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Anne Lavergne, Edith Darcissac, Hervé Bourhy, Sourakhata Tirera, Benoît De Thoisy, et al.. Complete Genome Sequence of a Vampire Bat Rabies Virus from French Guiana.. Genome Announcements, American Society for Microbiology, 2016, 4 (2), pii: e00188-16. <10.1128/genomeA.00188-16>. <pasteur-01429574>

HAL Id: pasteur-01429574

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Submitted on 8 Jan 2017

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Complete Genome Sequence of a Vampire Bat Rabies Virus from French Guiana

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A rabies virus was detected in a common vampire bat (*Desmodus rotundus*) in French Guiana. Its genomic sequence was obtained and found to be closely related to other hematophagous bat-related viruses that widely circulate in the northern Amazon region. This virus is named AT6.

Received 9 February 2016 Accepted 24 February 2016 Published 7 April 2016

Citation Lavergne A, Darcissac E, Bourhy H, Tirera S, de Thoisy B, Lacoste V. 2016. Complete genome sequence of a vampire bat rabies virus from French Guiana. *Genome Announc* 4(2):e00188-16. doi:10.1128/genomeA.00188-16.

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Rabies is a viral disease distributed all over the world, causing more than 55,000 deaths per year, principally in Africa and Asia (1). Most of the time, it is transmitted via rabid domestic animals, but the virus is also maintained and transmitted through sylvatic reservoirs, of which bats are a member. Vampire bats are now considered the main vector of the disease in South America (2, 3). In French Guiana, on the northern part of South America, 14 rabies cases were recorded in cattle and domestic carnivores between 1984 and 2011 (4). In 2008, a human rabies case was recorded (5). All cases were related to vampire bat-associated rabies viruses (RABV). RABV belongs to the *Rhabdoviridae* family, genus *Lyssavirus*. Its genome is a single-stranded negative-sense RNA of approximately 12 kb that encodes five structural proteins. A previous work on the circulation of rabies virus in wild bats in French Guiana allowed us to identify, among nearly 1,000 bats belonging to 30 species, one common vampire bat, *Desmodus rotundus*, which was positive for RABV (6).

We report here the full-genome sequence of the rabies virus isolate AT6. To generate the complete genome sequence, total RNA was extracted from the heart using the NucliSENS easyMAG bio-robot (bioMérieux). cDNA was prepared with the SuperScript III reverse transcriptase (Invitrogen). Sequences were generated by reverse transcription PCR (RT-PCR) using different combinations of primers. Overlapping amplicons were generated, cloned, and then sequenced by Beckman Coulter Genomics (Takeley, United Kingdom). One contig sequence was assembled using the MEGA5 software (7).

The complete genome of the strain is 11,922 nucleotides (nt) in length. Its genetic organization is consistent with that of previously sequenced rabies virus genomes, with five open reading frames unidirectionally transcribed and separated by intergenic regions of various sizes (8). The coding sequences are 1,353 nt for the nucleoprotein-encoding gene, 894 nt for the phosphoprotein, 609 nt for the matrix protein, 1,575 nt for the glycoprotein, and 6,387 nt for the RNA-dependent RNA polymerase, with the RNA-dependent RNA polymerase having a double start codon characteristic of RABV strains isolated from bats in the Americas (9).

We conducted a phylogenetic analysis based on the complete nucleotide sequence using a Bayesian approach with previously published rabies virus sequences. It showed that AT6 is closely related to a strain (accession no. KM594041) isolated from a *D. rotundus* bat in Brazil in 2013 with 98.79% nucleotide identity. These two sequences belong to a clade composed of sequences of desmodine origin from Brazil and French Guiana identified during the last two decades. All these strains belong to a large group of hematophagous bat-related viruses, named lineage II, which widely circulate in the northern Amazon region (10). Further analysis of RABV genomes detected in the northern Amazon region should enable an understanding of the circulation and transmission of RABV lineages in the bat populations.

Nucleotide sequence accession number. The complete genome sequence of RABV AT6 is available in the GenBank database under accession no. [KU523255](https://www.ncbi.nlm.nih.gov/nuclseq/KU523255).

