Human brucellosis is a neglected and underrecognized infection of widespread geographic distribution. Brucellosis is present on all inhabited continents and endemic in many areas of the world, including Kuwait and the Middle East. Here, we present draft genome assemblies of five Brucella melitensis strains isolated from patients in Kuwait.

**TABLE 1** Summary characteristics of whole-genome assemblies of five clinical B. melitensis strains isolated in Kuwait

<table>
<thead>
<tr>
<th>Strain</th>
<th>Mean coverage (×)</th>
<th>N50 contig length (bp)</th>
<th>No. of contigs</th>
<th>Assembly size (bp)</th>
<th>No. of genes</th>
<th>No. of tRNAs</th>
<th>No. of SNPs</th>
<th>Accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>KU/RCF-03</td>
<td>43.0</td>
<td>189,106</td>
<td>43</td>
<td>3,283,635</td>
<td>3,143</td>
<td>52</td>
<td>1,042</td>
<td>LDTY00000000</td>
</tr>
<tr>
<td>KU/RCF-31</td>
<td>40.0</td>
<td>176,881</td>
<td>49</td>
<td>3,289,202</td>
<td>3,151</td>
<td>51</td>
<td>1,487</td>
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</tr>
<tr>
<td>KU/RCF-64</td>
<td>52.6</td>
<td>268,511</td>
<td>40</td>
<td>3,290,511</td>
<td>3,154</td>
<td>52</td>
<td>1,501</td>
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</tr>
<tr>
<td>KU/RCF-84</td>
<td>69.0</td>
<td>293,285</td>
<td>34</td>
<td>3,289,577</td>
<td>3,150</td>
<td>52</td>
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</tr>
<tr>
<td>KU/RCF-96</td>
<td>67.2</td>
<td>195,560</td>
<td>41</td>
<td>3,289,620</td>
<td>3,150</td>
<td>52</td>
<td>1,487</td>
<td>LAQM00000000</td>
</tr>
</tbody>
</table>

**B**ruceellosis is a highly infectious zoonotic disease caused by the organisms of genus Brucella (1). Among the 10 known species of Brucella (2), Brucella melitensis is the most pathogenic organism and a biological threat to humans (3). Genotyping of B. melitensis isolates is important for contact tracing and epidemiological surveillance in regions endemic for the organism (4). Whole-genome sequencing, by using next-generation sequencing (NGS) technologies, is emerging as a rapid method for the genetic characterization of B. melitensis (5, 6). NGS-based assays are capable of identifying genetic variations in the form of single nucleotide polymorphisms (SNPs) and indels (5, 6). In order to identify genetic variations in strains from Kuwait, we did whole-genome sequencing of five B. melitensis strains isolated from patients residing in Kuwait. The sequence data were analyzed to determine the number of SNPs in the genomes.

Five clinical isolates of B. melitensis were grown on culture plates, and single colonies were suspended in saline. The bacterial suspensions were heated at 95°C for 10 min, and DNA was purified using the QIAamp DNA minikit (Qiagen, Hilden, Germany). DNA libraries were prepared using the Nextera XT DNA library preparation kit (Illumina, San Diego, CA). The genomic DNA was sequenced using Illumina MiSeq paired-end (2 × 150 bp) sequencing technology. The data quality was checked with FastQC (7). Reads were trimmed and quality filtered using FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/). The de novo assembly was performed using Velvet 1.2.10 (8). The best Velvet assembly was merged with SPAdes assembly by using SPAdes 3.8 (9). Quast was used to check the assembly quality (10). After ordering the obtained contigs against B. melitensis bv. 1 strain 16M using the Mauve contig aligner (11), each draft assembly was submitted to the NCBI for annotation with PGAP 3.3. SNPs were detected relative to the genome of reference strain B. melitensis bv. 1 strain 16M (GenBank assembly accession no. GCA_000007125.1) using BioNumerics 7.6 (Applied Maths, Belgium). All the assemblies have 57.2% G+C content and 3 rRNAs. Other assembly/genome characteristics, i.e., mean coverage, N50 contig length, number of contigs, assembly size, and number of genes, tRNAs, and SNPs are provided in Table 1. In-depth comparative analyses of these genomes are under way and will be published in an upcoming manuscript.

**Accession number(s).** All the genome sequences were submitted to NCBI under BioProject PRJNA278809 and are available with accession numbers listed in Table 1.

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REFERENCES


