Acinetobacter baumannii is recognized as an opportunistic nosocomial pathogen, mainly in immunocompromised patients being frequently associated with therapeutic failures, due to its multi-drug (MDR), extended-drug (XDR) or even pan-drug resistance (PDR) phenotypes. Carbapenemases were the antibiotics of choice for infections treatment caused by this organism, but resistance to carbapenems is becoming common, and very few therapeutic options remain. Mortality rates among patients associated with Carbapenem Resistant Acinetobacter baumannii (CRAB) isolates may facilitate the bla OXA23 dissemination. Our survey revealed a high drug resistance in A. baumannii isolates. Different plasmid groups containing CRAB isolates may facilitate the bla OXA23 dissemination.

**Keywords:** carbapenem resistance, virulence, community acquired, nosocomial infections

The acquisition of genes encoding aminoglycoside-modifying enzymes (AMES) has been a main cause of resistance to aminoglycosides in A. baumannii [8]. Different AME-encoding genes, such as aphA1, aphA6, aphA15, aacC1, aacC2, aacA4, aadB, aadA1, and aadA4, have been detected in clinical isolates of A. baumannii [8,9]. Many of these genes (for example, aac C1, aacA4, and aadA1) are located on class 1 integrons [10]. In contrast, the aphA1 and aphA6 genes have always been surrounded by IS elements, forming different composite transposon structures [7].

Numerous potential virulence factors have been revealed in A. baumannii strains, including biofilm formation [several factors contribute to biofilm formation such as the Csu pili [11] encoded by csuE gene, the autoinducer synthase AbaI, part of the quorum sensing (QS) system [12], the outer membrane protein A (encoded by OmpA gene) which facilitates the adhesion to host epithelial cells], complement resistance [13], iron acquisition characteristics, capsule, outer membrane protein phospholipases, alteration in penicillin-binding proteins [14]. Phospholipases C and D are responsible for epithelial cell invasion [15, 16]; the siderophore acinetobactin [17]; the polysaccharidic capsule [18]; and a penicillin-binding protein 7/8 [19] are important for...
survival and dissemination in human serum. Growth in serum has been demonstrated to upregulate iron acquisition systems, genes associated with epithelial cell adherence and DNA uptake, as well as numerous putative antibiotic efflux pumps, leading to increased antibiotic tolerance [20]. In addition, lipopolysaccharide (LPS) is an important cell envelope component, which influence the pathogenic potential of A. baumannii by the O-polysaccharide chain (O-antigen) [21].

Regarding A. baumannii infections the most predisposed are patients from ICU in which this pathogen may cause serious infection and, thus, contributes substantially to the considerable mortality of this population [22]. Although the attention of A. baumannii infections has been focused on hospitalized patients, there is another patient population that may be affected by this important pathogen, namely, patients in the community setting that have some form of morbidity, especially in the tropical and sub-tropical area [23].

Originally, we are interested in identifying the relationship between virulence and antimicrobial resistance in CRAB strains from both hospital settings and the community, the ARGs, their transfer and dissemination into the community.

**Experimental part**

**Material and methods**

The study included 93 recently isolated (Aug-Nov 2017) A. baumannii strains, which were isolated in majority from hospitalized patients (H) (n=75) and from CA infections (n=18). The hospital strains were identified by BD Phoenix and the CA ones by mass spectrometry using MALDI Biotyper and MicroScan Walk Away 96. Carbapenemases and virulence genes were searched by PCR.

**Antibiotic resistance**

The antibiotic susceptibility was determined by Kirby-Bauer standard disk diffusion method [using the antibiotics recommended by CLSI, 2017: meropenem (MEM), imipenem (IMP), ertapenem (ETP), cephalotin (CEF), ceftriaxone (CTX), cefuroxime (CXM), cefoxitin (FOX), ceftazidim (CAZ), aztreonam (ATM), cefepime (FEP), amoxicillin-clavulanic acid (AMC), piperacillin-tazobactam (PIP-TAZ), ciprofloxacin (CIP), levofloxacin (LEV) gentamycin (GEN), amikacin (AMK), nitrofurantoin (NIT), trimethoprim-sulfamethoxazole (SXT), tetracycline (TET), tigecycline (TIG) and colistin] and quality control was performed with Pseudomonas aeruginosa ATCC 27853 and automated methods (BD Phoenix and Vitek II).

