

# Genome Sequences of a Novel Vietnamese Bat Bunyavirus

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**To document the viral zoonotic risks in Vietnam, fecal samples were systematically collected from a number of mammals in southern Vietnam and subjected to agnostic deep sequencing. We describe here novel Vietnamese bunyavirus sequences detected in bat feces. The complete L and S segments from 14 viruses were determined.**

Received 25 October 2016 Accepted 28 October 2016 Published 22 December 2016

**Citation** Oude Munnink BB, Phan MVT, van der Hoek L, Kellam P, Cotten M, the VIZIONS Consortium. 2016. Genome sequences of a novel Vietnamese bat bunyavirus. *Genome Announc* 4(6):e01366-16. doi:10.1128/genomeA.01366-16.

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The *Bunyaviridae* is a diverse viral family comprising five genera. Some members are notorious for their zoonotic potential (hantavirus and Rift Valley fever virus), one can cause severe problems in cattle (Smallegen virus), and another infects plants (tomato spotted wilt virus). Members of the enveloped *Bunyaviridae* typically enclose a segmented negative-sense single-stranded RNA genome, with the L segment encoding an RNA-dependent RNA polymerase (RdRp), the M segment encoding glycoproteins, and the S segment encoding the nucleoprotein. The combined genomic length of the three segments is 11 to 19 kb (1).

We searched for novel members of the *Bunyaviridae* in 135 bat fecal samples collected from roosting sites using an agnostic deep-sequencing approach (2). Fecal samples were processed as previously described (3), followed by sequencing on an Illumina HiSeq platform yielding 3 to 4 million 250-nucleotide (nt) paired-end reads per sample, which were *de novo* assembled using SPAdes version 3.5.0 (4), followed by improve\_assembly (5). The resulting reads were subjected to a modified protein blast search using usearch (6) to identify *Bunyaviridae*-related sequences.

Fourteen of 135 samples (10%) yielded sequences with 51% amino acid identity to a small part of the RdRp of a *Rhinolophus pearsoni* bunyavirus. The M and S segments of this new Vietnamese bat bunyavirus could not be identified using simple homology searching. Therefore, Uclust (6) was used to cluster all consensus sequences of the bunyavirus-positive samples. Contigs present in over 70% of the samples were submitted to a conserved domain search (7), which yielded a putative S segment of the novel bunyavirus showing similarities to a conserved tenuivirus/phlebovirus nucleocapsid protein domain; however, no amino acid identity to known bunyaviruses could be identified. The genome lengths of the L segment of the novel Vietnamese bat bunyaviruses were 6,484 to 6,713 nucleotides (average sequence coverage, 78- to 2,619-fold). The nucleotide sequence of the L segment of the 14 isolates differed at 21 to 124 positions (98% to 100% nucleotide identity), while the S segments differed at 5 to 54 positions (97% to 100% nucleotide identity). The genome length of the S segment varied between 1,464 and 1,578 nucleotides (average sequence coverage, 47- to 849-fold).

Consistent with other studies (8,9), no contigs with similarities

to the *Bunyaviridae* M segment could be found. Either the M segment exists in these samples with greater sequence divergence precluding identification, or these viruses exist without a standard M segment, perhaps by complementation with functions from other coinfecting viruses.

In conclusion, we present the L and S genome segments of a novel Vietnamese bunyavirus. This novel virus was identified in 14 bat fecal samples, and for all viruses, the complete genome sequences of the L and S segments were determined. The lengths of the two segments of this novel unclassified bunyavirus are consistent with other members of *Phlebovirus* and the *Hantavirus* (1); however, additional research is needed to accurately classify this novel bunyavirus and resolve the M segment mystery.

**Accession number(s).** The complete genome sequences of the Vietnamese bat bunyaviruses are deposited in GenBank under the accession numbers [KX886759](https://www.ncbi.nlm.nih.gov/nuccore/KX886759) to [KX886786](https://www.ncbi.nlm.nih.gov/nuccore/KX886786).

