Draft genome sequence of Nocardia jinanensis, an opportunistic bacterial pathogen that causes cellulitis

Chakrabortti, Alolika; Li, Jinming; Liang, Zhao-Xun

2016

Chakrabortti, A., Li, J., & Liang, Z.-X. (2016). Draft genome sequence of Nocardia jinanensis, an opportunistic bacterial pathogen that causes cellulitis. Genome Announcements, 4(4), e00593-16-. doi:10.1128/genomeA.00593-16

https://hdl.handle.net/10356/80654

https://doi.org/10.1128/genomeA.00593-16

AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of *Nocardia jinanensis*, an Opportunistic Bacterial Pathogen That Causes Cellulitis

Alolika Chakrabortti,[a] Jinming Li,[b] Zhao-Xun Liang[a]

School of Biological Sciences, Nanyang Technological University, Singapore[a]; Department of Bioinformatics, School of Basic Medical Sciences, Southern Medical University, Guangzhou, Guangdong, China[b]

The draft genome sequence of *Nocardia jinanensis*, an opportunistic pathogen that can cause skin infections, reveals genes that may contribute to the lifestyle and pathogenicity of *N. jinanensis*. The genome also reveals the biosynthetic capacity of *N. jinanensis* in producing mycolic acids, siderophores, and other polyketide and nonribosomal peptide-derived secondary metabolites.

Received 6 May 2016 **Accepted** 26 May 2016 **Published** 21 July 2016

Citation Chakrabortti A, Li J, Liang Z-X. 2016. Draft genome sequence of *Nocardia jinanensis*, an opportunistic bacterial pathogen that causes cellulitis. Genome Announc 4(4): e00593-16. doi:10.1128/genomeA.00593-16.

Address correspondence to Zhao-Xun Liang, zxliang@ntu.edu.sg.

Nocardia is a genus of rare actinomycetes that is partially acid-fast in nature and characterized by a microscopic appearance of branching hyphae (1). Various *Nocardia* strains have been isolated from aquatic and terrestrial habitats as well as the tissue of infected patients. *Nocardia* are capable of producing secondary metabolites, some of which are likely to contribute to the pathogenicity of pathogenic *Nocardia* strains. The *Nocardia jinanensis* strain NBRC 108249 (CGMCC 4.3508, DSM 45048) was isolated from soil samples and is considered an opportunistic pathogenic strain that causes a form of skin infection called cellulitis (2). The pathogenesis of *N. jinanensis* seems to differ from that of the pathogenic *Nocardia* strains *N. farcinica* and *N. brasiliensis*. We sequenced the genome of *N. jinanensis* to gain a better understanding of the pathogenicity of *N. jinanensis* and its biosynthetic capacity.

The genomic DNA of *N. jinanensis* was isolated and purified using the TIANamp bacteria DNA kit. Genome sequencing was performed using a whole-genome shotgun technique (HiSeq Illumina platform), and the DNA fragments were assembled using SOAP*denovo* by Macrogen, Inc. (South Korea). The draft genome of *N. jinanensis* has a G+C content of 67.3% and a size of 5.04 Mb. The genome seems to be relatively small compared to the genomes of *N. farcinica* (6.3 Mb), *N. cyriacigeorgica* (6.2 Mb), and *N. brasiliensis* (9.4 Mb). Phylogenetic analysis of *Nocardia* spp. based on 16S RNA sequences suggests that *N. jinanensis* belongs to the same clade as the pathogenic *N. farcinica* and *N. cyriacigeorgica* in the phylogenetic tree consisting of 78 *Nocardia* species. The genome of *N. jinanensis* contains the orthologs of a large number of putative pathogenic genes of *N. farcinica* (3), such as the Mce and YbrE virulence factors used for mammalian cell invasion and infection, superoxide dismutases, antigenic proteins/transporters, esterases, and hemolysin. The presence of the putative pathogenic genes provides support for the lifestyle and pathogenicity of *N. jinanensis* as an opportunistic pathogen.

Mining of biosynthetic gene clusters using antiSMASH 3.0 (4) suggests that the genome contains more than 20 biosynthetic gene clusters that encode polyketide synthase (PKS), nonribosomal peptide synthase (NRPS), terpene cyclase, glycosyltransferases, and other enzymes. The genome contains several unique biosynthetic gene clusters that indicate that *N. jinanensis* can produce secondary metabolites that are unique to the strain. We identified eight NRPS gene clusters and two PKS gene clusters in the genome. One of the PKS gene clusters shares high similarity with the mycolic acid gene cluster from *Mycobacterium tuberculosis*. This cluster is likely to be involved in the biosynthesis of mycolic acids, considering that it contains all the genes required for mycolic acid biosynthesis, including the genes that code for the iterative PKS, AMP-dependent ligase, carboxyl transferase, and other essential enzymes (5). The genome also contains two PKS-NRPS hybrid gene clusters. One of the PKS-NRPS gene clusters bears resemblance to the nocobactin cluster of *N. farcinica* and is also conserved in *N. cyriacigeorgica* GUH-2 (6).

Nucleotide sequence accession numbers. The genome sequence can be found in GenBank with the accession numbers LNDA01000001 to LNDA01000107.

ACKNOWLEDGMENT

The project is supported by a Tier II ARC grant (to Z.-X.L.) from the Ministry of Education (MOE) of Singapore.

REFERENCES

1. **Wilson JW.** 2012. Nocardiosis: updates and clinical overview. Mayo Clinic Proc **87:**403–407.
2. **Tan CK, Lai CC, Lin SH, Liao CH, Chou CH, Hsu HL, Huang YT, Hsueh PR.** 2010. Clinical and microbiological characteristics of Nocardiosis including those caused by emerging Nocardia species in Taiwan, 1998-2008. Clin Microbiol Infect **16:**966–972. http://dx.doi.org/10.1111/j.1469-0691.2009.02950.x.
3. **Ishikawa J, Yamashita A, Mikami Y, Hoshino Y, Kurita H, Hotta K, Shiba T, Hattori M.** 2004. The complete genomic sequence of *Nocardia farcinica* IFM 10152. Proc Natl Acad Sci USA **101:**14925–14930. http://dx.doi.org/10.1073/pnas.0406410101.
4. **Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH.** 2015. antiSMASH 3.0–a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Res **43:**237–243.
5. **Marrakchi H, Lanéelle M.-A, Daffé M.** 2014. Mycolic acids: structures, biosynthesis, and beyond. Chem Biol **21:**67–85. http://dx.doi.org/10.1016/j.chembiol.2013.11.011.
6. **Hoshino Y, Chiba K, Ishino K, Fukai T, Igarashi Y, Yazawa K, Mikami Y, Ishikawa J.** 2011. Identification of nocobactin NA biosynthetic gene clusters in *Nocardia farcinica*. J Bacteriol **193:**441–448. http://dx.doi.org/10.1128/JB.00897-10.