

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

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| **Code assigned:** | **2020.010M** |  |
| **Short title:**  Create one new species (*Hyalomma lostrhavirus*) in the genus *Lostrhavirus (Mononegavirales*: *Rhabdoviridae*) | | |
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**Author(s) and email address(es)**

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

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| *Rhabdoviridae* Study Group |

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

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| Approved by all responding SG members (8 of 14) with minor revisions. |

**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 | 26 July 2020 |
| Date of this revision (if different to above) |  |

**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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| 2020.010M.R.Lostrhavirus\_1nsp |

**Abstract**

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| The new species *Hyalomma lostrhavirus* is proposed for Xinjiang tick rhabdovirus. The virus clusters phylogenetically with lone star tick rhabdovirus, the only existing member of the genus *Lostrhavirus.* Xinjiang tick rhabdovirus meets demarcation criteria for assignment to a new species in the genus. |

**Text of proposal**

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| |  | | --- | | Xinjiang tick rhabdovirus (XjTRV; strain 15-XJ) was detected in hard ticks (*Hyalomma asiaticum*) collected in Xinjiang Autonomous Region, China, in 2015. The near-complete genome sequence (11,472 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. We propose to assign XjTRV to a new species (*Hyalomma lostrhavirus)* in the genus *Lostrhavirus.*  **Genome organization**  The XjTRV genome is similar in organisation to that of lone star tick rhabdovirus (LSTRV), the only current member of the genus *Lostrhavirus*. Each genome contains the five canonical rhabdovirus structural protein genes (N, P, M, G and L) (**Figure 1**). Various small alternative ORFs (>180 nt) occur in various genes of each genome. However, it is not known if they are expressed and none are conserved in both viruses.  A Clustal X alignment indicates that lostrhavirus G proteins are similar in structure and length, and share identifiable sequence identity, with each containing all 12 conserved cysteine residues that in vesicular stomatitis Indiana virus (VSIV) form six disulphide bonds in the folded protein (**Figure 2**).  **Phylogeny and amino acid sequence relationships**  Based on ML trees generated from complete L protein sequences XjTRV and LSTRV form a well-supported clade that is distinct from the clades formed by viruses assigned to other genera (**Figure 3**). Amino acid sequence divergence between XjTRV and LSTRV in pair-wise alignments (p-distances) is 59.3 % in the N proteins, 58.0 % in the G proteins and 59.3 % in the L proteins.  **Ecology**  Lostrhaviruses have been isolated from hard ticks (Ixodidae) of different genera. XjTRV was isolated from Asiatic hyalomma ticks (*Hyalomma asiaticum*) in China. LSTRV was isolated from lone star ticks (*Amblyomma americanum)* in the USA.    **Species demarcation criteria**  Viruses assigned to different species within the genus *Lostrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N; B) minimum amino acid sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% in G; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  XjTRV meets demarcation criteria A, B, C and F. XjTRV has a similar genome organization to LSTRV (criterion D). Neutralisation tests (criterion E) have not been conducted as no virus isolates are currently available.  **Derivation of names**  The species name *Hyalomma lostrhavirus* has been selected as XjTRV was detected in ticks of the genus *Hyalomma*. | |

**Supporting evidence**

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**Figure 1.** Lostrhavirus genome organisations.

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**Figure 2.** A Clustal X alignment of the VSIV G protein with the lostrhavirus G proteins. Conserved cysteine residues in the VSIV G protein are marked (CI-CXII).

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**Figure 3.** The evolutionary history was inferred from a Clustal W alignment of 169 complete L protein sequences of 168 animal rhabdoviruses currently assigned or recently proposed for assignment to species in other genera and Xinjiang tick rhabdovirus which we propose to be assigned to a new species in the genus *Lostrhavirus*. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 915 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-127314.573) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.

**References**

XjTRV is reported only as a GenBank entry (MH688524); are no other published references to this virus.