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GENOME ANNOUNCEMENT

Genome Sequences of Four Divergent Multidrug-Resistant *Acinetobacter baumannii* Strains Isolated from Patients with Sepsis or Osteomyelitis

Daniel V. Zurawski,[a] Mitchell G. Thompson,[a] Christin N. McQueary,[a] Malcolm N. Matalka,[b] Jason W. Sahl,[b] David W. Craft,[a] and David A. Rasko[b]

Walter Reed Army Institute of Research (WRAIR), Department of Wound Infections, Silver Spring, Maryland, USA,[a] and Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, Maryland, USA[b]

***Acinetobacter baumannii* is a Gram-negative bacterium that causes nosocomial infections worldwide, with recent prevalence and higher frequency in wounded military personnel. Four *A. baumannii* strains from the Walter Reed Army Medical Center (WRAMC) isolated between 2008 and 2009 were sequenced, representing diverse, multidrug-resistant isolates from osteomyelitis or septic patients.**

Acinetobacter baumannii is a nonfermentative, Gram-negative coccobacillus that is the etiological agent of nosocomial infections resulting in septicemia, meningitis, endocarditis, pneumonia, and wound and urinary tract infections (7, 8, 10). The rapid development of antimicrobial resistance and nosocomial spread of this emerging pathogen have elicited great interest (5, 7, 8). *A. baumannii* isolates can typically be characterized into three identifiable clonal clusters, termed international clonal complexes I to III (4, 6, 9). In previous studies, U.S. military personnel have had representatives from each clonal complex (11, 13). The isolates sequenced for this report were part of a larger diversity set of *A. baumannii* isolates from 2005 to 2010 at the Walter Reed Army Medical Center (WRAMC) (our unpublished data).

A total of four strains were chosen, as they represented one of each clonal group and an outlier group based on pulsed-field gel electrophoresis (PFGE), multiplex PCR, and multilocus sequence type (MLST) analysis (http://www.pasteur.fr/recherche/genopole/PF8/mlst/Abaumannii.html), had different isolation sites (osteomyelitis of the tibia or ischium or blood), and had diverse phenotypes and virulence profiles (our unpublished data). The four strains were isolated within a year's time (2008 to 2009), determined to be multidrug resistant (MDR), and were obtained from the Multidrug-Resistant Organism Repository and Surveillance Network (MRSN). They are designated AB4857 (MRSN939), AB5075 (MRSN959), AB5256 (MRSN961), and AB5711 (MRSN1310).

Genomic DNA was prepared with the PureLink genomic DNA minikit (Invitrogen) according to the manufacturer's instructions and subjected to sequencing on a 454 GS-FLX Titanium system (454 Life Science Corporation) maintained at the University of Maryland School of Medicine, Institute for Genome Sciences, Genome Resource Center (http://www.igs.umaryland.edu/). Paired-end libraries with 3-kb inserts were sequenced for each of the isolates, yielding >320,000 reads for each isolate (range, 322,062 to 385,454 reads/isolate) and an average read size of 356.4 bp (range, 342.9 to 370.4); this results in ~24.8-fold coverage for each genome (range, 22.67 to 26.0). Assembly was performed using the Newbler software, which resulted in an average of 47 contigs per isolate (range, 36 to 55) and 12.5 scaffolds (range, 11 to 14). The contig data were annotated using the cloud computing pipeline CloVR (3).

The GC content of the strains, 36.6% (range, 36.4 to 36.78%), is within the deviation for *A. baumannii* genomes (2, 12, 14). The numbers of predicted genes from the draft genomes were also similar to those of previously sequenced *A. baumannii* genomes, with 4,903 genes/genome (range, 4,673 to 5,084). Each of the strains had at least one contig that mapped to *A. baumannii* plasmids (1, 2, 12). Phylogenetically, these isolates are not similar to other isolates from a comparable isolation source (data not shown). No one functional group of genes was overrepresented in the annotation. Additionally, there were no large gene clusters that could account for the observed tissue tropism associated with the site of isolation in the human body. These facts taken together suggest that *A. baumannii* is a generalist pathogen that takes advantage of opportunities to invade the human body at certain locations (11, 12). Further analysis is required to determine how the gene differences are related to the observed phenotypes and will provide insight into *A. baumannii* pathogenesis.

Nucleotide sequence accession numbers. The genome data have been deposited in GenBank under accession numbers AHAG00000000, AHAH00000000, AHAI00000000, and AHAJ00000000 for isolates AB4857, AB5075, AB5256, and AB5711, respectively.

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Address correspondence to Daniel V. Zurawski, daniel.zurawski@amedd.army.mil.

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