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# Draft Genome Sequence of a *Mycobacterium avium* Complex Isolate from a Broadbill Bird

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**We report the draft genome sequence of a *Mycobacterium avium* complex isolate. This isolate has an estimated genome size of 5.1 Mb with an average GC content of 68.9% and is predicted to carry 4,497 protein-encoding genes and 317 pseudogenes.**

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*Mycobacterium avium* complex (MAC) organisms cause opportunistic infections in humans, yet their epidemiology remains poorly understood. They are slowly growing environmental and animal-associated mycobacteria that have little notoriety except for the strains that cause disseminated infections in HIV-infected humans (1). Most MAC organisms are classified taxonomically as a single species, *M. avium*, which is divided into at least four subspecies, *M. avium* subsp. *avium*, *M. avium* subsp. *hominissuis*, *M. avium* subsp. *paratuberculosis*, and *M. avium* subsp. *silvaticum* (2). The only other species in this group is *M. intracellulare*. Genotyping of this diverse bacterial group has been achieved using intergenic spacers (3) and *rpoB* sequence analysis (4, 5).

The genome sequences of *M. avium* subsp. *hominissuis* strain 104 and *M. avium* subsp. *avium* ATCC 25291 have been made publically available, but neither has yet been formally published. Strain 104 was isolated from an immunocompromised human and ATCC 25291 was obtained from a bird. Here we present the draft genome sequence of another *M. avium* subspecies. This isolate was obtained from a broadbill bird (family Eurylaimidae; species not specified) from a Texas zoo in 2005. Analysis of the *rpoB* gene sequence using the method of Ben Salah et al. (4) shows that this isolate clusters with *M. avium* subsp. *hominissuis*.

Purified genomic DNA obtained from this isolate was subjected to whole-genome shotgun sequencing using the Ion PGM sequencing system (Ion Torrent) with 200-bp read chemistry (Life Technologies). Sequence coverage was 81.0×. A *de novo* assembly

of the ~5.15-Mbp sequence using MIRA assembly software version 3.2.0 yielded 190 contigs. The sequence was annotated with the NCBI Prokaryotic Genomes Automatic Annotation Pipeline ([http://www.ncbi.nlm.nih.gov/genome/annotation\\_prok/](http://www.ncbi.nlm.nih.gov/genome/annotation_prok/)). A total of 5 rRNA operons and 46 tRNA genes were identified.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project was deposited at DDBJ/EMBL/GenBank under the accession number [AYLW00000000](http://www.ncbi.nlm.nih.gov/nuclink/AYLW00000000). The version described in this paper is AYLW01000000.

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