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GENOME SEQUENCES

Genome Sequence of a *Salmonella enterica* subsp. *enterica* Serovar Corvallis Strain Isolated from Human Blood

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ABSTRACT *Salmonella enterica* subsp. *enterica* serovar Corvallis is commonly reported in avian populations and avian by-products. We report the draft genome sequence of a multidrug-resistant *S.* Corvallis strain (NPHL 15376). To our knowledge, this is the first reported case of this serovar isolated from human blood in the United States.

Salmonella enterica subsp. *enterica* serovar Corvallis is a cause of foodborne disease (1, 2). Recent publications have also reported highly resistant strains of this serovar, which makes this serovar a public health concern (2, 3). Historically, there have been limited data available for nonfecal *S.* Corvallis strains of human origin (4). Here, we report the draft genome sequence of a multidrug-resistant *S.* Corvallis strain (NPHL 15376) isolated from human blood from a patient in Nebraska. To our knowledge, this is the first reported case of this serovar isolated from human blood in the United States.

The *Salmonella* Corvallis strain was isolated from a routine blood culture using a Bactec instrument, followed by overnight culture on blood agar, MacConkey agar, and chocolate agar. The automated BD Phoenix system (Becton, Dickinson and Company, Franklin Lakes, NJ) was used for organism identification and susceptibility testing, as recommended by the manufacturer.

S. Corvallis NPHL 15376 was grown on blood agar plates overnight at 37°C. DNA was then extracted using the DNeasy UltraClean microbial kit (Qiagen, Germany), and libraries were constructed using the HyperPlus library preparation kit (Kapa Biosciences, Wilmington, MA, USA), both as per the manufacturers' directions. Whole-genome sequencing was performed as previously described (5) on a MiSeq platform (Illumina, CA, USA), producing 1,260,002 paired-end reads with an average length of 300 bp and insert size of 500 bp. Reads were merged using FLASH (version 1.2.11), with the –m 15 –M 50 parameters (6), and were trimmed using Btrim (version 0.3.0), with the parameters – b 300 – e 1 –P –Q –l 100 (7). The trimmed reads were then *de novo* assembled using Newbler (version 2.9), with default parameters. Genome annotations were done using the NCBI Prokaryotic Genome Annotation Pipeline (version 4.8) (8).

The *S.* Corvallis NPHL 15376 genome was assembled into 68 contigs with a total length of 5,013,778 bp, an N_{50} value of 381,703 bp, an average read depth of around 153×, and 52.1% GC content. The contigs contain 4,819 coding sequences (CDSs) and 99 RNA genes. *S.* Corvallis NPHL 15376 was confirmed to belong to serovar Corvallis *in silico* using the SISTR Web service (version 1) (https://omictools.com/sistr-tool). A total of 22 antibiotic resistance genes were identified (Table 1).

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TABLE 1 Antibiotic resistance profile for *Salmonella* serovar Corvallis

Resistance phenotype	Resistance gene	Identity (%)	Reference accession no.
Aminoglycosides	*aac(6′)-Iaa*	99.32	NC_003197
	aph(6)-Id	100	M28829
	aph(3″)-Ib	100	AF321551
	aph(3′)-Ia	100	V00359
	armA	100	AY220558
	aac(3)-IId	99.77	EU022314
	aadA2	100	JQ364967
Fluoroquinolones and aminoglycosides	*aac(6′)-Ib-cr*	100	DQ303918
Fluoroquinolones	*qnrS1*	100	AB187515
Beta-lactams	bla_{CMY-2}	100	X91840
	bla_{TEM-1B}	100	AY458016
	bla_{OXA-1}	100	HQ170510
Tetracycline	*tet*(A)	99.84	AF534183
Trimethoprim	*dfrA12*	100	AM040708
Sulfonamide	*sul1*	100	U12338
	sul2	100	AY034138
Macrolides	*mph*(E)	100	DQ839391
	msr(E)	100	FR751518
	mph(A)	100	D16251
Phenicol	*catB3*	100	U13880
	floR	98.19	AF118107
Rifampin	*arr-3*	100	JF806499

Data availability. The assembled contigs and sequencing reads of this isolate are deposited in the NCBI GenBank database under the BioSample accession number SAMN11179044. The Sequence Read Archive accession number is SRS5077420, and the whole-genome shotgun sequencing project number is SPQE00000000.

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