

Lawrence Berkeley National Laboratory

LBL Publications

Title

Permanent Improved High-Quality Draft Genome Sequence of *Nocardia casuarinae* Strain BMG51109, an Endophyte of Actinorhizal Root Nodules of *Casuarina glauca*

Permalink

<https://escholarship.org/uc/item/1kb17776>

Journal

Microbiology Resource Announcements, 4(4)

ISSN

2576-098X

Authors

Ghodhbane-Gtari, Faten

Beauchemin, Nicholas

Louati, Moussa

et al.

Publication Date

2016-08-25

DOI

10.1128/genomea.00799-16

Peer reviewed

Permanent Improved High-Quality Draft Genome Sequence of *Nocardia casuarinae* Strain BMG51109, an Endophyte of Actinorhizal Root Nodules of *Casuarina glauca*

Faten Ghodhbane-Gtari,^a Nicholas Beauchemin,^b Moussa Louati,^a Imen Nouioui,^a Amir Ktari,^a Karima Hezbri,^a Abdellatif Gueddou,^a Amy Chen,^c Marcel Huntemann,^c Natalia Ivanova,^c Nikos Kyrpides,^c Victor Markowitz,^c Kostas Mavrommatis,^c Ioanna Pagani,^c Arnab Sen,^d Luis Wall,^e Tanja Woyke,^c Maher Gtari,^a Louis S. Tisa^b

University of Tunis-El Manar, Tunis, Tunisia^a; University of New Hampshire, Durham, New Hampshire, USA^b; DOE Joint Genome Institute, Walnut Creek, California, USA^c; University of North Bengal, Siliguri, India^d; University of Quilmes, Quilmes, Argentina^e

Here, we report the first genome sequence of a *Nocardia* plant endophyte, *N. casuarinae* strain BMG51109, isolated from *Casuarina glauca* root nodules. The improved high-quality draft genome sequence contains 8,787,999 bp with a 68.90% GC content and 7,307 predicted protein-coding genes.

Received 13 June 2016 Accepted 15 June 2016 Published 4 August 2016

Citation Ghodhbane-Gtari F, Beauchemin N, Louati M, Nouioui I, Ktari A, Hezbri K, Gueddou A, 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 improved high-quality draft genome sequence of *Nocardia casuarinae* strain BMG51109, an endophyte of actinorhizal root nodules of *Casuarina glauca*. *Genome Announc* 4(4):e00799-16. doi:10.1128/genomeA.00799-16.

Copyright © 2016 Ghodhbane-Gtari et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Louis S. Tisa, louis.tisa@unh.edu.

Members of the genus *Nocardia* are ubiquitous soil-borne aerobic microorganisms belonging to a large group of actinobacteria that are best known for their pathogenicity and their harmful infections for humans or animals (1). However, several *Nocardia* spp. have been consistently reported as plant endophytes and isolated from disinfected roots (*N. callitridis* [2]), stems (*N. artemisiae* [3] and *N. endophytica* [4]), and actinorhizal root nodules (*N. autotrophica* [5], *N. casuarinae* [6], and *Nocardia* sp. [7–9]). The potential role of the *Nocardia* endophyte has been postulated, especially in the case of actinorhizal symbiosis (5, 10). To the best of our knowledge, these plant-associated *Nocardia* spp. have not had their genomes sequenced.

We report here the genome sequence of *Nocardia casuarinae* strain BMG51109, which was isolated from root nodules of *Casuarina glauca* growing in Tunisia (6). *N. casuarinae* strain BMG51109 was sequenced to provide new insights into the role that this microbe plays in actinorhizal plants.

The draft genome of *N. casuarinae* strain BMG51109 was generated at the DOE Joint Genome Institute (JGI; Walnut Creek, CA, USA) using Pacific Biosciences (PacBio) technology. A PacBio SMRTbell library was constructed and sequenced on the PacBio RS platform, which generated 583,909 filtered subreads totaling 1.4 Gbp. All general aspects of library construction and sequencing performed at the JGI can be found at <http://www.jgi.doe.gov>. The raw reads were assembled using HGAP version 2.0.0 (11). The final draft assembly contained 4 contigs in 4 scaffolds, totaling 8.8 Mbp in size. The input read coverage was 155.7×.

Project information is accessible in the Genomes Online Database (12). Genes were identified using Prodigal (13), followed by a round of manual curation using GenePRIMP (14) as part of the microbial annotation pipeline of the JGI (15). Additional gene prediction analysis and manual functional annotation were performed within the Integrated Microbial Genomes–Expert Review

(IMG-ER) platform (<http://img.jgi.doe.gov>) developed by JGI (16).

The high-quality draft genome of *N. casuarinae* strain BMG51109 was resolved to 4 scaffolds consisting of 7,730,817 bp, with a G+C content of 68.90%, 7,822 candidate protein-coding genes, 55 tRNA genes, and 3 rRNA regions.

