

3-21-2013

Draft Genome Sequence of Frankia sp. Strain QA3, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of *Alnus nitida*

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Recommended Citation

Sen, A., N. Beauchemin, D. Bruce, P. Chain, A. Chen, K. Walston Davenport, S. Deshpande, C. Detter, T. Furnholm, F. Ghodbhane-Gtari, L. Goodwin, M. Gtari, C. Han, J. Han, M. Huntemann, N. Ivanova, N. Kyrpides, M. L. Land, V. Markowitz, K. Mavrommatis, M. Nolan, I. Nouioui, I. Pagani, A. Pati, S. Pitluck, C. L. Santos, S. Sur, E. Szeto, F. Tavares, H. Teshima, S. Thakur, L. Wall, J. Wishart, T. Woyke, and L. S. Tisa. 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. (doi: 10.1128/genomeA.00103-13).

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Members of the actinomycete genus *Frankia* form a nitrogen-fixing symbiosis with 8 different families of actinorhizal plants. We report a high-quality draft genome sequence for *Frankia* sp. strain QA3, a nitrogen-fixing actinobacterium isolated from root nodules of *Alnus nitida*.

Received 16 February 2013 Accepted 25 February 2013 Published 21 March 2013

Citation Sen A, Beauchemin N, Bruce D, Chain P, Chen A, Walston Davenport K, Deshpande S, Detter C, Furnholm T, Ghodhbhane-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, Woyke T, Wishart J, 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. doi:10.1128/genomeA.00103-13.

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The genus *Frankia* consists of filamentous actinobacteria that form nitrogen-fixing symbiotic associations with a wide variety of woody angiosperms termed actinorhizal plants (1–3). The symbiosis allows actinorhizal plants to colonize harsh environmental terrains under diverse ecological conditions. Phylogenetic analysis based on several criteria, including the 16S rRNA gene (4), *glnII* (5, 6), and the 16S-23S rRNA intertranscribed spacer region (7), has identified four distinct clusters among the *Frankia* strains. Genomes for representatives from each of these clusters have been sequenced (8–10) and have provided vital baseline information for genomic approaches toward understanding these novel bacteria.

Members of cluster I *Frankia* strains are known to associate with *Betulaceae*, *Myricaceae*, and *Casuarinaceae* plants (except *Gymnostoma*) and include both narrow-host-range and mid-host-range symbionts. Since only two members of cluster I have been sequenced, strains ACN14a and CcI3 (8), another cluster I strain was sequenced to increase our understanding of this *Frankia* group and its host plant range. *Frankia* sp. strain QA3 was chosen for sequencing as another cluster I representative with mid-host-range properties. The strain was isolated from root nodules of *Alnus nitida* collected at an elevation of 1,240 m in the mountainous region of Bahrin, District Swat, Pakistan (11). *Frankia* sp. strain QA3 is also resistant to elevated levels of toxic heavy metals (12) and has potential applications in bioremediation. Strain QA3 was sequenced to provide information about the potential ecological roles of the *Frankia* strains and their interaction with actinorhizal plants.

The draft genome of *Frankia* sp. strain QA3 was generated at the Department of Energy (DOE) Joint Genome Institute (JGI)

using a combination of 454-GS-FLX-Titanium (13) and Illumina GAii (14) techniques. A standard 454 titanium standard library, which generated 261,792 reads, a paired-end 454 library with an average insert size of 8 kb, which generated 728,635 reads totaling 258.7 Mb of 454 data, and an Illumina GAii shotgun library, which generated 116,789,226 reads totaling 8,876 Mb were created. All techniques for DNA isolation, library construction, and sequencing were performed according to JGI standards and protocols (<http://www.jgi.doe.gov>). The 454 Titanium standard data and the 454 paired-end data were assembled together with Newbler, version 2.3 (13), and resulted in 177.9 Mb of 454 draft data, which provided an average 23.4× coverage of the genome. The Illumina sequencing data were assembled with Velvet, version 1.0.13 (15), and the resulting 8,345.8 Mb of Illumina draft data provided an average 1,098.1× coverage of the genome. For finishing, the gaps and misassemblies were resolved by editing in Consed, by PCR, and by bubble PCR primer walks.

The high-quality draft genome of *Frankia* QA3 was resolved to 1 scaffold containing 121 contigs consisting of 7,590,853 bp with a G+C content of 72.6%, 6,493 candidate protein-encoding genes, 46 tRNA genes, and 3 rRNA regions.

Nucleotide sequence accession number. The whole draft genome sequences of *Frankia* strain QA3 have been deposited in GenBank with accession number [AJWA00000000](http://www.ncbi.nlm.nih.gov/GenBank/BJWA00000000).

ACKNOWLEDGMENTS

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under contact number DE-AC02-05CH11231. This project (L.S.T.) was supported in part by Agriculture and Food Research Initiative

grant 2010-65108-20581 from the USDA National Institute of Food and Agriculture, Hatch grant NH530, and the college of Life Sciences and Agriculture at the University of New Hampshire, Durham, NH. M.G. and F.G.-G. were supported in part by a Visiting Scientist and Postdoctoral Scientist Program administered by the NH AES at the University of New Hampshire.

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