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Cecilia Nieves, Ignacio Ferrés, Florencia Díaz-Viraqué, Alejandro Buschiazzi, Leticia Zarantonelli, et al.. Draft Genome Sequences of 40 Pathogenic *Leptospira* Strains Isolated from Cattle in Uruguay. Microbiology Resource Announcements, American Society for Microbiology, 2019, 8 (47), pp.e00893-19. 10.1128/MRA.00893-19 . pasteur-02554324

HAL Id: pasteur-02554324

<https://hal-pasteur.archives-ouvertes.fr/pasteur-02554324>

Submitted on 25 Apr 2020



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Draft Genome Sequences of 40 Pathogenic *Leptospira* Strains Isolated from Cattle in Uruguay

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ABSTRACT Pathogenic *Leptospira* species represent a major concern for livestock but also for human health, as they cause zoonotic infections. Forty strains representing *L. interrogans*, *L. borgpetersenii*, and *L. noguchii* were isolated from naturally infected cattle in Uruguay. Here, we report the whole-genome sequences for these strains.

Leptospira is a bacterial genus whose taxonomic diversity has recently scaled up to over 60 described species, which can be grouped into four main phylogenetic lineages (1–3). Historically, these lineages were classified as “pathogens,” “intermediates,” and “saprophytes.” The pathogens (and intermediates to a lesser extent) are the recognized causative agents of human leptospirosis, an emerging zoonotic disease that accounts for more than 1 million severe cases and over 60,000 deaths every year worldwide (4). In cattle, leptospirosis causes reproductive problems, including abortions and stillbirths, constituting an important concern for livestock health and industries (5). In Uruguay, serologic studies of animals have historically shown high prevalence of exposure to *Leptospira*, with individual seropositivity ranging from 25 to 50% and herd prevalence from 50 to 70% (6, 7). In a recent study, we described the isolation, serotyping, and molecular characterization of 40 autochthonous pathogenic *Leptospira* strains recovered from cattle (7). Here, we report the whole-genome sequences and main genomic features of these strains.

Leptospira isolates were cultured in Ellinghausen-McCullough-Johnson-Harris (EMJH) medium supplemented with 100 µg/ml 5-fluorouracil at 29°C and observed under dark-field microscopy weekly for up to 6 months. In case of contamination, cultures were filtrated through a 0.22-µm sterile syringe filter and subcultured in fresh EMJH medium without 5-fluorouracil (6). Genomic DNA was purified with the PureLink genomic DNA minikit (Invitrogen). Whole-genome sequencing libraries were prepared with Nextera XT, and sequencing was performed using Illumina technology to produce paired-end reads (2 × 150 cycles) at the P2M core facility (Mutualized Platform for Microbiology) in the Institut Pasteur (Paris, France) or at the sequencing facility in the Institut Pasteur de Montevideo (Montevideo, Uruguay). Raw reads were quality filtered, assembled, and annotated as previously described (8). Species membership was confirmed by inspecting the 16S rRNA gene sequence and by calculating the average nucleotide identity (ANI) using in-house R scripts against public reference *Leptospira*

Citation Nieves C, Ferrés I, Díaz-Viraqué F, Buschiazzo A, Zaranonelli L, Iraola G. 2019. Draft genome sequences of 40 pathogenic *Leptospira* strains isolated from cattle in Uruguay. *Microbiol Resour Announc* 8:e00893-19. <https://doi.org/10.1128/MRA.00893-19>.

Editor David A. Baltus, University of Arizona

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Received 12 August 2019

Accepted 31 October 2019

Published 21 November 2019

genomes. In all cases, species coincided with previous determinations using molecular methods, representing 21 *L. interrogans*, 11 *L. borgpetersenii*, and 8 *L. noguchii* strains. For *L. interrogans*, the N_{50} value ranged from 10,222 to 49,707 bp, and the genome size ranged from 3.96 to 4.62 Mb. For *L. borgpetersenii*, the N_{50} value ranged from 31,998 to 44,974 bp, and the genome size, from 3.67 to 3.74 Mb. For *L. noguchii*, the N_{50} value ranged from 9,345 to 33,876 bp, and the genome size, from 3.86 to 4.75 Mb. More details on the assembly and annotation summary statistics are available at <https://doi.org/10.6084/m9.figshare.8277623.v3>.

An initial characterization of these strains obtained by recovering multilocus sequence typing (MLST) genes (scheme 3 available at PubMLST) from whole-genome sequences revealed that the *L. interrogans* strains were genetically monomorphic at this level, being assigned to the sequence type 58 (ST-58). In contrast, all of the *L. borgpetersenii* and *L. noguchii* strains harbored new combinations of previously described alleles or novel alleles representing new genotypes. This genomic data set represents the diversity of *Leptospira* species circulating in naturally infected cattle in Uruguay. The in-depth comparative analysis of these genomes together with those from strains isolated from humans and livestock will allow us to precisely determine epidemiological features of pathogenic *Leptospira* in this geographic region and improve our understanding of the genetic variability of circulating strains in naturally infected cattle and how this correlates with serotyping and other standard tools currently used to characterize *Leptospira* strains.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the BioProject numbers [PRJNA543681](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA543681) and [PRJEB29877](https://www.ncbi.nlm.nih.gov/bioproject/PRJEB29877). Specifically, the data are available under the accession numbers [ERS2975868](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975868), [ERS2975869](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975869), [ERS2975939](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975939), [ERS2975870](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975870), [ERS2975940](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975940), [ERS2975942](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975942), [ERS2975943](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975943), [ERS2975946](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975946), [ERS2975948](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975948), [ERS2975949](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975949), [ERS2976055](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976055), [ERS2976056](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976056), [ERS2976057](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976057), [ERS2976058](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976058), [ERS2976059](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976059), [ERS2976060](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976060), [ERS2976061](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976061), [ERS2975938](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975938), [ERS2975871](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975871), [ERS2975941](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975941), [ERS2976047](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976047), [ERS2976048](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976048), [ERS2976050](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976050), [ERS2976052](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976052), [ERS2976054](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976054), [ERS2976062](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976062), [ERS2975872](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975872), [ERS2975944](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975944), [ERS2975945](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975945), [ERS2975947](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2975947), [ERS2976049](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976049), [ERS2976051](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976051), [ERS2976053](https://www.ncbi.nlm.nih.gov/nuclseq/ERS2976053), [VCHF00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHF00000000), [VCHG00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHG00000000), [VCHH00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHH00000000), [VCHI00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHI00000000), [VCHJ00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHJ00000000), [VCHK00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHK00000000), and [VCHL00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VCHL00000000).

ACKNOWLEDGMENTS

All strains sequenced for this study were obtained from a collaborative work conducted by the consortium “Grupo de Trabajo Interinstitucional de Leptospirosis” (Institut Pasteur Montevideo/UdelaR/INIA/MGAP, Uruguay).

This work was supported by grants from the Agencia Nacional de Investigación e Innovación (ANII, Uruguay), ALI_1_2014_1_4982 and FSA_1_2013_1_12557. Partial support was also obtained through grants from the Institut Pasteur Paris (PTR Program) PTR30-17, Ministerio de Industria, Energía y Minería (MIEM, Industrial Funds program) 2016-8-2-002671, and FOCEM (MERCOSUR Structural Convergence Fund) COF03/1.

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