

GENOME ANNOUNCEMENTS

Genome Sequence of *Cronobacter sakazakii* E899, a Strain Associated with Human Illness

Y. Chen,^{1*} E. A. Strain,² M. Allard,¹ and E. W. Brown¹

Division of Microbiology¹ and Division of Mathematics,² Center for Food Safety and Applied Nutrition, Food and Drug Administration, 5100 Paint Branch Parkway, College Park, Maryland

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***Cronobacter* has caused numerous illnesses in neonates, infants, and children. Here we report the draft genome of *Cronobacter sakazakii* E899. Whole-genome sequence analysis of *Cronobacter* strains provides a tool for understanding the genomic regions specific to each individual species.**

Cronobacter (formerly *Enterobacter*) *sakazakii* is a Gram-negative rod of the family *Enterobacteriaceae*. In recent years, this bacterium has been associated with illnesses in neonates, infants, and children (from 3 months to 4 years old) (1). The pathogen causes neonatal meningitis, bacteremia, necrotizing enterocolitis, and in some cases death. A variety of foods were identified as possible sources of *Cronobacter* contamination, and powdered infant formula has been linked to neonatal meningitis cases. In 2004, the World Health Organization and Food and Agricultural Organization issued a report on a meeting that addressed the concern of *Cronobacter* as a pathogen (6).

There are six species of *Cronobacter*: *C. sakazakii*, *C. maloticus*, *C. turicensis*, *C. muytjensii*, *C. dublinensis*, and *Cronobacter* genomospecies 1. To date, the genome sequences of only one strain of *C. sakazakii* (ATCC BAA-894) (3) and one strain of *Cronobacter turicensis* (LMG 23827) (5) are available. The limited number of *Cronobacter* genome sequences makes it challenging to understand *Cronobacter* species and strain variability and subsequently develop rapid detection and subtyping techniques for the genus, as well as each individual species of *Cronobacter*. Here we announce the availability of the draft genome of another *C. sakazakii* strain, E899, a clinical strain from the United States.

Genomic DNA was isolated from an overnight culture of strain E899 using the DNeasy blood and tissue kit (Qiagen). The genome was sequenced using 454 Titanium pyrosequenc-

ing (Roche) according to the manufacturer's instructions at 20× coverage (4). Genomic sequence contigs for strain E899 were assembled using *C. sakazakii* ATCC BAA-894 (accession number AADR00000000) as a reference. Assemblies were performed using the Roche Newbler software version 2.3. The sequences were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) (2). Detailed analysis of a full comparison of the genomes of these strains and other available *Cronobacter* strains will be included in a future publication.

Nucleotide sequence accession number. The draft genome sequence of strain E899 is available in GenBank under accession number AFMO00000000.

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* Corresponding author. Mailing address: FDA, CFSAN, 5100 Paint Branch Parkway HFS-712, College Park, MD 20740. Phone: (240) 402-2783. Fax: (301) 436-2644. E-mail: yi.chen@fda.hhs.gov.