

University of New Hampshire

University of New Hampshire Scholars' Repository

Molecular, Cellular and Biomedical Sciences
Scholarship

Molecular, Cellular and Biomedical Sciences

12-17-2015

Permanent Draft Genome Sequence of Frankia sp. Strain ACN1ag, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Alnus glutinosa*

Erik Swanson

University of New Hampshire, Durham

Rediet Oshone

University of New Hampshire, Durham

Stephen Simpson

University of New Hampshire, Durham

Krystalynne Morris

University of New Hampshire, Durham

Feseha Abebe-Akele

University of New Hampshire, Durham

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

See next page for additional authors

Comments

This is an article published by American Society for Microbiology in Genome Announcements in 2015, available online: <https://dx.doi.org/10.1128/genomeA.01483-15>

Recommended Citation

Swanson, E., R. Oshone, K. Morris, F. Abebe-Akele, S. Simpson, W. K. Thomas, and L. S. Tisa. 2015. Draft Genome sequence of Frankia sp. strain ACN1ag, a nitrogen-fixing actinobacterium isolated from the root nodule of *Alnus glutinosa*. *Genome Announc* 3(6):e01483-15. doi:10.1128/genomeA.01483-15.

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

Erik Swanson, Rediet Oshone, Stephen Simpson, Krystalynne Morris, Feseha Abebe-Akele, W. Kelley Thomas, and Louis S. Tisa

Permanent Draft Genome Sequence of *Frankia* sp. Strain ACN1^{ag}, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Alnus glutinosa*

Erik Swanson, Rediet Oshone, Stephen Simpson, Krystalynne Morris, Feseha Abebe-Akele, W. Kelley Thomas, Louis S. Tisa

University of New Hampshire, Durham, New Hampshire, USA

Frankia strain ACN1^{ag} is a member of Frankia lineage Ia, which are able to re-infect plants of the Betulaceae and Myricaceae families. Here, we report a 7.5-Mbp draft genome sequence with a G+C content of 72.35% and 5,687 candidate protein-encoding genes.

Received 27 October 2015 Accepted 27 October 2015 Published 17 December 2015

Citation Swanson E, Oshone R, Simpson S, Morris K, Abebe-Akele F, Thomas WK, Tisa LS. 2015. Permanent draft genome sequence of *Frankia* sp. strain ACN1^{ag}, a nitrogen-fixing actinobacterium isolated from the root nodules of *Alnus glutinosa*. *Genome Announc* 3(6):e01483-15. doi:10.1128/genomeA.01483-15.

Copyright © 2015 Swanson 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 in a broad range of ecological and environmental conditions (4). The symbiosis allows actinorhizal plants to colonize harsh environmental terrains. The genus *Frankia* has not yet been described to the species level, but it has become an area of greater interest. Four major *Frankia* lineages have been identified (5–8), and genomes for representatives from each cluster have been sequenced (9–21).

Cluster I contains two subclusters: one subcluster (Cluster Ia) represents *Frankia* strains with the ability to infect a wider range of host plants, including member of the *Betulaceae* and *Myricaceae* families, and the other subcluster (Cluster Ib) contains strains limited to *Casuarina* and *Allocasuarina* host plants. As another member of Cluster Ia, *Frankia* sp. strain ACN1^{ag} was chosen for sequencing to provide more information on this lineage and its interaction with actinorhizal plants. *Frankia* sp. strain ACN1^{ag} is a re-isolate from root nodules of *Alnus glutinosa* inoculated from an isolate of *Alnus viridis crispa* collected from Atikokan, Ontario, Canada (22, 23).

The draft genome of *Frankia* sp. strain ACN1^{ag} was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH, USA) using Illumina technology (24) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq2000 platform, which generated 14,474,194 reads (260-bp insert size) totaling 2,127.7 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench version 8.0.1 and AllPaths-LG version r41043 (25). The final draft assembly contained 108 contigs with an N_{50} of 157.4 kb. The total size of the genome is 7.5 Mbp, and the final assembly is based on 2,127.17 Mb of Illumina draft data and provided an average 220× coverage of the genome.

The high-quality draft genome of *Frankia* sp. strain ACN1^{ag} was resolved to 108 contigs consisting of 7,505,639 bp with a G+C content of 72.35%. The assembled *Frankia* sp. strain ACN1^{ag} ge-

nome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (26, 27), and resulted in 5,687 candidate protein-encoding genes, 45 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 number [LJPA00000000](https://www.ncbi.nlm.nih.gov/nuccore/LJPA00000000). The version described in this paper is the first version, LJPA01000000.

ACKNOWLEDGMENTS

Partial funding was provided by the New Hampshire Agricultural Experiment Station. This is Scientific Contribution Number 2638. This work was supported by the USDA National Institute of Food and Agriculture Hatch 022821 (L.S.T.), Agriculture and Food Research Initiative Grant 2015-67014-22849 from the USDA National Institute of Food and Agriculture (L.S.T.), and the College of Life Science and Agriculture at the University of New Hampshire–Durham. Sequencing was performed on an Illumina HiSeq2500 purchased with NSF MRI Grant DBI-1229361 to W.K.T.