Nucleotide sequence accession numbers. The *Nocardia casuarinae* strain BMG51109 genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number JAFQ00000000. The version described in this paper is the first version, JAFQ01000000.

ACKNOWLEDGMENTS

Partial funding by the New Hampshire Agricultural Experiment Station. This is Scientific Contribution Number 2678. 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 contract no. 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, USA. M.G. and F.G.-G. were supported in part by the 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).

REFERENCES

1. Goodfellow M. 2014. Family *Nocardiaceae*, p 595–650. In Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson F (ed), *The prokaryotes—Actinobacteria*. Springer, Berlin.
2. Kaewkla O, Franco CM. 2010. *Nocardia callitridis* sp. nov., an endophytic

- actinobacterium isolated from a surface-sterilized root of an Australian native pine tree. *Int J Syst Evol Microbiol* 60:1532–1536. <http://dx.doi.org/10.1099/ijs.0.016337-0>.
3. Zhao GZ, Li J, Zhu WY, Klenk HP, Xu LH, Li WJ. 2011. *Nocardia artemisiae* sp. nov., an endophytic actinobacterium isolated from a surface-sterilized stem of *Artemisia annua* L. *Int J Syst Evol Microbiol* 61:2933–2937. <http://dx.doi.org/10.1099/ijs.0.029306-0>.
 4. Xing K, Qin S, Fei SM, Lin Q, Bian GK, Miao Q, Wang Y, Cao CL, Tang SK, Jiang JH, Li WJ. 2011. *Nocardia endophytica* sp. nov., an endophytic actinomycete isolated from the oil-seed plant *Jatropha curcas* L. *Int J Syst Evol Microbiol* 61:1854–1858. <http://dx.doi.org/10.1099/ijs.0.027391-0>.
 5. Dobritsa SV, Sharaya LS. 1986. Genome identity of different *Nocardia autotrophica* isolates from *Alnus* spp. root nodules and rhizosphere. In Szabo G, Biro S, Goodfellow M (ed), *Biological, biochemical and biomedical aspects of Actinomycetes Part B*, vol 32. Akadémiai Kiadó, Budapest.
 6. Ghodhbane-Gtari F, Nouioui I, Salem K, Ktari A, Montero-Calasanz Mdel C, Tisa LS, Klenk HP, Gtari M. 2014. *Nocardia casuarinae* sp. nov., an actinobacterial endophyte isolated from root nodules of *Casuarina glauca*. *Antonie Van Leeuwenhoek* 105:1099–1106. <http://dx.doi.org/10.1007/s10482-014-0168-6>.
 7. Malishkaite YB, Nechaeva GA, Kuimova TF, Evtushenko LI, Agre NS. 1987. *Nocardia* strains from actinorhizal plant nodules. *Microbiology* 56:100–106.
 8. Pariiskaya AN, Novik SN, Agre NS, Kalakutskii LV. 1982. *Nocardia* Isolated from nitrogen-fixing nodules on the roots of the gray and black alder. *Microbiology* 51:117–121.
 9. Ghodhbane-Gtari F, Essoussi I, Chattaoui M, Chouaia B, Jaouani A, Daffonchio D, Boudabous A, Gtari M. 2010. Isolation and characterization of non-*Frankia* actinobacteria from root nodules of *Alnus glutinosa*, *Casuarina glauca* and *Elaeagnus angustifolia*. *Symbiosis* 50:51–57. <http://dx.doi.org/10.1007/s13199-009-0029-7>.
 10. Ghodhbane-Gtari F, Tisa LS. 2014. Ecology and physiology of non-*Frankia* actinobacteria from actinorhizal plants, p 27–42. In Katsey EI (ed), *Plasticity in plant-growth-promoting and phytopathogenic bacteria*. Springer, New York.
 11. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <http://dx.doi.org/10.1038/nmeth.2474>.
 12. Reddy TB, Thomas AD, Stamatis D, Bertsch J, Isbandi M, Jansson J, Mallajosyula J, Pagani I, Lobos EA, Kyrpides NC. 2015. The Genomes OnLine Database (GOLD) v.5: a metadata management system based on a four level (meta)genome project classification. *Nucleic Acids Res* 43:D1099–D1106. <http://dx.doi.org/10.1093/nar/gku950>.
 13. Hyatt D, Chen GL, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <http://dx.doi.org/10.1186/1471-2105-11-119>.
 14. Pati A, Ivanova NN, Mikhailova N, Ovchinnikova G, Hooper SD, Lykidis A, Kyrpides NC. 2010. GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. *Nat Methods* 7:455–U462. <http://dx.doi.org/10.1038/nmeth.1457>.
 15. Mavromatis K, Ivanova NN, Chen IM, Szeto E, Markowitz VM, Kyrpides NC. 2009. The DOE-JGI standard operating procedure for the annotations of microbial genomes. *Stand Genomic Sci* 1:63–67. <http://dx.doi.org/10.4056/sigs.632>.
 16. Markowitz VM, Mavromatis K, Ivanova NN, Chen IM, 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>.