

University of New Hampshire
University of New Hampshire Scholars' Repository

Molecular, Cellular and Biomedical Sciences
Scholarship

Molecular, Cellular and Biomedical Sciences

5-22-2014

Draft Genome Sequence of Frankia sp. Strain Thr, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of Casuarina cunninghamiana Grown in Egypt

Sheldon G. Hurst IV
University of New Hampshire, Durham

Rediet Oshone
University of New Hampshire, Durham

Faten Ghodhbane-Gtari
Université de Tunis El-Manar

Krystalynne Morris
University of New Hampshire, Durham

Feseha Abebe-Akele
University of New Hampshire, Durham

See next page for additional authors

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

Recommended Citation

Hurst IV, S. G., F. Ghodhbane-Gtari, R. Oshone, K. Morris, F. Abebe-Akele, W. K. Thomas, A. Ktari, K. Salem, S. Mansour, M. Gtari, and L. S. Tisa. 2014. Draft Genome Sequence of Frankia sp. strain Thr, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of Casuarina cunninghamiana Grown in Egypt. *Genome Announc* 2 (3):e00493-14. doi:10.1128/genomeA.00493-14.

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 nicole.hentz@unh.edu.

Authors

Sheldon G. Hurst IV, Rediet Oshone, Faten Ghodhbane-Gtari, Krystalynne Morris, Feseha Abebe-Akele, W. Kelley Thomas, Amir Ktari, Karima Salem, Samira R. Mansour, Maher Gtari, and Louis S. Tisa

Draft Genome Sequence of *Frankia* sp. Strain Thr, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Casuarina cunninghamiana* Grown in Egypt

Sheldon G. Hurst IV,^a Rediet Oshone,^a Faten Ghodhbane-Gtari,^{a,b} Krystalynne Morris,^a Feseha Abebe-Akele,^a W. Kelley Thomas,^a Amir Ktari,^b Karima Salem,^b Samira Mansour,^c Maher Gtari,^{a,b} Louis S. Tisa^a

University of New Hampshire, Durham, New Hampshire, USA^a; Laboratoire Microorganismes et Biomolécules Actives, Université Tunis El Manar (FST) & Université Carthage (INSAT), Campus Universitaire, Tunis, Tunisia^b; Botany Department, Faculty of Science, Suez Canal University, Ismailia, Egypt^c

Nitrogen-fixing actinobacteria of the genus *Frankia* are symbionts of woody dicotyledonous plants termed actinorhizal plants. We report here a 5.3-Mbp draft genome sequence for *Frankia* sp. strain Thr, a nitrogen-fixing actinobacterium isolated from root nodules of *Casuarina cunninghamiana* collected in Egypt.

Received 2 May 2014 Accepted 6 May 2014 Published 22 May 2014

Citation Hurst SG IV, Oshone R, Ghodhbane-Gtari F, Morris K, Abebe-Akele F, Thomas WK, Ktari A, Salem K, Mansour S, Gtari M, Tisa LS. 2014. Draft genome sequence of *Frankia* sp. strain Thr, a nitrogen-fixing actinobacterium isolated from the root nodules of *Casuarina cunninghamiana* grown in Egypt. *Genome Announc.* 2(3):e00493-14. doi:10.1128/genomeA.00493-14.

Copyright © 2014 Hurst 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.

Among the *Actinobacteria*, the genus *Frankia* is well known for its facultative lifestyle as a plant symbiont of dicotyledonous plants, termed actinorhizal plants, and as a free-living soil dweller (1-3). Actinorhizal plants are ecologically important pioneer community plants that are found worldwide under a broad range of ecological and environmental conditions (4). The symbiosis allows actinorhizal plants to colonize harsh environmental terrains. Based on molecular phylogenetic analysis, four major clusters within the genus are recognized (5-9), and genomes for representatives from each cluster have been sequenced (10-16). Cluster I contains two subclusters: one subcluster (cluster Ia) represents *Frankia* strains with the ability to infect a wide range of host plants, including members of the *Betulaceae* and *Myricaceae* families, and the other subcluster (cluster Ib) contains strains limited to *Casuarina* and *Allocasuarina* host plants.

The fast growing and highly tolerant trees from the family *Casuarinaceae* have been used worldwide as windbreaks, dune stabilizers, fuel wood, and in soil regeneration (17). In North Africa, these actinorhizal plants are grow well under the harsh conditions. *Frankia* sp. strain Thr was isolated from root nodules of *Casuarina cunninghamiana* growing in Egypt and effectively reinfects its original host plant, one of the *Casuarina* spp. (18). *Frankia* sp. strain Thr has been used extensively in infection studies and is well characterized for its host plant interactions. Presently, two genomes from *Frankia* cluster Ib *Casuarina*-infecting strains are available (10, 16). *Frankia* sp. strain Thr was sequenced to increase our understanding of this subcluster Ib with restricted host plant range and to provide information about its potential ecological roles and interaction with actinorhizal plants.

