

Draft Genome Sequence of *Actinomadura madurae* LIID-AJ290, Isolated from a Human Mycetoma Case

Lucio Vera-Cabrera,^a Rocio Ortiz-Lopez,^{b,c} Ramiro Elizondo-González,^c Mayra Paola Campos-Rivera,^a Anabel Gallardo-Rocha,^a Carmen Amelia Molina-Torres,^a Jorge Ocampo-Candiani^a

Laboratorio Interdisciplinario de Investigación Dermatológica, Servicio de Dermatología, Hospital Universitario, UANL, Monterrey, México^a; Universidad Autónoma de Nuevo León, Departamento de Bioquímica y Medicina Molecular, Monterrey, México^b; Universidad Autónoma de Nuevo León, Centro de Investigación y Desarrollo en Ciencias de la Salud, Monterrey, México^c

Here we present the draft genome sequence of a member of the *Thermomonosporaceae*, *Actinomadura madurae* LIID-AJ290, isolated from a human case of mycetoma. The assembly contains 10,308,866 bp. This is to our knowledge the first reported genome of a human-pathogenic *Actinomadura* species.

Received 21 February 2014 Accepted 10 March 2014 Published 27 March 2014

Citation Vera-Cabrera L, Ortiz-Lopez R, Elizondo-González R, Campos-Rivera MP, Gallardo-Rocha A, Molina-Torres CA, Ocampo-Candiani J. 2014. Draft genome sequence of *Actinomadura madurae* LIID-AJ290, isolated from a human mycetoma case. *Genome Announc.* 2(2):e00201-14. doi:10.1128/genomeA.00201-14.

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Address correspondence to Lucio Vera-Cabrera, drluciovera@yahoo.com.

Mycetoma is a subcutaneous infection produced by fungi and aerobic actinomycetes. It is characterized by tumefaction of the affected region, production of abscesses and fistulae, and the presence of microcolonies of the etiologic agent. Although worldwide 50% of mycetoma is produced by eumycetes and 50% by actinomycetes (1), in Mexico actinomycetoma is more commonly reported, accounting for about 98% of the cases. *Nocardia brasiliensis* is found in 86% of the infections, followed by *Actinomadura madurae* and *Nocardia* spp., which produce the rest of the cases (2). The genome sequence of *N. brasiliensis* has been reported (3, 8). Herein, we report the first draft of the genomic sequence of *A. madurae*.

A. madurae LIID-AJ290 was isolated in 2011 from a mycetoma case in the foot. The isolate has <20 subcultures. The bacteria used for genome sequencing were isolated from a purified stock kept at -70°C. The bacterial culture was expanded on brain heart infusion at 37°C with shaking at 110 rpm for 72 h, and the bacterial mass was subjected to DNA extraction using the cetyltrimethylammonium bromide (CTAB) method. The bacterial identity was determined using a hydrolysis pattern (4) as well as nucleotide sequencing analysis of a fragment of the 16S RNA gene using primers NOC3 and NOC4 (5). The genome sequence was determined using the platforms Roche/454 GS Junior (428,248 reads) and Illumina/MiSeq (1,243,587 reads). Both sets of reads were combined and assembled using Newbler 2.7 software (Roche Diagnostics, Branford, CT).

The genome annotation was carried out using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). According to the NCBI, the PGAAP combines hidden Markov model (HMM)-based gene prediction methods with a sequence similarity-based approach which combines comparison of the predicted gene products with the nonredundant protein database Entrez Protein Clusters, the Conserved Domain database, and the Clusters of Orthologous Groups (COGs) database (6, 7).

The unclosed draft genome of *A. madurae* LIID-AJ290 consists of 149 contigs and is a total of 10.30 Mbp long, with a G+C content of 72.04%. According to the GenBank annotation system,

the draft genome contains 9,643 genes, 10 rRNAs, 80 tRNAs, and 1 CRISPR array.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AW000000000](https://www.ncbi.nlm.nih.gov/nuccore/AW000000000). The version described in this paper is version AW0002000000.

ACKNOWLEDGMENT

This work was supported by the Consejo Nacional de Ciencia y Tecnología (CONACYT) grant 155892.

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