Resistance Phenotypes of *Pseudomonas Aeruginosa* Strains of Human Origin in B – Lactamases

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**Abstract**

The use of β – lactam antibiotics is of utmost importance in medical practice. The natural resistance of *Ps. aeruginosa* strains to β-lactamases is important for clinical reasons, however, acquired resistance is very common (Pilly et al., 2006). Acquired resistance comprises either enzymatic mechanisms or non-enzymatic ones (Strateva T et al., 2009).

The aims is to identifying β-lactam profiles of resistance to *Ps. aeruginosa* strains and the last objective of this study is to evaluate the reliability and accuracy of the VITEK-2 Compact (Biome’rieux) automated identification and susceptibility testing system.

The batch studied included 793 multi-resistant strains of *Ps. aeruginosa*, which were isolated from the Institute of Cardiovascular Diseases in Iaşi during 2013 – 2014, the isolates being taken from sputa, urine, pus and blood. Those isolates have passed susceptibility test that resistant to one or more antibiotic from third generation cephalosporin and/or resistant to aztreonam and/or intermediate or resistant to one or more antibiotic from carbapenem class.

The results were interpreted with the help of the Vitek2 system, 61 beta-lactam resistance profiles being defined. Sputum is the primary source of isolates with almost 60%, the rest are from other sources i.e. urine, pus, blood, etc.

As a result of the investigations we carried out, out of the total of 793 strains isolated and identified as multi-resistant *Ps. aeruginosa*, 61 strains were confirmed as having beta-lactam resistance profile. The result of this study confirmed that anyone could be infected by β- lactams resistance profile regardless their age, gender, and clinical manifestation.

**Keywords:** *Pseudomonas aeruginosa*, β – lactamase, strains of human origin, VITEK® 2

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**INTRODUCTION**

β-Lactams are a group of antibiotics acting on the cell wall of a bacterial cell. These include the penicillins, cephalosporins, carbapenems and monobactems. These bind to and inhibit the carboxypeptidases and transpeptidases. All beta-lactam based on a common chemical structure: beta-lactam nucleus. From this nucleus there are four families: penicillins, cephalosporins or cephem, carbapenem, monobactams.

Beta- lactam have a synergistic effect when administered with aminoglycosides and have an additive effect when administered together with fluoroquinolones.

Resistance to beta-lactams can occur by three mechanisms: the target protein modification,
production of beta-lactam - especially observed in gram-negative bacteria - beta-lactamase is an enzyme which inactivates beta-lactam nucleus, decreased permeability of the outer membrane for Gram negative, so beta-lactam no longer have access to the internal wall. (Pilly et al., 2006)

Resistance to β-lactams has probably arisen throughout bacterial history but has become a useful and therefore selected trait since the β-lactam antibiotics came into clinical use.

Acquired resistances are related enzymatic mechanisms (penicillinases, cephalosporinases, ESBLs, metallo-enzymes) or non-enzymatic (impermeability, efflux and targets).

**MATERIALS AND METHODS**

There were studied strains of *Pseudomonas aeruginosa* isolated and identified during 2013-2014 in Iasi Cardiology hospital laboratory. The study group included 61 for phenotypic characterization resistant *Pseudomonas aeruginosa* strains of the Institute of Cardiovascular Diseases "Prof. Dr. G.I.M. Georgescu "Iași.

These strains came from urine, sputum, tracheal secretions, wounds, blood cultures.

Antibiotic sensitivity of strains included in the study were tested using automated systems 2 VITEK®.

Ensemble resistance phenotypes of *Pseudomonas aeruginosa* strains to β-lactams is summarized in Table 1:

**RESULTS AND DISCUSSIONS**

Between 2013 - 2014 the Institute of Cardiovascular Diseases "Prof. Dr. G.I.M. Georgescu "Iași were isolated and identified:

- 793 strains of *Pseudomonas aeruginosa* of which:

**Tab.1 The main resistance phenotypes of *Pseudomonas aeruginosa* strains to β-lactams**

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>Wild phenotype</th>
<th>Penicillins</th>
<th>CHN</th>
<th>ESBL</th>
<th>Carbapenemases</th>
<th>Efflux</th>
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<tbody>
<tr>
<td>Ticarcillin</td>
<td>S</td>
<td>R</td>
<td>R</td>
<td>R/R</td>
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<td>S</td>
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<tr>
<td>Tica-ac. clav</td>
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<td>R/S</td>
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<td>R</td>
<td>R</td>
<td>R/R</td>
<td>S</td>
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<tr>
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<td>S</td>
<td>S</td>
<td>R</td>
<td>R/S</td>
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<tr>
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<td>R/R</td>
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<td>R</td>
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<tr>
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<td>R</td>
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<td>Imipenem</td>
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<td>S</td>
<td>R</td>
<td>S/S</td>
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<td>Imipenem</td>
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**Fig. 1 Pseudomonas aeruginosa isolates from the total culture**
Ø Sputum: 3052 bacterial cultures - 227 strains of *Pseudomonas aeruginosa*
Ø Urinalysis: 3715 bacterial cultures - 331 strains of *Pseudomonas aeruginosa*
Ø Blood cultures: 784 bacterial culture - 70 strains of *Pseudomonas aeruginosa*
Ø Pus: 768 bacterial cultures - 165 strains of *Pseudomonas aeruginosa*

In this study we have identified 61 strains of *Pseudomonas aeruginosa* resistant strains being characterized these phenotypic test system using VITEK® 2 provides greater certainty of results, including:
Ø 19 strains show resistance phenotype of beta-lactam
Ø 2 strains acquired resistance phenotype type enzyme ESBL OXA
Ø 12 strains acquired resistance phenotype enzymatic: carbapenemases
Ø 8 strains acquired resistance phenotype enzymatic and non-enzymatic of waterproof type

**CONCLUSIONS**

- Phenotypic testing system using VITEK® 2 provides greater certainty of results and eliminating repetitive manual operations.
- The phenotypic confirmatory tests are highly sensitive and specific compared to genotypic confirmatory tests. However, there are a number of instances whereby the phenotypic confirmatory tests may be falsely positive or negative.
- The most common resistance phenotype in this study beta-lactam phenotype.
- The natural resistance of *Ps. aeruginosa* is important and acquired resistance are increasingly common. The bacteria may acquire additional resistance gene from the plasmid, transposon or phage (Jehl *et al.*, 2004).
- One additional important that contribute to the resistance of the strains of *Ps. especially aeruginosa* isolates from patients with cystic fibrosis (Hancock *et al.*, 1999) is its mode of growth in the lungs. The aggregates of bacteria in the lungs are surrounded by a layer of polysaccharide alginate (Nichols *et al.*, 1988).

. For this layer can bind cationic antibiotics such as aminoglycosides, restricting diffusion. These microcolonies or biofilms are extremely resistant to antibiotics, due to the mechanisms remain unclear.
- Resistance is mostly due to a combination of endogenous acquired beta-lactamases, along with natural up-regulated impermeability and efflux. (Livermore *et al.*, 2006)
- Many organisms now produce multiple beta-lactamases, which may reduce the effectiveness of beta-lactam / beta-lactamase inhibitor combinations.
- Antimicrobial resistance of the pathogens responsible for a majority of nosocomial infections continue to increase throughout the healthcare system. (Ciocan *et al.*, 2014)

**REFERENCES**

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