assuming that a certain fraction of sites are evolutionarily invariable (+I). The scale bars indicate an evolutionary distance of 0.1 substitutions per position in the sequence. Bootstrap values ≥70%, calculated from 1,000 replicates, are shown at the tree branches. SANGV is marked by gray box and an arrow.
ANDV, *Andes virus*; BAYV, *Bayou virus*; DOBV, *Dobrava-Belgrade virus*; HTNV, *Hantaan virus*; PHV, *Prospect Hill virus*; PUUV, *Puumala virus*; SANGV, *Sangassou virus*; SEOV, *Seoul virus*; SNV, *Sin Nombre virus*; THAIV, *Thailand virus*; TULV, *Tula virus*.

Annex 3. Results of typing of neutralizing antibodies in sera from mice immunized with brain suspension of suckling mice infected intracerebrally with SANGV strain SA14 or DOBV strain SK/Aa.

	Neutralizing titer against*:		
	SANGV	DOBV	HTNV
anti-SANGV	40	<20	<20
anti-DOBV	<20	160	<20

* Determined by focus reduction neutralization assay (FRNT)