A novel orthobunyavirus, Bellavista virus, was isolated from Culex (Melanoconion) portesi mosquitoes in the Bellavista neighborhood of Iquitos, Peru, in 2009. The assembled segment L, M, and S sequences of strain PRD0552 are 6,950, 4,469, and 1,256 bases in length, respectively, comprising complete protein-coding sequences and partial terminal untranslated sequences.

Received 14 September 2016 Accepted 21 September 2016 Published 10 November 2016

Citation Hang J, Yang Y, Kuschner RA, Evangelista J, Astete H, Halsey ES, Kochel TJ, Forshey BM. 2016. Genome sequence of Bellavista virus, a novel orthobunyavirus isolated from a pool of mosquitoes captured near Iquitos, Peru. Genome Announc 4(6):e01262-16. doi:10.1128/genomeA.01262-16.

Copyright © 2016 Hang et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Jun Hang, jun.hang.civ@mail.mil, or Brett M. Forshey, brett.m.forshey.ctr@mail.mil.

Many arthropod-borne viruses (arboviruses) are human pathogens (1, 2). Group C arboviruses were first isolated in acute febrile illness (AFI) patients in the 1950s and subsequently classified as members of genus Orthobunyavirus (family Bunyaviridae) (3). Orthobunyaviruses have been isolated from humans, other mammals, and arthropods in many regions worldwide (4–8). An epidemiological study in western South America identified AFI patients with orthobunyavirus infection in and around the city of Iquitos, located in the Amazon basin of northeastern Peru (9). To identify potential vectors of orthobunyviruses in the region, we collected mosquitoes using CO2-baited light traps in four sites in two neighborhoods, Bellavista-Nanay and San Juan, in peri-urban areas of Iquitos (10).

Mosquitoes were pooled by species, location, and date; triturated; and inoculated onto mosquito (Aedes albopictus C6/36) and mammalian (African green monkey Vero 76) cell cultures (10). In one pool of Culex (Melanoconion) portesi collected in the Bellavista-Nanay neighborhood in November 2009 (pool PRD0552), orthobunyavirus infection was indicated by cytopathic effect and indirect immunofluorescent assay in inoculated Vero 76 cells using polyclonal antibodies against group C orthobunyaviruses. Nucleic acids of isolate PRD0552 were extracted from the supernatant of Vero 76 cell culture and subjected to random reverse transcription, random PCR amplification and high-throughput pyrosequencing using GS FLX system (Roche 454 Life Sciences, Branford, CT) (11, 12). Sequence data were assembled and analyzed using Roche GS analysis software v2.9 (Roche 454 Life Sciences), BLAST programs (http://blast.ncbi.nlm.nih.gov/Blast.cgi), and software Geneious 8.1.7 (Biomatters, Auckland, New Zealand).

The genome sequence for PRD0552 was assembled using 34,931 reads, in total 8,389,524 bases, with average sequence alignment depth of 660-fold. The assembled large (L) segment sequence of the genome has 6,950 bases with a complete open reading frame (ORF) encoding a 2,248 amino acids protein. The L protein has amino acid identity of 67.3% with RNA-dependent RNA polymerase (RdRp) of Enseada virus (AMR89952), a mosquito orthobunyavirus identified in Brazil (13) and 66.5% with RdRp of Caraparu virus (AGW82149), a human orthobunyavirus pathogen identified in Peru (14). The medium (M) segment sequence has 4,469 bases encoding one complete ORF for a 1,436 amino acids polyprotein, consisting of nonstructural protein NSm and glycoproteins Gn and Gc. The polyprotein is homologous with M proteins of human and mosquito orthobunyaviruses, including Guama virus (AKO90175) and Catu virus (AL554743) (15), albeit with amino acid identity of 62% or lower. The small (S) segment sequence has 1,256 bases encoding two complete ORFs for a putative 236 amino acid nucleocapsid protein and a putative 95 amino acid nonstructural protein NSs. These two proteins had low similarity with known orthobunyaviruses, including 51.0% and 41.5% amino acid identities with the respective homologs (AMR98955 and AMR98954) in Enseada virus (14). The low identities with known orthobunyaviruses for the encoded gene products indicate that the isolate represents a novel virus, which we provisionally term Bellavista virus, after the neighborhood where the mosquitoes were collected.