REFERENCES

- Schwencke J, Carú 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>.
- Chaia EE, Wall LG, Huss-Danell K. 2010. Life in soil by the actinorhizal root nodule endophyte *Frankia*. A review. *Symbiosis* 51:201–226. <http://dx.doi.org/10.1007/s13199-010-0086-y>.
- Normand P, Benson DR, Berry AM, Tisa LS. 2014. Family *Frankiaceae*, p 339–356. In Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson F (ed), *The prokaryote—Actinobacteria*, 4th ed. Springer-Verlag, Berlin, Germany.
- 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>.
- 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>.
- 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. *Antonie 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. Normand P, Lapiere P, Tisa LS, Gogarten JP, Alloisio N, Bagnarol E, Bassi CA, Berry AM, Bickhart DM, Choisne N, Couloux A, Cournoyer B, Cruveiller S, Daubin V, Demange N, Francino MP, Goltzman E, Huang Y, Kopp OR, Labarre L, Lapidus A, Lavire C, Marechal J, Martinez M, Mastrorunzio JE, Mullin BC, Niemann J, Pujic J, Rawnsley T, Rouy Z, Schenowitz C, Sellstedt A, Tavares F, Tomkins JP, Vallet 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>.
10. Normand P, Queiroux C, Tisa LS, Benson DR, Rouy Z, Cruveiller S, Médigue C. 2007. Exploring the genomes of *Frankia*. *Physiol Plant* 130: 331–343. <http://dx.doi.org/10.1111/j.1399-3054.2007.00918.x>.
11. Persson T, Benson DR, Normand P, Vanden Heuvel B, Pujic J, Chertkov O, Teshima H, Bruce DC, Detter C, Tapia R, Han S, Han J, Woyke T, Pitluck S, Pennacchio L, Nolan M, Ivanova N, Pati A, Land ML, Pawlowski K, Berry AM. 2011. Genome sequence of “*Candidatus Frankia daticae*” 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 L, Woyke T, Tisa LS. 2013. Draft genome sequence of *Frankia* sp. strain CN3, an atypical, noninfective (Nod⁻) ineffective (Fix⁻) isolate from *Coriaria nepalensis*. *Genome Announc* 1(2):e00085-13. <http://dx.doi.org/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, 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 C-L, 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 IV SG, 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. <http://dx.doi.org/10.1128/genomeA.01205-13>.
17. Hurst IV SG, 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. <http://dx.doi.org/10.1128/genomeA.00493-14>.
18. Ghodhbane-Gtari F, Hurst IV SG, Oshone R, Morris K, Abebe-Akele F, Thomas WK, Ktari A, Salem K, Gtari M, Tisa LS. 2014. Draft genome sequence of *Frankia* sp. strain BMG5.23, a salt-tolerant nitrogen-fixing actinobacterium isolated from the root nodules of *Casuarina glauca* grown in Tunisia. *Genome Announc* 2(3):e00520-14. <http://dx.doi.org/10.1128/genomeA.00520-14>.
19. Tisa LS, Beauchemin N, Gtari M, Sen A, Wall LG. 2013. What stories can the *Frankia* genomes start to tell us? *J Biosci* 38:719–726. <http://dx.doi.org/10.1007/s12038-013-9364-1>.
20. Gtari M, Ghodhbane-Gtari F, Nouioui I, Ktari A, Hezbri K, Mimouni W, Sbissi I, Ayari A, Yamanaka T, Normand P, Tisa LS, Boudabous A. 2015. Cultivating the uncultured: growing the recalcitrant cluster-2 *Frankia* strains. *Sci Rep* 5:13112. <http://dx.doi.org/10.1038/srep13112>.
21. Tisa LS, Beauchemin N, Cantor MN, Furnholm T, Ghodhbane-Gtari F, Goodwin L, Copeland A, Gtari M, Huntemann M, Ivanova N, Kyrpides N, Markowitz V, Mavrommatis K, Mikhailova N, Nouioui I, Oshone R, Ovchinnikova G, Pagani I, Palaniappan K, Pati A. 2015. Draft genome sequence of *Frankia* sp. strain DC12, an atypical, noninfective, ineffective isolate from *Datisca cannabina*. *Genome Announc* 3(4):e00889-15. <http://dx.doi.org/10.1128/genomeA.00889-15>.
22. Baker D, Torrey JG, Kidd GH. 1979. Isolation by sucrose-density fractionation and cultivation *in vitro* of actinomycetes from nitrogen-fixing root nodules. *Nature* 281:76–78. <http://dx.doi.org/10.1038/281076a0>.
23. Lalonde M, Calvert HE, Pine S. 1981. Isolation and use of *Frankia* strains in actinorhizae formation, p 296–299. In Gibson AH, Newton WE (ed), *Current perspectives in nitrogen fixation*. Australian Academy of Science, Canberra, Australia.
24. Bennett S. 2004. *Solexa Ltd. Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
25. 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 USA* 108:1513–1518. <http://dx.doi.org/10.1073/pnas.1017351108>.
26. 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>.
27. Markowitz VM, Mavromatis K, Ivanova NN, Chen IA, Chu K, Kyrpides NC. 2009. IMG ER: a system for microbial genome annotation expert review and curation. *Bioinformatics* 25:2271–2278. <http://dx.doi.org/10.1093/bioinformatics/btp393>.