**Evaluation of the soluble enzymatic factors**

The virulence phenotypes were investigated by performing enzymatic tests for the expression of the following soluble virulence factors: haemolysins, pore forming toxins (lecithinase, lipase), proteases (caseinase, gelatinase), amylase and aesculin hydrolysis.

**Genetic support of AR and virulence in CRAB**

The genetic support of the resistance (carbapenemases and aminoglycosides table 1), Plasmid analysis included identification of replica genes:19 PCR amplifications were devised to detect 27 replica genes, which were grouped into 19 homology groups (GRs) on the basis of their nucleotide sequence similarities (table 2), BIOPFILM biofilm producing virulence factors (table 3) and global lineage in CRAB (table 4) was investigated by simplex and multiplex PCR, using a reaction mix of 20μL (PCR Master Mix 2X, Thermo Scientific) containing 1μL of bacterial DNA extracted using the alkaline extraction method. In this purpose, 1-5 colonies of bacterial cultures were suspended in 1.5 ml tubes containing 20 μL solution of NaOH (sodium hydroxide) and SDS (sodium dodecyl sulphate). The following step was the addition of 180 μL of TE buffer (TRIS+EDTA) 1X and centrifugation at 13000 rpm for 3 min. All PCR reactions were performed using the Thermal Cycler machine Bio-Rad.

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**Table 1**

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<th>Target gene</th>
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Results and discussions

The antibiotic resistance profiles in H and CA A. baumannii isolates revealed high percentages of carbapenem-resistance in both H and CA isolates, i.e. imipenem (82.66%/77.77%), meropenem (84%/83.33%) as well as for SXT (85.33%/77.77%) and aminoglycosides (85.33%/66.66%). The ciprofloxacin resistance was close in both types of isolates (84%/83.33%) (fig. 1). A. baumannii has acquired a huge genetic repertoire via horizontal gene transfer that makes it virulent and resistant to any environmental pressures [30-33]. Antibiotic susceptibility testing in this study showed that all A. baumannii isolates were resistant to the commercially available antibiotics with the exception of colistin. Previously in Romania, Vaduva et al., revealed the presence of beta-lactamase producers nosocomial A. baumannii strains from Timisoara hospital and a very closer aminoglycosides resistance profile [34].

CRAB H and CA isolates revealed the intrinsic carbapenemase OXA-51 (58.6%/55.5%) and the acquired
carbapenemases OXA-23 (50%/55.5%), OXA-24 (26.6%/16.6%), IMP (26.66%/22.22%) and VIM-2 (1.33%/0%) (fig. 2, 3).

In Bucharest, one study performed on A. baumannii nosocomial strains recovered from clinical infections in patients hospitalized in ICU between 2001-2003 demonstrated the association of class 1 integrons with blaIPM-1, blaVIM-2, blaOXA-24 and blaOXA-25 genes [35]. In Iasi hospitals the presence of blaIMP-13 in nosocomial A. baumannii strains was revealed [36]. Data revealed by our research team (2012-2013) demonstrated that A. baumannii strains that were investigated harboured the class D carbapenemase OXA-23 [37]. Previous studies in Timisoara, Arad and Resita indicated that CHLD in A. baumannii is encoded by chromosomally - located blaOXA-23, with the insertion sequence ISAba1 detected upstream and the strains belonged to the ST2 and ST1 clones [6]. More recently one study from our department highlights a remarkable mobility for blaOXA-23-Tn2008 and surrounding structures (identified in plasmid or chromosome of different clones) and also describes for the first time the spread of Tnaph6-carrying pACICU2-like plasmids in A. baumannii in Europe [27]. A pilot study from three Romanian hospitals - Iasi and Targu-Mures (2014-2015) demonstrated the presence of carbapenemases OXA-23, OXA-24/72 in A. baumannii nosocomial isolates [38].

