AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

First Draft Genome Sequence of *Leishmania* (*Viannia*) *lainsoni* Strain 216-34, Isolated from a Peruvian Clinical Case

Wuling Lin,[a,c] Dhwani Batra,[b] Vidhya Narayanan,[a,c] Lori A. Rowe,[b] Mili Sheth,[b] Yueli Zheng,[a,d] Phalasy Jueng,[b] Vladimir Loparev,[b] Marcos de Almeida[a]

[a]Reference Diagnostic Laboratory, Parasitic Diseases Branch/Department of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

[b]Biotechnology Core Facility, DSR/NCEZID, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

[c]IHRC, Inc., Atlanta, Georgia, USA

[d]Eagle Global Scientific, San Antonio, Texas, USA

ABSTRACT We present here the first draft genome sequence of *Leishmania* (*Viannia*) *lainsoni* strain 216-34, sequenced using PacBio and MiSeq platforms. PacBio contigs were generated from *de novo* assemblies using CANU version 1.6 and polished using Illumina reads.

In South and Central America, cutaneous leishmaniasis (CL) is caused by several *Leishmania* species in the *Leishmania* and *Viannia* subgenera (1, 2). Patients infected with some *Leishmania* (*Viannia*) strains of *L.* (*V.*) *braziliensis*, *L.* (*V.*) *guyanensis*, and *L.* (*V.*) *panamensis* can also develop mucocutaneous leishmaniasis (MCL), a mucosa-destructive sequela affecting the naso-oropharyngeal and laryngeal tracts (3). Other species in the *Viannia* subgenus, such as *L.* (*V.*) *lainsoni* and *L.* (*V.*) *peruviana*, are associated only with CL. Treatment is recommended for most cases of CL. However, the drugs typically used for treating CL are associated with several adverse side effects. In addition, the choice of therapeutic agents and their efficacy vary by clinical characteristics and parasite-specific factors (3–5). Therefore, DNA-based diagnostic tests that allow specific identification of infecting parasite species are critical for appropriate clinical management, including decisions regarding which treatment is indicated and how to monitor for relapse and sequelae.

As a part of our efforts to improve the quality of species-specific diagnostics for leishmaniasis, we present here the first draft genome sequence of *L.* (*V.*) *lainsoni*, that of strain 216-34, derived from a parasite isolated in our laboratory from a clinical case from Peru in 2016. Parasites grown in RPMI 1640 axenic medium (Life Technologies, CA) were initially identified on the basis of morphological analysis (6). Later, the species identity of *L.* (*V.*) *lainsoni* was confirmed using multilocus sequence analysis (MLSA) targeting glucose-6-phosphate dehydrogenase (G6PDH), isocitrate dehydrogenase (ICD), malate dehydrogenase (MDH), and mannose-6-phosphate isomerase (MPI) *Leishmania* sp. enzyme-coding genes. The sequencing data, generated on an ABI 3130xl DNA analyzer (Applied Biosystems, CA), were compared with the NCBI nucleotide database using the BLASTn algorithm (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch).

MiSeq and PacBio libraries were prepared with genomic DNA purified using the MagAttract high-molecular-weight (HMW) DNA kit (Qiagen, MD). For the short reads, libraries were prepared with NEBNext Ultra library prep reagents (New England BioLabs, MA), barcoded with indices produced at the CDC Biotechnology Core Facility, and sequenced using a MiSeq 2 × 250-cycle sequencing kit (Illumina, CA). Sequence reads were filtered for read quality, base called, and demultiplexed using bcl2fastq (version 2.19). Long-read sequencing data were obtained from a 20-kb DNA library and pre-

Citation Lin W, Batra D, Narayanan V, Rowe LA, Sheth M, Zheng Y, Jueng P, Loparev V, de Almeida M. 2019. First draft genome sequence of *Leishmania* (*Viannia*) *lainsoni* strain 216-34, isolated from a Peruvian clinical case. Microbiol Resour Announc 8:e01524-18. https://doi.org/10.1128/MRA.01524-18.

Editor Vincent Bruno, University of Maryland School of Medicine

Address correspondence to Marcos de Almeida, MdeAlmeida@cdc.gov.

Received 7 November 2018
Accepted 12 January 2019
Published 7 February 2019

pared using standard PacBio 20-kb library protocols (Pacific Biosciences, CA). The library was size selected with the BluePippin system (Sage Science, MA), bound to polymerase using the DNA/polymerase binding kit P6v2, loaded onto 6 single-molecule real-time (SMRT) cells, and sequenced with C4v2 chemistry for 360-min movies on the RS II instrument (Pacific Biosciences, CA).

The reads (246,178 reads; mean read length, 12,377 bp) from the RS II instrument were filtered and *de novo* assembled using Canu version 1.6 (7) with default parameters. Non-*Leishmania* contigs identified using the NCBI-BLASTn algorithm were removed, and the remaining contigs were polished and corrected using unicycler_polish (Unicycler package version 4.4) (8) with the 26,942,306 Illumina reads. The *L*. (*V*.) *lainsoni* genome assembly comprises 140 contigs covering 34,156,530 bp, with an L_{50} value of 17, N_{50} value of 638,860 bp, G+C content of 57.83%, and average read coverage of 75×.

The first draft genome sequence of *L*. (*V*.) *lainsoni* presented here is an important resource for diagnostic applications and research on the *Leishmania* genus.

Data availability. The draft genome contigs of *L*. (*V*.) *lainsoni* 216-34 have been deposited in GenBank under accession number RAIA00000000 and in the SRA under accession numbers SRR7883038, SRR7883039, SRR7883040, and SRR8179821 (BioProject number PRJNA484340).

ACKNOWLEDGMENT

This work was made possible through support from CDC's Office of Advanced Molecular Detection (OAMD).

REFERENCES

1. Herwaldt BL. 1999. Leishmaniasis. Lancet 354:1191–1199. https://doi.org/10.1016/S0140-6736(98)10178-2.
2. Van der Auwera G, Dujardin JC. 2015. Species typing in dermal leishmaniasis. Clin Microbiol Rev 28:265–294. https://doi.org/10.1128/CMR.00104-14.
3. Aronson N, Herwaldt BL, Libman M, Pearson R, Lopez-Velez R, Weina P, Carvalho E, Ephros M, Jeronimo S, Magill A. 2017. Diagnosis and treatment of leishmaniasis: clinical practice guidelines by the Infectious Diseases Society of America (IDSA) and the American Society of Tropical Medicine and Hygiene (ASTMH). Am J Trop Med Hyg 96:24–45. https://doi.org/10.4269/ajtmh.16-84256.
4. Oliveira LF, Schubach AO, Martins MM, Passos SL, Oliveira RV, Marzochi MC, Andrade CA. 2011. Systematic review of the adverse effects of cutaneous leishmaniasis treatment in the New World. Acta Trop 118:87–96. https://doi.org/10.1016/j.actatropica.2011.02.007.
5. Copeland NK, Aronson NE. 2015. Leishmaniasis: treatment updates and clinical practice guidelines review. Curr Opin Infect Dis 28:426–437. https://doi.org/10.1097/QCO.0000000000000194.
6. Silveira FT, Shaw JJ, Braga RR, Ishikawa E. 1987. Dermal leishmaniasis in the Amazon region of Brazil: Leishmania (Viannaia) [*sic*] lainsoni sp.n., a new parasite from the State of Pará. Mem Inst Oswaldo Cruz 82:289–291.
7. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res 27:722–736. https://doi.org/10.1101/gr.215087.116.
8. Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol 13:e1005595. https://doi.org/10.1371/journal.pcbi.1005595.