



HAL
open science

Genome Sequences of Three *Nocardia cyriacigeorgica* Strains and One *Nocardia asteroides* Strain

Florian Vautrin, Emmanuelle Bergeron, Audrey Dubost, Danis Abrouk, Christophe Martin, Benoit Cournoyer, Vanessa Louzier, Thierry Winiarski, Veronica Rodriguez-Nava, Petar Pujic

► **To cite this version:**

Florian Vautrin, Emmanuelle Bergeron, Audrey Dubost, Danis Abrouk, Christophe Martin, et al.. Genome Sequences of Three *Nocardia cyriacigeorgica* Strains and One *Nocardia asteroides* Strain. *Microbiology Resource Announcements*, 2019, 8 (33), pp.e00600-19. 10.1128/MRA.00600-19. hal-02386389

HAL Id: hal-02386389

<https://hal.science/hal-02386389>

Submitted on 26 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Genome Sequences of Three *Nocardia cyriacigeorgica* Strains and One *Nocardia asteroides* Strain

Florian Vautrin,^{a,b,d} Emmanuelle Bergeron,^{a,b} Audrey Dubost,^a Danis Abrouk,^a Christophe Martin,^a Benoit Cournoyer,^a Vanessa Louzier,^c Thierry Winiarski,^d Veronica Rodriguez-Nava,^{a,b} Petar Pujic^a

^aUMR CNRS 5557, INRA 1418 Ecologie Microbienne, Université Lyon 1, Villeurbanne, France

^bObservatoire Français des Nocardioses, Institut des Agents Infectieux (IAI), Centre de Biologie et Pathologie Nord, Hôpital de la Croix-Rousse, Lyon, France

^cAgressions Pulmonaires et Circulatoires dans le Sepsis (APCSe), VetAgro Sup–Campus Vétérinaire de Lyon, Marcy l'Etoile, France

^dUMR CNRS 5023, Laboratoire d'Ecologie des Hydrosystèmes Naturels et Anthropisés, Vaulx-en-Velin, France

ABSTRACT We report four draft genome sequences of *Nocardia* spp. The strains are the *Nocardia cyriacigeorgica* DSM 44484 pathogenic type strain; two environmental isolates, *Nocardia cyriacigeorgica* EML446 and EML1456; and the *Nocardia asteroides* ATCC 19247 nonpathogenic type strain, with estimated genome sizes of 6.3 to 6.8 Mb. The study of these isolates will provide insight into physiology, evolution, and pathogenicity of *Nocardia* spp.

Since Edmond Nocard first isolated *Nocardia* spp. in 1888 (1), 92 different species have been described (2). Most of them are pathogenic for human or animal infections worldwide. *Nocardia* spp. are Gram-positive, acid-fast actinobacteria and are ubiquitous in nature (2). Pathogenic *Nocardia* cells can infect different organs in humans, as well as disseminate from a primary infection site, such as the lungs, to distant organs and other sites, including the central nervous system (3). *Nocardia cyriacigeorgica* is one of the most often implicated species in human nocardiosis, including strain GUH-2 (4). This species, which derives from the *Nocardia asteroides* complex drug pattern type VI (5) and was described as *N. cyriacigeorgica* in 2001 (6), seems to be composed of three genotypes (2, 7–9).

Currently, only a few genomes of *N. cyriacigeorgica* strains have been entirely sequenced, and the genome of GUH-2, the model organism to study infections in animals, is the only one that is annotated (10). A genomic comparison of these three genotypes could untangle this clustering and maybe describe a new species within the former *N. asteroides* complex. Four strains have been sequenced, as follows: *Nocardia asteroides* type strain ATCC 19247, the type strain *N. cyriacigeorgica* DSM 44484, and two *N. cyriacigeorgica* environmental strains, EML446 and EML1456, isolated from infiltration basin urban sediments in France (coordinates 45°73'55.01"N, 4°95'74.65"E). Sediment suspensions were prepared according to Maldonado et al. (11), and serial dilutions were inoculated on brain heart infusion (BHI) agar containing cycloheximide.