Mammina et al., in 2012 revealed the presence in a high percentage of blaOXA-23 gene in nosocomial CRAB isolated ICU patients in Palermo Italy and belonging to ST2 [39]. Very recently Petrova et al., demonstrated a higher prevalence of OXA-23 A. baumannii producers isolated from different Bulgarian hospitals between 2010-2014 but opposite with our results they didn’t observe the presence of OXA-24 and overexpression of OXA-51 in any of the analysed isolates [40].

In our study blaOXA-23 gene was identified in different plasmid types (GR2-Aci1, GR6-pACICU2).
The multidrug resistant profile of the isolates was also heightened by the presence of AMEs namely the phosphotransferase AphA6 (24%/16.6% of the strains), and acetyltransferases aacB (9.3%/5.5%). Nowak et al., in 2014 reported in MDR A. baumannii isolated in Poland the following aminoglycoside resistance genes: aphA1, aphA6, and aacC1 [41]. The genes encoding AMEs can be disseminated via integrons, and expression of AMEs enable bacteria to catalyze the modification of amino and hydroxyl groups on sugar moieties, such as aminoglycosides [42].

Carbapenem and aminoglycosides resistance has been associated to nonenzymatic mechanisms revealed by changes on the outer membrane proteins [ompA biofilm-associated to nonenzymatic mechanisms revealed by changes on the outer membrane proteins], mechanism [43] demonstrated also by different authors. The outer membrane protein A of A. baumannii represents one of the most abundant surface protein essential for this organism's high levels of intrinsic resistance to different antibiotics [45]. Several reports have been demonstrated that A. baumannii possesses Omp's which interfere with carbapenem resistance, for e.g. in 2002, Limansky et al. demonstrated that imipenem susceptibility to carbapenems and the presence of AMEs enable bacteria to catalyze the modification of amino and hydroxyl groups on sugar moieties, such as aminoglycosides [42].

Regarding the soluble virulence factors, the decreasing frequency expressed were lipase (94.66%/88.88%), amylase (92%/87.87%), DN-ase (60%/30%), caseinase (8.08%/5.05%); aesculin hydrolysis (6.06%/6.06%), ascullin hydrolisys (6.06%/6.06%) and lecinthinase (3.03%/7.07%) (Fig. 4).

OXA-51-like alleles corresponding to the two main sequence groups were identified as blaOXA-51 (66.66% of the analysed strains) and respectively, blaOXA-66 (38.39%) and revealed the corresponding type of ompA and csuE sequence grouping (Fig. 2, 3). There have been revealed a link between the production of some of the naturally occurring OXA-51/69-like oxacillinase carbapenem resistance in A. baumannii. Despite the relatively weak ability of these enzymes to hydrolyse carbapenems, it has been shown that these oxacillinase may sometimes be overexpressed, resulting in a decreased level of susceptibility to carbapenems and the presence of ISAba1element upstream of the blaOXA-51-like gene ([J. Turton, N. Woodford and T. Pitt, personal communication].

Conclusions

The significant levels of antibiotic resistance in CARB strains highlights the need for continuous surveillance and epidemiological studies, of not only hospital, but also CA isolates. The elucidation of the genetic context of resistance in CRAB isolates with different origins could reveal further clinically important associations, and help to better understand the interaction between antimicrobial resistance and virulence in A. baumannii.

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Abbreviation

CRAB - Carbapenem Resistant Acinetobacter baumannii
AMEs - aminoglycoside-modifying enzymes
H - hospitalized patients
CA - Community-acquired infections

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