Microsporidia comprise a phylum of obligate intracellular pathogens related to fungi. Microsporidia *Nematocida* sp1 strain ERTm6 was isolated from wild-caught *Caenorhabditis briggsae* and causes a lethal intestinal infection in *Caenorhabditis* nematodes. We report the genome sequence of *N*. sp1 ERTm6, which will facilitate study of the *Nematocida* genus and other Microsporidia.

The genome size was estimated to be 4.28 Mb, with a GC content of 38.30%. The assembly was organized into 57 contigs, with an average insert size of 178 bases and 2.6 kb sequenced both strands. The assembly was organized by paired-end reads into 24 scaffolds. As found for other sequenced *Nematocida* (2), this is a compact genome and 67.48% of the genome sequence is predicted to be coding, with a mean distance between coding sequences of 578.63 bp. The average base is found in a scaffold with an N50 of 797.7 kb and a contig with an N50 of 219.3 kb. A total of 2,433 protein-coding genes, 51 RNA genes, and 9 rRNA genes were predicted as previously described (2).

We found that *N*. sp1 ERTm6 is likely diploid, although the heterozygous regions are not as polymorphic as ERTm2. The ERTm6 strain has 1 SNP every 989 bp, identified from BWA-MEM (10) alignments of the illumina reads using the GATK Unified Genotyper version 2.7 (11). This genome, together with the ERTm1, ERTm2, and ERTm3 genomes, provide an excellent resource for investigating microsporidium diversity and coevolution of parasites and hosts.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AKIJ00000000. The version described in this paper is version AKIJ01000000.

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