

## SHORT COMMUNICATION

# Genome of a Carbapenem Resistant *Acinetobacter baumannii* Isolate of a new Sequence Type ST1724 from Saudi Arabia

Ahmed M. Tolah<sup>1,2</sup>, Muhammad Yasir<sup>1,3</sup>, Asad Karim<sup>4</sup>, Asad M. Karim<sup>5</sup>,  
Hani A. Shukri<sup>6</sup>, Esam I. Azhar<sup>1,3</sup>

<sup>1</sup> Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

<sup>2</sup> Department of Medical Laboratory Technology, Faculty of Applied Medical Science, King Abdulaziz University, Rabigh, Saudi Arabia

<sup>3</sup> Department of Medical Laboratory Sciences, Faculty of Applied Medical Sciences, King Abdulaziz University, Jeddah, Saudi Arabia

<sup>4</sup> Jamil-Ur-Rahman Center for Genome Research, Dr. Panjwani Center for Molecular Medicine and Drug Research, International Center for Chemical and Biological Sciences (ICCBS), University of Karachi, Karachi, Pakistan

<sup>5</sup> Institute of Biopharmaceutical and Health Engineering, Tsinghua Shenzhen International Graduate School, Tsinghua University, Shenzhen, China

<sup>6</sup> Clinical and Molecular Microbiology Laboratories, King Abdulaziz University Hospital, Jeddah, Saudi Arabia

## SUMMARY

**Background:** The World Health Organization has classified carbapenem-resistant *Acinetobacter baumannii* as a pathogen of critical priority that poses a serious threat to human health. We report a draft genome sequence of colistin and carbapenem-resistant *A. baumannii* strain AB134 of a new sequence type ST1724.

**Methods:** *A. baumannii* strain AB34 was isolated from a tracheal aspirate specimen from a patient diagnosed with atherosclerotic disease and treated at a hospital in Saudi Arabia. Antimicrobial susceptibility was determined via microdilution using a VITEK 2 system. Genome sequencing was performed using a HiSeq 2500 platform (Illumina Inc., USA).

**Results:** *A. baumannii* strain AB134 was classified as a new sequence type (ST1724) comprised of 3,763 predicted genes and a guanine-cytosine content of 38.8%. The isolate was phenotypically resistant to 16 clinically important antibiotics, and 33 antimicrobial resistance genes were detected, including the beta-lactamase genes of *bla*<sub>OXA-23</sub>, *bla*<sub>OXA-66</sub>, *bla*<sub>ADC-25</sub>, and *bla*<sub>TEM-1D</sub>. It carries the colistin resistance gene *lpsB*. In addition, 49 genes associated with virulence factors (biofilm formation, adherence, quorum sensing, iron uptake, and two-component system), and seven insertion sequences were detected in the AB134 genome.

**Conclusions:** This report presents the first draft genome of ST1724 of carbapenem-resistant and extensively drug-resistant *A. baumannii*. The findings facilitate further understanding of the genomics of this pathogen, which is a leading cause of healthcare-associated infections worldwide.

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### Correspondence:

Muhammad Yasir  
King Fahd Medical Research Centre  
King Abdulaziz University  
Jeddah, 21589  
Saudi Arabia  
Phone: +966 563202241  
Email: yasirkhattak.mrl@gmail.com

