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Genome Sequence of *Coxiella*-Like Endosymbiont Strain CLE-RmD, a Bacterial Agent in the Cattle Tick (*Rhipicephalus microplus*) Deutsch Strain

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ABSTRACT We report a partial genome sequence for the *Coxiella*-like endosymbiont strain CLE-RmD, assembled from metagenomics data obtained from the southern cattle tick (*Rhipicephalus microplus*) Deutsch strain.

Many of the model species for investigating host-bacterial interactions include hematophagous, plant sap-sucking arthropods, and food-storage pests (1–4). These diets lack essential amino acids, vitamins, and cofactors, which also cannot be synthesized by the host arthropods. The endosymbiotic bacteria of these arthropods are hypothesized to provide those nutrients (5). Bacterial endosymbionts in hard and soft ticks related to *Coxiella burnetii*, the etiologic agent of Q fever, are known as *Coxiella*-like endosymbionts (CLEs) (6–8). The nutritional dependence of *Amblyomma americanum* on its CLE has been experimentally demonstrated (9) and further supported bioinformatically for CLEs from several other hard tick species whose symbiont genomes have been sequenced, namely, *Rhipicephalus turanicus* (CRt) (10), *Rhipicephalus sanguineus* (CLE-RsOK) (11), and *A. americanum* (CLEAA/CLE-AaGA) (11, 12). For most other tick CLE symbionts, only a few sequences have been obtained (7).

Illumina HiSeq-1000 (accession numbers SRX1668952, SRX1668960, and SRX1668961) and 454GS FLX (accession numbers SRX019998 and SRX019999) reads were generated from low-Cot and Cot 696 genomic DNA extracted from a pooled collection of eggs from the f7 and f10 to f12 generations of the *R. microplus* Deutsch strain colony from Webb County, Texas (13–16), and submitted by the Centre for Comparative Genomics, Murdoch University, Australia (BioProject numbers PRJNA312025 and PRJNA46685, respectively). All of the Illumina runs and 454 reads were merged independently and mapped against 38 *Coxiella* genome sequences (NCBI/DDBJ/EMBL) and NCBI contigs containing CLE sequences previously assembled from Illumina/PacBio/454 reads of *R. microplus* using BWA v0.7.12 (17). All of the Illumina and 454 mapped CLE-RmD reads were extracted using SAMtools v1.3.1 (18) and independently assembled into scaffolds using the state-of-the-art assemblers SPAdes v3.10.1 (19), Velvet v1.2.10 (20), and CLC Genomics Workbench v9.5.2 (Qiagen). The CISA v1.3 tool (21) was used to integrate the three *de novo* assemblies with the NCBI *R. microplus* CLE contigs into a hybrid set of scaffolds, from which duplicate regions were excluded.

The partial genome of CLE-RmD (1,296,618 bp, 89 contigs with 229× coverage) was annotated with Prokka (22) and BLAST (23). The size of CLE-RmD (1.30 Mb, 31.7% G+C) is 65.0% of the size of the genome of the human pathogen *C. burnetii* (1.99 Mb, 42.7% G+C) but 81.9% of CRt (1.58 Mb, 38.2% G+C; we excluded the near-exactly duplicated 150,764-bp region from coordinates 590,925 to 741,688, which is probably an artifact) (10) and 116.2% that of the partial CLE-RsOK genome assembly (1.12 Mb, 38.0%) (11, 12). All three CLEs from *Rhipicephalus* (CRt, CLE-RsOK, and CLE-RmD) are much larger than the complete CLEAA and CLE-AaGA genomes from *Amblyomma* (657 kb, 34.6% G+C) (11, 12). The partial CLE-RmD genome contained 742 protein genes, 28 tRNAs, 3

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rRNAs, and 3 small RNAs (sRNAs) (transfer-messenger RNA [tmRNA], single recognition particle [SRP], and RNaseP). CLE-RmD genes typically had 80 to 90% similarity to homologues in CRt and CLE-RsOK but had at least 10% lower similarity to those of CLEAA, CLE-AaGA, and *C. burnetii*.

Accession number(s). The genome of *Coxiella* endosymbiont strain CLE-RmD of *R. microplus* was submitted as a whole-genome shotgun (WGS) project at GenBank/DDBJ/ENA under the accession number DLUJ00000000. The WGS of the CLE-RmD version described in this paper is version DLUJ01000000.

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