The draft genome of *Frankia* sp. strain Thr was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH) using Illumina technology (19) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2000 platform, which generated 19,189,718 reads

(260-bp insert size) totaling 1,824.9 Mbp. The Illumina sequence data were assembled using the CLC Genomics Workbench (6.5.1) and AllPaths-LG (version r41043) (20). The final draft assembly contained 171 contigs, with an N_{50} of 71.6 kb. The total size of the genome is 5.3 Mbp, and the final assembly is based on 1,666.1 Mb of Illumina draft data, providing an average 248 \times coverage of the genome.

The high-quality draft genome of *Frankia* sp. strain Thr was resolved to 171 contigs consisting of 5,309,833 bp, with a G+C content of 69.95%. The assembled *Frankia* sp. strain Thr genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (21), and resulted in 4,805 candidate protein-coding genes, 46 tRNA genes, and 2 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JENI000000000](https://www.ncbi.nlm.nih.gov/nuccore/JENI000000000). The version described in this paper is version JENI01000000.

ACKNOWLEDGMENTS

This work was supported in part by the New Hampshire Agricultural Experimental Station (Hatch NH585), U.S.-Egypt Joint research grant BIO13-001, Agriculture and Food Research Initiative grant 2010-65108-20581 from the USDA National Institute of Food and Agriculture, and the College of Life Science and Agriculture at the University of New Hampshire-Durham. This is scientific contribution number 2557 from the NH Agricultural Experiment Station. M.G. and F.G.-G. were supported in part by a Visiting Scientist and Postdoctoral Scientist Program administered by the New Hampshire Agricultural Experimental Station at the University of New Hampshire.

REFERENCES

1. Benson DR, Silvester WB. 1993. Biology of *Frankia* strains, actinomycete symbionts of actinorhizal plants. *Microbiol. Rev.* 57:293-319.
2. 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>.
3. 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>.
 4. Benson DR, Dawson JO. 2007. Recent advances in the biogeography and genecology of symbiotic *Frankia* and its host plants. *Physiol. Plant.* 130: 318–330. <http://dx.doi.org/10.1111/j.1399-3054.2007.00934.x>.
 5. Normand P, Orso S, Cournoyer B, Jeannin P, Chapelon C, Dawson J, Evtushenko L, Misra AK. 1996. Molecular phylogeny of the genus *Frankia* and related genera and emendation of the family *Frankiaceae*. *Int. J. Syst. Bacteriol.* 46:1–9. <http://dx.doi.org/10.1099/00207713-46-1-1>.
 6. Cournoyer B, Lavire C. 1999. Analysis of *Frankia* evolution radiation using *glnII* sequences. *FEMS Microbiol. Lett.* 117:29–34.
 7. Nouioui I, Ghodhbane-Gtari F, Beauchemin NJ, Tisa LS, Gtari M. 2011. Phylogeny of members of the *Frankia* genus based on *gyrB*, *nifH* and *glnII* sequences. *American Van Leeuwenhoek* 100:579–587. <http://dx.doi.org/10.1007/s10482-011-9613-y>.
 8. Ghodhbane-Gtari F, Nouioui I, Chair M, Boudabous A, Gtari M. 2010. 16S-23S rRNA intergenic spacer region variability in the genus *Frankia*. *Microb. Ecol.* 60:487–495. <http://dx.doi.org/10.1007/s00248-010-9641-6>.
 9. Gtari M, Tisa LS, Normand P. 2013. Diversity of *Frankia* strains, *Actinobacteria* symbionts of actinorhizal plants, p 123–148. In Aroca R (ed), *Symbiotic endophytes, soil biology* 37. Springer Verlag, New York, NY. http://dx.doi.org/10.1007/978-3-642-39317-4_7.
 10. Normand P, Lapierre P, Tisa LS, Gogarten JP, Alloisio N, Bagnarol E, Bassi CA, Berry AM, Bickhart DM, Choisine 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. <http://dx.doi.org/10.1101/gr.5798407>.
 11. 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 datiscacae*” 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>.
 12. 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. doi: 10.1128/genomeA.00085-13.
 13. 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>.
 14. Nouioui I, 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, 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>.
 15. 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 C-L, 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>.
 16. Mansour SR, Oshone R, Hurst SG, IV, Morris K, Thomas WK, Tisa LS. 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. <http://dx.doi.org/10.1128/genomeA.01205-13>.
 17. Dommergues Y. 1997. Contribution of actinorhizal plants to tropical soil productivity and rehabilitation. *Soil Biol. Biochem.* 29:931–947. [http://dx.doi.org/10.1016/S0038-0717\(96\)00227-1](http://dx.doi.org/10.1016/S0038-0717(96)00227-1).
 18. Girgis MGZ, Ishac YZ, El-Haddad M, Saleh EA, Diem HG, Dommergues YR. 1990. First report on isolation and culture of effective *Casuarina*-compatible strains of *Frankia* from Egypt, p 156–164. In El-Lakany MH, Turnbull JW, Brewbaker JL (ed), 2nd International Casuarina Workshop, American University, Cairo, Egypt.
 19. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
 20. 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>.
 21. Markowitz VM, Korzeniewski F, Palaniappan K, Szeto E, Werner G, Padki A, Zhao X, 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>.