

8-4-2016

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Recommended Citation


Ghodhbane-Gtari F, Beauchemin N, Gueddou A, Hezbri K, Ktari A, Louati M, Nouioui I, Chen A, Huntemann M, Ivanova N, Kyrpidis N, Markowitz V, Mavrommatis K, Pagani I, Sen A, Wall L, Woyke T, Gtari M, Tisa LS. 2016. Permanent draft genome sequence of *Nocardia* sp. BMG111209, an actinobacterium isolated from nodules of *Casuarina glauca*. *Genome Announc* 4(4):e00770-16. <https://dx.doi.org/10.1128/genomeA.00770-16>

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Permanent Draft Genome Sequence of *Nocardia* sp. BMG111209, an Actinobacterium Isolated from Nodules of *Casuarina glauca*

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This is scientific contribution number 2677.

***Nocardia* sp. strain BMG111209 is a non-*Frankia* actinobacterium isolated from root nodules of *Casuarina glauca* in Tunisia. Here, we report the 9.1-Mbp draft genome sequence of *Nocardia* sp. strain BMG111209 with a G + C content of 69.19% and 8,122 candidate protein-encoding genes.**

Received 8 June 2016 Accepted 10 June 2016 Published 4 August 2016

Citation Ghodhbane-Gtari F, Beauchemin N, Gueddou A, Hezbri K, Ktari A, Louati M, Nouioui I, Chen A, Huntemann M, Ivanova N, Kyrpides N, Markowitz V, Mavrommatis K, Pagani I, Sen A, Wall L, Woyke T, Gtari M, Tisa LS. 2016. Permanent draft genome sequence of *Nocardia* sp. BMG111209, an actinobacterium isolated from nodules of *Casuarina glauca*. *Genome Announc* 4(4):e00770-16. doi:10.1128/genomeA.00770-16.

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Actinorhizal plants are well known for their symbiotic association with the actinobacteria, *Frankia*, which results in the formation of root nodule structures (1). Besides hosting these bacterial symbionts, root nodules have other occupants or plant endophytes that seem to aid plant growth and health. Many non-*Frankia* actinobacteria have been isolated from actinorhizal root nodules, occupying the same microniche as *Frankia* (2–14). These non-*Frankia* actinobacteria appear to have functional roles including plant growth-promoting activity (4). As early as 1981, *Nocardia* species were found associated with actinorhizal nodules (7, 8). *Nocardia* sp. strain BMG111209 was isolated from the root nodules of *Casuarina glauca* grown in Tunisia (2). This isolate was sequenced to provide a greater understanding of the metabolic potential of this microbe and its interaction with actinorhizal plants.

The draft genome of *Nocardia* sp. strain BMG111209 was generated at the DOE Joint genome Institute (JGI) using a hybrid of Illumina (15) and Pacific Biosciences (PacBio) technologies. An Illumina Std. shotgun library and long insert mate-pair library were constructed and sequenced using the Illumina HiSeq 2000 platform. This procedure generated 51,070,879 reads totaling 7,660.6 Mbp from the standard shotgun library and 47,626,505 reads totaling 4,134.5 Mb from the long insert mate-pair library. A PacBio SMRTbell library was constructed and sequenced on the PacBio RS platform, which generated 250,559 raw PacBio reads yielding 166,907 adapter trimmed and quality filtered subreads totaling 471.4 Mb. All techniques for DNA isolation, library construction, and sequencing were performed according to JGI standards and protocols (<http://www.jgi.doe.gov>). The Illumina and PacBio sequence data were assembled using Allpaths-LG (version r42328) (16). The final draft assembly contained six contigs in five scaffolds.

The total size of the genome is 9.1 Mbp. The final assembly is based on 7,660.9 Mbp of Illumina Standard PE, 4,143.5 Mb of Illumina CLIP and 471.4 Mb of PacBio post filtered data, which provides an average 1297.2× Illumina coverage and 51.8× PacBio coverage of the genome, respectively.

The assembled *Nocardia* BMG111209 genome was annotated using the JGI annotation pipeline (17, 18) and the data are available from the IMG data management system (19). The draft genome of *Nocardia* BMG111209 was resolved into 5 scaffolds consisting of 9,143,142 bp with a G + C content of 69.19%, 8,122 candidate protein-encoding genes, 52 tRNA genes, and 2 rRNA regions. Analysis of this genome for metabolism potential revealed phytohormone (i.e., IAA) biosynthesis pathways and the presence of a *hup* operon encoding an Ni-hydrogenase suggesting possible roles in their functioning as a plant-endophyte.

Nucleotide sequence accession numbers. This whole-genome shotgun sequence has been deposited at DDBJ/EMBL/GenBank under the accession number [ARMU000000000](https://www.ncbi.nlm.nih.gov/nuclink/ARMU000000000). The version described in this paper is the first version, ARMU01000000.

ACKNOWLEDGMENTS

Partial funding by the New Hampshire Agricultural Experiment Station. The work conducted by the U.S. Department of Energy Joint Genome Institute was supported by the Office of Science of the U.S. Department of Energy under contract DE-AC02-05CH11231. This project (L.S.T.) was supported in part by the USDA National Institute of Food and Agriculture, Hatch 022821, 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.

FUNDING INFORMATION

This work, including the efforts of Louis S. Tisa, was funded by USDA | National Institute of Food and Agriculture (NIFA) (Hatch 022821). This work, including the efforts of Tanja Woyke, was funded by U.S. Department of Energy (DOE) (DE-AC02--05CH11231).

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