



HAL
open science

Six Nearly Complete Genome Segments of a Novel Reovirus Identified in Laotian Batflies

Sarah Temmam, Khamsing Vongphayloth, Jeffrey C. Hertz, Ian Sutherland, Bounsavane Douangboubpha, Marc Grandadam, Thomas Bigot, Paul T. Brey, Marc Eloit

► **To cite this version:**

Sarah Temmam, Khamsing Vongphayloth, Jeffrey C. Hertz, Ian Sutherland, Bounsavane Douangboubpha, et al.. Six Nearly Complete Genome Segments of a Novel Reovirus Identified in Laotian Batflies. *Microbiology Resource Announcements*, 2019, 8 (46), pp.e00733-19. 10.1128/MRA.00733-19. pasteur-03240194

HAL Id: pasteur-03240194

<https://pasteur.hal.science/pasteur-03240194v1>

Submitted on 28 May 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Six Nearly Complete Genome Segments of a Novel Reovirus Identified in Laotian Batflies

Sarah Temmam,^a Khamsing Vongphayloth,^b Jeffrey C. Hertz,^c Ian Sutherland,^{c,d} Bounsavane Douangboubpha,^e Marc Grandadam,^f  Thomas Bigot,^{a,g} Paul T. Brey,^b Marc Eloit^{a,h}

^aInstitut Pasteur, Biology of Infection Unit, Inserm U1117, Pathogen Discovery Laboratory, Paris, France

^bLaboratory of Vector Borne Diseases, Institut Pasteur du Laos, Vientiane, Lao People's Democratic Republic

^cUnited States Naval Medical Research Unit Two, Singapore

^dUnited States Navy Entomology Center of Excellence, NAS Jacksonville, Jacksonville, Florida, USA

^eFaculty of Environmental Science, Lao National University, Vientiane, Lao People's Democratic Republic

^fArbovirology and Emerging Virus Laboratory, Institut Pasteur du Laos, Vientiane, Lao People's Democratic Republic

^gInstitut Pasteur–Bioinformatics and Biostatistics Hub–Computational Biology Department, Institut Pasteur, USR 3756 CNRS, Paris, France

^hNational Veterinary School of Alfort, Paris-Est University, Maisons-Alfort, France

ABSTRACT As part of the characterization of viral communities of Laotian batflies, we report here the sequencing of six nearly complete genome segments of a novel reovirus identified in Laotian batflies that is distantly related to reoviruses recently reported in various Diptera species.

Batflies are obligate bloodsucking Diptera (Hippoboscoidea) species belonging to two families, Streblidae and Nycteribiidae. Streblidae species have functional wings, whereas Nycteribiidae species are flattened, spiderlike flies that lack wings. Usually known as “batflies,” most species are highly host-specific and only feed on bats. Viruses belonging to the *Reoviridae* are double-stranded nonenveloped RNA viruses that present 9 to 12 genome segments. They have been found in many host species, from plants to vertebrate and invertebrate animals (1). Recently, six segments of two novel reoviruses in Diptera were sequenced (i.e., High Island virus in U.S. mosquitoes [2] and Hubei diptera virus 21 in a Chinese pool of Diptera species [3]). In order to characterize viral communities of bat ectoparasites in the Lao People's Democratic Republic, we report here the sequencing of 6 nearly complete segments of a novel divergent reovirus identified in Laotian batflies.

A total of 99 batflies (8 genera belonging to the families Streblidae and Nycteribiidae) collected in 2017 in the Vientiane Province of Lao People's Democratic Republic (Fueng, Hin Heup, and Van Vieng districts) were analyzed. Batflies were morphologically identified at the genus level. Individual specimens were suspended in 400 μ l of cold phosphate-buffered saline (PBS) and crushed for 1 min at 60 Hz in a TissueLyser homogenizer (Qiagen) in the presence of Lysing Matrix E beads (MP Biomedicals). Residual tissue fragments were pelleted by spinning the tubes at 10,000 $\times g$ for 5 min. Half of the supernatant (200 μ l) was used for total RNA purification using NucleoSpin RNA kits (Macherey-Nagel) according to the manufacturer's instructions. The rest of the lysates were kept frozen at -80°C for viral isolation assays. Nine minipools of 11 individuals were constituted to contain both batfly families and were further used for transcriptome sequencing (RNA-Seq) library preparation using the SMARTer stranded RNA-Seq Pico Input mammalian kit v2 (Clontech). The nine libraries were sequenced in a 2 \times 150-bp paired-end format on a NextSeq sequencer with the NextSeq 500/550 high-output v2 flow cell (Illumina). An average of 43 million clusters were obtained per library. An in-house bioinformatics pipeline was used, which comprised quality check

