This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.019M*** | | | | (to be completed by ICTV officers) |
| **Short title: One (1) new species in the genus *Tibrovirus* (*Mononegavirales*: *Rhabdoviridae*)** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Wiley, Michael R.  Prieto, Karla  Blasdell, Kim R.  Caì, Yíngyún  Campos Lawson, Christine  Walker, Peter J.  Chiu, Charles Y.  Palacios, Gustavo  Kuhn, Jens H. | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Kuhn, Jens H.; [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | | | | | |
| **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 *Rhabdoviridae* SG** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | August 25, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.019M.U.v1.Tibrovirus\_sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
|  |

Beatrice Hill virus (BHV) was first reported in 1984 as a novel virus of biting midges (*Culicoides peregrinus*) that had been collected at Beatrice Hill, Northern Territory, Australia (Standfast *et al*.). In 2016, a 5,734 nt-long contig of the BHV genome was published, which indicated that this virus most likely falls into the tibrovirus clade (genus *Tibrovirus*) of rhabdoviruses (*Mononegavirales*: *Rhabdoviridae*) (Huang *et al*.). Using a historical sample of brain tissue from a laboratory mouse that had been infected intracranially with BHV-containing material, the BHV genome sequence was finally completely sequenced in (Wiley *et al*.). Using PASC (Bao *et al*.), the determined complete BHV genome sequence (GenBank # KY073493) was found to be 72.79% identical to that of Tibrogargan virus (TIBV, GenBank #GQ294472.1) and 72.48% identical to that of Bivens Arm virus (BAV, GenBank # KM205019 or #KP688373.1) (Walker *et al*., Wiley *et al*.). Amino acid sequence identities indicate that BHV is most closely related to BAV in the N (95%), G (82%) and L (86%) proteins, respectively (Tables 1–3). These levels of sequence divergence exceed 20% at the nt level and ranges between 5–18% divergence at the aa level.

Tibrovirus species demarcation criteria have previously been defined as follows: “The species demarcation criteria are based on low-level or no cross-reaction in virus neutralisation tests, supported by phylogenetic analysis and genetic diversity estimations using L and N gene sequences to establish that the species represents a distinct lineage. Typically, there will be <5% amino acid sequence diversity (divergence) within species and >20% diversity (divergence) between species.” (*Tibrovirus* genus proposal, ICTV, 2011).

Like the viruses that have been assigned to established tibrovirus species (Bas Congo virus [BASB]: *Bas-Congo tibrovirus*; Coastal Plains virus [CPV]: *Coastal Plains tibrovirus*; Ekpoma virus 1 [EKV-1]: *Ekpoma 1 tibrovirus*; Ekpoma virus 2 [EKV-2]: *Ekpoma 2 tibrovirus*; Sweetwater Branch virus [SWBV]: *Sweetwater Branch tibrovirus*; and Bivens Arm virus [BAV] together with Tibrogargan virus [TIBV]: *Tibrogargan tibrovirus*), the virus we propose here to be assigned to new species in the genus *Tibrovirus* (Beatrice Hill virus [BHV]) shares the same unique genome organization (3´*N-P-M-U1-U2-G-U3-L*5´), comprising five genes encoding the canonical rhabdovirus structural proteins (*N*, *P*, *M*, *G*, and *L*), and three additional genes encoding long ORFs (*U1*, *U2*, and *U3*). ORF *U1* and ORF *U2* encode small proteins with unknown functions; ORF *U3* encodes a small viroporin-like transmembrane protein. Each ORF lies within an independent transcriptional unit bounded by consensus transcription initiation and transcription termination/polyadenylation sequences. All tibroviruses, including BHV, form a monophyletic clade in a maximum likelihood tree inferred from complete L protein sequences of 121 rhabdoviruses (Figure 1).

