

Draft Genome Sequences of Three Newly Identified Species in the Genus *Cronobacter*, *C. helveticus* LMG23732^T, *C. pulveris* LMG24059, and *C. zurichensis* LMG23730^T

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***Cronobacter helveticus*, *Cronobacter pulveris*, and *Cronobacter zurichensis* are newly described species in the *Cronobacter* genus, which is associated with serious infections of neonates. This is the first report of draft genome sequences for these species.**

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The *Cronobacter* genus until recently consisted of seven species, *C. sakazakii*, *C. malonaticus*, *C. turicensis*, *C. universalis*, *C. muytjensii*, *C. dublinensis*, and *C. condimenti* (1). In 2013, three new *Cronobacter* species were proposed, *C. zurichensis*, *C. pulveris*, and *C. helveticus* (2). 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 (Codex Alimentarius Commission, code of hygienic practice for powdered formulae for infants and young children, http://www.codexalimentarius.net/download/standards/11026/CXP_066e.pdf). Therefore, the genome sequencing of these newly described species is warranted for better understanding of the genus diversity and improved detection methodology. This was undertaken using *C. helveticus* strain LMG23732^T, *C. zurichensis* strain LMG23730^T, and *C. pulveris* strain LMG24059 isolated from powdered infant formula.

Bacterial DNA was extracted from 1-day cultures using a GenElute bacterial genome kit (Sigma-Aldrich) and sequenced using an Illumina HiSeq 2500 sequencing system. *De novo* assembly was performed using Velvet (3). For further annotation we used the SEED-based automated annotation system provided by the RAST server (4).

C. helveticus LMG23732^T, *C. pulveris* LMG24059, and *C. zurichensis* LMG23730^T generated 8,351,512, 5,000,582, and 6,613,368 high-quality paired-end reads of 150 bp in length, respectively. The genome sizes were 4,530,369 bp, 4,900,556 bp, and 4,246,797 bp with G+C contents of 56%, 56.6%, and 57.8%, respectively. These were in 79, 125, and 103 contigs with 4,315, 4,630, and 3,883 coding sequences (CDS), respectively, and 30-fold coverage. The CDS include traits previously described in *Cronobacter* (5). These included genes associated with iron acquisition, stress response, heavy metal resistance (arsenic, copper cobalt, zinc and cadmium), and phages. Genes encoding proteins associated with several virulence-associated traits such as adhesion and antibiotic resistance, including fluoroquinolones, fosfomycin, β -lactamases, and multi-drug efflux pumps, were also determined.

Nucleotide sequence accession numbers. The genome sequences of *C. helveticus*, *C. pulveris*, and *C. zurichensis* have been deposited in GenBank under the accession numbers AWFEX00000000, AWFY00000000, and AWFZ00000000, respectively.

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REFERENCES

- Joseph S, Chtinkaya E, Drahovska H, Levican A, Figueras MJ, Forsythe SJ. 2012. *Cronobacter condimenti* sp. nov., isolated from spiced meat, and *Cronobacter universalis* sp. nov., a species designation for *Cronobacter* sp. genomospecies 1, recovered from a leg infection, water, and food ingredients. *Int. J. Syst. Evol. Microbiol.* 62:1277–1283.
- Brady C, Cleenwerck I, Venter S, Coutinho T, De Vos P. 2013. Taxonomic evaluation of the genus *Enterobacter* based on multilocus sequence analysis (MLSA): proposal to reclassify *E. nimipressuralis* and *E. amnigenus* into *Lelliottia* gen. nov. as *Lelliottia nimipressuralis* comb. nov. and *Lelliottia amnigena* comb. nov., respectively, *E. gergoviae* and *E. pyrinus* into *Pluralibacter* gen. nov. as *Pluralibacter gergoviae* comb. nov. and *Pluralibacter pyrinus* comb. nov., respectively, *E. cowanii*, *E. radincincitans*, *E. oryzae* and *E. arachidis* into *Kosakonia* gen. nov. as *Kosakonia cowanii* comb. nov., *Kosakonia radincincitans* comb. nov., *Kosakonia oryzae* comb. nov. and *Kosakonia arachidis* comb. nov., respectively, and *E. turicensis*, *E. helveticus* and *E. pulveris* into *Cronobacter* as *Cronobacter zurichensis* nom. nov., *Cronobacter helveticus* comb. nov. and *Cronobacter pulveris* comb. nov., respectively, and emended description of the genera *Enterobacter* and *Cronobacter*. *Syst. Appl. Microbiol.* 36:309–319.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. doi:10.1186/1471-2164-9-75.
- Joseph S, Desai P, Ji Y, Cummings CA, Shih R, Degoricija L, Rico A, Brzoska P, Hamby SE, Masood N, Hariri S, Sonbol H, Chuzhanova N, McClelland M, Furtado MR, Forsythe SJ. 2012. Comparative analysis of genome sequences covering the seven *Cronobacter* species. *PLoS One* 7:e49455.