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Draft Genome Sequences of 112 *Salmonella enterica* Serovar Dublin Strains Isolated from Humans and Animals in Brazil

Fábio Campioni,[a] Felipe Pinheiro Vilela,[b] Guojie Cao,[c] George Kastanis,[c] Daniela Miller,[c] Maria Sanchez Leon,[c] Monique Ribeiro Tiba-Casas,[d] Sueli Aparecida Fernandes,[d] Dália dos Prazeres Rodrigues,[e] Renata Garcia Costa,[e] Marc William Allard,[c] Juliana Pfrimer Falcão[a]

[a]Departamento de Análises Clínicas, Toxicológicas e Bromatológicas, Faculdade de Ciências Farmacêuticas de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, São Paulo, Brazil

[b]Faculdade de Odontologia de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, São Paulo, Brazil

[c]Division of Microbiology, Office of Regulatory Science, Center for Food Safety and Applied Nutrition, U.S. Food and Drug Administration, College Park, Maryland, USA

[d]Instituto Adolfo Lutz, Centro de Bacteriologia, São Paulo, São Paulo, Brazil

[e]Laboratório de Enterobactérias, FIOCRUZ/Fundação Instituto Oswaldo Cruz, Rio de Janeiro, Rio de Janeiro, Brazil

ABSTRACT *Salmonella enterica* serovar Dublin is a strongly adapted serovar that causes enteritis and/or systemic disease in cattle and results in high rates of mortality. Here, we report the draft genome sequences of 112 *S.* Dublin strains isolated from humans and animals in Brazil. These draft genome sequences will help enhance our understanding of this serovar in Brazil.

Salmonellosis by nontyphoidal serovars is among the most common foodborne infections worldwide, causing around 93.8 million cases of gastroenteritis and 155,000 deaths annually (1). *Salmonella enterica* serovar Dublin is a strongly adapted serovar that causes enteritis and/or systemic disease in cattle and results in high rates of mortality. However, sporadically, it can be isolated from humans, usually causing serious disease, especially in patients with underlying chronic diseases (2–4).

In this report, we announce 112 draft genome sequences from a collection of *S.* Dublin strains isolated from humans and animals in several states of Brazil.

DNA from each strain was extracted according to Campioni and Falcão (5). Libraries were prepared using 1 ng of genomic DNA with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA). The genomes were then sequenced using the Illumina NextSeq 500 desktop sequencer using the NextSeq 500/500 high-output kit version 2 (300 cycles; Illumina) at 2 × 151 cycles, according to the manufacturer's recommendations. *De novo* assemblies were generated from all the Illumina sequence data using CLC Genomics Workbench version 9.5.2 (Qiagen Bioinformatics, Denmark). The contigs for each isolate (draft genomes) were annotated using NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) (6). The genomes ranged between 4.7 and 5.0 Mb in size, as described for other *Salmonella* genomes (4.6 Mb to almost 5.1 Mb) (7). The number of contigs per assembly for each isolate ranged from 46 to 179.

The data provided will help in the understanding of the epidemiology of *Salmonella* Dublin strains isolated in Brazil from different sources. It will also provide phylogenetic insights into the evolution of these strains. A more detailed report of these genomic features will be addressed in a future publication.

Accession number(s). The draft genome sequences for these 112 *S.* Dublin isolates are available in GenBank and are listed in Table 1.

Received 27 April 2018 **Accepted** 7 May 2018 **Published** 14 June 2018

Citation Campioni F, Vilela FP, Cao G, Kastanis G, Miller D, Sanchez Leon M, Tiba-Casas MR, Fernandes SA, Rodrigues DDP, Costa RG, Allard MW, Falcão JP. 2018. Draft genome sequences of 112 *Salmonella enterica* serovar Dublin strains isolated from humans and animals in Brazil. Genome Announc 6:e00405-18. https://doi.org/10.1128/genomeA.00405-18.

Address correspondence to Marc William Allard, marc.allard@fda.hhs.gov, or Juliana Pfrimer Falcão, jufalcao@fcfrp.usp.br.

