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GENOME ANNOUNCEMENTS

Complete Genome Sequence of *Mycoplasma hyorhinis* Strain HUB-1▽

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***Mycoplasma hyorhinis* is generally considered a swine pathogen yet is most commonly found infecting laboratory cell lines. An increasing body of evidence suggests that chronic infections with *M. hyorhinis* may cause oncogenic transformation. Here, we announce the complete genome sequence of *M. hyorhinis* strain HUB-1.**

Mycoplasma hyorhinis is generally considered to be a swine pathogen causing lung lesions, inflammation in the chest and abdominal lining, and arthritis (8). This agent also frequently contaminates laboratory cell cultures, impinging on many aspects of biological research (3). Recent studies have demonstrated that *M. hyorhinis* infections induce a malignant phenotype in human prostate (7) and gastric (4) cells, suggesting that *M. hyorhinis* infections are associated with oncogenic transformation. These properties of *M. hyorhinis* have increased its profile to researchers. The complete genome sequence of this microbe has yet to be determined.

We sequenced the genome of *M. hyorhinis* strain HUB-1, a pathogenic strain isolated from the respiratory tract of swine. Whole-genome sequencing was performed by combining GS FLX (6) and Solexa paired-end sequencing technologies (1). Genomic libraries containing 3-kb inserts were constructed, and 308,604 reads (79.7% paired end) were produced using the GS FLX system, giving 65.9-fold coverage of the genome. About 93.4% of reads were assembled into one large scaffold using Newbler software (454 Life Sciences, Branford, CT). A total of 822,579 reads were generated using an Illumina Solexa Genome Analyzer IIx and were mapped to the scaffold using the Burrows-Wheeler alignment (BWA) tool (5). Gaps were filled by local assembly of the Solexa/Roche 454 reads or by sequencing PCR products by using an ABI 3730 capillary sequencer. Open reading frames containing more than 30 amino acid residues were predicted using Glimmer 3.0 (2) and verified by comparison with six other closely related genome sequences.

The complete genome of *M. hyorhinis* HUB-1 consists of an 839,615-bp single circular chromosome with an average G+C content of 25.88%. A total of 654 protein-encoding genes are predicted. The average protein size is 364 amino acids, and the mean coding percentage is 85.2%. The genome includes 30 tRNA genes, and only a single copy of the 16S-23S rRNA operon can be found. The 5S rRNA operon is separate from the 16S-23S rRNA operon. Protein secretion occurs through a truncated membrane protein secretion system, consisting of SecA, SecD, SecY, PrsA, DnaK, Tig, and LepA. Additionally, 20 pseudogenes, which become truncated or inactivated, are identified in the genome.

M. hyorhinis contains a special variable lipoprotein (Vlp) system that constitutes its major coat protein (9) and provides a mutational strategy for evasion of the host immune system. Different *M. hyorhinis* strains carry a variable number of *vlp* genes (9). *M. hyorhinis* HUB-1 is characterized to contain seven *vlp* genes displayed in the order 5′-*vlpD*-*vlpE*-*vlpF*-insertion sequence (IS)-*vlpG*-*vlpA*-IS-*vlpB*-*vlpC*-3′.

This is the first complete genome sequence of *M. hyorhinis*, and its availability will provide a better-defined genetic background for future studies of gene expression and regulation.

Nucleotide sequence accession number. The genome sequence of *M. hyorhinis* HUB-1 has been deposited in GenBank under the accession number CP002170.

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