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4-6-2017

Permanent draft genome sequence of *Ensifer* sp. strain LCM 4579, a salt-tolerant, nitrogen-fixing bacterium isolated from Senegalese soil

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This is an article published by American Society for Microbiology in Genome Announcements in 2017, available online: <https://dx.doi.org/10.1128/genomeA.00117-17>

Recommended Citation

Diagne N, Swanson E, Pesce C, Fall F, Diouf F, Bakhoum N, Fall D, Ndigue Faye M, Oshone R, Simpson S, Morris K, Thomas WK, Moulin L, Diouf D, Tisa LS. 2017. Permanent draft genome sequence of *Ensifer* sp. strain LCM 4579, a salt-tolerant, nitrogen-fixing bacterium isolated from Senegalese soil. *Genome Announc* 5:e00117-17. <https://dx.doi.org/10.1128/genomeA.00117-17>

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Permanent Draft Genome Sequence of *Frankia* sp. Strain Allo2, a Salt-Tolerant Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Allocasuarina*

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***Frankia* sp. strain Allo2 is a member of *Frankia* lineage Ib, which is able to reinfect plants of the *Casuarinaceae* family, and exhibits a high level of salt tolerance compared to other isolates. Here, we report the 5.3-Mbp draft genome sequence of *Frankia* sp. strain Allo2 with a G+C content of 70.0% and 4,224 candidate protein-encoding genes.**

Received 25 March 2016 Accepted 29 March 2016 Published 19 May 2016

Citation Oshone R, Ngom M, Abebe-Akele F, Simpson S, Morris K, Sy MO, Champion A, Thomas WK, Tisa LS. 2016. Permanent draft genome sequence of *Frankia* sp. strain Allo2, a salt-tolerant nitrogen-fixing actinobacterium isolated from the root nodules of *Allocasuarina*. *Genome Announc* 4(3):e00388-16 doi:10.1128/genomeA.00388-16.

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Salinization of soils and groundwater is a serious problem, especially in arid and semiarid lands, and has resulted in a drastic reduction in agricultural production (1). Worldwide, over 800 million hectares of land are affected (2). One potential solution for dealing with salt stress problems is reclaiming saline soils with fast-growing, multipurpose, salt-tolerant trees like the actinorhizal plants. Among the actinorhizal plants, the genus *Casuarina* grows well under these conditions and has been used in North Africa for these purposes. Actinorhizal plants form a nitrogen-fixing symbiosis with the genus *Frankia* that results in the ability of these plants to colonize harsh environments (3–5).

Based on phylogenetic markers, four major clusters are recognized within the genus (6–9), and genomes for representatives from each cluster have been sequenced (10–26). Cluster I contains two subclusters: one subcluster (cluster Ia) consists of *Frankia* spp. strains that associate with host plants in the *Betulaceae* and *Myricaceae* families, while the other subcluster (cluster Ib) is limited to *Casuarina* and *Allocasuarina* host plants. *Frankia* sp. strain Allo2 was isolated from root nodules of *Allocasuarina verticillata* (27). This strain showed an increased level of NaCl tolerance (R. Oshone and L. S. Tisa, unpublished data) and was sequenced to increase our understanding of salt-tolerance mechanisms and to provide insight about its interaction with actinorhizal plants. A comparative analysis of sequenced genomes among the salt-tolerant and salt-sensitive *Casuarina* strains may provide a clear picture of the role that these symbionts play in allowing these actinorhizal plants to colonize harsh environments, including saline soils.

The draft genome sequence of *Frankia* sp. strain Allo2 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 26,647,886 reads (260-bp insert size), totaling 3,866.4 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench version 8.0.1 and AllPaths-LG version r41043 (29). The final draft assembly for *Frankia* sp. Allo2 consisted of 133 contigs in 110 scaffolds with an N_{50} contig size of 96.9 kb. The final assembled genome contained a total sequence of 5,352,211 bp with a G+C content of 70.0% and is based on 3,120.3 Mb of Illumina draft data, providing an average 583× coverage of the genome.

The assembled *Frankia* sp. strain Allo2 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 4,224 candidate protein-encoding genes and 45 tRNA and 3 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JPH000000000](https://www.ncbi.nlm.nih.gov/nuccore/JPH000000000). The version described in this paper is the first version, JPHT01000000.

ACKNOWLEDGMENTS

Partial funding was provided by the New Hampshire Agricultural Experiment Station. This is Scientific Contribution Number 2665. 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, M.N. was supported by an ARTS (Allocation de Recherche pour une Thèse au Sud) PhD grant from the Institut de recherche pour le développement (IRD). Sequencing was performed on an Illumina HiSeq2500 purchased with NSF MRI Grant DBI-1229361 to W.K.T.

FUNDING INFORMATION

This work, including the efforts of Mariama Ngom, was funded by Institut de Recherche pour le Développement (ARTS). This work, including the efforts of W. Kelley Thomas, was funded by National Science Foundation (NSF) (DBI-1229361). This work, including the efforts of Louis S. Tisa, was funded by USDA | National Institute of Food and Agriculture (NIFA) (Hatch 022821 and 2015-67014-22849).

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