Whole-Genome Sequence of Nocardiopsis alba Strain ATCC BAA-2165, Associated with Honeybees

Jianjun Qiao,ab Lei Chen,abc Yongli Li,a Jiangxin Wang,a,bb Weiwen Zhang,ab and Shawn Chenac
School of Chemical Engineering & Technology, Tianjin University, Tianjin, People’s Republic of China; Key Laboratory of Systems Bioengineering, Ministry of Education, Tianjin, People’s Republic of China; and Molecular and Cellular Biology Program, Department of Biological Sciences, Ohio University, Athens, Ohio, USA

The actinomycete Nocardiopsis alba was reportedly associated with honeybees in separate occurrences. We report the complete genome of Nocardiopsis alba ATCC BAA-2165 isolated from honeybee guts. It will provide insights into the metabolism and genetic regulatory networks of this genus of bacteria that enable them to live in a range of environments.

Nocardiopsis alba is a high-G+C, Gram-positive, filamentous actinomycete belonging to the family Nocardiopsaceae (9), previously represented by the genome-sequenced Nocardiopsis dassonvillei (10) and Thermobifida fusca (4). Nocardiopsis species are ecologically versatile and have been isolated from a variety of habitats (2, 3, 7). We have observed a year-round presence of Nocardiopsis alba ATCC BAA-2165 in a survey of actinomycetes from honeybee guts at a North American location (6). We found that it produces inhibitory bioactivities against several Bacillus isolates and some Gram-positive human pathogens. Coincidentally, an international team also isolated Nocardiopsis alba from beehives in Thailand (8). They found that a strain which could produce antibiotic activities against the growth of honeybee pathogens Paenibacillus larvae and Melissococcus plutonius that cause the American and European foulbrood, respectively. We therefore sequenced the whole genome of our strain (aka BE74) to provide a foundation for studies of the phylogenetically diverse group of bacteria on an important ecological basis.

The genome was sequenced with Illumina Solexa paired-end technology at BGI-Shenzhen, China. Three shotgun sequencing libraries (500 bp, 5 kb, and 10 kb) were constructed. Ninety-base-pair reads totalling 4.34 Gbp were assembled into 13 scaffolds and 21 contigs using the BGI SOAPdenovo protocol. The gaps and holes were filled by further PCR experiments. All sequences were assembled into one closed cyclic contig that is 5,848,211 bp with a GC content of 69.65%. Gene prediction was based on Glimmer 3.0, rRNAmer, and tRNAscanSE provided in the IGS Annotation Engine (http://e.igs.umaryland.edu/cgi/ae_pipeline_outline.cgi). The genome contains 5,539 protein genes, 54 tRNA genes, and 5 tRNA operons. The genome was entered into the Antibiotics and Secondary Metabolites Analysis Shell (antiSMASH) (http://antismash.secondarymetabolites.org/) (5), which identified 18 biosynthetic gene clusters. At least 8 clusters are for known antibiotics and secondary metabolites. The bioactivities of these small molecular metabolites are significant against Gram-positive bacteria.

The RAST server (http://rast.nmpdr.org) (1) was used to perform a preliminary comparison between the BE74 genome and that of Nocardiopsis dassonvillei DSM 43111 or Thermobifida fusca YX. In a gene sequence-based comparison with BE74 as the reference, 4,323 genes (~82.12%) of BE74 are homologous to the genes in DSM 43111 with identities of >21%, while 941 (~17.87%) genes are unique to BE74; 3,644 genes (~69.22%) of BE74 are homologous to the genes in YX with identities of >21%, while 1,620 genes (~30.77%) were unique to BE74. In a function-based comparison in RAST, ~81.29% (1,565/1,929) functional genes were found in both BE74 and DSM 43111 and ~77.32% (1,507/1,949) in both BE74 and YX.

The high-quality genome sequence of the Nocardiopsis alba strain isolated from honeybee guts should advance our understanding of the physiology and genetics of the Nocardiopsaceae family. We are interested in fundamental aspects, such as nutrient acquisition and osmotic, oxidative, and thermal tolerance of the Nocardiopsis species, facilitation of planning to use this strain as a model to study the primary and secondary metabolisms, and genetic regulatory mechanisms.

Nucleotide sequence accession number. The Nocardiopsis alba ATCC BAA-2165 Whole Genome Shotgun Sequencing project has been deposited in the NCBI GenBank database under accession number CP003788.

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REFERENCES


