



Draft Genome Sequences of Seven *Streptococcus agalactiae* Strains Isolated from *Camelus dromedarius* at the Horn of Africa

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ABSTRACT We present draft whole-genome sequences of seven *Streptococcus agalactiae* strains isolated from *Camelus dromedarius* in Kenya and Somalia. These data are an extension to the group B *Streptococcus* (GBS) pangenome and might provide more insight into the underlying mechanisms of pathogenicity and antibiotic resistance of camel GBS.

The natural colonizer of human gastrointestinal and genitourinary tracts *Streptococcus agalactiae*, also known as Lancefield's group B *Streptococcus* (GBS), is an emerging pathogen of serious clinical concern (1). As a main causative agent of meningitis, sepsis, and respiratory diseases in neonates, GBS is strongly linked to child mortality and morbidity (2). *S. agalactiae* has also been isolated from both healthy and diseased camels in countries from the Horn of Africa (3–7). Given the fundamental role of camels for human nutrition and financial safety in these regions, GBS-associated diseases, such as mastitis or udder abscesses resulting in significant losses in milk production, can have a devastating impact (5). Here, we report the whole-genome sequences of seven GBS strains, isolated from Kenyan and Somalian camels (*Camelus dromedarius*). Previous genomic analysis of these isolates by multilocus sequence typing (MLST) indicated a detached phylogenetic relationship compared to GBS strains of human or bovine origin (5). The three isolates ILRI025, ILRI030, and ILRI067 were isolated from healthy camels, while ILRI037 (causing gingivitis), ILRI054 (causing wound infection), ILRI120 (causing chronic cough), and ILRI127 (causing periarticular abscess) were associated with disease.

Genomic DNA was extracted from a single bacterial colony cultivated on Columbia sheep blood agar using the QIAamp DSP DNA minikit (Qiagen, Hilden, Germany). DNA was fragmented by ultrasonication using the Covaris S2 instrument (Covaris, Inc., Woburn, MA, USA). Barcoded libraries were generated with the Ion fragment library kit and Ion Xpress DNA barcode adaptors (Life Technologies, Inc., Carlsbad, CA, USA). Sequencing was performed on an Ion Torrent Personal Genome Machine (PGM) system, with the Ion PGM sequencing 400 kit and the Ion 318 Chip version 2 (Life Technologies, Inc.). After sequencing, single processing and base calling were performed using Torrent Suite 3.6 (Life Technologies, Inc.), and barcode-separated FASTQ files were generated. For *de novo* assemblies, we used MIRA version 4.0 (8). Contigs were sorted along the already published (9) GBS genomes of ILRI112 (accession no. HF952106) and

Received 22 May 2017 Accepted 25 May 2017 Published 13 July 2017

Citation Rothen J, Schindler T, Pothier JF, Younan M, Certa U, Daubenberg C, Pflüger V, Jores J. 2017. Draft genome sequences of seven *Streptococcus agalactiae* strains isolated from *Camelus dromedarius* at the Horn of Africa. *Genome Announc* 5:e00525-17. <https://doi.org/10.1128/genomeA.00525-17>.

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TABLE 1 List of *Streptococcus agalactiae* draft whole genomes released to GenBank

Strain	GenBank accession no.	Multilocus ST ^a	Serotype	Genome size (bp)	No. of proteins
ILRI025	NDGG000000000	610	VI	2,013,384	1,876
ILRI030	NDGF000000000	617	VI	1,999,626	1,883
ILRI037	NDGE000000000	612	Ia	2,020,002	1,895
ILRI054	NDGD000000000	615	II	2,021,031	1,867
ILRI067	NDGC000000000	614	V	1,980,469	1,812
ILRI120	NDGB000000000	618	Ia	2,049,911	1,954
ILRI127	NDGA000000000	613	Ia	1,973,342	1,875

^aST, sequence type.

ILRI005 (accession no. HF952105) (only for isolate ILRI067) using the Move Contigs function in Mauve version 2.3.1 (10). SeqMan Pro from the Lasergene genomics package version 12.1.0 (DNASTar, Madison, WI) was used to check and manually close gaps between contigs. Genome annotation was added using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The seven genomes displayed an overall size between 1,973,342 and 2,049,911 bp, with 1,812 to 1,954 proteins detected (Table 1).

The draft genome sequences of cameloid GBS isolates presented here are a valuable addition to the pangenome of *S. agalactiae* (11). These genomic data provide a basis for the investigation of adaptive factors in GBS host colonization as well as underlying mechanisms of antibiotic resistance development and pathogenicity of camel *S. agalactiae*.

Accession number(s). The annotated draft whole-genome sequences of the seven *S. agalactiae* isolates were deposited in GenBank under BioProject no. PRJNA382326. The accession numbers for each isolate are shown in Table 1.

ACKNOWLEDGMENTS

This work was supported by funding from the Swiss Tropical and Public Health Institute and Mabritec AG.

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