Genome sequences of a novel vietnamese bat bunyavirus

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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 (Snoellenberg virus), and another infects plants (hantavirus and Rift Valley fever virus), one can cause severe pulmonary disease in humans (hantavirus) (1); however, additional research is needed to accurately classify this novel bunyavirus and resolve the M segment mystery.

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.

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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.

**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.

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 segments exist 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 coinfected 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.
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