## ACKNOWLEDGMENTS

The VIZIONS Consortium members (alphabetical order by surname) from the Oxford University Clinical Research Unit are Bach Tuan Kiet, Stephen Baker, Alessandra Berto, Maciej F. Boni, Juliet E. Bryant, Bui Duc Phu, James I. Campbell, Juan Carrique-Mas, Dang Manh Hung, Dang Thao Huong, Dang Tram Oanh, Jeremy N. Day, Dinh Van Tan, H. Rogier van Doorn, Duong An Han, Jeremy J. Farrar, Hau Thi Thu Trang, Ho Dang Trung Nghia, Hoang Bao Long, Hoang Van Duong, Huynh Thi Kim Thu, Lam Chi Cuong, Le Manh Hung, Le Thanh Phuong, Le Thi Phuc, Le Thi Phuong, Le Xuan Luat, Luu Thi Thu Ha, Ly Van Chuong, Mai Thi Phuoc Loan, Behzad Nadjm, Ngo Thanh Bao, Ngo Thi Hoa, Ngo Tri Tue, Nguyen Canh Tu, Nguyen Dac Thuan, Nguyen Dong, Nguyen Khac Chuyen, Nguyen Ngoc An, Nguyen Ngoc Vinh, Nguyen Quoc Hung, Nguyen Thanh Dung, Nguyen Thanh Minh, Nguyen Thi Binh, Nguyen Thi Hong Tham, Nguyen Thi Hong Tien, Nguyen Thi Kim Chuc, Nguyen Thi Le Ngoc, Nguyen Thi Lien Ha, Nguyen Thi Nam Lien, Nguyen Thi Ngoc Diep, Nguyen Thi Nhung, Nguyen Thi Song Chau, Nguyen Thi Yen Chi, Nguyen Thieu Trinh, Nguyen Thu Van, Nguyen Van Cuong, Nguyen Van Hung, Nguyen Van Kinh, Nguyen Van Minh Hoang, Nguyen Van My, Nguyen Van Thang, Nguyen Van Thanh, Nguyen Van Vinh Chau, Nguyen Van Xang, Pham Ha My, Pham Hong Anh, Pham Thi Minh Khoa, Pham Thi Thanh Tam, Pham Van Lao, Pham Van Minh, Phan Van Be Bay, Phan Vu Tra My, Maia A. Rabaa, Motiur Rahman, Corinne Thompson, Guy Thwaites, Ta Thi Dieu Ngan, Tran Do

Hoang Nhu, Tran Hoang Minh Chau, Tran Khanh Toan, Tran My Phuc, Tran Thi Kim Hong, Tran Thi Ngoc Dung, Tran Thi Thanh Thanh, Tran Thi Thuy Minh, Tran Thua Nguyen, Tran Tinh Hien, Trinh Quang Tri, Vo Be Hien, Vo Nhut Tai, Vo Quoc Cuong, Voong Vinh Phat, V. U. Thi Lan Huong, and Vu Thi Ty Hang, Heiman Wertheim; from the Centre for Immunity, Infection and Evolution, University of Edinburgh: Carlijn Bogaardt, Margo Chase-Topping, A. L. Ivens, Lu Lu, Dung Nyugen, Andrew Rambaut, Peter Simmonds, and Mark Woolhouse; from the Wellcome Trust Sanger Institute, Hinxton, United Kingdom: Matthew Cotten, Bas Oude Munnink, Paul Kellam, and My Vu Tra Phan; from the Laboratory of Experimental Virology, Department of Medical Microbiology, Center for Infection and Immunity Amsterdam (CINIMA), Academic Medical Center of the University of Amsterdam, Amsterdam, The Netherlands: Martin Deijs, Lia van der Hoek, Maarten F. Jebbink, and Seyed Mohammad Jazaeri Farsani; and from Metabiota, Inc., San Francisco, CA: Kimberly Dodd, Jason Euren, Ashley Lucas, Nancy Ortiz, Len Pennacchio, Edward Rubin, Karen E. Saylor, Tran Minh Hai, and Nathan D. Wolfe.

#### FUNDING INFORMATION

This work was supported by the Wellcome Trust of the United Kingdom through the VIZIONS strategic award WT/093724. M.C. and B.B.O.M. were additionally funded by the European Union's Horizon 2020 research and innovation program under grant agreements 643476 (COMPARE) and 634650 (Virogenesis).

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