

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.022M** |  |
| **Short title:** Create four new species in the genus *Phlebovirus (Bunyavirales*: *Phenuiviridae)* | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Marklewitz M, Tchouassi DP, Torto B, Sang R, Junglen S | [marco.marklewitz@charite.de](mailto:marco.marklewitz@charite.de);  [dtchouassi@icipe.org](mailto:dtchouassi@icipe.org);  [btorto@icipe.org](mailto:btorto@icipe.org);  [rsang@icipe.org](mailto:rsang@icipe.org);  [sandra.junglen@charite.de](mailto:sandra.junglen@charite.de) |

**Corresponding author**

|  |
| --- |
| Sandra Junglen; sandra.junglen@charite.de |

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

|  |
| --- |
| ICTV *Phenuiviridae* Study Group |

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

|  |
| --- |
| None. |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | August 21, 2020 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2020.022M.R.Plebovirus\_4sp.xlsx |

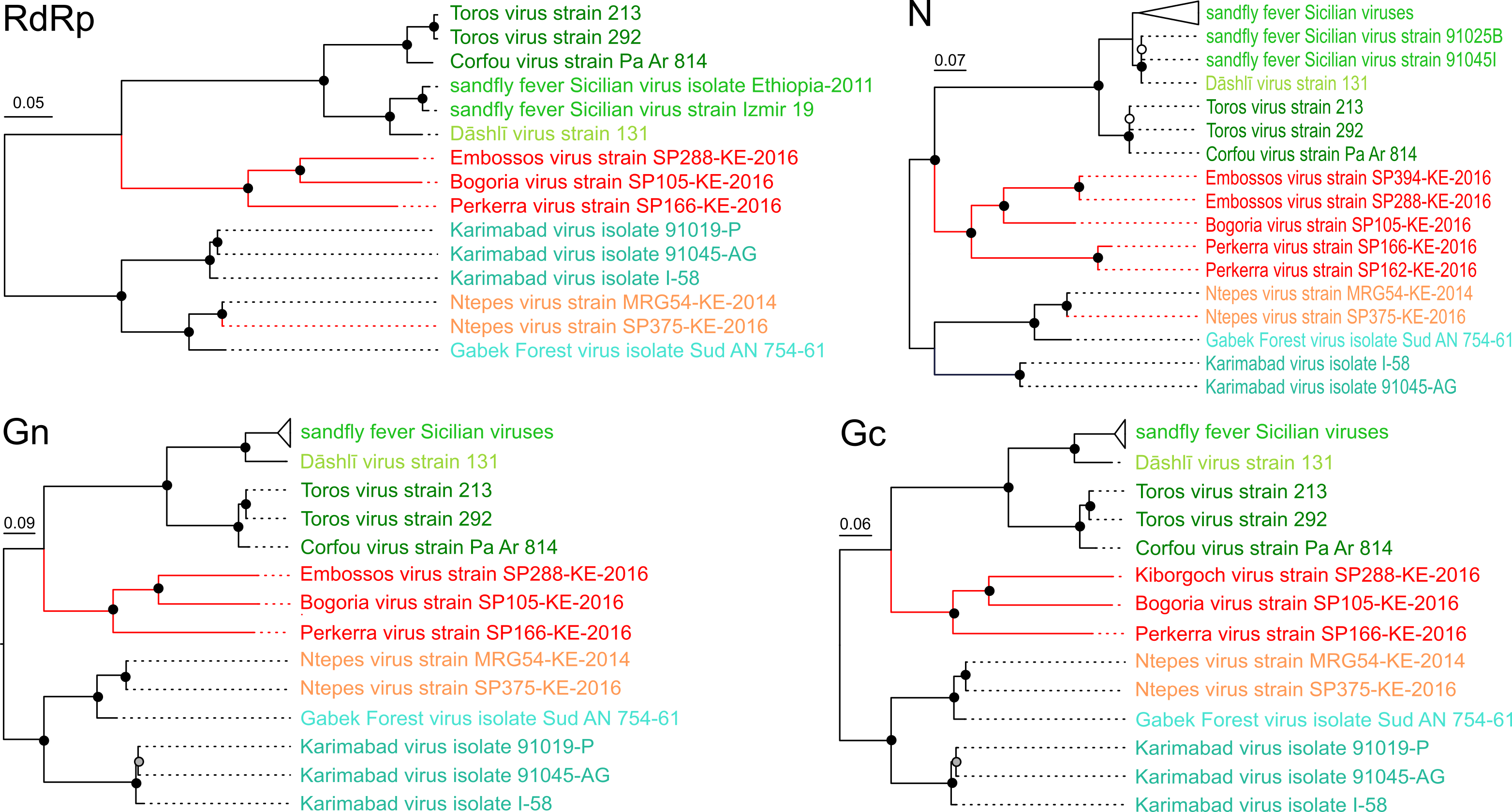
**Abstract**

|  |
| --- |
| We propose the creation of 4 new species in the genus *Phlebovirus.* Species demarcation is based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparison according to the established species demarcation criteria for the genus *Phlebovirus*. |

|  |  |
| --- | --- |
| **Text of proposal**   |  | | --- | | Four previously unknown viruses have been detected in sandflies collected in the Kenyan Rift Valley and named after geographic references in the area of Baringo County where the phlebovirus-positive sandfly specimens were collected: Bogoria virus (BGRV), named after Lake Bogoria, Embossos virus (EMBV), named after Embossos River, Perkerra virus (PERV), named after Perkerra River, and Kiborgoch virus (KBGV) named after the Community Wildlife and Wetlands Conservancy south of Marigat. Species demarcation criteria for the genus phlebovirus are <95% identity in the amino acid sequence of the RdRp, thus viruses with <95% sequence identity represent unique species. Maximum pairwise identities among the identified new viruses and established phleboviruses range between 84 – 55% identity in the amino acid sequence of the entire RdRp. The low genetic identity of coding-complete genome (CCG) sequences to known viruses and phylogenetic reconstructions support the need to create four novel species within the genus *Phlebovirus* (Figure 1). We propose the creation of 4 new species within the genus *Phlebovirus*, namely *Bogoria phlebovirus* (with Bogoria virus (BGRV) as exemplar virus), *Embossos phlebovirus* (with Embossos virus (EMBV) as exemplar virus), *Perkerra phlebovirus* (with Perkerra virus (PERV) as exemplar virus), and *Kiborgoch phlebovirus* (with Kiborgoch virus (KBGV) as exemplar virus). | |

**Supporting evidence**

****

****

**Figure 1:** Phylogenetic relationship of established and proposed phleboviruses. The phylogenetic tree is based on a MAFFT-alignment of the RdRp amino acid sequences using the E-INS algorithm and was inferred using the PhyML and the LG substitution model. Numbers on branch nodes represent bootstrap values (1,000 replicates). Proposed new phleboviruses are shown in red. Separate subtrees of newly identified and related viruses due to the low bootstrap support in phylogenies containing all phleboviruses.

**References**

Marklewitz M, Tchouassi DP, Hieke C, Heyde V, Torto B, Sang R, Junglen S (2020) Insights into the evolutionary origin of Mediterranean sandfly fever viruses.

*mSphere* in press