

University of New Hampshire

University of New Hampshire Scholars' Repository

Molecular, Cellular and Biomedical Sciences
Scholarship

Molecular, Cellular and Biomedical Sciences

1-1-2014

Draft Genome Sequence of Frankia sp. Strain Ccl6, a Salt-Tolerant Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of Casuarina cunninghamiana

Samira R. Mansour
Suez Canal University

Rediet Oshone
University of New Hampshire, Durham

Sheldon G. Hurst IV
University of New Hampshire, Durham

Krystalynne Morris
University of New Hampshire, Durham

W. Kelley Thomas
University of New Hampshire, Durham, Kelley.Thomas@unh.edu

Follow this and additional works at: https://scholars.unh.edu/mcbs_facpub

Comments

See next page for additional authors

This is an article published by American Society for Microbiology in Genome Announcements in 2014, available online: <https://dx.doi.org/10.1128/genomeA.01205-13>

Recommended Citation

Mansour, S.R, R. Oshone , S. G. Hurst IV, K. Morris, W. K. Thomas, and L. S. Tisa. 2014. Draft Genome Sequence of Frankia sp. strain Ccl6, a Salt-tolerant Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of Casuarina cunninghamiana. Genome Announc. 2(1) e01205-13 (doi:10.1128/genomeA.01205-13).

This Article is brought to you for free and open access by the Molecular, Cellular and Biomedical Sciences at University of New Hampshire Scholars' Repository. It has been accepted for inclusion in Molecular, Cellular and Biomedical Sciences Scholarship by an authorized administrator of University of New Hampshire Scholars' Repository. For more information, please contact Scholarly.Communication@unh.edu.

Authors

Samira R. Mansour, Rediet Oshone, Sheldon G. Hurst IV, Krystalynne Morris, W. Kelley Thomas, and Louis S. Tisa

Draft Genome Sequence of *Frankia* sp. Strain CcI6, a Salt-Tolerant Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of *Casuarina cunninghamiana*

Samira R. Mansour,^a Rediet Oshone,^b Sheldon G. Hurst IV,^b Krystalynne Morris,^b W. Kelley Thomas,^b Louis S. Tisa^b

Suez Canal University, Ismailia, Egypt^a; University of New Hampshire, Durham, New Hampshire, USA^b

Members of the actinomycete genus *Frankia* form a nitrogen-fixing symbiosis with 8 different families of actinorhizal plants. We report a 5.57-Mbp draft genome sequence for *Frankia* sp. strain CcI6, a salt-tolerant nitrogen-fixing actinobacterium isolated from root nodules of *Casuarina cunninghamiana* grown in Egyptian soils.

Received 11 December 2013 Accepted 13 December 2013 Published 16 January 2014

Citation Mansour SR, Oshone R, Hurst SG, IV, Morris K, Thomas WK, Tisa LS. 2014. Draft genome sequence of *Frankia* sp. strain CcI6, a salt-tolerant nitrogen-fixing actinobacterium isolated from the root nodule of *Casuarina cunninghamiana*. *Genome Announc.* 2(1):e01205-13. doi:10.1128/genomeA.01205-13.

Copyright © 2014 Mansour et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Louis S. Tisa, louis.tisa@unh.edu.

Members of the genus *Frankia* are well known for their facultative lifestyles as free-living soil dwellers and as plant symbionts of wood angiosperms termed actinorhizal plants (1–3). Actinorhizal plants are ecologically important as pioneer community plants, are distributed worldwide under a broad range of ecological conditions, and have economic significance for land reclamation, reforestation, soil stabilization, landscaping, and fuel. Their symbiosis allows actinorhizal plants to colonize harsh environmental terrains under diverse ecological conditions. The genomes for representatives from four major lineages have been sequenced (4–9) and have provided vital baseline information for genomic approaches toward understanding these novel bacteria.

In arid and semiarid areas, the salinization of soils and groundwater is a serious problem (10). Egypt, which occupies the northeastern corner of Africa, has arid and semiarid climates and greatly suffers from high soil salinity. Among the actinorhizal plants, the genus *Casuarina* has been shown to have the ability to grow well under such conditions, and it is widely distributed in Egyptian soil. *Frankia* sp. strain CcI6 was isolated from root nodules of *Casuarina cunninghamiana* grown in Egypt and shown to reinfect *C. cunninghamiana*, *Casuarina glauca*, and *Casuarina equisetifolia* (11). This strain showed an increased level of NaCl tolerance (12). Based on 16S phylogenetic analysis, this strain is close to *Frankia* sp. strain CcI3, another narrow-host range symbiont, whose genome has been sequenced. *Frankia* sp. CcI6 has the potential to be used as a large-scale inoculum for *Casuarina* trees involved in land reclamation of Egyptian saline soils. *Frankia* sp. CcI6 was sequenced to increase our understanding of its salt tolerance mechanisms and to provide information about its potential ecological roles and interactions with actinorhizal plants.

