

P0943 Draft genome sequences of four clinical isolates of multidrug-resistant *Acinetobacter baumannii* from Romanian hospitals

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Background:

An increased incidence of carbapenem- and multidrug-resistant *Acinetobacter baumannii* nosocomial strains is reported lately, due to a high number of resistance and virulence genes located on mobile genetic elements (MGE). This is the first report on the draft genome analysis of four MDR *A. baumannii* strains isolated in Romanian hospitals from bloodstream infections, in two hospitals from Bucharest, Romania.

Materials/methods: The genomes of four *A. baumannii* strains (1s, 14s, A7, A14) were sequenced using HiSeqX Ten, Illumina (GenBank accession numbers: SRX4094320, SRX4094321, SRX4094322, SRX4094323). The paired reads were assembled by using SPADes 3.12.0 and the quality of assembling was checked by QUAST program. Annotation was performed with RAST; the analysis of resistance and virulence profiles was achieved by using multiple programs (ResFinder, PlasmidFinder, PathogenFinder, CARD, PubMLST, IS finder, Virulence Factor Database).

Results: All strains present resistance genes for beta-lactams (*bla*_{OXA-66}, *bla*_{OXA-72}, *bla*_{ADC-25}, *bla*_{TEM-1D}, and *bla*_{OXA-23}), aminoglycosides [aph(3')-VIa, ANT(3'')-IIa, aph(6)-Id, ANT(3'')-IIa, APH(3'')-Ib, aadA2, armA, aph(3')VIj, aph(3')-Ia, aadA1, aac(3)-Ia] and sulphonamides (sul1, sul2). Additionally, the 14s and A14 isolates carry resistance genes to macrolides, streptogramin B [msr(E), mph(E)], and tetracyclines (tetB, tetR). The genes involved in resistance to chloramphenicol, aminoglycosides, trimethoprim, sulphonamides, macrolides and tetracyclines were detected on MGE. Genes encoding heavy metal resistance to Cu (cutE), Co, Zn, Cd (czdABD), Cr (chrA) and As (ArsH, ACR3) were detected in all strains. All four strains harbor virulence markers associated with adherence, biofilm formation, enzyme and serum resistance, while some of them also contain genes involved in host immune system evasion (pgi, PMM, wza and weeH), iron uptake (entE, hemO) and regulation (abaIR). The 14s and A14 strains contain hemO (hemoxigenase) gene, which was associated with a hypervirulent phenotype of *A. baumannii* LAC.

Conclusions: The analyzed *A. baumannii* harbored between 23 and 28 antibiotic and heavy metals resistance genes, many of them located on MGE as well as, 3-11 virulence genes, an arsenal which explains their multi-drug resistance and capacity to persist and multiply in the human host, making them a serious threat for hospitalized patients.

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