Genome sequences of three *Acinetobacter baumannii* strains assigned to ST2, ST25 and ST78 multilocus sequencing typing genotypes.

Raffaele Zarrilli,¹* Maria Giannouli,¹ Francesco Rocco,² Nicholas J. Loman,³ Anthony S. Haines,³ Chrystala Constantinidou,³ Mark J. Pallen,³ Maria Triassi,¹ and Pier Paolo Di Nocera.²

Department of Preventive Medical Sciences, University of Napoli Federico II, Naples, Italy,¹ Department of Cellular and Molecular Biology and Pathology, University of Napoli Federico II, Naples, Italy,² Centre for Systems Biology, School of Biosciences, University of Birmingham, Birmingham, B15 2TT UK.³

*Corresponding author. Mailing address: Dipartimento di Scienze Mediche Preventive, Università di Napoli Federico II, Via Pansini 5, 80131, Napoli, Italy. Phone: 39-081-7463026. Fax: 39-081-7463352. E-mail: rafzarri@unina.it
Abstract

*Acinetobacter baumannii* is an emerging opportunistic gram-negative pathogen responsible for hospital-acquired infections. *A. baumannii* epidemics described in Europe and worldwide were caused by a limited number of genotypic clusters of multidrug-resistant strains. Here we report the availability of draft genome sequences for three multidrug-resistant *A. baumannii* strains assigned to ST2, ST25 and ST78 multilocus sequencing typing genotypes, that were more frequently isolated during outbreaks occurred in Greece, Italy, Lebanon and Turkey.
Acinetobacter baumannii is an emerging opportunistic pathogen, causing a variety of nosocomial infections, (13). Outbreaks of A. baumannii were caused by few genotypic clusters of strains that were initially named European clones I, II and III and are now regarded as international (7,10,13), and referred to, according to multilocus sequence typing, as ST1, ST2 and ST3, respectively (7). Epidemiological studies showed the prevalence of international clone II lineage during the last few years (7,8,10,13) and the occurrence of epidemics caused by multidrug-resistant strains belonging to novel genotypes ST25 and ST78 in several Mediterranean hospitals (8,9).

The whole genome sequences of six ST1 (1,2,15), and single ST2, ST3 and ST77 A. baumannii strains were available so far (2,11,14,15). Here we announce the availability of three draft genome sequences for carbapenem-resistant A. baumannii ST2 strain 3990, ST78 strain 3909 and ST25 strain 4190, isolated during cross-transmission episodes occurred at the Monaldi Hospital, Naples, Italy during 2006, 2007 and 2009, respectively (8,9).

The genomes were sequenced to at least 10-fold coverage using 454 FLX Titanium emPCR pyrosequencing (Roche) according to the manufacturer’s recommendations. Draft genomes were assembled using Newbler and automatically annotated using xBASE2 bacterial genome annotation service (4). The draft genome sequences of the ST2, ST25 and ST78 strains consisted of 96, 396 and 236 contigs, comprised 4,015,011 bases, 4,032,291 bases and 3,954,832 bases and generated 3,806, 3,910 and 3,721 protein coding sequences by automated annotation against A. baumannii AB0057 genome, respectively. Comparative analysis of ST2, ST25 and ST78 genomes with ACICU, AB0057, ABAYE and ATCC17978 genomes using Mauve software (6) identified 3,068 homologous protein coding sequences at the same relative position in the seven genomes. Sixty-three DNA segments, ranging in size from 3 to 126 kb, were present only in some of the seven genomes, but were either missing or replaced by non-homologous DNA sequences in others. Consistent with their close genetic relatedness, both the ST2 3990 and the ACICU strains carried a 15.4-kb region containing antimicrobial resistance genes inserted in the ATPase gene locus. At the
corresponding chromosomal location, a 12.7 kb region flanked by transposases but devoid of resistance genes was identified in the ST78, but not in the ST25 strain.

Complete plasmid sequences for ST2, ST25 and ST78 strains were obtained by comparing DNA sequences of contigs with those determined by a primer-walking technique on purified plasmid preparations. Genome annotations were manually verified and corrected using the Artemis viewer (3). The ST2 3990 strain contained two plasmids, p1-ABST2 (63,320 bp) carrying a complete tra locus and p2-ABST2 (21,846 bp) carrying one copy of the carbapenem-hydrolyzing oxacillinase (CHDL) \( \text{bla}_{\text{OXA-58}} \) gene, homologous to plasmids pACICU2 and pACICU1, respectively (11). The ST25 strain contained two distinct plasmids, p1-ABST25 (15,267 bp) and p2-ABST25 (8,970 bp), that both carried one copy of the CHDL \( \text{bla}_{\text{OXA-72}} \) gene and were homologous to plasmids carrying the \( \text{bla}_{\text{OXA-24}} \) gene (5,12). The single plasmid p1-ABST78 (26,411 bp) identified in the ST78 strain contained one copy of the \( \text{bla}_{\text{OXA-58}} \) gene and was homologous to plasmids p2-ABST2 and pACICU1 (11).

Nucleotide sequence accession numbers. The draft genome sequences of strains 3990, 4190 and 3909 have been deposited at GenBank under accession numbers AEOY0000000, AEPA0000000, AEOZ0000000, respectively.

This work was supported in part by grants from Agenzia Italiana del Farmaco, Italy (AIFA2007 contract no. FARM7X9F8K) and from Ministero dell’Istruzione, dell’Università e della Ricerca, Italy (PRIN 2008 to RZ).

We thank people at the Birmingham Science City funded 454 sequencing facility for genome sequencing.
REFERENCES