The draft genome of *Frankia* sp. CcI6 was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH) using Illumina technology (13) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2000 platform, which generated 17,617,450 reads (260-bp insert size) totaling 1,665.7 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench (version

6.5.1) and AllPaths-LG (version r41043) (14). The final draft assembly contains 138 contigs, with an N₅₀ of 103 kb. The total size of the genome is 5.6 Mbp, and the final assembly is based on 1,243.2 Mb of Illumina draft data, providing an average 222× coverage of the genome.

The high-quality draft genome of *Frankia* sp. CcI6 was resolved to 138 contigs consisting of 5,565,969 bp, with a G+C content of 67.6%. The assembled *Frankia* sp. CcI6 genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA (15), and resulted in 4,900 candidate protein-encoding genes, 46 tRNA genes, and 3 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AYTZ000000000](https://www.ncbi.nlm.nih.gov/nuccore/AYTZ000000000). The version described in this paper is version AYTZ01000000.

ACKNOWLEDGMENTS

This work was supported in part by United States-Egypt Joint Research grant no. BIO13-001 (to S.R.M. and L.S.T.) and Hatch grant no. NH585 (to L.S.T.).

REFERENCES

- Benson DR, Silvester WB. 1993. Biology of *Frankia* strains, actinomycete symbionts of actinorhizal plants. *Microbiol. Rev.* 57:293–319.
- Schwencke J, Caru M. 2001. Advances in actinorhizal symbiosis: host plant-*Frankia* interactions, biology, and applications in arid land reclamation. A review. *Arid Land Res. Manag.* 15:285–327. [http://dx.doi.org/10.1080/153249801753127615](https://doi.org/10.1080/153249801753127615).
- Chaia EE, Wall LG, Huss-Danell K. 2010. Life in soil by actinorhizal root nodule endophyte *Frankia*. A review. *Symbiosis* 51:201–226. [http://dx.doi.org/10.1007/s13199-010-0086-y](https://doi.org/10.1007/s13199-010-0086-y).
- Normand P, Lapiere P, Tisa LS, Gogarten JP, Alloisio N, Bagnarol E, Bassi CA, Berry AM, Bickhart DM, Choise N, Couloux A, Cournoyer B, Cruveiller S, Daubin V, Demange N, Francino MP, Goltsman E, Huang Y, Kopp OR, Labarre L, Lapidus A, Lavire C, Marechal J, Martinez M, Mastrorunzio JE, Mullin BC, Niemann J, Pujic P, Rawnsley T, Rouy Z, Schenowitz C, Sellstedt A, Tavares F, Tomkins JP, Vallenet D, Valverde C, Wall LG, Wang Y, Medigue C, Benson DR. 2007. Genome characteristics of facultatively symbiotic *Frankia* sp. strains reflect host range and host plant biogeography. *Genome Res.* 17:7–15.

