

# Draft Genome Sequence of “*Candidatus Cronobacter colletis*” NCTC 14934<sup>T</sup>, a New Species in the Genus *Cronobacter*

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**Members of the *Cronobacter* genus are associated with serious infections in neonates. This is the first report of the draft genome sequence for the newly proposed species *Cronobacter colletis*.**

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Due to the association of *Cronobacter* with fatal neonatal infections, there is an international requirement for powdered infant formula to be microbiologically tested for all members of the *Cronobacter* genus (1). “*Candidatus Cronobacter colletis*” is a previously undescribed species closely related to *Cronobacter zurichensis*. Therefore, genome sequencing and public access of this newly described species are warranted for a better understanding of the diversity of the genus and improved detection methodology. This was undertaken using the type strain “*Candidatus Cronobacter colletis*” NCTC 14934.

Bacterial DNA was extracted from 1-day cultures using a GenElute bacterial genome kit (Sigma-Aldrich) and sequenced using an Illumina HiSeq 2500 sequencing platform. A total of 1,501,270 high-quality paired-end reads were generated, with 16-fold coverage. *De novo* assembly was performed using Velvet (version 1.1.09) (2). The genome was distributed in 42 contigs, with a total size of 4,261,112 bp and a G+C content of 57.07%.

A phylogenetic tree based on seven housekeeping genes (3,036 bp concatenated length) from *Cronobacter* BIGSdb (<http://www.pubMLST.org/cronobacter>; <http://dx.doi.org/10.6084/m9.figshare.1032771>) suggests that “*Candidatus Cronobacter colletis*” is a member of the *Cronobacter* genus, with a near match to *C. zurichensis*. A comparison of the “*Candidatus Cronobacter colletis*” genome with the genome sequence available for *C. zurichensis* LMG 23730<sup>T</sup> (3) revealed an average nucleotide identity (ANI) of 87.18%. A formal description of “*Candidatus Cronobacter colletis*” is currently in progress.

For further annotation, we used the SEED-based automated annotation system provided by the RAST server (4), which iden-

tified 3,967 coding sequences (CDSs) and 109 RNAs. The CDSs included those for copper homeostasis, iron acquisition, multi-drug efflux pumps, arsenic, cobalt, zinc, and cadmium resistance, stress response associated with cold shock, osmotic and oxidative stress, and several phage-associated traits.

**Nucleotide sequence accession number.** The genome sequence of “*Candidatus Cronobacter colletis*” NCTC 14934<sup>T</sup> has been deposited in GenBank under the accession no. [JMSQ00000000](https://www.ncbi.nlm.nih.gov/nuclink/JMSQ00000000).

## ACKNOWLEDGMENT

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