Complete Closed Genome Sequences of a *Mannheimia haemolytica* Serotype A1 Leukotoxin Deletion Mutant and Its Wild-Type Parent Strain

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*Mannheimia haemolytica* is a bacterial pathogen that secretes leukotoxin (LktA) which binds to leukocyte membranes via CD18, causing bacterial pneumonia in ruminants. We report the complete closed genome sequences of a leukotoxin mutant and its parent strain that are frequently used in respiratory disease studies.

Frozen cultures were grown 16 h on brain heart infusion (BHI) agar plates at 37°C and 5% CO2, inoculated in 10-mL BHI broth, and dant overlapping sequences were removed from the 3’ ends (/H11022 99% identity) indicating circular chromosomes. Redundant consensus sequences revealed circularized sequences. The origins of replication were determined for genome assembly with Quiver (35). The error-corrected reads were assembled on a Pacific Biosciences RSII instrument (Pacific Biosciences, Menlo Park, CA) with libraries prepared from manufacturer’s kits. Reads were error-corrected and sequenced using a blood and cell culture DNA kit (Qiagen, Valencia, CA). Sequencing was performed on a Pacific Biosciences RSII instrument (Pacific Biosciences, Menlo Park, CA). The respective genome sizes of *M. haemolytica* strains USDA-ARS-USMARC 56470 and 56467 (89010807 N, LktA+ and LktA−) were 2,705,355 and 2,704,219, with CDS counts of 2749 and 2750; tRNA counts of 65; rRNA counts of 20; and a GC content of 41.0%. The 7.6-kb lktA operon was identical between strains, excluding the replacement of LktA with a beta-lactamase gene. The parent lktA operon was identical to *M. haemolytica* strains 183, 2286, D153, D174, and M42548 (CP004752, CP006619, CP005972, CP006574, and CP005383, respectively).

Nucleotide sequence accession numbers. Sequences of parent and mutant strains were deposited in GenBank under the accession numbers CP011098 and CP011099, respectively.

ACKNOWLEDGMENTS
The contributions of M.P.H., G.P.H., T.P.L.S., J.L.B., and C.G.C.-M. were funded by the Agricultural Research Service of the United States Department of Agriculture.

Cultures of the parent strain (89010807N, LktA+) and mutant strain (89010807N, LktA−) were kindly provided by Anthony W. Confer, Oklahoma State University.

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REFERENCES


