This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| --- | --- | --- |
| **Code assigned:** | ***2018.013M*** | (to be completed by ICTV officers) |
| **Short title:** One (1) new species in the genus *Banyangvirus* (*Bunyavirales*: *Phenuiviridae*) |
|  |
| **Author(s):** |
| Shu ShenXiaomei DuanBo WangLiying ZhuYanfang ZhangJingyuan ZhangJun WangTao LuoChun KouDan LiuChuanwei LvLei ZhangChenchen ChangZhengyuan SuShuang TangJie QiaoAbulimiti MomingCheng WangAbulikemu AbudurexitiHualin WangZhihong HuYujiang ZhangSurong SunFei Deng |
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| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | **ICTV *Phenuiviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
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| Date first submitted to ICTV: | June 6, 2018 |
| Date of this revision (if different to above): |       |

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

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2018.013M.N.v1.Banyangvirus\_sp |

**Supporting material:**

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Guertu virus (GTV) is most closely related to two other tick-borne viruses, severe fever with thrombocytopenia syndrome virus (SFTSV) and Heartland virus (HRTV), and therefore belongs to the currently proposed genus *Banyangvirus* in the family bunyaviral family *Phenuiviridae*. The three viruses have same genome organization (L, M, and S segments) but have significant sequence differences. Sequence pairwise identities between GTV, SFTSV and HRTV are 76% and 67% for the L segment, 72% and 59% for the M segment, and 74% and 60% for the S segment, respectively. Amino acid pairwise identities between GTV, SFTSV, and HRTV are 89% and 73% for the RNA-dependent RNA polymerase (RdRp), 78% and 60% for the glycoprotein (G), 88% and 60% for the nucleoprotein (NP), and 74% and 59% for the non-structural protein (NSs), respectively. To date, GTV has only been found in *Dermacentor nuttalli* ticks and can infect and replicate in human- and animal-derived cells, which indicated the possibility of interspecies transmission.

The previous species demarcation criteria for bunyaviruses suggested that species should be defined on the criterion that the ≈1 kb sequence fragment containing the core polymerase domain (premotif A to motif E) of the third conserved region of the L protein should be less than 90% identical on the amino acid level compared to that of any other related bunyaviruses (2016.030a-vM.A.v6.Bunyavirales). The aa similarities of core polymerase regions of GTV RdRp to SFTSV is 92%, a little higher than the <90% threshold value, and to HRTV is 79%. Nevertheless, GTV RdRp shows <90% aa similarities to both SFTSV and HRTV. However, the phylogenetic trees built using the nucleotide sequences of L, M, and S segments from GTV and the relatives show that SFTSV, GTV, HRTV and Hunter Island group virus (HIGV) cluster within a branch with different evolutionary distances, suggesting that GTV is a distinct member of genus *Banyangvirus* (Figure 1).

**Figure 1: The ML phylogenetic trees of banyangviruses (shaded in yellow) and phleboviruses (shaded in orchid) were built based on the genomic sequences of the L, M, and S segments.** The branches are labeled with different colors. GTV is shown in bold red characters. HRTV sequences are indicated by bold black characters. SFTSV sequences are shown in bold characters, and five genotypes are distinguished by different colors: C1 in green, C2 in chocolate, C3 in khaki, C4 in purple, and J in cyan. Trees were constructed using Mega 5.0 and tested by the bootstrap method with 1,000 replications. Bootstrap values greater than 50% are shown at each node. The Gouléako virus sequences (genus *Goukovirus*) are used as the outgroup control.

| **References:** |
| --- |
| [A novel tick-borne phlebovirus, closely related to severe fever with thrombocytopenia syndrome virus and Heartland virus, is a potential pathogen.](https://www.ncbi.nlm.nih.gov/pubmed/29802259)Shen S, Duan X, Wang B, Zhu L, Zhang Y, Zhang J, Wang J, Luo T, Kou C, Liu D, Lv C, Zhang L, Chang C, Su Z, Tang S, Qiao J, Moming A, Wang C, Abudurexiti A, Wang H, Hu Z, Zhang Y, Sun S, Deng F.Emerg Microbes Infect. 2018 May 25;7(1):95. doi: 10.1038/s41426-018-0093-2.PMID:29802259 |