TABLE 1 Metadata for the 112 *Salmonella* Dublin strains isolated from humans and animals in Brazil

CFSAN no.	WGS accession no.[a]
CFSAN060419	QBMT00000000
CFSAN060420	QBMU00000000
CFSAN060421	QBMV00000000
CFSAN060422	QBMW00000000
CFSAN060423	QBMX00000000
CFSAN060424	QBMY00000000
CFSAN060425	QBMZ00000000
CFSAN060426	QBNA00000000
CFSAN060427	QBNB00000000
CFSAN060428	QBNC00000000
CFSAN060429	QBND00000000
CFSAN060430	QBNE00000000
CFSAN060431	QBNF00000000
CFSAN060432	QBNG00000000
CFSAN060433	QBNH00000000
CFSAN060434	QBNI00000000
CFSAN060435	QBNJ00000000
CFSAN060436	QBNK00000000
CFSAN060437	QBNL00000000
CFSAN060438	QBNM00000000
CFSAN060439	QBNN00000000
CFSAN060440	QBNO00000000
CFSAN060441	QBNP00000000
CFSAN060442	QBNQ00000000
CFSAN060443	QBNR00000000
CFSAN060444	QBNS00000000
CFSAN060445	QBNT00000000
CFSAN060446	QBNU00000000
CFSAN060447	QBNV00000000
CFSAN060449	QBNW00000000
CFSAN060450	QBNX00000000
CFSAN060451	QBNY00000000
CFSAN060452	QBNZ00000000
CFSAN060453	QBOA00000000
CFSAN060454	QBOB00000000
CFSAN060455	QBOC00000000
CFSAN060456	QBOD00000000
CFSAN060457	QBOE00000000
CFSAN060458	QBOF00000000
CFSAN060459	QBOG00000000
CFSAN060460	QBOH00000000
CFSAN060461	QBOI00000000
CFSAN060462	QBOJ00000000
CFSAN060463	QBOK00000000
CFSAN060464	QBOL00000000
CFSAN060465	QBOM00000000
CFSAN060466	QBON00000000
CFSAN060467	QBOO00000000
CFSAN060468	QBOP00000000
CFSAN060469	QBRY00000000
CFSAN060470	QBRZ00000000
CFSAN060471	QBSA00000000
CFSAN060472	QBSB00000000
CFSAN060473	QBSC00000000
CFSAN060474	QBSD00000000
CFSAN060475	QBSE00000000
CFSAN060476	QBSF00000000
CFSAN060477	QBSG00000000
CFSAN060478	QBSH00000000
CFSAN060479	QBSI00000000
CFSAN060480	QBSJ00000000
CFSAN060481	QBSK00000000
CFSAN060482	QBSL00000000
CFSAN060483	QBSM00000000
CFSAN060484	QBSN00000000

(Continued on next page)

TABLE 1 (Continued)

CFSAN no.	WGS accession no.[a]
CFSAN060485	QBSO00000000
CFSAN060486	QBSP00000000
CFSAN060487	QBSQ00000000
CFSAN060488	QBSR00000000
CFSAN060489	QBSS00000000
CFSAN060491	QBST00000000
CFSAN060492	QBSU00000000
CFSAN060493	QBSV00000000
CFSAN060494	QBSW00000000
CFSAN060495	QBSX00000000
CFSAN060496	QBSY00000000
CFSAN060497	QBSZ00000000
CFSAN060498	QBTA00000000
CFSAN060499	QBTB00000000
CFSAN060500	QBTC00000000
CFSAN060501	QBTD00000000
CFSAN060502	QBTE00000000
CFSAN060503	QBTF00000000
CFSAN060504	QBTG00000000
CFSAN060505	QBTH00000000
CFSAN060506	QBTI00000000
CFSAN060507	QBTJ00000000
CFSAN060508	QBTK00000000
CFSAN060509	QBTL00000000
CFSAN060510	QBTM00000000
CFSAN060511	QBTN00000000
CFSAN060512	QBTO00000000
CFSAN060513	QBTP00000000
CFSAN060514	QBTQ00000000
CFSAN060515	QBTR00000000
CFSAN060516	QBTS00000000
CFSAN060517	QBTT00000000
CFSAN060518	QBTU00000000
CFSAN060519	QBTV00000000
CFSAN060520	QBPE00000000
CFSAN060521	QBPD00000000
CFSAN060522	QBPC00000000
CFSAN060523	QBPB00000000
CFSAN060524	QBPA00000000
CFSAN060526	QBOZ00000000
CFSAN060527	QBOY00000000
CFSAN060528	QBOX00000000
CFSAN060529	QBOW00000000
CFSAN060530	QBOV00000000
CFSAN060531	QBOU00000000
CFSAN060532	QBOT00000000
CFSAN060533	QBOS00000000

[a]WGS, whole-genome sequencing.

ACKNOWLEDGMENTS

The study was supported by FDA/CFSAN under Marc William Allard's supervision and by the Sao Paulo Research Foundation-FAPESP (Proc. 2016/24716-3) and CNPq (473043/2013-0) under Juliana Pfrimer Falcão's supervision. During the course of this work, Fabio Campioni was supported by a fellowship from the Sao Paulo Research Foundation-FAPESP (grants 2013/25191-3 and 2016/05817-3) and Felipe Pinheiro Vilela by a scholarship from the Sao Paulo Research Foundation-FAPESP (grants 2015/10818-6 and 2017/05756-7).

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