



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**

<b>Code assigned:</b>	<b>2009.001abV</b> (to be completed by ICTV officers)
<b>Short title:</b> Create the species named Chapare virus in the genus Arenavirus, in the family Arenaviridae (e.g. 6 new species in the genus <i>Zetavirus</i> )	
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>

**Author(s) with e-mail address(es) of the proposer:**

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Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	<b>Yes</b>
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**ICTV-EC or Study Group comments and response of the proposer:**

Discrepancy between species demarcation criteria of more than 12% divergence in the nucleoprotein amino acid sequence. and the 8<sup>th</sup> report figure of 26%. Otherwise, has support of EC.

Checked with SG Chair, 12% figure will appear in 9<sup>th</sup> report. 26% was just an example of how divergent species can be.

Date first submitted to ICTV:	12.03.09
Date of this revision (if different to above):	22.06.09

MODULE 2: **NEW SPECIES**

**Part (a)** to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	<b>2009.001aV</b>	(assigned by ICTV officers)
<b>To create a new species with the name: <i>Chapare virus</i></b>		

**Part (b)** assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	<b>2009.001bV</b>	(assigned by ICTV officers)
<b>To assign the species listed in section 2(a) as follows:</b>		
Genus:	<i>Arenavirus</i>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write "<b>(new)</b>" after its proposed name.</li> <li>• If no genus is specified, enter "<b>unassigned</b>" in the genus box.</li> </ul>
Subfamily:		
Family:	<i>Arenaviridae</i>	
Order:		

**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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

After a localized outbreak of hemorrhagic fever in Bolivia, Chapare virus (CHAV) was isolated in 2004 from tissues of an afflicted person (Delgado et al., 2008). Two other arenaviruses in Bolivia, Machupo virus and Latino virus, are hosted by the rodent *Calomys callosus*, but the reservoir for Chapare virus is not known. Chapare virus cross-reacted with a rabbit polyvalent hyperimmune serum raised against Guanarito virus, Machupo virus and Sabia virus. The complete sequence of the large and small genomic segments has been determined (Delgado et al., 2008, CHAV S segment - GenBank Accession No. EU260463; CHAV L segment - GenBank Accession No. EU260464) and used to analyze the genetic distances between full-length gene sequences of Chapare virus and other arenavirus species. This reveals that Chapare virus is most closely related to Sabia virus, with a genetic divergence in the amino acid sequence of the nucleoprotein of 15% (see Annex for phylogenetic trees). All these points indicate that Chapare virus should be classified as a new species in the genus *Arenavirus*.

Species demarcation criteria

Members of an arenavirus species:

- share a specific host in the same species or genus,
- share a similar geographic distribution,

- are / are not an agent of disease in humans,
- share antigenic cross-reactivity,
- show a divergence of no more than 12% in the nucleoprotein amino acid sequence.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Delgado S, Erickson BR, Agudo R, Blair PJ, Vallejo E, Albariño CG, Vargas J, Comer JA, Rollin PE, Ksiazek TG, Olson JG, Nichol ST. 2008. Chapare virus, a newly discovered arenavirus isolated from a fatal hemorrhagic fever case in Bolivia. PLoS Pathog. 2008 Apr 18;4(4):e1000047.

**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.

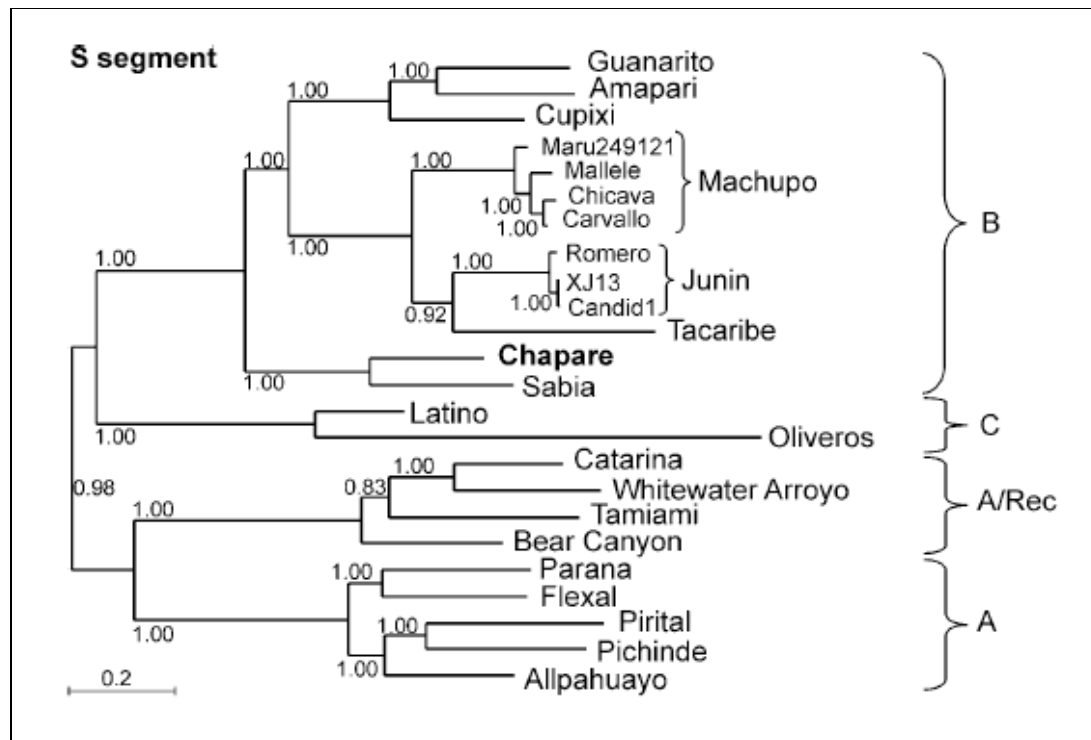


Fig.1. Phylogenetic tree showing the relationship between arenavirus species and the proposed species *Chapare virus* (ChPV), using complete nucleoprotein amino acid sequences.