FUNDING INFORMATION

This work, including the efforts of Anne Lavergne, Benoît de Thoisy, and Vincent Lacoste, was funded by ERDF (ViRUSES and CAROLIA). This work, including the efforts of Anne Lavergne, Benoît de Thoisy, and Vincent Lacoste, was funded by EC REGPOT (REGPOT-CT-2011-285837-STRonGer). This work, including the efforts of Anne Lavergne, Benoît de Thoisy, and Vincent Lacoste, was funded by ANR Investissements d'Avenir (CEBA Ref. ANR-10-LABX-25-01).

This work was conducted within the ViRUSES and CAROLIA programmes, supported by European funds (FEDER/ERDF) and assistance from the Région Guyane and Direction Régionale pour la Recherche et la Technologie. It has also benefited from a European Commission REGPOT-CT-2011-285837-STRonGer grant within the FP7 and an Investissement d'Avenir grant managed by Agence Nationale de la Recherche (CEBA ref. ANR-10-LABX-25-01).

REFERENCES

1. World Health Organization. 2005. WHO Expert Committee on Rabies, 2004. First report, WHO technical report series 931. World Health Organization, Geneva, Switzerland.
2. Barbosa TF, Medeiros DB, Travassos da Rosa ES, Casseb LM, Medeiros

- R, Pereira Ade S, Vallinoto AC, Vallinoto M, Begot AL, Lima RJ, Vasconcelos PF, Nunes MR. 2008. Molecular epidemiology of rabies virus isolated from different sources during a bat-transmitted human outbreak occurring in Augusto Correa municipality, Brazilian Amazon. *Virology* 370:228–236. <http://dx.doi.org/10.1016/j.virol.2007.10.005>.
3. Da Rosa ES, Kotait I, Barbosa TF, Carrieri ML, Brandão PE, Pinheiro AS, Begot AL, Wada MY, de Oliveira RC, Grisard EC, Ferreira M, Lima RJ, Montebello L, Medeiros DB, Sousa RC, Bensabath G, Carmo EH, Vasconcelos PF. 2006. Bat-transmitted human rabies outbreaks, Brazilian Amazon. *Emerg Infect Dis* 12:1197–1202. <http://dx.doi.org/10.3201/eid1208.050929>.
 4. Berger F, Desplanches N, Baillargeaux S, Joubert M, Miller M, Ribadeau-Dumas F, Spiegel A, Bourhy H. 2013. Rabies risk: difficulties encountered during management of grouped cases of Bat bites in 2 isolated villages in French Guiana. *PLoS Negl Trop Dis* 7:e2258.
 5. Meynard JB, Flamand C, Dupuy C, Mahamat A, Eltges F, Queuche F, Renner J, Fontanella JM, Hommel D, Dussart P, Grangier C, Djossou F, Dacheux L, Goudal M, Berger F, Ardillon V, Krieger N, Bourhy H, Spiegel A. 2012. First human rabies case in French Guiana, 2008: epidemiological investigation and control. *PLoS Negl Trop Dis* 6:e1537. <http://dx.doi.org/10.1371/journal.pntd.0001537>.
 6. De Thoisy B, Bourhy H, Pontier D, Darcissac E, Delaval M, Guidez A, Lavenir R, Salmier A, Lacoste V, Lavergne A. 2016. Bioecological drivers of rabies virus circulation in a Neotropical bat community. *PLoS Negl Trop Dis* 10:e0004378.
 7. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. 2011. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* 28:2731–2739. <http://dx.doi.org/10.1093/molbev/msr121>.
 8. Delmas O, Holmes EC, Talbi C, Larrous F, Dacheux L, Bouchier C, Bourhy H. 2008. Genomic diversity and evolution of the lysaviruses. *PLoS One* 3:e2057. <http://dx.doi.org/10.1371/journal.pone.0002057>.
 9. Mochizuki N, Kobayashi Y, Sato G, Hirano S, Itou T, Ito FH, Sakai T. 2011. Determination and molecular analysis of the complete genome sequence of two wild-type rabies viruses isolated from a haematophagous bat and a frugivorous bat in Brazil. *J Vet Med Sci* 73:759–766. <http://dx.doi.org/10.1292/jvms.10-0238>.
 10. Condori-Condori RE, Streicker DG, Cabezas-Sanchez C, Velasco-Villa A. 2013. Enzootic and epizootic rabies associated with vampire bats, Peru. *Emerg Infect Dis* 19:1463–1469. <http://dx.doi.org/10.3201/eid1809.130083>.