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Complete Genome Sequence of *Ehrlichia canis* Strain YZ-1, Isolated from a Beagle with Fever and Thrombocytopenia

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ABSTRACT We report the complete genome sequence of *Ehrlichia canis* strain YZ-1, which was isolated from a beagle with fever, anorexia, depression, lethargy, weight loss, and thrombocytopenia. *E. canis* is the tick-borne agent of canine and human monocytic ehrlichiosis.

Ehrlichia species, which are important tick-borne pathogens in humans and animals, are obligate intracellular Gram-negative bacteria of the family *Anaplasmataceae*. Five *Ehrlichia* species are recognized, namely *E. chaffeensis*, *E. ewingii*, *E. canis*, *E. ruminantium*, and *E. muris*, with three (*E. canis*, *E. chaffeensis*, and *E. ewingii*) causing canine ehrlichiosis (1–3). Complete genome sequences have previously been reported for *E. chaffeensis* strain Arkansas (4), *E. muris* strain AS145 (5), *E. canis* strain Jake (6), three strains of *E. ruminantium* (7), and *E. mineirensis*, a novel organism closely related to *E. canis* (8). Here, we describe the second complete genome sequence of *E. canis*, made from strain YZ-1, which was isolated from an adult female beagle (*Canis lupus familiaris*) living in a commercial dog farm in Taizhou, Jiangsu, China. The dog was clinically ill, with signs that included fever (41.4°C), depression, lethargy, anorexia, and thrombocytopenia (1.2×10^{10} platelets/liter).

The *E. canis* YZ-1 strain isolate has been maintained in our laboratory by continuous passage in the DH82 canine monocytic cell line (ATCC CRL-10389) for 20 passages. For genome sequencing, the organisms were extracted from DH82 cells and purified by Percoll density-gradient centrifugation. The *E. canis* YZ-1 DNA was extracted using the Qiagen DNA minikit (Qiagen, Valencia, CA) and a 1-μl aliquot quantified using the Qubit fluorometric quantification system (Thermo Fisher Scientific, Waltham, MA). The genome of *E. canis* strain YZ-1 was sequenced by single molecule real-time (SMRT) technology using PacBio systems (Pacific Biosciences, USA) at Beijing Novogene Bioinformatics Technology Co., Ltd. (Beijing, China). A total of 146,443 pass-filter quality reads of 1.8×10^9 bp in length were generated, showing an average read score of 84%. The *de novo* assembly of the reads using SMRT Portal resulted in 156 polished contigs and 2,735,875 bases, with an N_{50} value of 129,950. A single contig status without gaps was achieved for the genome, and the circular chromosomal structure was validated.

The genome of *E. canis* strain YZ-1 consists of a single circular chromosome containing 1,314,789 nucleotides with an overall G+C content of 29%. The origin of replication (*oriC*) was predicted using the Ori-Finder program to be a 425-nucleotide region upstream of a hypothetical protein (locus tag EC-YZGM000006), and 1 bp was assigned to be the beginning of the *oriC* (9). The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline version 4.3, which used GeneMarkS+ for gene prediction (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/). The genome of *E. canis* YZ-1 is predicted to contain 994 genes, including 924 protein-coding sequences (CDSs), one copy of each of the rRNA genes (5S, 16S, and 23S), 36 tRNA genes, 29 pseudogenes, and two small noncoding RNAs. The availability of the complete genome

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of *E. canis* YZ-1 will enable divergence with other *Ehrlichia* spp. to be determined and studied and enable more reliable insights into the evolution of the species and mechanisms of their host specificity.

Accession number(s). The *E. canis* strain YZ-1 whole-genome sequence has been deposited in GenBank under the accession number CP025749.

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