Genome Sequence of *Mycoplasma hyorhinis* Strain GDL-1

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***Mycoplasma hyorhinis* impacts swine health and production in many countries, either as a primary pathogen or as a component of a polymicrobial infection. Isolates of this species are also common contaminants of tissue culture lines. The genome sequence of the cell culture isolate *M. hyorhinis* GDL-1 is presented herein.**

Mycoplasma hyorhinis is a pathogen of swine (4) as well as a notorious contaminant of mammalian tissue cultures (5). With regard to its role as an obligate parasite of swine, the factors that contribute to the pathologies of rhinitis, pneumonia, polyserositis, and arthritis are incompletely known, and possible features that distinguish field isolates from tissue culture strains have only recently begun to be explored at the genome level. Following the recent release of the sequence for a respiratory isolate of *M. hyorhinis* from China (3), we undertook the determination of the genome sequence of *M. hyorhinis* strain GDL-1, a tissue culture isolate for which several antigens have been characterized (1, 6). While this work was in progress, the genome sequence of an additional cell line isolate was published (2), thus expanding opportunities for intraspecies comparisons.

The genome sequence was determined by Titanium sequencing on the 454 platform (3-kb paired-end library), carried out by The Genome Center at Washington University, St. Louis, MO. The resulting sequence reads, representing 128× genome coverage, were assembled into a single scaffold (454 Newbler software), within which were 39 gaps, predominantly due to multiple copies of the previously characterized IS unit IS1221. PCR and Sanger sequencing together with molecular cloning and sequencing of restriction fragments resulted in the generation of a single molecule of 837,480 bp. Through the Institute of Genome Sciences Annotation Engine (University of Maryland, Baltimore, MD), open reading frames (ORFs) (GLIMMER), tRNAs (tRNAscan-SE), and rRNAs (Blastn) were delineated and autoannotated. Each gene was subsequently manually curated.

The resulting gene set contains 741 genes, of which 707 are ORFs and 34 are RNA genes. Approximately 8% of genes are pseudogenes (60 total) with confirmed degeneracy or frameshift mutations. A single multicopy IS element is present; all but one of the 21 full-length IS1221 transposase genes contain frameshift mutations, consistent with a previous survey of coding potential (7). Remarkably, all 21 elements are located in the same locations as those in the *M. hyorhinis* HUB-1 isolate from China, and all 19 copies in strain MCLD have insertion sites identical to those in strain GDL-1. Comparison of the coding potential of each *M. hyorhinis* genome disclosed only limited differences in gene repertoire; the *M. hyorhinis* HUB-1 chromosome contains one additional copy of IS1221, a one-gene expansion in the tandem array of *mod* genes encoding related type III DNA methyltransferases and one extra phase-variable surface lipoprotein gene (*vlpG*) in relation to strain GDL-1. The overall similarity in ORF complement indicates that any differ-

ences in source adaptation are not encoded by large genomic islands but are encrypted within highly similar gene sets.

Sequence analysis of additional isolates is warranted to confirm the limited species pangenome identified to date and to determine whether distinctive patterns of pseudogenes exist and correlate with tissue tropism in swine or cell culture. Nevertheless, the current data sets are a critical adjunct for post-genomic analyses of the deduced proteome (including immunoproteome) and transcriptional networks, which have yet to be systematically explored.

Nucleotide sequence accession number. The genome sequence of *M. hyorhinis* GDL-1 has been deposited in GenBank under accession number [CP003231](https://www.ncbi.nlm.nih.gov/nuccore/CP003231).

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