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# Molecular epidemiology of multidrug-resistant Acinetobacter baumannii in Hungary, 2011-2016: spread of an OXA-72-producing Acinetobacter baumannii clone

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**Background:** Multidrug-resistant *Acinetobacter baumannii* (MACI) is one of the most difficult antimicrobial-resistant Gram-negative bacilli to control and treat, especially due to their carbapenem-resistance. In *A. baumannii* the prevalent carbapenem resistance mechanism is the production of a carbapenem-hydrolyzing Ambler class D β-lactamase (CHDL). The main acquired CHDLs belong to the OXA-23, OXA-24/40 and OXA-58 groups. Molecular typing of isolates obtained from various locations in Europe has shown the existence of three distinct lineages of MACI that have been termed European clone I (EUI), EUII, and EUIII. Scarce information is available on molecular epidemiology of MACI in Hungary, thus investigation was conducted on MACI isolates in order to define the prevalent clones in Hungary, 2011-2016.

**Material/methods:** Suspected MACI isolates from patients of entire country submitted to the National Center for Epidemiology between January 2011 and September 2016 were investigated. The antimicrobial susceptibility testing to imipenem, meropenem, ciprofloxacin, amikacin, gentamicin and tobramycin was performed and interpreted using EUCAST guidelines and only carbapenem resistant isolates were included in this study. The presence of different CHDL encoding genes was verified using conventional PCR. The possible clonal relationships were investigated by PFGE analysis and by MLST-Pasteur. Whole-genome sequencing (WGS) of selected isolates of two OXA-40-like CHDL producing MACI strains was performed by Illumina 251-bp paired-end sequencing. From WGS data acquired antimicrobial resistance genes were retrieved using ResFinder tool, and the IS elements associated to OXA-40-like genes using ISFinder tool.

**Results:** Altogether 754 MACI isolates from 40 hospitals were subjected to molecular typing where EUI clone (31.2%) and EUII clone (61.4%) proved prevalent in Hungary. Six different sequence types (STs) were identified associated with variable CHDL group distribution (Table 1). Based on the WGS results both OXA-40-like CHDL in ST78 and ST636 proved OXA-72 associated with ISAba1 and ISAba17, respectively. The ST78/OXA-72 (n=8) was found only in 2014-2015. Except of 2011, the EUII was the most prevalent, however between 2012-2015 the ST-2/EUII was the dominant sequence type, while ST636/EUII/OXA-72 introduced in 2015 became widespread (12 hospitals in seven counties) by 2016.

**Conclusions:** We described for the first time OXA-72 CHDL among Hungarian MACI isolates. It is highly likely that its introduction was consequence of independent emergence of two ST types. The widespread of ST636 in a very short time period is of a great concern. Thus enhanced survey is recommended in order to restrict its further expansion.

Table 1. Distribution of ST types and CHDLs of A. baumannii isolates in Hungary, 2011-2016

| ST type/EU clone | No of isolates | Distribution of CHDL groups by STs(%) | | |
|---|---|---|---|---|
| | | OXA-23 | OXA-40 | OXA-58 |
| ST1/EUI | 174 | 65 | 0 | 35 |
| ST81/EUI | 23 | 100 | 0 | 0 |
| ST2/EUII | 279 | 56 | 0 | 44 |
| ST45/EUII | 15 | 67 | 0 | 33 |
| ST636/EUII | 45 | 0 | 100 | 0 |
| ST78/singleton | 8 | 0 | 100 | 0 |