

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.010S** |  |
| **Short title:** Create one new species (*Caaingua virus*) in the genus *Alphavirus* (*Martellivirales*: *Togaviridae*) | | |
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**Author(s) and email address(es)**

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| Tschá MK, Suzukawa AA, Gräf T, Piancini LDS, Silva AM, Faoro H, Riediger IN, Medeiros LC, Wowk PF, Zanluca C, Duarte dos Santos CN | tschamarcel@gmail.com;andreia.suzukawa@fiocruz.br; akograf@gmail.com;laerciopiancini@gmail.com; allan.silva@sesa.pr.gov.br;helisson.faoro@fiocruz.br; irinariediger@sesa.pr.gov.br;[irinariediger@sesa.pr.gov.br](mailto:irinariediger@sesa.pr.gov.br); pryscilla.wowk@fiocruz.br;camila.zanluca@fiocruz.br; claudia.dossantos@fiocruz.br |

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**Corresponding author**

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**List the ICTV Study Group(s) that have seen this proposal**

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| *Togaviridae* Study Group |

**ICTV study group comments and response of proposer**

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| Our study group has reviewed and discussed the proposal. We agree that the new Gaaingua virus can be classified as a species in *Togaviridae*. However, the figure provided in the proposal is not correctly done. Since there is a major recombination event in *Togaviridae*, we cannot use phylogenetic trees based on whole genome sequence. Rather, two trees based on structural and non-structural genes respectively should be provided.  Response: The required trees have been added to the proposal, as requested by the SG. |

**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 25/09/2019 |
| Date of this revision (if different to above) | 21/08/2020 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.010S.R.Caaingua\_virus\_1nsp.xlsx |

**Abstract**

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| *Caaingua virus*, is proposed as a new species in the genus *Alphavirus* (*Martellivirales*: *Togaviridae*). Phylogenetic analysis showed that it is distinct from all existing alphavirus species. |

**Text of proposal**

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| |  | | --- | | Caainguá virus (CAAV) was isolated from pools of *Culex* mosquitoes collected at Marilena municipality, Brazil (22°44'09′′ S, 53°02′24′′ W) (Tschá et al., 2019). Next generation sequencing of the third passage of the isolated virus in C6/36 cells yielded the viral genome in a single contig containing 12,096 bp with an average coverage of 1,846X. Comparison of the complete genome sequence (GenBank accession MK353339) with the GenBank nucleotide database using BLASTn showed a 73% identity with equine encephalitis complexes.  Phylogenetic trees generated from the non-structural protein and structural protein genomic regions were compared to identify potential recombination events within CAAV genome, but recombination breakpoints were not identified in CAAV. A maximum likelihood tree constructed using the complete genome sequence is shown in Fig. 1 [taken from (Tschá et al., 2019)].    Caainguá virus is a tribute to the indigenous tribe of the Guarani Indians that inhabited the region. Caainguá is a variant of the name, which in the Tupi Guarani language means “who lives in the wood/jungle.” | |

**Supporting evidence**



Figure 1. Comparative phylogenies between structural (left) and non-structural (right) genomic regions of the genus *Alphavirus*. Maximum likelihood trees were co-plotted using phytools R package and nodes were rotated to maximize tips matching. Branches were colored to highlight the four main alphavirus complexes and bootstrap support are shown for key branches.

**References**

Tschá, MK, Suzukawa AA, Gräf T, Piancini L, da Silva AM, Faoro H, Riediger IN, Medeiros LC, Wowk PF, Zanluca C, Duarte Dos Santos CN (2019) Identification of a novel alphavirus related to the encephalitis complexes circulating in southern Brazil. Emerg Microbes Infect 8: 920-933. PMID: 31237479; PMCID: PMC6598490. <https://doi.org/10.1080/22221751.2019.1632152>.