Draft Genome Sequence of Citrobacter freundii UFMG-H9, Isolated from Urine from a Healthy Bovine Heifer (Gyr Breed)

Silvia Giannattasio-Ferraz  
*Loyola University Chicago*

Laura Maskeri  
*Loyola University Chicago*

André P. Oliveira  
*Loyola University Chicago*

Edel F. Barbosa-Stancioli  
*Loyola University Chicago*

Catherine Putonti  
*Loyola University Chicago*, cputonti@luc.edu

Follow this and additional works at: https://ecommons.luc.edu/bioinformatics_facpub

Part of the Bioinformatics Commons, and the Biology Commons

**Recommended Citation**

Giannattasio-Ferraz, Silvia; Maskeri, Laura; Oliveira, André P.; Barbosa-Stancioli, Edel F.; and Putonti, Catherine. Draft Genome Sequence of Citrobacter freundii UFMG-H9, Isolated from Urine from a Healthy Bovine Heifer (Gyr Breed). Microbiology Resource Announcements, 9, : , 2020. Retrieved from Loyola eCommons, Bioinformatics Faculty Publications, http://dx.doi.org/10.1128/MRA.00387-20

This work is licensed under a Creative Commons Attribution 4.0 License. © Giannattasio-Ferraz et al., 2020.
Draft Genome Sequence of *Citrobacter freundii* UFMG-H9, Isolated from Urine from a Healthy Bovine Heifer (Gyr Breed)

Silvia Giannattasio-Ferraz,a Laura Maskeri,b André P. Oliveira,c Edel F. Barbosa-Stancioli,a Catherine Putontib,d,e,f

aDepartamento de Microbiologia, Instituto de Ciências Biológicas, Universidade Federal Minas Gerais, Belo Horizonte, MG, Brazil
bBioinformatics Program, Loyola University Chicago, Chicago, Illinois, USA
cEmpresa de Pesquisa Agropecuária de Minas Gerais–EPAMIG, Uberaba, MG, Brazil
dDepartment of Biology, Loyola University Chicago, Chicago, Illinois, USA
eDepartment of Computer Science, Loyola University Chicago, Chicago, Illinois, USA
fDepartment of Microbiology and Immunology, Stritch School of Medicine, Loyola University Chicago, Maywood, Illinois, USA

**ABSTRACT** *Citrobacter freundii* is a pathogen associated with antibiotic resistance and severe infections in humans. Here, we report the draft genome sequence of *C. freundii* strain UFMG-H9, an isolate from urine from a healthy Gyr heifer.

*Citrobacter freundii* is a known human pathogen highly associated with the occurrence of bacteremia and antibiotic resistance (1). This species has been reported as a contaminant of wastewater (2) and food of animal origin such as milk and cheese (3). Strains of *C. freundii* have also been reported to cause urinary infections in humans (4). Here, we report the draft genome sequence of *C. freundii* strain UFMG-H9, isolated from urine from a healthy heifer belonging to a Gyr herd pure in origin, from the Agricultural Research Company of Minas Gerais State (EPAMIG) in Brazil.

Samples were collected in May 2019, and the methodology was previously approved by the Ethics Committee in Animal Experimentation of the Universidade Federal de Minas Gerais, Brazil (CEUA/UFMG; approval number 40/2019). All experiments were performed in accordance with relevant guidelines. To collect the urine, the vulva of the animal was washed with distilled water and soap, and then midstream urine was collected using a 50-ml sterile tube. The urine was kept at –20°C until processing (within 48 h). Aliquots of 2 ml were centrifuged. The supernatant was plated on lysogeny broth (LB) agar plates and incubated at 37°C overnight. Single colonies were picked, grown in LB at 37°C overnight, and then replated. This process of plating and liquid culture was repeated 3 times in order to obtain pure colonies. Following this, a single colony was inoculated in LB liquid medium and grown overnight with shaking at 37°C. A 1-ml aliquot was centrifuged, and the pellet was used for DNA extraction with the DNeasy UltraClean microbial kit (Qiagen, Hilden, Germany) according to the manufacturer’s instruction. The DNA was quantified using a Qubit fluorometer. The genus and species were determined prior to whole-genome sequencing by sequencing the 16S rRNA gene sequence. Next, the DNA was sent to the Microbial Genomic Sequencing Center (MiGS) at the University of Pittsburgh for library preparation and whole-genome sequencing. Briefly, the DNA was fragmented using an Illumina tagmentation enzyme, and indices were attached using PCR. The genome sequencing was conducted using the NextSeq 550 platform. Sequencing produced 2,854,920 pairs of 150-bp reads that were trimmed using Sickle v1.33 (https://github.com/najoshi/sickle). The genome was assembled using SPAdes v3.13.0 with the “only-assembler” option for k values of 55, 77, 99, and 127 (5). Then, the genome coverage was calculated using BBMap v38.47 (https://sourceforge.net/projects/bbmap/). Finally, the genome was annotated by the NCBI

---


**Editor** Julie C. Dunning Hotopp, University of Maryland School of Medicine

**Copyright © 2020 Giannattasio-Ferraz et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.**

**Address correspondence to Catherine Putonti, cputonti@luc.edu.**

**Received** 12 April 2020

**Accepted** 14 April 2020

**Published** 7 May 2020
Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (6). Default parameters were used for all software tools unless otherwise noted. 

*C. freundii* strain UFMG-H9 is 4,744,381 bp long with a GC content of 50.77%. The assembly includes 20 contigs with an N₅₀ value of 525,854 bp, and the genome coverage is 164×. Annotation identified 4,315 coding genes and 75 tRNAs. Further analysis of this strain can increase our understanding of the urogenital tract of this species.

**Data availability.** This whole-genome sequencing (WGS) project has been deposited in GenBank under accession number JAAVMN000000000. The raw reads can be found in SRA under accession number SRR11455638. This sequencing is part of BioProject accession number PRUNA615899.

**REFERENCES**


