The genus *Bordetella* is reportedly a human or animal pathogen and environmental microbe. We report the draft genome sequence of *Bordetella trematum* strain HR18, which was isolated from the rumen of Korean native cattle (Hanwoo; *Bos taurus coreanae*). It is the first genome sequence of a *Bordetella* sp. isolated from the rumen of cattle.

The HR18 genome was sequenced using an Illumina HiSeq 2000 system at the Genome Research Center of the Korea Research Institute of Bioscience and Biotechnology (KRIBB). A total of 14,222,221 paired-end reads (341.62-fold coverage) were obtained from the HiSeq 100-bp paired-end library and were pre-processed and *de-novo*-assembled using the CLC Genomics Workbench (CLC bio), version 7.5. The genome sequence was assembled into 21 scaffolds (23 contigs). The sizes of the largest and the longest contigs were 542,107 and 398,472 bp, respectively. The open reading frames (ORFs) of the assembled genome were predicted and annotated using the Integrated Microbial Genomes—Expert Review (IMG-ER) (5), NCBI Clusters of Orthologous Groups (COG) (6), Pfam (7), and EzTaxon-e (8) databases and the rRNA genes and tRNA genes were identified by utilizing the RNAmmer 1.2 (9) and tRNAscan-SE 1.23 (10) tools, respectively. The draft genome of *B. trematum* strain HR18 was 4,204,757 bp. The G+C content was 65.8%, and the ORF number was 3,882. The numbers of tRNA and rRNA, and the protein coding genes with functions were 58, 3, and 2,612, respectively. The genome is estimated to contain 3,292 coding sequences, with the majority of the sequences coding for amino acid transport and metabolism. Approximately 183 genes are predicted to be involved in membrane transport. Interestingly, two genes coding for cytotoxic lymphocyte distending toxin (CDT) were found in the genome of *B. trematum* strain HR18. CDT is a heterotrimeric B-type glycoprotein produced by certain gammaproteobacterial mucocutaneous bacterial pathogens (11). Thus far, no research has shown that betaproteobacteria, *Bordetella* species produce CDT. The potential pathogenicity of *B. trematum* strain HR18 against Korean native cattle requires further investigation.

**Nucleotide sequence accession number.** The draft genome sequence of *B. trematum* is available in DDBJ/EMBL/GenBank under the accession no. JPQP00000000.

**ACKNOWLEDGMENTS**

This work was supported by the Research Program for Agricultural Science & Technology Development (project PJ010168) and was partially supported by grants from the National Research Foundation of Korea (NRF) (2008-2004721 and 2013M3A9A0766001), the KRIBB Research Initiative Programs (KGM4111443 and KCM1051413), and the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHD1), funded by the Ministry of Health & Welfare of the Republic of Korea (grant HI14C03680200).

**REFERENCES**