Citation Temmam S, Vongphayloth K, Hertz JC, Sutherland I, Douangboubpha B, Grandadam M, Bigot T, Brey PT, Eloit M. 2019. Six nearly complete genome segments of a novel reovirus identified in Laotian batflies. *Microbiol Resour Announc* 8:e00733-19. <https://doi.org/10.1128/MRA.00733-19>.

Editor Jelle Matthijssens, KU Leuven

Copyright © 2019 Temmam et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Paul T. Brey, ptb1957@yahoo.com, or Marc Eloit, marc.eloit@pasteur.fr.

Received 19 June 2019

Accepted 18 October 2019

Published 14 November 2019

TABLE 1 Matrix showing the amino acid identity of Lao batfly reovirus with representative closest members of the *Reoviridae* family^a

Sequence no.	Species	% amino acid identity (segment) by sequence no. and species ^b :										
		1 (Lao batfly reovirus)	2 (Shelly Beach virus)	3 (High Island virus)	4 (Hubei diptera virus 21)	5 (Eccles virus)	6 (Operophtera brumata reovirus)	7 (Hubei reo-like virus 3)	8 (Cimodo virus)	9 (Lutzomyia reovirus 2)	10 (Torrey Pines virus)	11 (Maize rough dwarf virus)
2	Shelly Beach virus	61.83 (S1), 57.04 (S2), 36.65 (S5)										
3	High Island virus	65.27 (S1), 54.78 (S2), 41.58 (S5)	64.89 (S1), 56.89 (S2), 42.55 (S5)									
4	Hubei diptera virus 21	55.43 (S1), 52.18 (S2), 33.19 (S5)	56.38 (S1), 50.68 (S2), 34.82 (S5)	58.10 (S1), 49.57 (S2), 35.17 (S5)	66.09 (S1), 61.77 (S2), 50.64 (S5)							
5	Eccles virus	61.07 (S1), 51.18 (S2), 35.11 (S5)	60.69 (S1), 50.81 (S2), 37.15 (S5)	60.11 (S1), 48.94 (S2), 36.65 (S5)	66.09 (S1), 61.77 (S2), 50.64 (S5)							
6	Operophtera brumata reovirus	37.17 (S1)	37.55 (S1)	37.36 (S1)	38.87 (S1)	37.24 (S1)						
7	Hubei reo-like virus 3	22.10 (S1)	22.28 (S1)	20.97 (S1)	21.76 (S1)	21.58 (S1)	19.14 (S1)					
8	Cimodo virus	22.37 (S1)	21.62 (S1)	22.74 (S1)	22.41 (S1)	21.58 (S1)	19.81 (S1)	44.23 (S1)				
9	Lutzomyia reovirus 2	20.00 (S1)	19.43 (S1)	18.15 (S1)	19.09 (S1)	18.71 (S1)	18.16 (S1)	17.41 (S1)	17.05 (S1)			
10	Torrey Pines virus	19.62 (S1)	18.49 (S1)	20.04 (S1)	20.60 (S1)	18.71 (S1)	16.54 (S1)	20.00 (S1)	20.08 (S1)	32.19 (S1)		
11	Maize rough dwarf virus	21.38 (S1)	20.63 (S1)	21.56 (S1)	20.19 (S1)	19.81 (S1)	18.73 (S1)	21.59 (S1)	19.96 (S1)	15.62 (S1)	17.18 (S1)	
12	Rice black streaked dwarf virus	21.19 (S1)	21.00 (S1)	21.56 (S1)	20.19 (S1)	19.44 (S1)	18.35 (S1)	21.40 (S1)	19.96 (S1)	15.81 (S1)	17.37 (S1)	96.46 (S1)

