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Complete Genome Sequence of Multidrug-Resistant *Acinetobacter baumannii* Strain 1656-2, Which Forms Sturdy Biofilm

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***Acinetobacter baumannii* is a Gram-negative bacterium causing nosocomial infections worldwide. To gain quick insight into the molecular basis of biofilm formation in *A. baumannii*, we determined the complete genome sequence of *A. baumannii* strain 1656-2, which forms sturdy biofilm and is resistant to multiple drugs.**

Acinetobacter baumannii is a nonfermentative Gram-negative coccobacillus that causes nosocomial infections, particularly in immunocompromised individuals, resulting in septicemia, meningitis, endocarditis, pneumonia, wound infection, and urinary tract infection (6, 11). In the 1970s, this organism was susceptible to most antimicrobial agents. It has now become a major cause of nosocomial infection worldwide because of its remarkable ability to acquire resistance determinants to various kinds of antimicrobial agents (3, 4).

We recently investigated the biofilm-forming ability of 23 multidrug-resistant (MDR) *A. baumannii* strains isolated from a university hospital in South Korea. Our results showed that most strains have the ability to form a considerable amount of biofilm (9, 12). To gain quick insight into the molecular basis of biofilms and antimicrobial resistance of MDR *A. baumannii*, we determined the complete genome sequence of *A. baumannii* strain 1656-2, which showed the highest ability to form biofilm in the study (9), using a 454 GS-FLX (454 Life Science Corporation). A total of 862,301 high-quality reads with an average read length of 369.5 bp were produced. Assembly was performed using the Newbler software, which resulted in 219 contigs. The order of contigs was confirmed by PCR and combinatorial PCR. The completed genome sequence had 78.4× sequence coverage for chromosome, 275× for plasmid 1 (p1) and 130× for plasmid 2 (p2). The complete sequence was analyzed using GLIMMER3 (2) for the protein-coding gene, tRNAscan-SE (10) for the tRNA, and RNAmmer (8) for the rRNA. The functions of predicted protein-coding genes were then annotated through comparisons with the databases of UniRef90 (13), NCBI-NR (1), COG (14), and KEGG (7).

The genome size of *A. baumannii* 1656-2 was 3,940,614 bp with a G+C content of 39.2% and a coding region of 88.0% with 3,715 open reading frames. There are 18 predicted rRNA genes and 71 predicted tRNA genes. The 1656-2 strain has two plasmids, p1 and p2, with sizes of 74,451 bp with 101 open reading frames and 8,041 bp with 8 open reading frames, respectively. The G+C contents of the two plasmids together were 33.5%. For the genomic analysis of multidrug resistance of strain 1656-2, 39 genes, including $bla_{\text{PER-1}}$, $bla_{\text{OXA-109}}$, and tellulite resistance gene were found. A total of 17 IS*Aba1* copies were found in the chromosome (15 copies) and p1 plasmid (2 copies), which has been known to be related to antibiotic resistance only in *Acinetobacter* spp. (5). Thirteen genes, including the polyglutamic acid (PGA) synthesis protein-coding gene, were predicted for sturdy-biofilm formation, and 34 genes related to cell adhesion were searched. Compared to other *A. baumannii* genomes, such as *A. baumannii* ACICU (GenBank accession no. NC010611), AYE (GenBank accession no. NC010410), ATCC 17978 (GenBank accession no. NC009085), and SDF (GenBank accession no. NC010400), we found more genes involved in cell motility, cell traffic, secretion, and vesicular transport and more copies of IS elements in the 1656-2 genome than in the genomes of other *A. baumannii* strains. Further in-depth analysis of this genome with other *A. baumannii* genomes could give more valuable information on biofilm formation in *A. baumannii*.

Nucleotide sequence accession number. The complete genome sequence of *Acinetobacter baumannii* strain 1656-2 has been deposited in GenBank under accession no. CP001921.

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