**Complete Genome Sequence of *Mycobacterium chimaera* Strain AH16**

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*Mycobacterium chimaera* is a nontuberculous mycobacterial species that causes cardiovascular, pulmonary, and postsurgical infections. Here, we report the first complete genome sequence of *M. chimaera*. This genome is 6.33 Mbp, with a G+C content of 67.56%, and encodes 4,926 protein-coding genes, as well as 74 tRNAs, one ncRNA, and three rRNA genes.

Whole-genome alignments of *M. chimaera* AH16 and six MAC genomes revealed 511,189 variable single nucleotide polymorphisms (SNPs), including: 459,672 SNPs compared to *M. avium* subsp. *hominis suis* TH135; 64,709 SNPs compared to *M. intracellulare* ATCC 13950; 50,875 SNPs compared to *Mycobacterium* sp. MOTT 36Y; 49,805 SNPs compared to *M. yongonense* 05-0390; and 49,524 SNPs compared to *Mycobacterium* sp. H4Y. Comparing the *M. chimaera* AH16 genome against the *M. avium* subsp. *hominis suis* TH135, *M. intracellulare* ATCC 13950, *M. yongonense* 05-0390, *Mycobacterium* sp. MOTT 36Y, and *Mycobacterium* sp. H4Y genomes, the average nucleotide identities (ANIs) were 85.55%, 96.87%, 97.14%, 97.16%, and 97.22%, respectively. The limited SNP variation (0.78 to 7.26% of the genome) and ANI values observed between *M. chimaera* AH16 and MAC species suggests that the non-*M. avium* MAC species have limited genomic variation. Furthermore, intraspecies genome comparisons of *M. chimaera* AH16 to *M. chimaera* MCIMRL6, MCIMRL4, and MCIMRL2 (accession nos. LJHN00000000, LJHM00000000, and LJHL00000000) have 99.14%, 99.11%, and 99.18% ANIs, respectively, which are within the 95 to 96% cutoff for species boundaries (11).

**Accession number(s).** The genome sequence of *M. chimaera* AH16 is deposited in NCBI GenBank under the accession numbers CP012885 to CP012888.

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REFERENCES