^aAccession numbers are given here for segments 1, 2, and 5, respectively, for viruses numbered 1 to 5, and for segment 1 for viruses numbered 6 to 12. Sequence numbers, species, and accession numbers are as follows:

1, Lao batfly reovirus (GenBank accession numbers [QBA09477](#), [QBA09478](#), and [QBA09481](#)); 2, Shelly Beach virus ([AYP67577](#), [AYP67578](#), and [AYP67581](#)); 3, High Island virus ([AVO64750](#), [MF094129](#) [translation in amino acids of the nucleotide sequence], and [AVO64753](#)); 4, Hubei diptera virus 21 ([APG79176](#), [APG79177](#), and [APG79180](#)); 5, Eccles virus ([AWA82237](#), [AWA82238](#), and [AWA82241](#)); 6, Operophtera brumata reovirus ([YP_392501](#)); 7, Hubei reo-like virus 3 ([APG79172](#)); 8, Cimodo virus ([AHF20715](#)); 9, Lutzomyia reovirus 2 ([AKP18622](#)); 10, Torrey Pines virus ([AWY11145](#)); 11, Maize rough dwarf virus ([ANG56321](#)); and 12, Rice black streaked dwarf virus ([AO558315](#)).

^bS1 refers to segment 1, coding for the RNA-dependent RNA polymerase; S2 refers to segment 2 complete coding sequence (CDS); S5 refers to segment 5 complete CDS.

and trimming (based on AlienTrimmer package v0.4.0, using default parameters except for $-p = 80$ [4]), *de novo* assembly (using MEGAHIT v1.1.2 with default parameters, except for the minimum contig length being defined as 100 bp [5]), and open reading frame (ORF) prediction (https://figshare.com/articles/translateReads_py/7588592). A BLAST-based similarity search (v2.2.26) was performed for all contigs and singletons against the protein Reference Viral Database (RVDB) (6), followed by the verification that no better hit than a virus was found when a BLAST search was performed against the whole NCBI nonredundant (nr) protein database.

Six out of nine pools of batflies included sequences related to the family *Reoviridae*. Although one pool contained only 6 singletons, which were assigned to 3 segments belonging to members of the *Reoviridae*, the other 5 pools presented large contigs with distant similarity (<65% amino acid identity) to Hubei diptera virus 21, High Island virus, Eccles virus, and Shelly Beach virus, respectively identified in Diptera, mosquitoes, *Drosophila*, and tick arthropods (Table 1). We combined reads belonging to pools BF02, BF07, and BF10 to *de novo* assemble viral segments of this novel reovirus, tentatively named Lao batfly reovirus. This virus includes at least 6 segments that present distant homologies with Hubei diptera virus 21 and High Island virus, but additional highly divergent segments may have been missed by the usual BLAST-based methods of taxonomic assignation of reads. To date, it is therefore impossible to conclusively state the number of segments comprising Lao batfly reovirus. To help with segment annotation, we aligned the 5' and 3' putative termini of Lao batfly reovirus with Hubei diptera virus 21 and High Island reovirus segments. Segments 4 and 6 were partially sequenced, whereas the complete ORFs were obtained for segments 1, 2, 3, and 5, with high coverage (> 500× per segment). Segment 1 encodes a protein of 1,373 amino acids (aa), and segments 2, 3, and 5 code for hypothetical proteins of 1,174, 1,076, and 595 aa, respectively (4,160 bp, 3,654 bp, 3,334 bp, and 1,898 bp, respectively, for segments 1, 2, 3, and 5). To assign a function to the segment 1 viral protein, we used the Swiss-Model program (7) to predict the tertiary structure of Lao batfly reovirus segment 1. The closest structure determined by Swiss-Model was the RNA-dependent RNA polymerase of cytoplasmic polyhedrosis virus (CPV), a reovirus that infects insects. No significant hit was obtained for other proteins coded by segments 2 to 6, leading us to propose them as hypothetical proteins. Further biochemical characterizations will help define functions for these viral proteins.

