



Draft Genome Sequence of an *Acinetobacter baumannii* Isolate Recovered from a Horse with Conjunctivitis in Germany

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ABSTRACT Here, we announce the draft genome sequence of *Acinetobacter baumannii* strain 161514, which was recovered from a horse with conjunctivitis, and determine the genetic basis of its antimicrobial resistance phenotype. The genome has a size of 3,839,365 bp and a G+C content of 38.93% and is predicted to contain 3,529 coding sequences. The isolate belongs to sequence type 462 (ST462) according to the Oxford scheme (Abaumannii1) and to ST46 according to the Pasteur scheme (Abaumannii2).

Acinetobacter baumannii is a Gram-negative, opportunistic pathogen from the genus *Acinetobacter* and a member of the family *Moraxellaceae*. It is a serious and emerging pathogen that causes nosocomial and community-acquired infections in humans, with a high incidence among immunocompromised patients (1). In animals, it is associated with mastitis, wound infections, septicemia, bronchopneumonia, and eye infections. Horses have been reported to develop wound infections, septicemia, and bronchopneumonia, as well as neonatal encephalopathy and eye infections (2).

A. baumannii strain 161514 was isolated in Germany in 2016 from a horse with conjunctivitis. The sample was a part of a resistance monitoring system aimed at collecting resistance data on animal-pathogenic bacteria (GERM-Vet-2016). The sample was cultured on Columbia blood agar at 37°C, and initial microbial species identification was done using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS; Bruker Daltonik GmbH, Bremen, Germany) and PCR by detection of the *bla*_{OXA-51-like} carbapenemase gene (3).

MICs were determined by the microdilution method using the Micronaut MDR large animal 3, MRGN-screening 3, and β -lactamase plates (Merlin Diagnostika GmbH, Bornheim-Hersel, Germany). The susceptibility to the panel of antimicrobial agents was determined as described in the manufacturer's instructions and interpreted automatically according to the CLSI guidelines (Table 1).

Genomic DNA was extracted according to the manufacturer's instructions using the Qiagen Genomic-tip 100/G kit (Qiagen, Hilden, Germany) from a single colony grown in LB medium supplemented with 1% glucose at 37°C. The paired-end sequencing library was prepared with the Nextera XT DNA library prep kit (Illumina, Inc., San Diego, CA, USA). The library was sequenced using a MiSeq sequencer (Illumina, Inc.). Raw reads were processed using the shovill pipeline v1.04 (<https://github.com/tseemann/shovill>) to produce assembled FASTA files of more than 500 bp in length and with a kmer coverage greater than 3 (enabled options, -trim, -minlen 500, -mincov 3). Quality assessment of the assembled data was conducted with QUAST v4.3 using standard settings (4). Genome annotation was performed using PGAP v4.9 and the NCBI database (5). The distribution of genes (including resistance genes) assigned to the SEED subsystems and the initial metabolic reconstruction were analyzed using RAST (6)

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somal mutations in the isolated strain were determined using the SRST2 tool v0.2.0 (10) and the databases ResFinder v3.1 (11) and ARG-ANNOT (12) (Table 1). Default parameters were used for all software tools unless stated differently.

Acinetobacter baumannii is a serious and emerging pathogen that causes nosocomial and community-acquired infections in humans. The data on the impact of *A. baumannii* strains from (companion) animal origin on human health are still inconclusive. Further comprehensive studies are needed to assess the possible zoonotic risk of this agent for human and animal health.

Data availability. The sequence data of *A. baumannii* 161514 were deposited in the NCBI archive under GenBank accession number [RPDK000000000](https://www.ncbi.nlm.nih.gov/nuccore/RPDK000000000), SRA accession number [SRR8191030](https://www.ncbi.nlm.nih.gov/sra/SRR8191030), BioProject accession number [PRJNA505595](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA505595), and BioSample accession number [SAMN10426731](https://www.ncbi.nlm.nih.gov/biosample/SAMN10426731).

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