Genome Sequences of Two Tunisian Field Strains of Avian Mycoplasma, M. meleagridis and M. gallinarum

Elhem Yacoub, a Plymouth Sirand-Pugnet, b,c Aurélien Barre, d Alain Blanchard, b,c Christophe Hubert, e Florence Maurier, d Emmanuel Bouilhô, f Boutheina Ben Abdelmoumen Mardassi a

Unit of Mycoplasmas, Laboratory of Molecular Microbiology, Vaccinology and Biotechnology Development, Institut Pasteur de Tunis, University of Tunis El Manar, Tunisia; INRA, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France; Université de Bordeaux, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France; Centre de bioinformatique et de génomique fonctionnelle, CBiB, Université de Bordeaux, Bordeaux, France, Plateforme Génome-Transcritpome de Bordeaux, CGFB, Université de Bordeaux, Bordeaux, France.

Mycoplasma meleagridis and Mycoplasma gallinarum are bacteria that affect birds, but little is known about the genetic basis of their interaction with chickens and other poultry. Here, we sequenced the genomes of M. meleagridis strain MM_26B8_IPT and M. gallinarum strain Mgn_IPT, both isolated from chickens showing respiratory symptoms, poor growth, reduction in hatchability, and loss of production.

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Address correspondence to Boutheina Ben Abdelmoumen Mardassi, boutheina.mardassi@pasteur.rns.tr.

Mycoplasma meleagridis and Mycoplasma gallinarum belong to the hominis phylogenetic group within the Mollicutes class. Turkey was considered to be, for a long time, the specific host for M. meleagridis (1), until its isolation from chickens was reported (2). The ubiquitous nature of M. gallinarum in poultry as well as mammals has been reported by many investigators (3). It is considered to have a commensal relationship with its hosts. In poultry, M. gallinarum is commonly thought to be unable to cause disease by itself. Currently, the only available information that can provide us with data on genetic factors that might explain the host tropism and pathogenic potential of M. meleagridis and M. gallinarum is limited to the information given by the genome narum M. meleagridis Turkey was considered to be, for a long time, the specific host for tropism and pathogenic potential of provide us with data on genetic factors that might explain the host disease by itself. Currently, the only available information that can MM_26B8_IPT and Mgn_IPT, both isolated from chickens showing respiratory symptoms, poor growth, reduction in hatchability, and loss of production.

The MM_26B8_IPT genome has a size of 658,083 bp (assembled in 32 contigs), whereas the Mgn_IPT one is smaller, consisting of 800,663 bp (organized in 56 contigs). The G+C content in the two genomes was almost the same, around 26% A total of 539 and 601 coding sequences (CDSs) were identified in MM_26B8_IPT and Mgn_IPT, respectively. The more the genome was reduced, the greater was the coding density (90.44% in MM_26B8_IPT versus 87.40% in Mgn_IPT). Both strains were found to contain 33 tRNAs and a single copy of tmRNA.

Among the 9 and 10 genes involved in the stress response determined in MM_26B8_IPT and Mgn_IPT, respectively, 8 heat shock proteins (DnaK, DnaJ, GrpE, HrcA, LepA, SmpB, and 2 rRNA methyltransferase subunits) were shared. In addition, 17 and 14 genes potentially implicated in virulence and resistance to antibiotics and toxic compounds were identified in MM_26B8_IPT and Mgn_IPT, respectively.

Further analyses of the genome sequences of these two avian field strains, M. meleagridis and M. gallinarum, isolated from Tunisian chickens will help further the study of their host specificity and pathogenic potential.

Nucleotide sequence accession numbers. These whole-genome shotgun projects of M. meleagridis and M. gallinarum field strains have been deposited at DDBJ/EMBL/GenBank under the accession numbers LVWOO0000000 and LVLH0000000, respectively. The versions described in this paper are versions LVWOO00000001 for M. meleagridis MM_26B8_IPT and LVLH00000001 for M. gallinarum Mgn_IPT.

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