Complete Genome Sequence of *Mycoplasma hyopneumoniae* Strain 168[▽]

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Mycoplasma hyopneumoniae **strain 168, a pathogenic strain prevalent in China, was isolated in 1974. Although this strain has been widespread for a long time, the genome sequence had not been determined. Here, we announce the complete genome sequence of *M. hyopneumoniae* strain 168.**

Mycoplasma hyopneumoniae is the causative agent of porcine enzootic pneumonia, which results in a mild, chronic pneumonia of swine (8). The primary mycoplasmal infection often becomes complicated by secondary bacterial and viral infections (2). *M. hyopneumoniae* strain 168 was isolated from the no. 168 Er-hua-nian pig (a Chinese local breed very sensitive to *M. hyopneumoniae*) in 1974, which had typical clinical and pathogenic characteristics of mycoplasmal pneumonia of swine (MPS) (4). As a prevalent strain in China, *M. hyopneumoniae* strain 168 causes considerable economic losses in the swine industry.

Whole-genome sequencing was performed by a hybrid sequencing method using both GS FLX (7) and Solexa technologies (1). Genomic libraries containing 3-kb inserts were constructed and 342,540 reads (83.7% paired ends) were produced with the GS FLX system, giving 71.1-fold coverage of the genome. About 94.6% of reads were assembled into one large scaffold with Newbler (454 Life Sciences, Branford, CT). A total of 2,041,937 reads were generated with an Illumina Solexa genome analyzer IIx and were mapped to the scaffold with the Burrows-Wheeler Alignment (BWA) tool (5). Gaps were filled by local assembly of the Solexa/Roche 454 reads or by sequencing PCR products with an ABI 3730 capillary sequencer. Open reading frames containing more than 30 amino acids were predicted by Glimmer 3.0 (3). The analysis of the genome was performed as described previously (6).

The complete genome of *M. hyopneumoniae* 168 consists of a 925,576-bp single circular chromosome with 28.46% GC content. A total of 695 protein-coding genes are predicted. The average protein size is 357 amino acids, and the mean coding percentage is 80.6%. Approximately 51% of genes were assigned to specific COG (cluster of orthologous groups) functional groups, and 28% were assigned an enzyme classification number. The genome contains 30 tRNA genes, and only a single copy of the 16S-23S rRNA operon was found. The 5S rRNA is separate from the 16S-23S rRNA operon.

The genome of *M. hyopneumoniae* 168 harbors 13 copies of IS-like elements, all of which belong to the family IS*1634*. Cilium adhesin p97 is regarded as the major cell adhesion determinant and is commonly linked to p102, forming a two-gene operon (9). Interestingly, p102, the companion gene in this operon, was truncated at 564 bp by a 1-base insertion in strain 168. Another intact copy of p102 (99% identity) was found 85 kb away from this operon. This indicates that p102 can be translated separately and that this gene may, at least partially, replace the role of the copy downstream of p97.

Initial comparative genomic analysis of strain 168 confirms it to be a member of the *M. hyopneumoniae* species, sharing 658 orthologous genes with the other three publicly available genomes in this species. Thirteen genes are uniquely present in *M. hyopneumoniae* strain 168. However, most of them have not been well characterized according to functional category, which highlights the need for better characterization.

Nucleotide sequence accession number. The genome sequence of *M. hyopneumoniae* strain 168 has been deposited in GenBank under accession no. CP002274.

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▽ Published ahead of print on 10 December 2010.

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