

# Whole-Genome Shotgun Sequencing of a Colonizing Multilocus Sequence Type 17 *Streptococcus agalactiae* Strain

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**This report highlights the whole-genome shotgun draft sequence for a *Streptococcus agalactiae* strain representing multilocus sequence type (ST) 17, isolated from a colonized woman at 8 weeks postpartum. This sequence represents an important addition to the published genomes and will promote comparative genomic studies of *S. agalactiae* recovered from diverse sources.**

Neonates and young infants are susceptible to *Streptococcus agalactiae* or group B streptococcus (GBS) infections during birth and up to 3 months of age. The most common complications include respiratory infections, sepsis, and meningitis, which can lead to long-term disabilities and death (1, 12). GBS acquisition typically occurs via vertical transmission, as up to 36% of asymptomatic mothers can be colonized with GBS in the genitourinary tract (4). Prior studies have demonstrated that some GBS strains are associated with neonatal disease. Specifically, GBS strains representing multilocus sequence type (ST) 17 were found to disproportionately affect neonates (2, 5–8) and more frequently cause meningitis than strains of other STs (10). Because ST 17 strains were suggested to have enhanced virulence (6), it is imperative to identify genetic characteristics unique to this lineage that may be important for invasive disease. At present, only one ST 17 genome and 10 additional GBS genomes are publicly available, though the J. Craig Venter Institute recently published short read archive (SRA) sequences for 231 GBS strains ([gsc.jcvi.org/status.shtml](http://gsc.jcvi.org/status.shtml)). Because of this, comparative genomic studies can more easily be conducted to better understand genomic differences between GBS isolated from different sources.

GBS strain GB00112 was selected for genome sequencing because genomic data from colonized women have been lacking. GB00112 was isolated in 1999 from a married woman in Calgary, Canada, during an 8-week postpartum visit (3). As described in our prior study of persistent GBS colonization (9), this GB00112 strain persistently colonized the woman before and after childbirth, despite the fact that she received intrapartum antibiotic prophylaxis. Genomic DNA was isolated using the UltraClean microbial DNA isolation kit (MO BIO Laboratories, Inc., Carlsbad, CA) and was submitted to the Research Training Support Facility at Michigan State University ([rtsf.msu.edu](http://rtsf.msu.edu)). Whole-genome sequencing was performed using the Roche 454 Life Sciences GS-FLX system, which resulted in 25× coverage and was assembled *de novo* using the Newbler Roche gsAssembler (version 1.1.03) (11). Draft genome assembly consisted of 63 contigs, ranging from 112 bp to 242,817 bp in size. The genome was annotated by the Prokaryotic Genomes Automatic Annotation Pipeline ([ncbi.nlm.nih.gov/genomes/static/Pipeline](http://ncbi.nlm.nih.gov/genomes/static/Pipeline)).

The GB00112 sequence data will be useful for future studies that aim to examine genetic variation among GBS strains from diverse sources and may enhance our understanding of genetic factors that aid in persistent colonization and are unique to the ST 17 lineage.

**Nucleotide sequence accession numbers.** The annotated draft genome has been deposited in GenBank under the accession number [AKXO00000000](http://ncbi.nlm.nih.gov/GenBank/entry/1000000000). The raw sequence reads have also been sub-

mitted to the Short Read Archive database of the National Center for Biotechnology Information (NCBI) under the accession number [SRR517012](http://ncbi.nlm.nih.gov/SRA/entry/SRR517012).

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