7-7-2016

Permanent Draft Genome Sequence for Frankia sp. Strain EI5c, a Single-Spore Isolate of a Nitrogen-Fixing Actinobacterium, Isolated from the Root Nodules of Elaeagnus angustifolia

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This is an article published by American Society for Microbiology in Genome Announcements in 2016, available online: https://dx.doi.org/10.1128/genomeA.00660-16

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c tinorhizal plants form a nitrogen-fixing symbiosis with the
genus Frankia that results in the ability of these plants to
colonize harsh environments (1–3). These important pioneer
community plants are found worldwide under a wide range of
ecological and environmental conditions, especially in poor and
marginal fertile soils (3,4). Actinorhizal plants represent 8 differ-
nent families of angiosperms and over 200 species of woody dicot-
yledonous plants.

Based on phylogenetic markers, four major clusters are recog-
nized within the genus (5–8). Cluster I consists of Frankia strains
that associate with host plants in the Cassarinaraceae, Betulaceae,
and Myricaceae families, while members of cluster II are infective
on Rosaceae, Coriariaceae, Datisaceae, and the genus Ceonothus
(Rhamnaceae). Cluster III members are the most promiscuous
and are infective on Eleagnaceae, Rhamnaceae, Myricaceae, Gym-
nostoma, and occasionally the genus Alnus. Cluster IV consists of
“atypical” Frankia strains that are unable to reinfect actinorhizal
host plants or form ineffective root nodule structures that are
unable to fix nitrogen. Genomes for representatives from each
cluster have been sequenced (9–25) and have provided a rich da-
table. Analysis of that resource has revealed several physiological
properties, including metabolic diversity, natural product biosyn-
thesis, and stress tolerance.

Besides being broad-host-range symbionts, members of
cluster III have the greatest metabolic diversity and possess
larger genomes than the other clusters. Many of these strains
have adapted to harsh environmental conditions. Frankia sp.
strain EI5c was obtained from a single-spore colony isolation
from cultures of Frankia sp. strain EI5 (UFI 132715) (26),
which was isolated from root nodules of Elaeagnus angustifolia
(27). This strain uses both intracellular (root hair infection)
and intercellular pathways of infection. Frankia sp. strain EI5c
was sequenced to provide information on this lineage and its
interactions with actinorhizal plants. Furthermore, this data-
base will also be used to help clarify the diversity of cluster III
members with the goal of speciation.

The draft genomes of Frankia sp. strain EI5c were generated
at the Hubbard Genome Center (University of New Hamp-
shire, Durham, NH, USA) using Illumina technology (28)
techniques. A standard Illumina shotgun library was con-
structed and sequenced using the Illumina HiSeq2000 plat-
form, which generated 24,085,096 reads (260-bp insert size)
totaling 3,612.7 Mbp. The Illumina sequence data were assem-
bled using CLC Genomics workbench version 8.0.1 and
AllPaths-LG version r41043 (29). The final draft assembly for
Frankia EI5c consisted of 159 contigs with an N50 contig size of
128.2 kb. The final assembled genome contained a total se-
quence of 6,617,243 bp with a G+C content of 72.14 % and is
based on 1,290.3 Mb of Illumina draft data, providing an aver-
age 195× coverage of the genome.

The assembled Frankia sp. strain EI5c 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 5,458 candidate protein-encoding genes and 46
tRNA and 2 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome
shotgun project has been deposited at DDBJ/EMBL/GenBank un-
der the accession number LRTK00000000. The version described
in this paper is the first version, LRTK01000000.

ACKNOWLEDGMENT

Partial funding was provided by the New Hampshire Agricultural Ex-
periment Station. This is Scientific Contribution Number 2672. This work
was also supported by the USDA National Institute of Food and Agricul-
ture Hatch 022821 (L.S.T.), by Agriculture and Food Research Initiative
Grant 2015-67014-22849 from the USDA National Institute of Food and
Agriculture (L.S.T.), and by the College of Life Sciences and Agriculture at
the University of New Hampshire–Durham. Sequencing was performed
on an Illumina HiSeq2500 purchased with NSF MRI Grant DBI-
1229361to W.K.T.
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