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GENOME ANNOUNCEMENT

Draft Genome Sequence of the Human Pathogen *Streptomyces somaliensis*, a Significant Cause of Actinomycetoma

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We report the draft genome sequence of the human pathogen *Streptomyces somaliensis* (DSM 40738), a pathogen within a genus of largely saprophytic organisms. *S. somaliensis* causes severe and debilitating deep tissue and bone infections. The genome sequence is deposited in DDBJ/EMBL/GenBank with the accession number AJJM01000000.

Streptomyces somaliensis is a Gram-positive, aerobic, filamentous human-pathogenic actinomycete that is a significant cause of actinomycetoma (4, 9). Actinomycetomas are severe and debilitating infections that can spread to affect deep tissue and bone and are characterized by the formation of tissue masses, which may result in tissue destruction and deformity and may be fatal without surgical intervention. *S. somaliensis* strain DSM 40738, the type strain for the species, was isolated in a case of mycetoma in the foot of a 20-year-old male (5). This strain will provide a good foundation for the study of human-pathogenic *Streptomyces* species.

Genome sequencing of *S. somaliensis* strain DSM 40738 was carried out using a whole-genome shotgun sequencing approach performed on a Roche GS-FLX/454 apparatus at the National Yang-Ming University VYM Genome Research Centre (Tapei, Taiwan). Using single-ended runs, we obtained 970,529 reads with an average length of 455 bp after trimming. The reads were assembled using a GS *de novo* assembler (Roche), which led to a final assembly of 243 contigs of >1,000 bp each. The total size of the assembly was 5,176,903 bp, with a mean contig size of 21,304 bp (an average coverage of 84-fold) and a G+C content of 74.1%. Automatic functional annotation results were obtained by using the Rapid Annotation using Subsystem Technology (RAST) server software (1).

The uncompleted draft genome sequence of *S. somaliensis* is estimated by RAST to have a total of 4,679 protein-coding genes, along with 62 tRNAs and 6 rRNA operons. The genome is smaller than previously sequenced *Streptomyces* genomes (3, 7, 8), which are usually in the 7- to 10-Mbp range (www.genomesonline.org). This finding is consistent with pulsed-field gel electrophoresis (PFGE) estimations of the genome size (K. Wierzbicka and J. Zakrzewska-Czerwińska, unpublished data) and may reflect the previously observed reductions in the genome sizes of pathogens (10). Interestingly, there do not appear to be any obvious genomic islands with genes for specific virulence functions, such as adhesion or toxin production. There are, however, two gene clusters associated with the production of siderophores, one of which shows high-level homology to the desferrioxamine cluster of *S. coelicolor* (2). There are multiple antibiotic resistance genes present within the genome, including multiple β-lactamase genes and genes for aminoglycoside phosphotransferases and monooxygenases. These are similar to those present in *Nocardia farcinica* (6) and may contribute to the observed difficulty in antibiotic treatment of this organism in the clinic.

The genome sequence of *S. somaliensis* should advance our knowledge of the biology of pathogenic *Streptomyces* species, facilitate more rapid diagnosis of infections, and improve the development of urgently required treatment regimens.

Nucleotide sequence accession numbers. The *S. somaliensis* (DSM 40738) Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJJM00000000. The version described in this paper is the first version, AJJM01000000.

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