

Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code † To designate the following viruses as species in the genus:

belonging to the family[°] :

BeAn 119303 AF512832

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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New Taxonomic Order

Order	
Family	<i>Arenaviridae</i>
Genus	<i>Arenavirus</i>
Type Species	<i>Lymphocytic choriomeningitis virus</i>
List of Species in the genus	<i>Ippy virus</i> <i>Lassa virus</i> <i>Lymphocytic choriomeningitis virus</i> <i>Mobala virus</i> <i>Mopeia virus</i> <i>Amapari virus</i> <i>Flexal virus</i> <i>Guanarito virus</i> <i>Junín virus</i> <i>Latino virus</i> <i>Machupo virus</i> <i>Oliveros virus</i> <i>Paraná</i> <i>Pichinde virus</i> <i>Sabiá virus</i> <i>Tacaribe virus</i> <i>Tamiami virus</i> <i>Whitewater Arroyo virus</i>
List of Tentative Species in the Genus	Pampa virus
List of Unassigned Species in the Family	None reported

Argumentation to justify the designation of new species in the genus

Species demarcation criteria in the genus

Members of an arenavirus species:

- share a specific host in the same species or genus,
- share a similar geographic distribution,
- are / are not agent of disease in humans,
- share an antigenic cross-reactivity,
- show a divergence of no more than 12% in the nucleoprotein amino acid sequence.

Argumentation to justify the designation of new species in the genus

Cupixi virus was isolated from an *Oryzomys capito* rodent in northeastern Brazil in 1970. The complete genome sequence of the small genomic segment has been determined (Charrel et al., 2002). Sequence and phylogenetic analyses showed that it is most closely related to *Guanarito virus*, the etiological agent of Venezuelan hemorrhagic fever, and *Amapari virus* from Brazil, which is not known to be pathogenic in humans. Accordingly, *Cupixi virus* should be included in lineage B of the New World (Tacaribe serocomplex) arenaviruses. There is no information on the capability of *Cupixi virus* to infect humans or to cause disease, but serious investigations remain to be conducted. No data concerning antigenic cross-reactivity are available. The genetic distance of *Cupixi virus* from *Guanarito virus* and *Amapari virus* in the amino acid sequences of the nucleoproteins is 17.1% in each case. Although *Cupixi virus* shares the same reservoir host and country of origin as *Amapari virus*, the genetic distances between the two viruses (17.1 and 31.4% for the amino acid sequences of the nucleoprotein and glycoprotein precursor protein respectively) are comparable to those between currently accepted arenavirus species, and clearly justify classifying *Cupixi virus* as a distinct species (see phylogenetic trees in annex).

List of created Species in the genus

Cupixi virus (CPXV)

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References

Charrel RN, Feldmann H, Fulhorst CF, Khelifa R, de Chesse R, de Lamballerie X (2002).

Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intra-segmental recombination. *Biochem Biophys Res Commun.* 296:1118-1124.

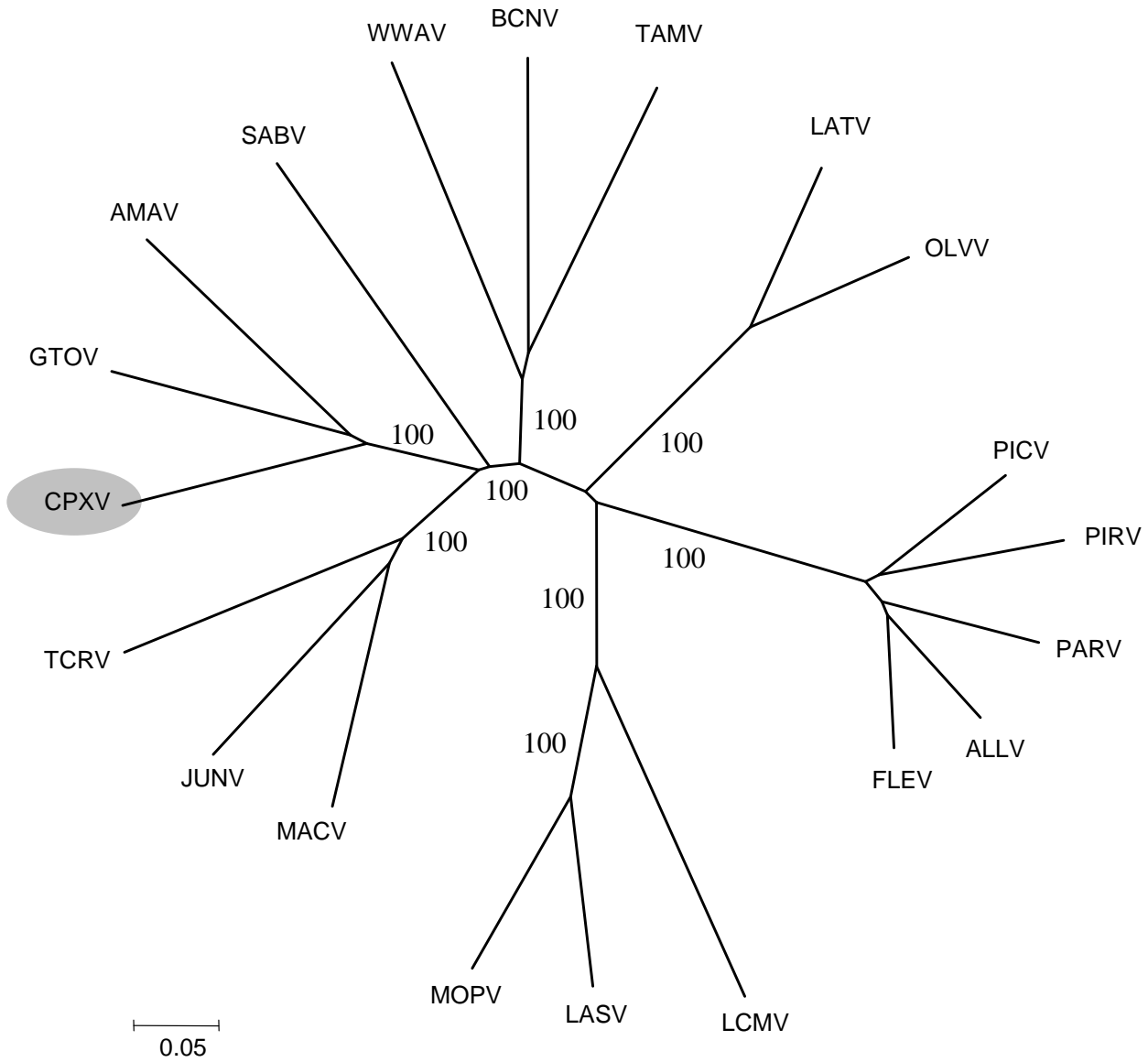


Fig.2. Phylogenetic tree showing the relationship between arenavirus species and the proposed species *Cupixi virus* (CPXV), using complete glycoprotein precursor amino acid sequences.