The first cases of Israeli spotted fever were reported in the late 1940s in the Haifa Bay area, Israel. In 1971, the agent of this disease was isolated from a patient and later described as a *Rickettsia conorii*-related bacterium named Israeli spotted fever rickettsia (14). The geographic distribution of the disease appears to be more widely spread in the Mediterranean countries than previously thought, as cases from Italy, Portugal, Tunisia, and, supposedly, Libya have been reported (4, 6, 7, 18). Israeli spotted fever rickettsia was proposed to be classified as one of four *R. conorii* subspecies, under the name *R. conorii* subsp. *israelensis* (17). To date, the genomes of three other proposed *R. conorii* subspecies have been sequenced (12, 15, 16). Here, we report the genome of *R. conorii* subsp. *israelensis* strain ISTT CDC1.

Genomic DNA of *R. conorii* subsp. *israelensis* strain ISTT CDC1 (deposited in the CDC collection, Atlanta, GA, and in the CSUR collection under reference number CSUR R119), isolated in 1974 from a *Rhipicephalus sanguineus* tick collected in Israel and grown in Vero cells, was pyrosequenced using the 454 GS FLX Titanium platform (Roche, Branford, CT) (11). The single-read shotgun sequencing resulted in 94,182 reads ranging in length from 40 to 716 bases, with 309.2 bases on average. These reads were then analyzed using the Newbler version 2.3 (Roche) *de novo* assembler module (gsAssembler). Potential coding sequences (CDSs) were predicted using AMIGene (3), and split genes or nonpredicted genes were detected and corrected manually where appropriate using Artemis (5) and BLASTN (1). Assignment of protein functions was performed by searching against the Rick-Base, GenBank, and Pfam databases using BLASTP (1, 2, 13), while rRNAs, tRNAs, and other RNAs were identified using BLASTN (1). Assignment of protein functions was performed by searching against the Rick-Base, GenBank, and Pfam databases using BLASTP (1, 2, 13), while rRNAs, tRNAs, and other RNAs were identified using BLASTN, tRNAscan-SE version 1.21 (10), and RNAmer 1.2 (8).

The draft genome of *R. conorii* subsp. *israelensis* consists of 33 contigs ranging in size from 1,004 to 110,058 bases (21.8-fold genome coverage), resulting in a total genome of 1,252,815 nucleotides. No plasmid was detected. The GC content of the genome was 32%, and the total number of predicted CDSs was 1,806. Like *R. conorii*, almost perfectly syntenic. However, we were not able to detect the genes for NADH dehydrogenase I chain B (NuoB), glycerol-3-phosphate cytidyltransferase (TagD), and MazG-like protein in the *R. conorii* subsp. *israelensis* genome, while they were present in those of the other three *R. conorii* subspecies. Whether this difference explains the differences in clinical expression observed among subspecies remains to be determined.

**Nucleotide sequence accession numbers.** The whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJVP00000000. The version described in this paper is the first version, AJVP01000000.

**ACKNOWLEDGMENT**

This research did not benefit from any external funding.

**REFERENCES**


**Received** 22 June 2012 **Accepted** 29 June 2012

Address correspondence to Pierre-Edouard Fournier, pierre-edouard.fournier@univmed.fr

Copyright © 2012, American Society for Microbiology. All Rights Reserved.
doi:10.1128/JB.01118-12