JOURNAL OF GENERAL VIROLOGY

ICTV VIRUS TAXONOMY PROFILE

Kuhn *et al.*, *Journal of General Virology* 2023;104:001932

DOI 10.1099/jgv.0.001932

MICROBIOLOGY SOCIETY

OPEN ACCESS

ICTV Virus Taxonomy Profile: *Wupedeviridae* 2023

Jens H. Kuhn[1], Scott Adkins[2], Katherine Brown[3], Juan Carlos de la Torre[4], Michele Digiaro[5], Holly R. Hughes[6], Sandra Junglen[7], Amy J. Lambert[6], Piet Maes[8], Marco Marklewitz[9], Gustavo Palacios[10], Takahide Sasaya (笹谷孝英)[11], Massimo Turina[12] and Yong-Zhen Zhang (张永振)[13,*]

Abstract

Wupedeviridae is a family of negative-sense RNA viruses with genomes of about 20.5 kb that have been found in myriapods. The wupedevirid 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 *Wupedeviridae*, which is available at ictv.global/report/wupedeviridae.

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

Example	**Wǔhàn millipede virus 2 (S: KM817757; M: KX650645; L: KM817696), species *Wumivirus millepedae*, genus *Wumivirus***
Virion	Unknown
Genome	About 20.5 kb of trisegmented negative-sense RNA
Replication	Unknown
Translation	Unknown
Host range	Polydesmid myriapods (millipedes)
Taxonomy	Realm *Riboviria*, kingdom *Orthornavirae*, phylum *Negarnaviricota*, class *Ellioviricetes*, order *Bunyavirales*; the family includes the genus *Wumivirus* and the species *Wumivirus millepedae*

VIRION

Unknown.

GENOME

The wupedevirid genome comprises three RNA segments (small [S], medium [M], and large [L]) of linear negative-sense RNA with a total length of about 20.5 kb (S segment: about 1.9 kb; M segment: about 7.0 kb; and L segment: about 11.6 kb) (Table 1). Each segment contains an ORF that encodes an NP (S segment), a GP (M segment), and an L protein containing an RdRP domain (L segment) [1] (Fig. 1).

REPLICATION

Unknown.

Received 22 November 2023; Accepted 23 November 2023; Published 20 December 2023

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

Keywords: ICTV Report; taxonomy; *Wupedeviridae*; wumivirus; Wǔhàn millipede virus 2.
Abbreviations: L, large; M, medium; NP, nucleoprotein; RdRP, RNA-directed RNA polymerase; S, small.
001932 © 2023 The Authors

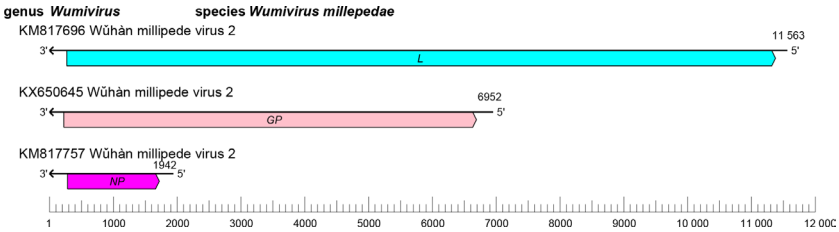

Fig. 1. Genome organisation of Wǔhàn millipede virus 2. ORFs are coloured according to the predicted protein function (*GP*, glycoprotein gene; *L*, large protein gene; *NP*, nucleoprotein gene).

TAXONOMY

Current taxonomy: ictv.global/taxonomy. Wupedevirids are most closely related to arenavirids, discovirids, leishbuvirids, mypoviruses, nairovirids, and phenuivirids [2–4] (Fig. 2). The family includes the genus *Wumivirus* for viruses that infect myriapods (millipedes). Like most closely related viruses [3, 5], wupedevirids (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.

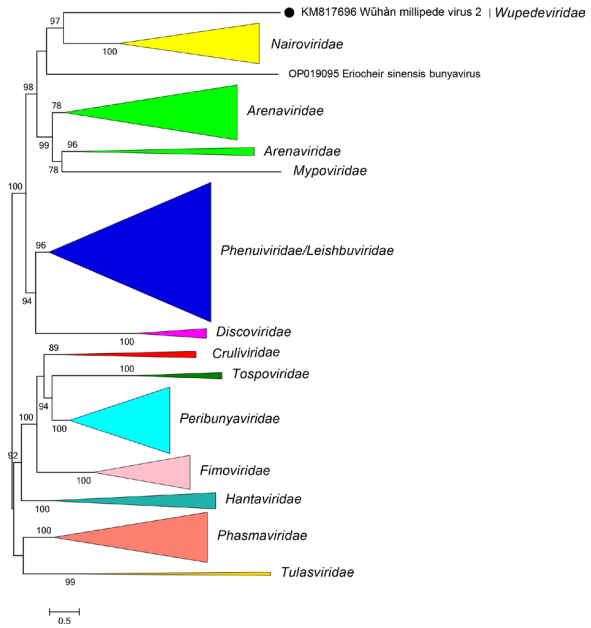

Fig. 2. Phylogenetic relationships of Wǔhàn millipede virus 2. Family branches have been collapsed. Numbers at nodes indicate bootstrap support >70%. For details of viruses and methods see the full ICTV Report on the family *Wupedeviridae*.

RESOURCES

Full ICTV Report on the family *Wupedeviridae*: ictv.global/report/wupedeviridae.

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. **Li C-X**, **Shi M**, **Tian J-H**, **Lin X-D**, **Kang Y-J**, ***et al***. Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. *Elife* 2015;4:e05378.
2. **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.
3. **Herath V**, **Romay G**, **Urrutia CD**, **Verchot J**. Family level phylogenies reveal relationships of plant viruses within the order *Bunyavirales*. *Viruses* 2020;12:1010.
4. **Olendraite I**, **Brown K**, **Firth AE**. Identification of RNA virus-derived RdRp sequences in publicly available transcriptomic data sets. *Mol Biol Evol* 2023;40:1093.
5. **Sun Y**, **Li J**, **Gao GF**, **Tien P**, **Liu W**. Bunyavirales ribonucleoproteins: the viral replication and transcription machinery. *Crit Rev Microbiol* 2018;44:522–540.