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Genome Note

Draft genome sequence of a clinical *Acinetobacter baumannii* isolate of new sequence type ST1688 from Saudi Arabia

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ABSTRACT

Objectives: *Acinetobacter baumannii* has emerged as a prevalent multidrug-resistant nosocomial pathogen worldwide. Here we report the draft genome sequence of *A. baumannii* strain Ab174 isolated from a neonatal patient diagnosed with acute peritonitis.
Methods: The draft genome sequence of *A. baumannii* Ab174 was determined using a MiSeq platform (Illumina Inc., San Diego, CA) using v.3, 2 × 30-bp chemistry. Genomic assembly was performed using SPAdes 3.9 algorithm.
Results: The draft genome of *A. baumannii* Ab174 is 3 747 065 bp in length and was classified as a new sequence type (ST1688). The genome of *A. baumannii* Ab174 has a G + C content of 39% and harbours two plasmids. The antimicrobial resistance gene bla_{ADC-25} and the virulence factor gene for penicillin-binding protein G (*pbpG*) as well as 17 genomic islands and 14 insertion sequences were identified in the genome of *A. baumannii* Ab174.
Conclusion: The genome sequence of *A. baumannii* strain Ab174 can be used as a reference sequence for the new ST1688. These data will facilitate further understanding of genomic variation in isolates from different geographical regions.

Until around 40 years ago, *Acinetobacter baumannii* was susceptible to most antibiotics [1], however in the past two decades the tendency to develop a multidrug-resistant (MDR) phenotype has increased tremendously [2]. Evolution of *A. baumannii* is driven by horizontal gene transfer and recombination owing to its highly malleable genome [3]. A. *baumannii* is widespread in the environment owing to its capacity to persist on dry surfaces. In addition, this bacterium is able to survive well in the hospital environment owing to its relative resistance to disinfectants, causing nosocomial infections such as pneumonia, septicaemia, meningitis and endocarditis [4]. Here we report the draft genome sequence of *A. baumannii* strain Ab174 isolated from a neonatal patient in Saudi Arabia.

A. baumannii strain Ab174 was isolated from a urine catheter specimen of a neonatal patient diagnosed with acute peritonitis in King Abdulaziz University Hospital (Jeddah, Saudi Arabia). The purified isolate was freshly cultured on a blood agar plate at 37 °C for 20 h and was identified using a MALDI Biotyper (Bruker Daltonics, Billerica, MA) [5]. Antimicrobial susceptibility testing was performed using an automated VITEK®2 system (bioMérieux, Marcy-l'Étoile, France) with a specific AST-N291 card for Gram-negative bacteria. Genomic DNA was extracted from *A. baumannii* Ab174 using an UltraClean® Microbial DNA Isolation Kit (MO BIO Laboratories, Inc., Carlsbad, CA). A genomic library was prepared using a Nextera XT DNA Library Preparation Kit (Illumina Inc.) and sequencing was performed on a MiSeq platform (Illumina Inc.) using v.3, 2 × 300-bp chemistry. The generated reads from genome

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sequencing were filtered according to the read qualities. De novo assembly of the genome was performed using SPAdes 3.9 algorithm. Annotation of the genome of *A. baumannii* Ab174 was performed by Rapid Annotation using Subsystem Technology (RAST) (http://rast.theseed.org/FIG/rast.cgi) and PATRIC web resources (https://www.patricbrc.org/). Antimicrobial resistance genes were identified using ResFinder 3.1, ARG-ANNOT (Antibiotic Resistance Gene-ANNOTation) and CARD (Comprehensive Antibiotic Resistance Database). The sequence type (ST) of the isolate was identified using a multilocus sequence typing (MLST) scheme based on seven housekeeping genes (https://cge.cbs.dtu.dk//services/MLST/). Virulence genes were identified through the Virulence Factors Database (VFDB) of pathogenic bacteria (http://www.mgc.ac.cn/VFs/main.htm). The genome sequence was deposited into the European Nucleotide Archive (ENA) under accession no. **PRJEB32440**.

The draft genome of *A. baumannii* Ab174 is 3 747 065 bp in length, has a G+C content of 39% and contains two circular plasmids (pABVA01 and p3ABSDF). A total of 3705 coding sequences were identified in the genome comprising 2878 proteins with functional assignments and 827 hypothetical proteins. Moreover, 72 RNA genes were detected comprising 63 tRNAs and 9 rRNAs. *A. baumannii* Ab174 was classified into a new sequence type (ST1688) based on new combinations of the known alleles (*gltA* 21, *gyrB* 12, *gdhB* 40, *recA* 26, *cpn60* 32, *gpi* 144 and *rpoD* 4). The isolate was resistant to aztreonam but was susceptible to ampicillin, ceftriaxone, ceftazidime, cefepime, piperacillin/tazobactam, imipenem, meropenem, gentamicin, tobramycin, ciprofloxacin, levofloxacin, minocycline, tigecycline, colistin, trimethoprim/sulfamethoxazole and nitrofurantoin. The antimicrobial resistance gene $bla_{\text{ADC-25}}$ linked with β-lactam resistance was detected in *A. baumannii* Ab174 and might be responsible for the observed aztreonam resistance (Table 1). Moreover, genes were identified from the genome linked with the resistance–nodulation–cell division (RND) efflux pump family (CzcCBA) associated with metal ion efflux. Several virulence factor genes were found in the genome, including biofilm-associated protein (*bap*), type IV pili (*pilE*), acinetobactin, penicillin-binding protein (*pbp*G), capsular polysaccharide (*wbjD*/*wecB*) and polysaccharide poly-*N*-acetylglucosamine (*pgaA*, *pgaB*, *pgaC* and *pgaD*). In total, 17 genomic islands and 14 insertion sequences from three families were detected by IslandViewer 4 and ISfinder, respectively. This is the first report of the genome of *A. baumannii* ST1688 and can be used as a reference sequence for future comparative analysis of various features, including acquisition and mobilisation of antimicrobial resistance genes in isolates belonging to ST1688.

Table 1
Antimicrobial resistance and virulence genes in *Acinetobacter baumannii* strain Ab174.

Gene	Class	Node	Length	Position
Antimicrobial resistance gene				
$bla_{\text{ADC-25}}$	Beta-lactam	156	1152	22289 . . . 23440
Virulence genes				
pgaA	PNAG	90	2439	57530 . . . 59968
pgaB		90	1830	55701 . . . 57530
pgaC		90	1248	54454 . . . 55701
pilE	Type IV pili	269	438	876 . . . 1313
pbpG	PbpG	34	1008	55020 . . . 56027
lpxM	Lipopolysaccharide	32	984	7044 . . . 8027
wbjD/*wecB*	Capsular polysaccharide	34	1008	55020 . . . 56027

PNAG, poly-*N*-acetylglucosamine; PbpG, penicillin-binding protein G.

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Competing interests

None declared.

Ethical approval

This study was reviewed and approved by the Ethical Research Committee of the Faculty of Medicine at King Abdulaziz University (Jeddah, Saudi Arabia) [ref. no. 235–15].

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