Accession number(s). The segment L, M, and S sequences for the Bellavista virus genome were deposited in GenBank under accession numbers KX161718 to KX161720.

ACKNOWLEDGMENTS

The views expressed here are those of the authors and do not reflect the official policy of the Department of the Army, Department of the Navy, Department of Defense, or U.S. Government. We declare that no conflict of interest exists. JH, RAK, JE, HA, ESH, and TJK are military service members or employees of the U.S. 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 a work prepared by a military service member or employee of the U.S. Government as part of that person’s official duties.

FUNDING INFORMATION

This work was funded by the Armed Forces Health Surveillance Branch Global Emerging Infections Surveillance and Response System.
REFERENCES

1. Gall A. 2015. Bugs full of viruses. Nat Rev Microbiol 13:253. http://dx.doi.org/10.1038/nrmicro3479.

2. Bolling BG, Weaver SC, Tesh RB, Vasilakis N. 2015. Insect-specific virus discovery: significance for the arbovirus community. Viruses 7:4911–4928. http://dx.doi.org/10.3390/v7092851.

3. Walter CT, Barr JN. 2011. Recent advances in the molecular and cellular biology of bunyaviruses. J Gen Virol 92:2467–2484. http://dx.doi.org/10.1099/vir.0.035105-0.

4. Lanciotti RS, Kosoy OI, Bosco-Lauth AM, Pohl J, Stuchlik O, Reed M, Lambert AJ. 2013. Isolation of a novel orthobunyavirus (Brazoran virus) with a 1.7 kbs S segment that encodes a unique nucleocapsid protein possessing two putative functional domains. Virology 444:55–63. http://dx.doi.org/10.1016/j.virol.2013.05.031.

5. Treangen TJ, Schoeler G, Phillippy AM, Bergman NH, Turell MJ. 2016. Identification and genomic analysis of a novel group C orthobunyavirus isolated from a mosquito captured near Iquitos, Peru. J Gen Virol 94:1676–1687. http://dx.doi.org/10.1099/vir.0.028308-0.

6. Beer M, Conraths FJ, van der Poel WH. 2013. “Schmallenberg virus”—a novel orthobunyavirus emerging in Europe. Epidemiol Infect 141:1–8. http://dx.doi.org/10.1017/S0950268812002245.

7. hang J, Forshey BM, Kochel TJ, Li T, Solórzano VF, Halsey ES, Kuschner RA. 2012. Random amplification and pyrosequencing for identification of novel viral genome sequences. J Biomol Tech JBT 23:4–10. http://dx.doi.org/10.7171/jbt.12-2301-001.

8. De Souza WM, Acrani GO, Romeiro MF, Reis O, Jr, Tolardo AL, da Silva SP, de Almeida Medeiros DB, Varela M, Nunes MR, Figueiredo LT. 2016. Molecular characterization of Capim and Enseada orthobunyaviruses. Infect Genet Evol 40:47–53. http://dx.doi.org/10.1016/j.meegid.2016.02.024.

9. Richer SM, Smedema ML, Durkin MM, Herman KM, Hage CA, Fuller D, Wheat LJ. 2016. Improved diagnosis of acute pulmonary histoplasmosis by combining antigen and antibody detection. Clin Infect Dis 62:896–902. http://dx.doi.org/10.1093/cid/ciw007.

10. Shchetinin AM, Lvov DK, Deriabin PG, Botikov AG, Gitelman AK, Kuhn JH, Alkhovsky SV. 2015. Genetic and phylogenetic characterization of Tataguine and Witwatersrand viruses and other orthobunyaviruses of the anopheles A, Capim, Guama, Koongol, Mapputta, Tete, and Turlock serogroups. Viruses 7:5987–6008. http://dx.doi.org/10.3390/v7112918.