

Complete Genome Sequence of *Nocardia brasiliensis* HUJEG-1

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In Mexico, actinomycetoma is mainly caused by *Nocardia brasiliensis*, which is a soil inhabitant actinobacterium. Here, we report for the first time the draft genome of a strain isolated from a human case that has largely been found in *in vitro* and experimental models of actinomycetoma, *N. brasiliensis* HUJEG-1.

In Mexico, actinomycetes are the main etiologic agent of mycetoma, 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 (7, 8, 14). To date, from the more than 30 *Nocardia* species reported (2, 10), only one genome sequence has been published: *N. farcinica* IFM 10152 (5). In the present report, we describe the genome sequence of *N. brasiliensis* HUJEG-1 (ATCC 700358), a strain that has largely been used for *in vitro* and *in vivo* experiments (1, 4, 9, 12).

The genome sequence was determined using the Roche/454 GS (FLX Titanium) sequencing platform (8-kb library). A total of 786,647 reads were obtained, providing about 27-fold genome coverage. The Roche/454 GS reads were assembled using Newbler 2.5.3 software (Roche Diagnostics, Branford, CT).

The unclosed draft genome of *N. brasiliensis* HUJEG-1 is constituted of 53 contigs, for a total length of 9,489,024 bp with 68% G+C content, and it contains three copies of 5S, 16S, and 23S rRNA genes.

By using the BLAST program we detected five genes (including *katN*, described previously [13]) for catalase and three for superoxide dismutase (SOD); both enzymes have been implicated in resistance to bacterial destruction by oxygen-derivative radicals (3). Virulence factors such as lipases, phospholipase genes, phosphatases, alkaline phosphatase, proteases (including metalloproteases and several caseinolytic peptidases [*clp*]), and hemolysin/cytolysin enzymes were also found. These factors may explain the typical caseinase activity, as well as the high *in vivo* proteolytic activity of this pathogen. The immunogenic Mce (mammalian cell entry) family of proteins is composed of virulence factors which are involved in mycobacterial entry and survival in macrophages (6). In *N. brasiliensis*, we found 33 ortholog genes of this gene family.

We also found about 17 cytochrome P450 monooxygenases, which may explain the previously demonstrated susceptibility of *N. brasiliensis* to azoles (11). Abundant penicillin-binding proteins and some beta-lactamases were also found, a finding which supports the already known *N. brasiliensis* resistance to beta-lactams. Two copies of GroEl and one copy of GroEs were observed.

When we compared this sequence with the *N. farcinica* genome sequence, we observed that it shares 2,737 genes, with a mean homology of 81.6%, a maximum of 100%, and a minimum of 70%. The *N. brasiliensis* genome sequence also showed homology to 412 genes of the well-known pathogenic actinobacterium *Mycobacterium tuberculosis*, most of them related to metabolic functions, including a pyrazinamidase gene and a secretory Ag85B.

Only one PE/PPE/PGRS gene family ortholog was found. The BLAST analysis with the *Mycobacterium leprae* TN genome sequence showed similarity to 157 genes of this human pathogen, including immunogen 84.

In conclusion, we believe that the analysis of the genome sequence data of *N. brasiliensis* can provide us with excellent tools to study the host-pathogen relationship, as well as to determine its use to obtain novel antimicrobial or cytostatic compounds.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AIHV000000000](https://www.ncbi.nlm.nih.gov/nuccore/AIHV000000000). The version described in this paper is the first version, AIHV01000000.

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