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**Draft genome sequence of *Cronobacter sakazakii* GP 1999, sequence type 145, an epiphytic isolate obtained from the tomato's rhizosphere/rhizosphere continuum**

Chase, H R; Eberl, L; Stephan, Roger; Jeong, H J; Chaeyoon Lee, C; Finkelstein, S; Negrete, F; Gangiredla, J; Patel, I; Tall, B D; Gopinath, G R; Lehner, Angelika

**Abstract:** We present here the draft genome of *Cronobacter sakazakii* GP1999, a sequence type 145 strain isolated from the rhizosphere of tomato plants. Assembly and annotation of the genome resulted in a genome of 4,504,670 bp in size, with 4,148 coding sequences, and a GC content of 56.8%.

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1 Draft genome sequence of *Cronobacter sakazakii* GP 1999, sequence type 145, an epiphytic  
2 isolate obtained from the tomato's rhizoplane/rhizosphere continuum

3

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11

12 Keywords: *Cronobacter sakazakii*, ST145, Tomato rhizosphere, whole genome sequencing

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14

15 **Abstract.**

16           We present the draft genome of *Cronobacter sakazakii* GP 1999, a sequence type 145  
17 strain isolated from the rhizosphere of tomato plants. Assembly and annotation of the genome  
18 resulted in a genome of 4,504,670 bp in size, with 4,148 coding sequences, and a G-C content  
19 of 56.8 %.

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21

22 *Cronobacter* species are food associated pathogens that cause rare but severe cases of  
23 meningitis, necrotising enterocolitis, sepsis and pneumonia in preterm and/or  
24 immunocompromised infants[1-3]. The genus comprises seven species - *C. sakazakii*, *C.*  
25 *malonaticus*, *C. turicensis*, *C. universalis*, *C. condimenti*, *C. muytjensii* and *C. dublinensis*, all  
26 capable of infecting humans, with the exception of *C. condimenti* [4,5]. *Cronobacter* have  
27 been isolated from a variety of environmental sources like soil, household dust and powdered  
28 infant formula production lines, as well as from fruits, vegetables, herbs, cereals, grains [6-8],  
29 and it has also been isolated from lemon tree, wheat, rice and soybean  
30 plant rhizosphere/rhizosphere continuums [9-12].

31 Several lines of evidence suggest an environmental origin for *Cronobacter* with plants  
32 as ancestral niche promoting the diversification of this genus [13, 14]. In this report, we  
33 are presenting the genome sequence of *C. sakazakii* GP1999 - originally isolated in 1999 from  
34 the roots of a *Lycopersicon esculentum* (tomato) plant by Schmid *et al.* [13].

35 GP1999 genomic DNA was subjected to whole genome sequencing (WGS) using the  
36 MiSeq platform (Illumina, San Diego, CA, USA), and a Nextera XT library kit. *De novo*  
37 assembly with CLC Genomics Workbench version 7.0 (CLC bio, Aarhus, Denmark) resulted  
38 in a genome of 4,504,670 bp, with 22 contigs, and a G-C content of 56.8 %. The genome was  
39 annotated using the RAST annotation server and 4,148 CDS were identified [15,16].  
40 *Cronobacter* MLST website (<http://pubmlst.org/cronobacter/>) showed that it belonged to the  
41 sequence type 145 [17].

42 The strain harbours a pESA3/pSP291-like plasmid, which was found by comparison of  
43 the genome assembly with whole-genome sequences of strains *C. sakazakii* BAA-894  
44 (NC\_00978) and *C. turicensis* z3032 (NC\_01328) and confirmed by PCR analysis. However,  
45 pESA2-like and pCTU-3 plasmid replicons were not detected by PCR [18].

46 Other mobilome genes found in the assembly include a total of eleven  
47 integrase/transposase genes, eight genes encoding unspecified mobile element proteins, and

48 63 genes encoding phage-associated proteins. Notably, a gene encoding resistance to the  
49 antibiotic fosfomycin, was found downstream of a transposase.

50 Other genes identified in GP1999 include virulence-associated genes encoding protein  
51 MsgA and factors VirL and MviM [15,16], multidrug resistance efflux pump-related genes  
52 belonging to *acrAB* operon, RND family, MFS superfamily and tripartite systems.  
53 Additionally, genes encoding heavy metal resistance to copper-, organic hydroperoxide,  
54 fusaric acid, and tellurite were found. Interestingly, an arsenic resistance operon repressor  
55 gene was identified downstream to an arsenic efflux pump operon and an arsenate reductase.  
56 An albicidin (a phytotoxin that blocks DNA gyrase in chloroplasts) resistance protein [19]  
57 was also observed. Furthermore, GP1999 contains a 16,771 bp operon encoding a xylose  
58 utilization pathway, supporting the hypothesis that plants represent the ancestral econiche of  
59 *Cronobacter* spp.

60 To the best of our knowledge, this is the first genome of a plant isolate of *C. sakazakii*  
61 being reported. The availability of the GP1999 genome will enable comparison with other  
62 genomes of *C. sakazakii* strains, thereby providing better insights into genetic features linked  
63 to plant association and possibly the natural history of this important foodborne pathogen.

64

#### 65 **Nucleotide sequence accession numbers.**

66 The whole genome sequence of *C. sakazakii* GP1999 has been submitted to NCBI under the  
67 *Cronobacter* GenomeTrakr FDA-CFSAN bioproject number PRJNA258403, Accession#:  
68 NHTW00000000. The version described in this paper is version NHTW01000000.

69

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82

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100 nov., *Cronobacter turicensis* sp. nov., *Cronobacter muytjensii* sp. nov., *Cronobacter*  
101 *dublinensis* sp. nov., *Cronobacter* genomospecies 1 and of three subspecies, *Cronobacter*  
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