Complete Genome Sequence of *Moraxella catarrhalis* Strain CCRI-195ME, Isolated from the Middle Ear

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**ABSTRACT** *Moraxella catarrhalis* is an important bacterial pathogen that causes otitis media and exacerbations of chronic obstructive pulmonary disease. Here, we report the complete genome sequence of *M. catarrhalis* strain CCRI-195ME, which contains the phase-variable epigenetic regulator ModM3.

*Moraxella catarrhalis* is a human-specific pathogen that causes otitis media and exacerbations of chronic obstructive pulmonary disease (1, 2), but it can also be carried asymptptomatically in the nasopharynx. The reason for differences in clinical presentation remains unclear, as genome analysis of *M. catarrhalis* isolates suggests a highly conserved genome with virulence determinants present in strains of both pathogenic and nonpathogenic origins (3, 4).

One potential explanation for the differences in pathology is differential regulation. Previous studies show that *M. catarrhalis* strains have a phase-variable DNA methyltransferase, ModM, that can alter the expression of a phase-variable regulon, known as a phasevarion (5, 6). Three alleles of ModM have been identified that have distinct DNA recognition domains and are hypothesized to alter different phasevarions. The modM3 allele is more frequently associated with strains isolated from the middle ear during otitis media than the nasopharynx during asymptomatic carriage (5). We report here the complete genome sequence of strain CCRI-195ME, an *M. catarrhalis* strain isolated from the middle ear of a 16-month-old child prone to otitis media (approved by Nationwide Children’s Hospital Institutional Review Board). CCRI-195ME contains the modM3 allele (MC195_06605), and this is the first closed genome of an *M. catarrhalis* strain with this allele.

Sequenced DNA was extracted from *M. catarrhalis* CCRI-195ME and grown on GC agar overnight at 37°C with 5% CO2, using the GenElute bacterial genomic DNA kit (Sigma-Aldrich), per the manufacturer’s instructions. The DNA was sequenced with the PacBio RSII platform using two SMRT cells and 180-min acquisition (Pacific Biosciences). Genome sequences were assembled de novo using the hierarchical genome assembly process (HGAP) (7). Consensus sequences generated using Quiver were submitted to NCBI for annotation with the Prokaryotic Genome Annotation Pipeline (PGAP), and annotated sequences were submitted to GenBank.

The CCRI-195ME genome resolved into a complete 1,954,607-bp chromosome (41.6% G+C) and a 39,779-bp plasmid (39.5% G+C). The genome consists of 1,782 predicted coding genes and 66 RNA genes (16 rRNAs and 50 tRNAs). CCRI-195ME belongs to 16S rRNA subtype I, as described in (8), and contains many of the known *M. catarrhalis* virulence determinants and vaccine candidates, including MID/Hag, CopB, UspA2H, and the transferrin-binding proteins TbpA and TbpB (9). The CCRI-195ME plasmid contains 44 predicted open reading frames. Overall, the plasmid does not show...
similarity to any plasmids in the NCBI databases. However, it does contain a number of putative homologues to transfer operon (Tra locus) components (10), suggesting that the plasmid may be conjugative.

PacBio methylome analysis determined that the ModM3 DNA methylation site 5’-ACm6ATC-3’ is present 4,529 times in the genome (4,446 in the chromosome and 83 in the plasmid) and is methylated to 100% when ModM3 is expressed. Collectively these data will aid in the understanding of how ModM3 mediates regulation and will help define the stably expressed immunological target repertoire of this organism. This will provide insight into the pathobiology of *M. catarrhalis* and aid the development of antibacterial strategies and vaccines.

**Accession number(s).** The CCRI-195ME genome has been deposited in GenBank under the accession numbers CP018059 (chromosome) and CP018060 (plasmid).

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**REFERENCES**