The bat study was approved by the Institutional Animal Care and Use Committee (IACUC) of the Department of Forest Resource Management (DFRM). For the Lao People's Democratic Republic side, the authorization agreement for carrying out bat capture was approved by the wildlife authorities of the DFRM and by the Ministry of Agriculture and Forestry, Lao People's Democratic Republic (approval number 0174/DFRM, issued January 2017).

Data availability. The genome sequence of Lao batfly reovirus strain BF02/7/10 was deposited in GenBank under accession numbers [MK468721](#) to [MK468726](#). Raw data corresponding to Lao batfly reovirus were deposited in the SRA database under accession number [SRR8592028](#).

ACKNOWLEDGMENTS

We thank the Ministry of Health and the Ministry of Agriculture and Forestry, Lao People's Democratic Republic, for their authorization of our field work. We also thank the local officials in Vientiane and all of the villagers who facilitated our field collection. Staff of the Faculty of Environmental Sciences, National University of Laos, provided expert assistance in bat collections, and Institut Pasteur du Laos (IP-Laos) staff provided expert assistance in DNA/RNA extraction.

The opinions and assertions contained here are those of the authors and do not reflect official views or policy of the U.S. Departments of the Army and Navy, the U.S. Department of Defense, or the U.S. Government.

J.C.H. and I.S. are military service members or federal/contracted employees of the United States government. This work was prepared as part of their official duties. Title

17 U.S.C. 105 provides that “copyright protection under this title is not available for any work of the United States Government.” Title 17 U.S.C. 101 defines a U.S. Government work as work prepared by a military service member or employee of the U.S. Government as part of that person’s official duties.

This work was supported by the United States Naval Medical Research Unit Two, work unit number D1425, in support of the Armed Forces Health Surveillance Branch–Global Emerging Infections Surveillance and Response System (AFHSB-GEIS), by the Institute Pasteur du Laos, by Laboratoire d’Excellence “Integrative Biology of Emerging Infectious Diseases” grant ANR-10-LABX-62-IBEID, and by the Direction Internationale de l’Institut Pasteur.

REFERENCES

1. Attoui H, Mohd Jaafar F, Belhouchet M, Biagini P, Cantaloube JF, de Micco P, de Lamballerie X. 2005. Expansion of family *Reoviridae* to include nine-segmented dsRNA viruses: isolation and characterization of a new virus designated *Aedes pseudoscutellaris* reovirus assigned to a proposed genus (*Dinovirnavirus*). *Virology* 343:212–223. <https://doi.org/10.1016/j.virol.2005.08.028>.
2. Sadeghi M, Popov V, Guzman H, Phan TG, Vasilakis N, Tesh R, Delwart E. 2017. Genomes of viral isolates derived from different mosquitos species. *Virus Res* 242:49–57. <https://doi.org/10.1016/j.virusres.2017.08.012>.
3. Shi M, Lin XD, Tian JH, Chen LJ, Chen X, Li CX, Qin XC, Li J, Cao JP, Eden JS, Buchmann J, Wang W, Xu J, Holmes EC, Zhang YZ. 2016. Redefining the invertebrate RNA virosphere. *Nature* 540:539–543. <https://doi.org/10.1038/nature20167>.
4. Criscuolo A, Brisse S. 2014. AlienTrimmer removes adapter oligonucleotides with high sensitivity in short-insert paired-end reads. *Commentary on Turner (2014) Assessment of insert sizes and adapter content in FASTQ data from NexteraXT libraries*. *Front Genet* 5:130. <https://doi.org/10.3389/fgene.2014.00130>.
5. Li D, Liu CM, Luo R, Sadakane K, Lam TW. 2015. MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics* 31:1674–1676. <https://doi.org/10.1093/bioinformatics/btv033>.
6. Bigot T, Temmam S, Pérot P, Eloit M. 2019. RVDB-prot, a reference viral protein database and its HMM profiles [version 1; peer review: 2 approved with reservations]. *F1000Res* 8:530. <https://doi.org/10.12688/f1000research.18776.1>.
7. Waterhouse A, Bertoni M, Bienert S, Studer G, Tauriello G, Gumienny R, Heer FT, de Beer TAP, Rempfer C, Bordoli L, Lepore R, Schwede T. 2018. SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Res* 46:296–303. <https://doi.org/10.1093/nar/gky427>.