Complete Genome Sequence of *Mycoplasma hyorhinis* Strain SK76

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*Mycoplasma hyorhinis* is a eubacterium belonging to the *Mollicutes* class and is responsible for porcine respiratory and arthritic diseases. It is also the major contaminant of mammalian tissue cultures in laboratories worldwide. Here, we report the complete genome sequence of *M. hyorhinis* strain SK76.

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The complete genome of *M. hyorhinis* strain SK76 is composed of a single circular chromosome of 836,897 bp with an overall G+C content of 26%. The genome contains 753 putative coding DNA sequences (CDSs). The average size of a CDS in this genome is 1,002 bp, with an average of one gene every 1,110 bp. This is similar to the gene density seen with the smaller genomes of many species of Gram-positive bacteria. The 5S rRNA gene is located in a distant region.

**Nucleotide sequence accession number.** The complete genome sequence of *M. hyorhinis* strain SK76 has been deposited in the NCBI GenBank database under the accession no. CP003914.

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**REFERENCES**

6. Namiki K, Goodison S, Porvasnik S, Allan RW, Iczkowski KA, Urbanek

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