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Permanent Draft Genome Sequence for *Frankia* sp. Strain CeD, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Casuarina equisetifolia* Grown in Senegal

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***Frankia* strain CeD is a member of *Frankia* lineage Ib that is able to reinfect plants of the *Casuarina* families. Here, we report a 5.0-Mbp draft genome sequence with a G+C content of 70.1% and 3,847 candidate protein-encoding genes.**

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Members of the genus *Frankia* are soil-dwelling actinobacteria that are well known for their facultative lifestyle as a plant symbiont of dicotyledonous plants, termed actinorhizal plants (1–3). As ecologically important pioneer community plants, actinorhizal plants are found worldwide in 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 (5–8) and genomes for representatives from each cluster have been sequenced (9–24). 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. Members of cluster II infect host plants of the subfamily *Dryadoideae* (*Rosaceae*), the families *Coriariaceae* and *Datisaceae*, and the genus *Ceanothus* (*Rhamnaceae*). Members of cluster III are the most promiscuous and are infective on *Eleagnaceae*, *Rhamnaceae*, *Myricaceae*, *Gymnostoma* (*Casuarinaceae*), and occasionally *Alnus*. The fourth *Frankia* lineage consists of the “atypical” strains which are unable to reinfect actinorhizal host plants or form ineffective root nodule structures that are unable to fix nitrogen.

Under tropic and subtropic conditions, fast growing and highly tolerant trees from the family *Casuarinaceae* have been used as windbreaks, dune stabilizers, fuel wood, and soil regeneration and these actinorhizal plants grow well under the harsh conditions including high salinity (25). *Frankia* sp. strain CeD was isolated from root nodules of *Casuarina equisetifolia* growing in Senegal and effectively reinfects its original host plant, *Casuarina* spp. (26). *Frankia* sp. strain CeD has been used extensively in

infection studies and is well characterized for its host plant interactions (27).

The draft genome of *Frankia* sp. strain CeD was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH, USA) using Illumina technology (28) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq2000 platform, which generated 29,802,574 reads (260 bp insert size) totaling 4,381.0 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench (8.0.1) and AllPaths-LG (version r41043) (29). The final draft assembly for *Frankia* CeD consisted of 154 contigs in 120 scaffolds containing a total sequence of 5,004,600 bp with an N_{50} contig size of 73.6 kb and G+C content of 70.1%. This assembled draft resulted in 703× coverage of the genome.

The assembled *Frankia* sp. strain CeD genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (30, 31) and resulted in 3,847 candidate protein-encoding genes, 45 tRNA, and 2 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JPGU00000000](https://www.ncbi.nlm.nih.gov/nuccore/JPGU00000000). The version described in this paper is version [JPGU01000000](https://www.ncbi.nlm.nih.gov/nuccore/JPGU01000000).

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REFERENCES

- 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>.
- 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 Heidelberg.
- 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>.
- Benson DR, Dawson JO. 2007. Recent advances in the biogeography and genealogy 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 JO, 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* 177:29–34.
- 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. *Ant Van Leeuw* 100:579–587. <http://dx.doi.org/10.1007/s10482-011-9613-y>.
- 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>.
- 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, noninfective (nod⁻) ineffective (fix⁻) isolate from *Coriaria nepalensis*. *Genome Announc* 1(2):00085–13. <http://dx.doi.org/10.1128/genomeA.00085-13>.
- Ghodhbane-Gtari F, Hurst SG, IV, 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>.
- Gtari M, Ghodhbane-Gtari F, Nouioui I, Ktari A, Hezbri K, Minouni W, Sbissi I, Ayari A, Sghaier H, Normand P, Tisa LS, Yamanaka T, Boudabous A. 2015. Cultivating the uncultured: growing the recalcitrant cluster-2 *Frankia* strains. *Sci Rep* 5:13112. <http://dx.doi.org/10.1038/srep13112>.
- Hurst SG, IV, Ghodhbane-Gtari F, Oshone R, 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): <http://dx.doi.org/10.1128/genomeA.00493-14>.
- Mansour SR, Oshone R, Hurst SG, IV, Morris K, Thomas WK, Tisa LS. 2014. Draft genome sequence of *Frankia* sp. strain Cc16, a salt-tolerant nitrogen-fixing actinobacterium isolated from the root nodule of *Casuarina cunninghamiana*. *Genome Announc* 2(1): <http://dx.doi.org/10.1128/genomeA.01205-13>.
- 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.
- 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. 2013. Draft genome sequence of *Frankia* sp. strain BMG5.12, a nitrogen-fixing actinobacterium isolated from Tunisian soils. *Genome Announc* 1(4): <http://dx.doi.org/10.1128/genomeA.00468-13>.
- Oshone R, Hurst SG, IV, Abebe-Akele F, Simpson S, Morris K, Thomas WK, Tisa LS. 2016. Permeant draft genome sequences for two variants of *Frankia* sp. strain Cp11, the first *Frankia* strain isolated from the root nodule of *Comptonia peregrina*. *Genome Announc* 4(1):e01588–15. <http://dx.doi.org/10.1128/genomeA.01588-15>.
- 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 T, Pitlock S, Pennacchio L, Nolan M, Ivanova N, Pati A, Land ML, Pawlowski K, Berry AM. 2011. Genome sequence of “*Candidatus Frankia datiscae*” 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>.
- Pujic P, Bolotin A, Fournier P, Sorokin A, Lapidus A, Richau KH, Briolay J, Mebarki F, Normand P, Sellstedt A. 2015. Genome sequence of the atypical symbiotic *Frankia* R43 strain, a nitrogen-fixing and hydrogen-evolving actinobacterium. *Genome Announc* 3(6):e01387–15. <http://dx.doi.org/10.1128/genomeA.01387-15>.
- 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>.
- Swanson E, Oshone R, Simpson S, Morris K, Abebe-Akele F, Thomas WK, Tisa LS. 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. <http://dx.doi.org/10.1128/genomeA.01483-15>.
- Swanson E, Oshone R, Simpson S, Morris K, Abebe-Akele F, Thomas WK, Tisa LS. 2015. Permeant draft genome sequence of *Frankia* sp. strain Avc11, a nitrogen-fixing actinobacterium isolated from the root nodule of *Alnus viridis* ssp. *crispa* grown in Canada. *Genome Announc* 3(6):e01511–15. <http://dx.doi.org/10.1128/genomeA.01511-15>.
- 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>.
- 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>.
- 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): <http://dx.doi.org/10.1128/genomeA.00503-13>.

25. Dommergues YR. 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).
26. Diem HG, Dommergues Y. 1983. The isolation of *Frankia* from nodules of *Casuarina*. *Can J Bot* 61:2822–2825.
27. Ngom M, Diagne N, Laplaze L, Champion A, Sy MO. 2 December 2015. Symbiotic ability of diverse *Frankia* strains on *Casuarina glauca* plants in hydroponic conditions. *Symbiosis*. <http://dx.doi.org/10.1007/s13199-015-0366-7>.
28. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
29. 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>.
30. 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>.
31. Markowitz VM, Mavromatis K, Ivanova NN, Chen IMA, 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>.