**Table 1. Amino acid sequence identities of tibrovirus N protein sequences as determined in Geneious 10.2.3.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | TIBV | BAV | BHV | SWBV | CPV | EKV-1 | EKV-2 | BASV |
| TIBV | 100 |  |  |  |  |  |  |  |
| BAV | 99.1 | 100 |  |  |  |  |  |  |
| BHV | 94.4 | 94.6 | 100 |  |  |  |  |  |
| SWBV | 75.2 | 75.9 | 74.8 | 100 |  |  |  |  |
| CPV | 66.4 | 66.8 | 66.6 | 68.2 | 100 |  |  |  |
| EKV-1 | 47.6 | 47.8 | 47.1 | 45.9 | 46.6 | 100 |  |  |
| EKV-2 | 40.2 | 40.2 | 39.7 | 38.6 | 40 | 41.4 | 100 |  |
| BASV | 39.6 | 39.8 | 38.6 | 39.6 | 40.3 | 40.5 | 45.2 | 100 |

**Table 2. Amino acid sequence identities of tibrovirus G protein sequences as determined in Geneious 10.2.3.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | TIBV | BAV | BHV | SWBV | CPV | EKV-1 | EKV-2 | BASV |
| TIBV | 100 |  |  |  |  |  |  |  |
| BAV | 96.4 | 100 |  |  |  |  |  |  |
| BHV | 81 | 81.6 | 100 |  |  |  |  |  |
| SWBV | 62.6 | 62.1 | 61.7 | 100 |  |  |  |  |
| CPV | 55.1 | 55.1 | 53.9 | 55.7 | 100 |  |  |  |
| EKV-1 | 32.4 | 32.7 | 32.5 | 31.2 | 29.8 | 100 |  |  |
| EKV-2 | 28.7 | 29.2 | 29.1 | 27.3 | 28.3 | 23.3 | 100 |  |
| BASV | 28.1 | 28.2 | 28.1 | 26.1 | 25.9 | 27.4 | 32.7 | 100 |

**Table 3. Amino acid sequence identities of tibrovirus L protein sequences as determined in Geneious 10.2.3.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | TIBV | BAV | BHV | SWBV | CPV | EKV-1 | EKV-2 | BASV |
| TIBV | 100 |  |  |  |  |  |  |  |
| BAV | 97.2 | 100 |  |  |  |  |  |  |
| BHV | 86.4 | 85.9 | 100 |  |  |  |  |  |
| SWBV | 63.3 | 62.9 | 63.5 | 100 |  |  |  |  |
| CPV | 55 | 55 | 54 | 54.7 | 100 |  |  |  |
| EKV-1 | 45.1 | 45.2 | 45.1 | 45.7 | 47.8 | 100 |  |  |
| EKV-2 | 41.6 | 41.6 | 41.1 | 42.9 | 41.6 | 44.6 | 100 |  |
| BASV | 43 | 43.3 | 43.1 | 43.3 | 42.3 | 44.1 | 50.8 | 100 |

**Fig. 1.** A maximum-likelihood phylogenetic tree inferred from a MUSCLE alignment of the full-length L protein sequences of **Beatrice Hill virus (BHV)**, 121 rhabdoviruses assigned to 18 genera and one rhabdovirus (Moussa virus, MOUV) which is currently classified to an unassigned rhabdovirus species. Full-length L protein sequences are not currently available for other rhabdoviruses assigned to species. Ambiguously aligned amino acid residues were removed using Gblocks with 484 positions remaining in the final dataset. The evolutionary history was inferred by using the WAG + frequency model. The initial tree for the heuristic search was obtained automatically by applying the neighbor-joining algorithm to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree with the highest log likelihood (-48495.5959) is shown. Asterisks (\*) indicate well-supported nodes in the tree (bootstrap proportion ≥ 75%) following 1000 iterations. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site, the scale bar indicating a value of 0.2. Evolutionary analyses were conducted in MEGA7.

**C:\Users\kuhnjens\AppData\Local\Microsoft\Windows\INetCache\Content.Word\Tree with BHV 220817.tiff**

**References:**

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