5. Persson T, Benson DR, Normand P, Vanden Heuvel B, Pujic P, Chertkov O, Teshima H, Bruce DC, Detter C, Tapia R, Han S, Han J, Woyke, Pitlock S, Pennacchio L, Nolan M, Ivanova N, Pati A, Land ML, Pawlowski K, Berry AM. 2011. Genome sequence of “*Candidatus Frankia datiscaae*” Dg1, the uncultured microsymbiont from nitrogen-fixing root nodules of the dicot *Datisca glomerata*. *J. Bacteriol.* 193:7017–7018. <http://dx.doi.org/10.1128/JB.06208-11>.
6. Ghodhbane-Gtari F, Beauchemin N, Bruce D, Chain P, Chen A, Walston Davenport K, Deshpande S, Detter C, Furnholm T, Goodwin L, Gtari M, Han C, Han J, Huntemann M, Ivanova N, Kyrpides N, Land ML, Markowitz V, Mavrommatis K, Nolan M, Nouioui I, Pagani I, Pati A, Pitluck S, Santos CL, Sen A, Sur S, Szeto E, Tavares F, Teshima H, Thakur S, Wall LG, Woyke T, Tisa LS. 2013. Draft genome sequence of *Frankia* sp. strain CN3, an atypical, non-infective (nod⁻) ineffective (Fix⁻) isolate from *Coriaria nepalensis*. *Genome Announc.* 1(2):00085–13. <http://dx.doi.org/10.1128/genomeA.00085-13>.
7. Sen A, Beauchemin N, Bruce D, Chain P, Chen A, Walston Davenport K, Deshpande S, Detter C, Furnholm T, Ghodhbane-Gtari F, Goodwin L, Gtari M, Han C, Han J, Huntemann M, Ivanova N, Kyrpides N, Land ML, Markowitz V, Mavrommatis K, Nolan M, Nouioui I, Pagani I, Pati A, Pitluck S, Santos CL, Sur S, Szeto E, Tavares F, Teshima H, Thakur S, Wall L, Wishart J, Woyke T, Tisa LS. 2013. Draft genome sequence of *Frankia* sp. strain QA3, a nitrogen-fixing actinobacterium isolated from the root nodule of *Alnus nitida*. *Genome Announc.* 1(2):e00103-13. <http://dx.doi.org/10.1128/genomeA.00103-13>.
8. Nouioui I, Beauchemin N, Cantor MN, Chen A, Detter JC, Furnholm T, Ghodhbane-Gtari F, Goodwin L, Gtari M, Han C, Han J, Huntemann M, Hua SX, Ivanova N, Kyrpides N, Markowitz V, Mavrommatis K, Mikhailova N, Nordberg HP, Ovchinnikova G, Pagani I, Pati A, Sen A, Sur S, Szeto E, Thakur S, Wall L, Wei CL, Woyke T, Tisa LS. 2013. Draft genome sequence of *Frankia* sp. strain BMG5.12, a nitrogen-fixing actinobacterium isolated from Tunisian soils. *Genome Announc.* 1(4):e00468-13. <http://dx.doi.org/10.1128/genomeA.00468-13>.
9. Wall LG, Beauchemin N, Cantor MN, Chaia E, Chen A, Detter JC, Furnholm T, Ghodhbane-Gtari F, Goodwin L, Gtari M, Han C, Han J, Huntemann M, Hua SX, Ivanova N, Kyrpides N, Markowitz V, Mavrommatis K, Mikhailova N, Nordberg HP, Nouioui I, Ovchinnikova G, Pagani I, Pati A, Sen A, Sur S, Szeto E, Thakur S, Wei CL, Woyke T, Tisa LS. 2013. Draft genome sequence of *Frankia* sp. strain BCU110501, a nitrogen-fixing actinobacterium isolated from nodules of *Discaria trinervis*. *Genome Announc.* 1(4):e00503-13. <http://dx.doi.org/10.1128/genomeA.00503-13>.
10. Rengasamy P. 2006. World salinization with emphasis on Australia. *J. Exp. Bot.* 57:1017–1023. <http://dx.doi.org/10.1093/jxb/erj108>.
11. Mansour SR, Moussa LAA. 2005. Role of gamma-radiation on spore germination and infectivity of *Frankia* strains CeI523 and CcI6 isolated from Egyptian *Casuarina*. *Isotope Rad. Res.* 37:1023–1038.
12. Oshone R, Mansour SR, Tisa LS. 2013. Effect of salt stress on the physiology of *Frankia* sp. strain CcI6. *J. Biosci.* 38:699–702. <http://dx.doi.org/10.1007/s12038-013-9371-2>.
13. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
14. Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Burton JN, Walker BJ, Sharpe T, Hall G, Shea TP, Sykes S, Berlin AM, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander ES, Jaffe DB. 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc. Natl. Acad. Sci. U. S. A.* 108:1513–1518. <http://dx.doi.org/10.1073/pnas.1017351108>.
15. Markowitz VM, Korzeniewski F, Palaniappan K, Szeto E, Werner G, Padki A, Zhao XL, Dubchak I, Hugenholtz P, Anderson I, Lykidis A, Mavromatis K, Ivanova N, Kyrpides NC. 2006. The integrated microbial genomes (IMG) system. *Nucleic Acids Res.* 34:D344–D348. <http://dx.doi.org/10.1093/nar/gkj024>.