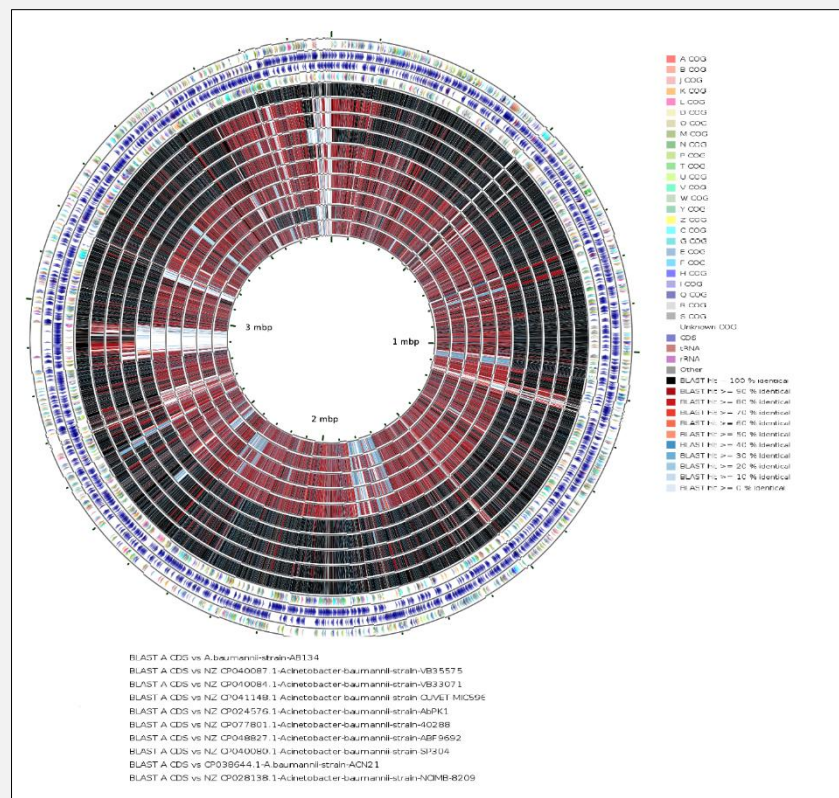
## Supplementary Data

Table S1. Virulence genes detected in the genome of *Acinetobacter baumannii* strain AB134.

| Virulence Factors                              | Genes         |
|------------------------------------------------|---------------|
| <b>Adherence</b>                               |               |
| Outer membrane protein                         | <i>ompA</i>   |
| <b>Biofilm formation</b>                       |               |
| AdeFGH efflux pump/transport autoinducer       | <i>adeF</i>   |
| AdeFGH efflux pump/transport autoinducer       | <i>adeG</i>   |
| AdeFGH efflux pump/transport autoinducer       | <i>adeH</i>   |
| Biofilm-associated protein                     | <i>bap</i>    |
| Csu pili                                       | <i>csuA/B</i> |
| Csu pili                                       | <i>csuA</i>   |
| Csu pili                                       | <i>csuB</i>   |
| Csu pili                                       | <i>csuC</i>   |
| Csu pili                                       | <i>csuD</i>   |
| Csu pili                                       | <i>csuE</i>   |
| PNAG (Polysaccharide poly-N-acetylglucosamine) | <i>pgaA</i>   |
| PNAG (Polysaccharide poly-N-acetylglucosamine) | <i>pgaB</i>   |
| PNAG (Polysaccharide poly-N-acetylglucosamine) | <i>pgaC</i>   |
| PNAG (Polysaccharide poly-N-acetylglucosamine) | <i>pgaD</i>   |
| <b>Enzyme</b>                                  |               |
| Phospholipase C                                | <i>plc</i>    |
| Phospholipase D                                | <i>plcD</i>   |
| <b>Immune evasion</b>                          |               |
| LPS                                            | <i>lpsB</i>   |
| LPS                                            | <i>lpxA</i>   |
| LPS                                            | <i>lpxB</i>   |
| LPS                                            | <i>lpxC</i>   |
| LPS                                            | <i>lpxD</i>   |
| LPS                                            | <i>lpxL</i>   |
| LPS                                            | <i>lpxM</i>   |
| <b>Iron uptake</b>                             |               |
| Acinetobactin                                  | <i>barA</i>   |
| Acinetobactin                                  | <i>barB</i>   |
| Acinetobactin                                  | <i>basA</i>   |
| Acinetobactin                                  | <i>basB</i>   |
| Acinetobactin                                  | <i>basC</i>   |
| Acinetobactin                                  | <i>basD</i>   |
| Acinetobactin                                  | <i>basF</i>   |
| Acinetobactin                                  | <i>basG</i>   |
| Acinetobactin                                  | <i>basH</i>   |
| Acinetobactin                                  | <i>basI</i>   |
| Acinetobactin                                  | <i>basJ</i>   |
| Acinetobactin                                  | <i>bauA</i>   |
| Acinetobactin                                  | <i>bauB</i>   |

**Table S1. Virulence genes detected in the genome of *Acinetobacter baumannii* strain AB134 (continued).**

| Virulence Factors       | Genes       |
|-------------------------|-------------|
| Iron uptake (continued) |             |
| Acinetobactin           | <i>bauC</i> |
| Acinetobactin           | <i>bauD</i> |
| Acinetobactin           | <i>bauE</i> |
| Acinetobactin           | <i>bauF</i> |
| Acinetobactin           | <i>entE</i> |
| Heme utilization        | <i>hemO</i> |
| Regulation              |             |
| Quorum sensing          | <i>abaI</i> |
| Quorum sensing          | <i>abaR</i> |
| Two-component system    | <i>bfmR</i> |
| Two-component system    | <i>bfmS</i> |
| Serum resistance        |             |
| PbpG                    | <i>pbpG</i> |
| Stress adaptation       |             |
| Catalase                | <i>katA</i> |



**Figure S1.** The coding region BLAST map of *Acinetobacter baumannii* genomes. *A. baumannii* strain AB134 was used as a reference genome against the other nine *A. baumannii* strains.

