

Draft Genome Sequence of the First Pathogenic *Leptospira* Isolates from Ecuador

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Pathogenic *Leptospira* spp. cause leptospirosis upon contact with mucosa through wounds or ingestion, leading to headaches, fever, jaundice, kidney or liver failure, or death in about 1.3 million people each year. Here, we present the draft genomes of one *L. santarosai* isolate and two *L. interrogans* isolates from Ecuador.

Received 9 March 2016 Accepted 11 March 2016 Published 5 May 2016

Citation Barragan V, Sahl JW, Wiggins K, Chiriboga J, Salinas A, Cantos NE, Loor MN, Intriago BI, Morales M, Trueba G, Pearson T. 2016. Draft genome sequence of the first pathogenic *Leptospira* isolates from Ecuador. *Genome Announc* 4(3):e00271-16. doi:10.1128/genomeA.00271-16.

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Leptospirosis is a zoonotic disease with worldwide distribution (1), responsible for 1.03 million human cases per year around the world (2). Leptospirosis infection occurs by direct contact with urine or flesh from infected animals or by contact with contaminated soil or water (3). Ten out of 22 *Leptospira* spp. are classified in the “pathogenic clade” of the genus: *L. alexanderi*, *L. weilii*, *L. borgpetersenii*, *L. santarosai*, *L. kmetyi*, *L. alstonii*, *L. interrogans*, *L. kirschneri*, *L. mayottensis*, and *L. noguchii* (4). Most of these have been reported to cause high human morbidity. To date, 334 whole genome *Leptospira* sequences have been published, from which most of them (65%) belong to *L. interrogans*, followed by *L. santarosai* (8%), *L. kirschneri* (8%), and *L. borgpetersenii* (6%) (5).

Here, we announce the first three *Leptospira* whole-genome sequences from Ecuador. These isolates are from human blood collected in 2014 from Portoviejo, Ecuador (isolate C216), and cow urine (isolates ZV013 and ZV016) from Portoviejo collected in 2014. Isolates were obtained by culturing human blood (isolate C216) and cow urine (isolates ZV013, ZV016) in EMJH culture media. Research on human samples was approved by the Northern Arizona University Institutional Review Board (482212-1). Dual-indexed Illumina MiSeq libraries were prepared from genomic DNA as described in Keim et al. (6). Genome assembly

was performed by using SPAdes version 3.60 (7). Comparative analysis of the 16S rRNA gene identified isolate C216 as *L. santarosai*, and isolates ZV013 and ZV016 as *L. interrogans*. A detailed list of genome assembly details is shown in Table 1. We used Prokka software (8) to annotate the genome and determine the total number of coding sequences, tRNAs, and rRNAs.

Nucleotide sequence accession numbers. All three genomes have been deposited in GenBank under the accession numbers listed in Table 1. The versions in this paper are the first versions.

ACKNOWLEDGMENTS

This work was funded by the National Institute of Allergy and Infectious Diseases, National Institutes of Health grant R15AI101913; a SENESCYT scholarship from the Ecuadorian government; and Universidad San Francisco de Quito, Ecuador. The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

FUNDING INFORMATION

This work, including the efforts of Veronica Barragan, was funded by Universidad San Francisco de Quito. This work, including the efforts of Talima Pearson, was funded by HHS | NIH | National Institute of Allergy and Infectious Diseases (NIAID) (R15AI101913). This work, including the efforts of Veronica Barragan, was funded by Secretaría de Educación Superior, Ciencia, Tecnología e Innovación (SENESCYT).

TABLE 1 Three *Leptospira* sp. genomes released to NCBI

Isolate ID	Accession no.	Source	Genome size (bp)	No. of contigs	No. of CDSs ^a	No. of tRNAs	No. of rRNAs
C216	LSSR00000000	Human sera	3,983,958	95	3,547	37	1
ZV013	LSSQ00000000	Cow urine	4,414,224	87	3,586	38	1
ZV016	LSSS00000000	Cow urine	4,416,860	117	3,590	38	1

^a CDSs, coding sequences.

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