



ICTV Virus Taxonomy Profile: *Leishbuviridae* 2023

Scott Adkins¹, Katherine Brown², Juan Carlos de la Torre³, Michele Digiario⁴, Holly R. Hughes⁵, Sandra Junglen⁶, Amy J. Lambert⁵, Piet Maes⁷, Marco Marklewitz⁸, Gustavo Palacios⁹, Takahide Sasaya (笹谷孝英)¹⁰, Massimo Turina¹¹, Yong-Zhen Zhang (张永振)¹² and Jens H. Kuhn^{13,*}

Abstract

Leishbuviridae is a family of negative-sense RNA viruses with genomes of about 8.0 kb that have been found in protists. The leishbuvirid genome consists of three monocistronic RNA segments with open reading frames (ORFs) that encode a nucleoprotein (NP), a glycoprotein (GP), and a large (L) protein containing an RNA-directed RNA polymerase (RdRP) domain. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Leishbuviridae*, which is available at [ictv.global/report/leishbuviridae](https://www.ictv.global/report/leishbuviridae).

Table 1. Characteristics of members of the family *Leishbuviridae*

Example	<i>Leptomonas moramango</i> virus (S: KX280014; M: KX280013; L: KX280012), species <i>Shilevirus leptomonadis</i> , genus <i>Shilevirus</i>
Virion	Unknown
Genome	About 8.0 kb of trisegmented negative-sense RNA
Replication	Unknown
Translation	Unknown
Host range	Kinetoplastean protists
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Negarnaviricota</i> , class <i>Ellioviricetes</i> , order <i>Bunyavirales</i> ; the family includes the genus <i>Shilevirus</i> and the species <i>Shilevirus leptomonadis</i>

VIRION

Unknown.

a total length of about 8.0 kb (S segment: 0.7–0.8 kb; M segment: about 1.2 kb; and L segment: about 6.0 kb) with ORFs that encode an NP, a GP, and an L protein containing an RdRP domain [1, 2] (Table 1, Fig. 1).

GENOME

The leishbuvirid genome comprises three RNA segments (small [S], medium [M], and large [L]) of linear negative-sense RNA with

REPLICATION

Unknown.

Received 22 November 2023; Accepted 23 November 2023; Published 08 December 2023

Author affiliations: ¹United States Department of Agriculture, Agricultural Research Service, US Horticultural Research Laboratory, Fort Pierce, FL 34945, USA; ²Division of Virology, Department of Pathology, Addenbrookes Hospital, University of Cambridge, Cambridge CB2 0QN, UK; ³Department of Immunology and Microbiology IMM-6, The Scripps Research Institute, La Jolla, CA 92037, USA; ⁴CIHEAM, Istituto Agronomico Mediterraneo di Bari, 70010 Valenzano, Italy; ⁵Centers for Disease Control and Prevention, Fort Collins, CO 80521, USA; ⁶Institute of Virology, Charité-Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Berlin 10117, Germany; ⁷KU Leuven, Rega Institute, Zoonotic Infectious Diseases Unit, 3000 Leuven, Belgium; ⁸FIND, 1202 Geneva, Switzerland; ⁹Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, NY 10029, USA; ¹⁰Institute for Plant Protection, National Agriculture and Food Research Organization, Tsukuba, Ibaraki 305-8517, Japan; ¹¹Institute for Sustainable Plant Protection, National Research Council of Italy (IPSP-CNR), 10135 Torino, Italy; ¹²School of Life Sciences and Human Phenome Institute, Fudan University, Shanghai 201052, PR China; ¹³Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, MD 21702, USA.

***Correspondence:** Jens H. Kuhn, kuhnjens@mail.nih.gov

Keywords: ICTV Report; *Leishbuviridae*; *Leptomonas moramango* virus; shilevirus; taxonomy.

Abbreviations: GP, glycoprotein; L, large; M, medium; NP, nucleoprotein; RdRP, RNA-directed RNA polymerase; S, small.

001934 © 2023 The Authors



This is an open-access article distributed under the terms of the Creative Commons Attribution License.

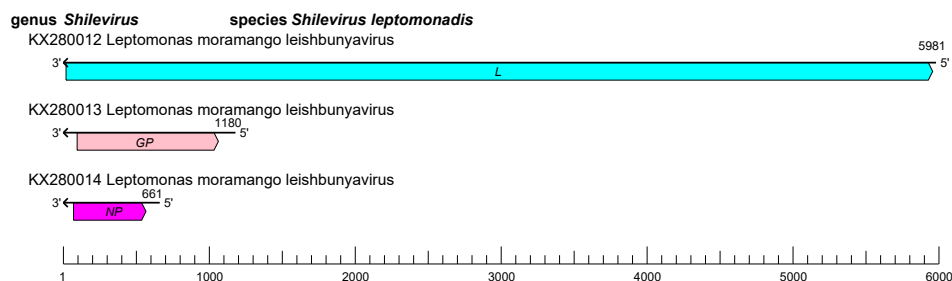


Fig. 1. Genome organisation of *Leptomonas moramango* virus. ORFs are coloured according to the predicted protein function (GP, glycoprotein gene; L, large protein gene; NP, nucleoprotein gene).

