Genome Sequence of Poultry Pathogen *Riemerella anatipestifer* Strain RA-YM[▽]

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***Riemerella anatipestifer* is a Gram-negative, rod-shaped bacterium associated with epizootic infections in poultry. *R. anatipestifer* strain RA-YM, belonging to the serotype 1 prevalent in China, is a clinically isolated strain with high-level virulence. Here, we report the first genome sequence of this species.**

Riemerella anatipestifer is a Gram-negative, rod-shaped bacterium that causes an epizootic, contagious, and often primary septicemic disease in domestic ducks, turkeys, and various other birds (14, 15). Presently, 21 serotypes of *R. anatipestifer* have been identified and no significant cross-protection was reported (10, 12, 13). Despite the devastating losses it causes in poultry production, not much is known about the pathogenesis and few data on virulence factors are available (4, 16, 18). Here, we sequenced the genome of *R. anatipestifer* strain RA-YM, a highly virulent field isolate of serotype 1 (9).

The genome sequence of strain RA-YM was determined by using the high-throughput Solexa sequencing technology (Illumina GA2x) in Shenzhen, China. Filtered paired-end reads totaling 245.90 Mb (mean read length, 90 bp) were obtained, providing about 119-fold coverage of the genome. The sequence reads were assembled, using SOAPdenovo (<http://soap.genomics.org.cn/soapdenovo.html>), into a total of 36 contigs (N50 length, 124,430 bp) distributed over 29 scaffolds (N50 length, 185,480 bp). The remaining intrascaffold gaps were closed by Sanger sequencing of PCR products. Protein-coding genes were predicted using Glimmer 3.0 (5). tRNA and rRNA genes were identified by tRNAScan and RNAmmer, respectively (8, 11). Functional annotation was performed by searching against protein databases, including NR, Swiss-Prot, TrEMBL, COG, and KEGG.

The RA-YM chromosome is 2,140,468 bp in length, with an average G+C content of 34.97% and a coding percentage of 90.78. There are 2,019 putative open reading frames with an average length of 957 bp, 42 rRNA operons, 1 microRNA gene, and 40 tRNA genes.

Numerous virulence-associated factors were identified in this genome. *sspA*, a novel gene, encodes a surface-localized, subtilisin-like serine protease that shows homology to C5a pro-

teases of pathogenic streptococci, which specifically inactivate C5a and act in adhesion to fibronectin type III and invasion of epithelial cells (1, 2, 3). The product of *hagA1*, a gene encoding a serine protease/hemagglutinin identified in the RA-YM genome, contains a 280-amino acid C-terminal region with 43% similarity to the HagA of *Porphyromonas gingivalis*, which may play a pivotal role in host colonization by *R. anatipestifer* and, thus, in infection (7). The gene *prtC*, which encodes an extracellular collagenase that could induce host cells to synthesize and secrete inflammatory cytokines to exert a destructive effect on periodontal tissue by *P. gingivalis*, may play an important role in RA-YM's pathogenicity (17). Five gene clusters involved in polysaccharide biosynthesis and export were identified, and the products of a gene cluster which are similar to alginate O-acetyltransferases of *P. aeruginosa* probably function in biofilm formation (6).

This is the first genome sequence of the *R. anatipestifer* species, and its availability will facilitate the understanding of virulence mechanisms of this pathogen and open new perspectives for the development of more efficient disease control strategies.

Nucleotide sequence accession number. The genome sequence of *R. anatipestifer* strain RA-YM has been deposited at DDBJ/EMBL/GenBank under the accession number AENH000000000.

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