



Draft Genome Sequences of Six Multidrug-Resistant Clinical Strains of *Acinetobacter baumannii*, Isolated at Two Major Hospitals in Kuwait

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ABSTRACT *Acinetobacter baumannii* is an important opportunistic pathogen in global health care settings. Its dissemination and multidrug resistance pose an issue with treatment and outbreak control. Here, we present draft genome assemblies of six multidrug-resistant clinical strains of *A. baumannii* isolated from patients admitted to one of two major hospitals in Kuwait.

Acinetobacter baumannii has steadily raised concerns in the medical field over the past decade as one of the most dangerous multidrug-resistant (MDR) human pathogens in health care settings and conflict zones (1). This opportunistic Gram-negative organism is the most pathogenic of the four genotypically related species in the *Acinetobacter calcoaceticus*-*Acinetobacter baumannii* (ACB) complex (2). Identification and genotyping of *A. baumannii* isolates are important for contact tracing and epidemiologic surveillance in outbreak conditions (3).

Whole-genome sequencing, by using next-generation DNA sequencing technologies, offers an increasingly attainable new path of bacterial investigation and outbreak control, through which partial or complete genomes can be examined based on nucleotide differences at a single site (single nucleotide polymorphisms [SNPs]) across the entire genome (4). In order to identify genetic variations in strains from Kuwait, we performed whole-genome sequencing of six multidrug-resistant *A. baumannii* strains isolated from patients admitted to one of two major hospitals in Kuwait. The sequence data were analyzed to determine the number of SNPs in the genomes.

Six clinical isolates of *A. baumannii*, three isolates each from Al-Sabah Hospital (KUSSH13, KUSSH35, and KUSSH36) and Farwaniya Hospital (KUFAR40, KUFAR42, and KUFAR44) (Table 1), were grown on blood agar plates, and single colonies were suspended in nuclease-free water. The bacterial suspensions were heated at 95°C for 25 min, and DNA was purified using the QIAamp DNA minikit (Qiagen, Hilden, Germany) and quantified using the Qubit double-stranded DNA (dsDNA) broad-range assay (Thermo Fisher Scientific). 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 (5). Output reads from MiSeq were checked for quality using FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc>), and low-quality sequences were removed from the ends using FASTX trimmer (http://hannonlab.cshl.edu/fastx_toolkit/). Retained high-quality reads were assembled *de novo* using Velvet 1.2.10 (6) and SPAdes 3.9.0 (7). Assembly statistics were checked by QAST (8). The contigs were ordered by Abacus 1.3.1 using *A. baumannii* strain AYE, a multidrug-resistant strain isolated in France (9) (GenBank assembly accession number GCA_000069245), as a reference. Assembled

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TABLE 1 Summary characteristics of whole-genome assemblies of six multidrug-resistant clinical *A. baumannii* strains isolated in Kuwait

| Strain | Mean coverage (x) | N ₅₀ contig size (bp) | No. of contigs | Assembly size (bp) | No. of genes | No. of tRNAs | No. of SNPs (AYE) | No. of SNPs (KUSSH36) | GenBank accession no. |
|---------|-------------------|----------------------------------|----------------|--------------------|--------------|--------------|-------------------|-----------------------|-----------------------|
| KUSSH13 | 55 | 175,365 | 80 | 3,887,021 | 3,811 | 65 | 5,327 | 2,416 | NEPY00000000 |
| KUSSH35 | 52 | 167,975 | 60 | 3,881,261 | 3,756 | 63 | 4,897 | 2 | NEPN00000000 |
| KUSSH36 | 62 | 184,821 | 60 | 3,882,939 | 3,758 | 63 | 4,899 | 0 | NEPM00000000 |
| KUFAR40 | 44 | 141,709 | 64 | 3,914,902 | 3,810 | 63 | 4,901 | 19 | NEPJ00000000 |
| KUFAR42 | 38 | 138,282 | 89 | 3,916,090 | 3,826 | 63 | 4,899 | 17 | NEPH00000000 |
| KUFAR44 | 64 | 153,110 | 69 | 3,940,599 | 3,857 | 62 | 4,895 | 11 | NEPG00000000 |

genomes were submitted to NCBI Prokaryotic Genome Annotation Pipeline 4.1 for genome annotation. Assembly statistics and annotation parameters are provided in Table 1. SNPs were detected using BioNumerics 7.6 (Applied Maths, Belgium), relative to the genome of reference strain AYE and one of the strains included in this study (KUSSH36). The SNP analysis showed that five of the six Kuwaiti isolates were genetically close to each other, but all of them were quite distinct from *A. baumannii* strain AYE (Table 1).

Accession number(s). All genome sequences discussed here were submitted to NCBI under BioProject number PRJNA380997 and are available with the accession numbers listed in Table 1.

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