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Draft Genome Sequences of Clinical Isolates of Multidrug-Resistant *Acinetobacter baumannii*

Keesha E. Erickson,[a] Nancy E. Madinger,[b] Anushree Chatterjee[a,c]

Chemical and Biological Engineering, University of Colorado Boulder, Boulder, Colorado, USA[a]; Division of Infectious Diseases, University of Colorado Anschutz Medical Campus, Aurora, Colorado, USA[b]; BioFrontiers Institute, University of Colorado Boulder, Boulder, Colorado, USA[c]

ABSTRACT We report here the draft genome sequences of two clinically isolated *Acinetobacter baumannii* strains. These samples were obtained from patients at the University of Colorado Hospital in 2007 and 2013 and encode an estimated 20 and 13 resistance genes, respectively.

Address correspondence to Anushree Chatterjee, chatterjee@colorado.edu.

Pathogens in the genus *Acinetobacter* have been named as a serious threat to public health (1), with *Acinetobacter baumannii* in particular capable of increasing risk of mortality up to 70% (2). *A. baumannii* is a decidedly adaptive species, demonstrating a wealth of mechanisms for evading diverse antibiotic classes, including on horizontally transferred resistance islands in the genome (2, 3) and resistance-conferring plasmids (4). *A. baumannii* is also able to survive for extended durations on dry surfaces (5). These factors together have allowed for a high frequency of multidrug-resistant nosocomial *A. baumannii* infections worldwide, with diminishing options for treatment. Characterization of clinically isolated *A. baumannii* strains will enable development of more effective treatment strategies.

We sequenced two *A. baumannii* strains from the University of Colorado Hospital Clinical Microbiology Laboratory organism bank. Strain CU060707 was isolated from the bloodstream of a 47-year-old male in 2007, and strain CU032113 was isolated from a hardware-associated bone infection in a 44-year-old female in 2013.

Colonies were grown aerobically in cation-adjusted Mueller-Hinton broth for 16 h at 37°C. Approximately two micrograms of DNA were isolated per strain (Wizard DNA purification kit, Promega). The Nextera XT DNA library kit was used to build paired-end 250-bp libraries, which were sequenced on an Illumina MiSeq, generating 1,644,910 and 1,081,729 reads for CU060707 and CU032113, respectively. FASTQ files were filtered using the sliding window mode in Trimmomatic (6). *De novo* assembly was performed with SPAdes version 1.0.0 (7) and Rescaf version 1.0.1; then annotation was executed with Prokka version 1.0.0 (8) in BaseSpace (https://basespace.illumina.com). Antibiotic resistance genes were identified with ARG-ANNOT (9).

The draft assembly of *A. baumannii* CU060707 is 4,119,754 bp in length (94× coverage, 39% GC content) in 240 contigs with an N_{50} of 150,723 bp. The genome contains 56 tRNAs, seven rRNAs, one CRISPR, and 3,831 coding sequences. The 20 resistance genes detected include six aminoglycosides [*ant(3″)-Ih*, *aadA1*, *aph(3″)-Ia*, *armA*, *strA*, and *strB*], nine β-lactams (ADC-30, *blaA1*, *blaA2*, *mbl*, OXA-235, OXA-66, TEM-1D, a penicillin-binding protein, and a zinc-dependent hydrolase), two macrolide-lincosamide-streptogramins (*mphE*, *msrE*), one chloramphenicol (*catB8*), one sulfon-amide (*sulI*), and one tetracycline (*tetB*). Most resistance genes are encoded on the genome, though OXA-235 appears to be on a plasmid, similar to GenBank CP015486.1.

The draft assembly of *A. baumannii* CU032113 is 4,182,411 bp in length (61× coverage, 39% GC content) in 322 contigs with an N_{50} of 59,362 bp. There are 70 tRNAs,

nine rRNAs, two CRISPRs, and 3,882 coding sequences. The 13 resistance genes found include two aminoglycosides (*strA* and *strB*), eight β-lactams (ADC-76, *blaA1*, *blaA2*, *mbl*, OXA-24, OXA-65, TEM-116, and a zinc-dependent hydrolase), two chloramphenicols (*catA1* and *cmlB1*), and one sulfonamide (*sulII*). OXA-24 is the only gene not on the genome; it appears to be on a plasmid, similar to GenBank JN207494.1 (4).

We validated resistances by plating on solid media with antibiotics and found that both strains are able to grow in tetracycline, ampicillin, and chloramphenicol. CU060707 cannot grow in meropenem. CU032113 grows in meropenem, but not in gentamicin or erythromycin. Both isolates are resistant to ciprofloxacin, indicating that *gyrA* and/or *parC* are mutated (10, 11).

Accession number(s). This whole-genome shotgun sequencing project has been deposited in GenBank under the accession numbers LXWY00000000 (for CU060707) and LXYW00000000 (for CU032113).

ACKNOWLEDGMENTS

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