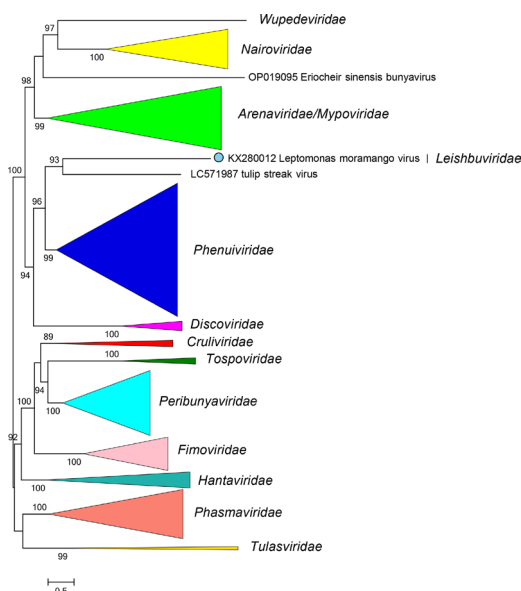


Fig. 2. Phylogenetic relationships of *Leptomonas moramango* virus with closely related viruses. Family branches are collapsed. Numbers at nodes indicated bootstrap support >70%. Details of the virus sequences and methods used are available in the full ICTV Report on the family *Leishbuviridae*.

TAXONOMY

Current taxonomy: [ictv.global/taxonomy](https://www.ictv.global/taxonomy). Leishbuvirids are most closely related to arenavirids, discovirids, mypovirids, nairovirids, phenuivirids, and wupedevirids [3, 4] (Fig. 2). The family includes the genus *Shilevirus* for viruses that infect protists; additional taxa may be represented among the numerous leishbuvirid-like sequences that have been described [5]. Leishbuvirids (i) have

multisegmented, negative-sense single-stranded RNA genomes; (ii) encode proteins with high sequence identity to proteins of other bunyavirals; (iii) and have five conserved motifs (A–E) in their RdRP domain.

RESOURCES

Full ICTV Report on the family *Leishbuviridae*: [ictv.global/report/leishbuviridae](https://www.ictv.global/report/leishbuviridae).

Funding information

Production of this Profile, the ICTV Report, and associated resources was supported by the Microbiology Society. This work was supported in part through the Laulima Government Solutions, LLC, prime contract with the U.S. National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN272201800013C. J.H.K. performed this work as an employee of Tunnell Government Services (TGS), a subcontractor of Laulima Government Solutions, LLC, under Contract No. HHSN272201800013C. The content of this publication should not be interpreted as necessarily representing the official policies, either expressed or implied, of the U.S. Department of Health and Human Services, including the Centres for Disease Control and Prevention, or of the institutions and companies affiliated with the authors, nor does mention of trade names, commercial products, or organisations imply endorsement by the U.S. Government. The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centres for Disease Control and Prevention.

Acknowledgements

We thank Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, Peter Simmonds, F. Murilo Zerbini, Evelien Adriaenssens, Mart Krupovic, Luisa Rubino, Arvind Varsani (ICTV Report Editors), and Donald B. Smith (Managing Editor, ICTV Report). We thank Anya Crane (Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, MD, USA) for critically editing the manuscript.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Akopyants NS, Lye L-F, Dobson DE, Lukeš J, Beverley SM. A novel bunyavirus-like virus of trypanosomatid protist parasites. *Genome Announc* 2016;4:e00715–16.
2. Grybchuk D, Akopyants NS, Kostygov AY, Konovalovas A, Lye L-F, et al. Viral discovery and diversity in trypanosomatid protozoa with a focus on relatives of the human parasite *Leishmania*. *Proc Natl Acad Sci U S A* 2018;115:E506–E515.

3. Huang P, Zhang X, Ame KH, Shui Y, Xu Z, et al. Genomic and phylogenetic characterization of a bunya-like virus from the freshwater Chinese mitten crab *Eriocheir sinensis*. *Acta Virol* 2019;63:433–438.
4. Herath V, Romay G, Urrutia CD, Verchot J. Family level phylogenies reveal relationships of plant viruses within the order *Bunyavirales*. *Viruses* 2020;12:e1010.
5. Macedo DH, Grybchuk D, Režnarová J, Votýpka J, Kloczek D, et al. Diversity of RNA viruses in the cosmopolitan monoxenous trypanosomatid *Leptomonas pyrrocoris*. *BMC Biol* 2023;21:191.