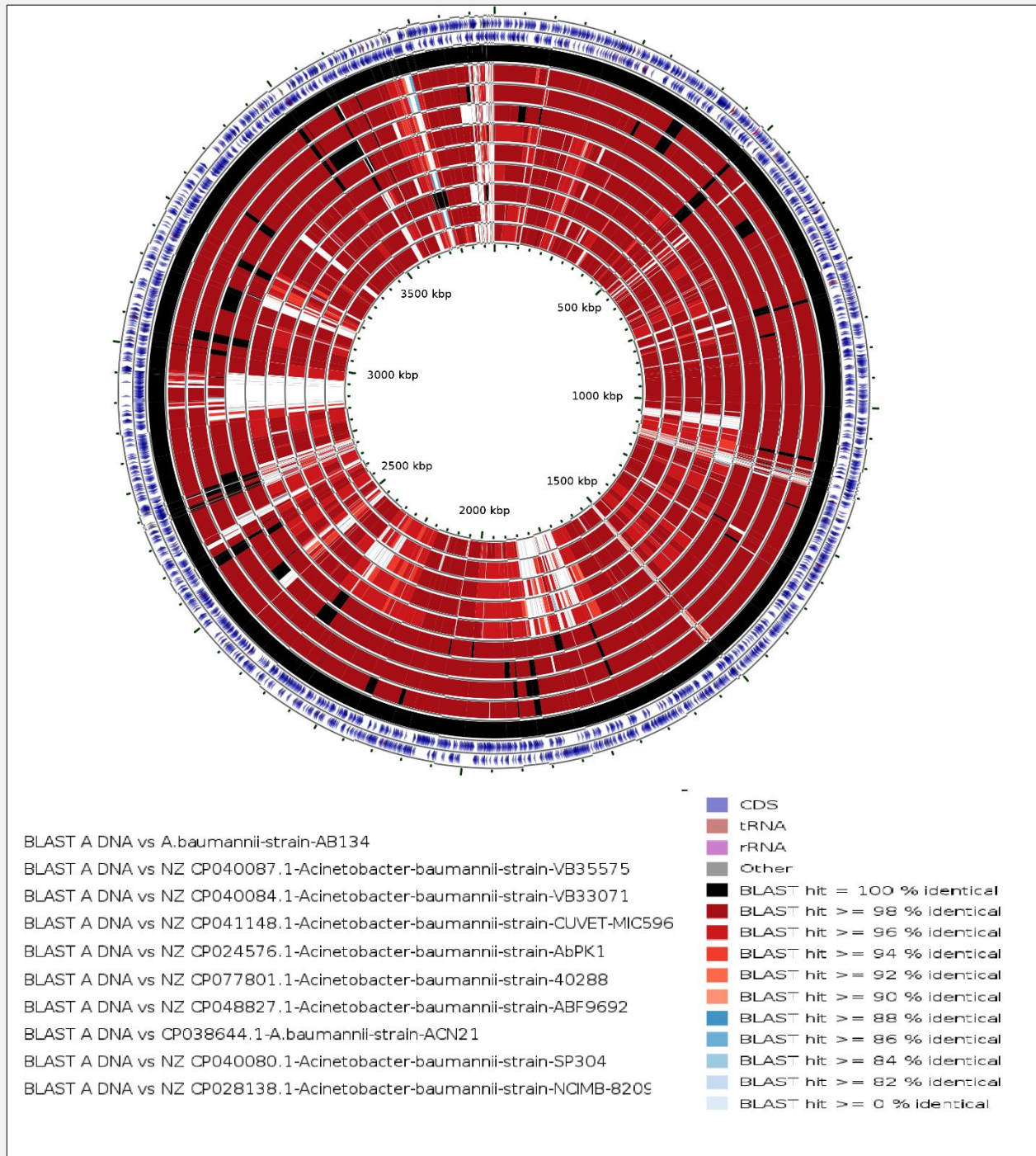


Figure S2: The DNA BLAST map of *Acinetobacter baumannii* genomes. *A. baumannii* strain AB134 was used as a reference genome against the other nine *A. baumannii* strains.