Strains were grown in BHI medium according to Beaman and Maslan (12), and genomic DNA was extracted from 50 ml cell culture during the exponential-growth phase. Cells were collected by centrifugation and pellet solubilized in 8 ml of 10 mM Tris-HCl, 1 mM EDTA (pH 8.2), 5 mg/ml lysozyme, and 10 µg/ml RNase A. After a 1-h period of cell lysis, 8 ml of 2% SDS and 2 mg/ml of proteinase K were added and incubated at 55°C for 5 h. Protein and cellular debris were eliminated by adding 16 ml phenol-chloroform-isoamyl alcohol, 25:24:1 (vol/vol/vol), at pH 8.2. After centrifugation, genomic DNA was precipitated by adding 1.5 ml of 3 M sodium acetate (pH 5.2) and absolute ethanol. Genomic DNA was collected by centrifugation, and the DNA pellet

Citation Vautrin F, Bergeron E, Dubost A, Abrouk D, Martin C, Cournoyer B, Louzier V, Winiarski T, Rodriguez-Nava V, Pujic P. 2019. Genome sequences of three *Nocardia cyriacigeorgica* strains and one *Nocardia asteroides* strain. *Microbiol Resour Announc* 8:e00600-19. <https://doi.org/10.1128/MRA.00600-19>.

Editor Irene L. G. Newton, Indiana University, Bloomington

Copyright © 2019 Vautrin 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 Veronica Rodriguez-Nava, veronica.rodriguez-nava@univ-lyon1.fr, or Petar Pujic, petar.pujic@univ-lyon1.fr.

Received 24 May 2019

Accepted 21 July 2019

Published 15 August 2019

TABLE 1 Characteristics of draft genomes and accession numbers of *N. asteroides* ATCC 19247^T and *N. cyriacigeorgica* DSM 44484^T, EML446, and EML1456

Isolate	BioProject no.	Accession no.	Genome size (Mbp)	G+C content (%)	No. of contigs	No. of reads	<i>N</i> ₅₀ value (Mbp)	Coverage level (×)	No. of CDS ^a	% coding proteins	No. of tRNAs	No. of rRNAs
<i>N. asteroides</i> ATCC 19247 ^T	PRJNA542835	VBUS00000000	6.6	70.0	18	13,451,664	1.51	301	6,498	91.4	50	2
<i>N. cyriacigeorgica</i> EML1456	PRJNA542859	VBUE00000000	6.8	68.0	108	16,883,270	0.15	370	6,906	89.7	49	2
<i>N. cyriacigeorgica</i> EML446	PRJNA542857	VBUT00000000	6.5	68.2	41	18,841,320	0.61	433	6,531	89.91	51	3
<i>N. cyriacigeorgica</i> DSM 44484 ^T	PRJNA542831	VBUR00000000	6.3	58.2	64	10,182,338	0.19	487	6,072	89.8	48	3

^a CDS, coding sequences.

was washed in 70% ethanol, air dried, and solubilized in 200 μ l of Tris-EDTA (TE) buffer (pH 8).

The genomes were sequenced using Illumina MiSeq technology by GATC (Mulhouse, France) and Biofidal (Vaulx-en-Velin, France). Libraries with 2 \times 300-bp and 2 \times 125-bp reads were constructed for Biofidal and GATC, respectively. The reads were processed using Unicycler v0.4.3 (13), quality controls were assessed with FastQC and Trimmomatic, and contigs shorter than 200 bp were removed, resulting in genomes of 6.6 Mb for *N. asteroides* ATCC 19247^T, 6.3 Mb for *N. cyriacigeorgica* DSM 44484^T, 6.5 Mb for *N. cyriacigeorgica* EML446, and 6.8 Mb for *N. cyriacigeorgica* EML1456. The genomes were annotated on MicroScope (14). The characteristics of the draft genomes are summarized in Table 1. These genome sequences provide valuable data to study the ecology, evolution, pathogenicity, phylogeny, and physiology of *Nocardia cyriacigeorgica* complex species.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1. The versions described in this paper are the first versions. Data for EML446 and EML1456 are available at the CRB-EML (<http://eml-brc.org/> and <https://brclims.pasteur.fr/brcWeb/>).

ACKNOWLEDGMENTS

Florian Vautrin held a doctoral fellowship from the region Auvergne-Rhône-Alpes.

The LABGeM (CEA/Genoscope and CNRS UMR8030), the France Génomique, and The French Institute of Bioinformatics (funded as part of the Investissement d'Avenir program managed by the Agence Nationale pour la Recherche, contracts ANR-10-INBS-09, ANR-11-INBS-0013) are all thanked for their support to the MicroScope annotation platform.

