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Draft Genome Sequence of an Actinobacterium, *Brachybacterium muris* Strain UCD-AY4

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Here we present the draft genome of an actinobacterium, *Brachybacterium muris* UCD-AY4. The assembly contains 3,257,338 bp and has a GC content of 70%. This strain was isolated from a residential bath towel and has a 16S rRNA gene 99.7% identical to that of the original *B. muris* strain, C3H-21.

Members of the *Brachybacterium* genus have been found in a variety of environments, including salt-fermented seafood (1), poultry deep litter (2), and deteriorated medieval wall paintings (3). *Brachybacterium* bacteria are characterized as Gram positive, nonsporulating, and nonmotile. They are coccoid shaped during the stationary phase and oval rod shaped when transferred to fresh medium (2).

*Brachybacterium muris* strain UCD-AY4 was isolated from a residential bath towel in Davis, California, in an effort to provide microbial reference genomes from the built environment. Fibers from a residential bath towel were incubated overnight in Luria broth (LB) at 37°C and then plated out on LB agar. Single colonies were picked for serial dilution streaking and the organism was identified by Sanger sequencing of the 16S PCR product produced during the stationary phase and oval rod shaped when transferred to fresh medium (2).

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自动化注释是使用RAST注释服务器（5）。*B. muris* UCD-AY4的全长（1,512 bp）16S rRNA序列是根据这个注释，并且用于识别物种的*Brachybacterium*。一个phylogenetic tree was produced using the Riboosomal Database Project (RDP)，which implements a weighted neighbor-joining tree-building algorithm (6)。In this tree, *B. muris* UCD-AY4 falls within a monophyletic clade of *B. muris* strains with 100% bootstrap support (doi: 10.6084/m9.figshare.628054). This sequence was 99.7% identical to *B. muris* C3H-21 isolated from mouse liver (7).

The genome sequences of only two other *Brachybacterium* species have been published, *B. faecium* (8) and *B. squillarum* (9). The 16S RNA gene from *B. muris* UCD-AY4 has 97% identity to that from *B. faecium* and 98% identity to that from *B. squillarum*.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AOUC0000000. The version described in this paper is the first version, number AOUC0100000. Illumina reads available at http://dx.doi.org/10.6084/m9.figshare.157178.

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**REFERENCES**