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 (Smallenburs 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 1,576 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 to KX886786.

ACKNOWLEDGMENTS

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 Thu Minh, Tran Thu Nguyen, Tran Tinh Hien, Trinh Quang Tri, Vo Be Hien, Vo Nhu 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).

REFERENCES