We thank the Infiltron project ANR-17-CE04-0010-03.

We thank Gonzalo Bermejo Miranda for his English grammar revision and help in the review of the manuscript.

REFERENCES

- Nocard E. 1888. Note sur la maladie des bœufs de la Guadeloupe connue sous le nom de farcin. *Ann Inst Pasteur* 2:293–302.
- Schlaberg R, Huard RC, Della-Latta P. 2008. *Nocardia cyriacigeorgica*, an emerging pathogen in the United States. *J Clin Microbiol* 46:265–273. <https://doi.org/10.1128/JCM.00937-07>.
- Lebeaux D, Bergeron E, Berthet J, Djadi-Prat J, Mounié D, Boiron P, Lortholary O, Rodriguez-Nava V. 2018. Antibiotic susceptibility testing and species identification of *Nocardia* isolates: a retrospective analysis of data from a French expert laboratory, 2010–2015. *Clin Microbiol Infect* 25:489–495. <https://doi.org/10.1016/j.cmi.2018.06.013>.
- Beaman BL, Maslan S. 1977. Effect of cyclophosphamide on experimental *Nocardia asteroides* infection in mice. *Infect Immun* 16:995–1004.
- Wallace RJ, Steele LC, Sumter G, Smith JM. 1988. Antimicrobial susceptibility patterns of *Nocardia asteroides*. *Antimicrob Agents Chemother* 32:1776–1779. <https://doi.org/10.1128/aac.32.12.1776>.
- Yassin AF, Rainey FA, Steiner U. 2001. *Nocardia cyriacigeorgica* sp. nov. *Int J Syst Evol Microbiol* 51:1419–1423. <https://doi.org/10.1099/00207713-51-4-1419>.
- McTaggart LR, Richardson SE, Witkowska M, Zhang SX. 2010. Phylogeny and identification of *Nocardia* species on the basis of multilocus sequence analysis. *J Clin Microbiol* 48:4525–4533. <https://doi.org/10.1128/JCM.00883-10>.
- Xiao M, Pang L, Chen S-A, Fan X, Zhang L, Li H-X, Hou X, Cheng J-W, Kong F, Zhao Y-P, Xu Y-C. 2016. Accurate identification of common pathogenic *Nocardia* species: evaluation of a multilocus sequence analysis platform and matrix-assisted laser desorption ionization-time of flight mass spectrometry. *PLoS One* 11:e0147487. <https://doi.org/10.1371/journal.pone.0147487>.
- Rudramurthy SM, Kaur H, Samanta P, Ghosh A, Chakrabarti A, Honnavar P, Ray P. 2015. Molecular identification of clinical *Nocardia* isolates from India. *J Med Microbiol* 64:1216–1225. <https://doi.org/10.1099/jmm.0.000143>.
- Zoropogui A, Pujic P, Normand P, Barbe V, Beaman B, Beaman L, Boiron P, Colinon C, Deredjian A, Graindorge A, Manganot S, Nazaret S, Neto M, Petit S, Roche D, Vallenet D, Rodriguez-Nava V, Richard Y, Cournoyer B, Blaha D. 2012. Genome sequence of the human- and animal-pathogenic strain *Nocardia cyriacigeorgica* GUH-2. *J Bacteriol* 194:2098–2099. <https://doi.org/10.1128/JB.00161-12>.

11. Maldonado L, Hookey JV, Ward AC, Goodfellow M. 2000. The *Nocardia salmonicida* clade, including descriptions of *Nocardia cummidelens* sp. nov., *Nocardia fluminea* sp. nov. and *Nocardia soli* sp. nov. *Antonie Van Leeuwenhoek* 78:367–377. <https://doi.org/10.1023/A:1010230632040>.
12. Beaman BL, Maslan S. 1978. Virulence of *Nocardia asteroides* during its growth cycle. *Infect Immun* 20:290–295.
13. Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Comput Biol* 13:e1005595. <https://doi.org/10.1371/journal.pcbi.1005595>.
14. Vallenet D, Calteau A, Cruveiller S, Gachet M, Lajus A, Josso A, Mercier J, Renaux A, Rollin J, Rouy Z, Roche D, Scarpelli C, Médigue C. 2017. MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. *Nucleic Acids Res* 45: D517–D528. <https://doi.org/10.1093/nar/gkw1101>.