Genome Sequence of a Mycoplasma meleagridis Field Strain

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Mycoplasma meleagridis is a major cause of disease and economic loss in turkeys. Here, we report the genome sequence of an M. meleagridis field strain, which enlarges the knowledge about this bacterium and helps the identification of possible coding sequences for drug resistance genes and specific antigens.

Mycoplasma meleagridis is widespread in turkey flocks, causing poor growth, air sacculitis, osteodystrophy, and immunosuppression (1,2). A recent work provided the first evidence that M. meleagridis could also establish a natural infection in chickens (3). Moreover, a number of antigens appear to be shared between M. meleagridis and the more important poultry mycoplasmas (Mycoplasma gallisepticum and Mycoplasma synoviae) resulting in cross-reactivity that complicates serological investigations (2).

The M. meleagridis strain used in this study was isolated in 2011 at the Istituto Zooprofilattico Sperimentale delle Venezie, Italy, from a turkey with typical mycoplasma symptoms, including skeletal alterations, by using traditional microbiological methods and denaturing gradient gel electrophoresis-PCR (DGGE-PCR) for confirmation.

The M. meleagridis genome was sequenced by using paired-ends Illumina MiSeq technology for 600 cycles and resulted in a total of 27,001,860 reads. ABySS assembly showed the best compromise to be Kmer equal to 63, resulting in 157 scaffolds and maximum scaffold length, 181,832 bp; number of scaffolds covering the N50, 90,728 bp; number of scaffolds covering the N50, 3 scaffolds). Nine of the scaffolds were >1 kb and used for the further analyses. The average coverage of reads on each scaffold was around 8,000×. The genome annotation was using RAST/SEED software and manually reviewed. Five hundred fifty-one putative open reading frames (ORFs) were identified: 513 of them were coding sequences, and 38 were tRNA genes. The metabolic pathways were constructed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database.

As a result, a total of 276 coding sequences have been assigned a putative functional identity. Two genes were identified as YjeE, which are predicted to have essential role in cell wall biosynthesis; another 16 genes were responsible for membrane transport; 15 genes code for amino acids and derivatives; and 132 genes were responsible for protein metabolism, including two responsible for lipoprotein biosynthesis, which represents important information for future studies regarding possible specific antigens for M. meleagridis diagnostics.

Also, four genes for fluoroquinolone resistance (parC, parE, gyrA, and gyrB) were identified and determined to be active together with one multidrug resistance gene belonging to the multidrug and toxic compound extrusion (MATE) superfamily. Their sequences were subjected to a BLAST search against the previously sequenced genome of an M. meleagridis reference strain (4), and we observed some mismatches in the gyrA and multidrug resistance genes. This feature is important since we are working with a sample field, and mutations in defined regions of the DNA gyrase genes, gyrA and gyrB, and the topoisomerase IV genes, parC and parE, have been linked to high-level fluoroquinolone resistance in various bacteria, including Neisseria gonorrhoeae and Mycoplasma genitalium (5).

The availability of high-quality genome sequences for an M. meleagridis field strain and comparative analyses with related species will improve our understanding of the genes encoding antibiotic resistance and immunodominant antigens for this bacteria that until today have not yet been well characterized.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LOHQ00000000. The version described in this paper is version LOHQ01000000.

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