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GENOME ANNOUNCEMENT

Draft Genome Sequences of Four Axenic *Mycoplasma genitalium* Strains Isolated from Denmark, Japan, and Australia

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The DNA genome of *Mycoplasma genitalium* currently represents the smallest of all known human bacterial pathogens. Despite their clinical importance in sexually transmitted infection and relevance as model bacterial pathogens, genomic diversity among *M. genitalium* strains worldwide is unknown. Herein we present the complete draft genome sequences of four geographically diverse strains of *M. genitalium*.

Mycoplasma genitalium is a pathogenic member of the *Mollicutes* class of bacteria. Although unique in its small genome, *M. genitalium* is among a few mycoplasmas that have been isolated from the urogenital tract (12) and the only one unequivocally implicated in male urethritis (11). *M. genitalium* is transmitted sexually, and infection has also been associated with inflammatory syndromes in females such as cervicitis, pelvic inflammatory disease, and tubal-factor infertility (2, 10, 11). The genome of the G37 type strain of *M. genitalium* was the second bacterial genome to be completely sequenced (1), but investigation of additional isolates is necessary to define genomic heterogeneity and understand the plasticity of the reduced genome.

Consistent with the small genome, *M. genitalium* has marked metabolic restrictions exemplified by a lack of almost all of the enzymes necessary for the biosynthesis of amino acids, *de novo* nucleic acid synthesis, and fatty acid biosynthesis (1). Similar to other mycoplasmas, *M. genitalium* is largely dependent on growth factors obtained from the host, such as sterols for the plasma membrane, and seems to target mucosal environments where infection can persist. It is hypothesized that long-term infections are in part facilitated by antigenic variation of membrane proteins encoded by the MG191 (*mgpB*) and MG192 (*mgpC*) genes, which is due to recombination with nine partial, noncoding loci termed MgPars throughout the genome (4, 5, 7, 8).

Herein we report the draft genome sequences of four geographically distinct *M. genitalium* strains isolated originally from males with symptomatic urethritis. Two strains originated from subjects in Copenhagen, Demark (designated M2288 and M2321), and one strain each was from Miyazaki, Japan (M6282), and Melbourne, Australia (M6320). All isolates were cloned by the standard filtration or limiting-dilution method (3, 6) prior to this study. Genomic DNA was extracted from axenic cultures of each strain and then sequenced using the Roche 454 GS FLX pyrosequencer (454 Life Sciences/Roche Diagnostics, Branford, CT). Sequencing reads were mapped to the *M. genitalium* G37 genome (GenBank accession no. NC_000908.2) as a reference for assembly using the CLC Genomics Workbench software package (CLC bio, Cambridge, MA). Functional annotation was carried out by using both the Joint Genome Institute's Integrated Microbial Genomes Expert Review (9) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline).

The draft genome lengths were 579,558, 579,977, 579,504, and 579,796 bp for strains M2288, M2321, M6282, and M6320, with average coverage depths of 137-, 124-, 133-, and 76-fold, respectively. Details of genomic features, architecture, and comparative analyses are forthcoming in a separate report.

Nucleotide sequence accession numbers. The nucleotide sequences of *M. genitalium* strains M2288, M2321, M6282, and M6320 generated as part of this project have been deposited in the DDBJ/EMBL/GenBank databases and assigned accession numbers CP003773, CP003770, CP003771, and CP003772, respectively. The four genome projects were also deposited individually into the Genomes OnLine Database as projects Gi04585, Gi04590, Gi04584, and Gi04583, respectively.

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