Occurrence of *bla* genes encoding carbapenem-resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii* from Intensive Care Unit in a tertiary care hospital

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**Abstract:**

**CONTEXT:** ICU shows increasing incidence of infection associated with the use of invasive procedures for the diagnostic purpose as well as the indiscriminate use of antibiotics. *Pseudomonas aeruginosa* and *Acinetobacter species* are “very successful” pathogen and the emergence of the Metallo-β-Lactamases (MBL) is becoming a therapeutic challenge.

**AIMS:** To isolate the Nonfermenting Gram negative bacilli from the ICU samples. To identify the metallo betalactamase producers and to detect the *bla* gene presence among the *Pseudomonas aeruginosa* and *Acinetobacter baumannii*.

**SETTINGS AND DESIGN:** The Nonfermenting Gram negative bacilli isolates from the ICU samples were taken over for 5 years (2009-2014) in a tertiary care hospital.

**METHODS AND MATERIALS:** The isolates of *Pseudomonas species* and *Acinetobacter species* were confirmed by API analyser and processed according to standard procedures. Detection of the MBL producers were done by E strip method and subjected for *bla* gene detection by PCR method.

**RESULTS:** In our study a total of 195 isolates of NFGNB were obtained from various ICU. Of these MBL producers, 26 % were *Pseudomonas aeruginosa* and 25 % were *Acinetobacter baumannii*. The subtypes of *bla*VIM MBL producing *P.aeruginosa* were 26%.The predominant gene coding for MBL activity in *A.baumannii* were found to be *bla*OXA gene 11.9%. The gene accession numbers were KF975367, KF975372.

**CONCLUSIONS:** We have to control the development and dissemination of these superbugs among the ICU’s.

**Key words:** *Acinetobacter baumanni*, *bla* genes, ICU, Metallo-β-lactamases, *Pseudomonas aeruginosa*

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**Introduction**

Isolation of nonfermenters from the clinical specimens obtained from Intensive Care Unit (ICU) shows that increasing incidence of infection associated with the use of invasive procedures, indiscriminate use of antibiotics, inadequate sterilization, and immune compromised condition due to lifestyle disease have also contributed.[1]

Among the nonfermenters, *Pseudomonas aeruginosa* is inherently resistant and *Acinetobacter* species capable of surviving in various environmental conditions are adapted at acquiring resistance.[2,3] The digestive tracts of patients within ICUs often serve as reservoirs for multidrug-resistant (MDR) isolates.[4,5]

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P. aeruginosa resistance is a global disease burden[6] and it is a therapeutic challenge.[8] The Acinetobacter baumannii complex is emerging multidrug resistant nosocomial and community acquired pathogen. The incidence of infection by these species among the patients receiving the mechanical ventilation are quite increasing.[8] These organisms are “very successful” pathogen which possesses both acquired and intrinsic mechanisms of resistance to various classes of antibiotics.[9-11]

Infections in the ICU patients were commonly associated with ventilator-associated pneumonia, urinary tract infection, and bacteremia caused by MDR organism Gram-negative bacilli with increasing morbidity and mortality.[12,13] The emergence of the metallo-β-lactamases (MBL) is becoming a therapeutic challenge.[12] Antimicrobial resistance pattern has emerged as an important determinant of the outcome for patients in the ICUs.[14]

In our study, drug-resistant isolates in the ICUs were detected and the gene encoding carbapenem resistance in P. aeruginosa and Acinetobacter baumannii was identified. The resulting sequences were compared with those available in GenBank.

**Methods**

All the suspected colonies of the NFGNB were identified by Gram staining, colony characteristics, oxidase test, motility, and standard biochemical reactions, and further confirmation of the species was carried out by API analyzer. The study was carried out in a tertiary care hospital (2009–2014). All the organisms identified were tested for the susceptibility according to the standard Clinical and Laboratory Standards Institute guidelines.[15] The sensitivity pattern of first- and second-line drugs was tested.

For *Pseudomonas* species, the following 15 drugs were used: amikacin (Ak-30 μg), aztreonam (Az-30 μg), colistin (Cl-10 μg), ciprofloxacin (Cip-5 μg), ceftazidime (Caz-5 μg), cefepime (Cpm-5 μg), carbenicillin (Cb-100 μg), gentamicin (G-10 μg), imipenem (Im-10 μg), meropenem (Mr-10 μg), netilmicin (Net-30 μg), ofloxacin (Of-5 μg), piperacillin-tazobactam (Pit-100 μg/10 μg), polymyxin B (Pb-300 units), tobramycin (Tb-10 μg).

For *Acinetobacter* species, amikacin (Ak-30 μg), cefepime (Cpm-5 μg), ceftazidime (Caz-5 μg), ciprofloxacin (Cf-5 μg), cefotaxime (Ce-5 μg), colistin (E strip), cotrimoxazole (Cot-5 μg), gentamicin (G-10 μg), imipenem (IMP-10 μg), meropenem (Mr-10 μg), piperacillin-tazobactam (Pt-100 μg/10 μg), and polymyxin B (E strip) were used, and in case of urine samples, nitrofurantoin (Nit-300 μg) disks were used.

The study was confined to the MBL-producing *P. aeruginosa* and *A. baumannii* species. The antibiotic discs used in our study were purchased from HiMedia. The E strip was purchased from HiMedia, Biomerieux, and Radianz biotechnologies. Screening for MBL production was done in imipenem-resistant isolates by the E strip method using the ceftazidime and ceftazidime + ethylendiaminetetraacetic acid.[16]

The MBL-producing resistant strains of *P. aeruginosa* were screened for the *bla* genes – *bla* 

| Table 1: The primers used for bla gene detection in *Pseudomonas aeruginosa* |
|---------------|-------------------|-----------------|
| Gene | Primers | Product size |
| blaVIM | Forward primer | 5’TCT ACA TGA CCG CTG CTG TC-3’ | 748 bp |
| blaVIM | Reverse primer | 5’TGT GCT TTA ACA ACG TGC GC-3’ | 587bp |
| blaIMP | Forward primer | 5’CCA GAT TTA AAA GAA GAG AAG CT-3’ | 522 bp |
| blaIMP | Reverse primer | 5’TGG CCA AGC TTC TAC ATT TCG T-3’ | 989bp |
| blaNDM | Forward primer | 5’GGT TTT GGC GAT CTG GTC CT-3’ | 522 bp |
| blaNDM | Reverse primer | 5’CGG AAT GGC TCA CGA TCA TCC GC-3’ | 989bp |
| blaKPC | Forward primer | 5’GCT ACA CCT AGC TCC ACC TTC-3’ | 442bp |
| blaKPC | Reverse primer | 5’ACA GTT GTT GGT AAT CCA TGC-3’ | 442bp |

Table 2: The primers used for bla gene detection in *Acinetobacter baumannii* |

| Gene | Primers | Product size |
| blaVIM | Forward primer | -5’GTCTTGGACAACGTTGTC-3’ | 442 bp |
| blaVIM | Reverse primer | -5’TCCACGCATTTCATGGCA-3’ | 220 bp |
| blaIMP | Forward primer | -5’TTCAGCAGTCTGATTCA-3’ | 220 bp |
| blaIMP | Reverse primer | -5’ACAGCTCACAACAAAGTGC-3’ | 220 bp |
| blaNDM | Forward primer | -5’AGTATGGGGCTTGTGCT-3’ | 398bp |
| blaNDM | Reverse primer | -5’AATACCTGATGCATTTG-3’ | 660 bp |
| blaKPC | Forward primer | 5’GTT GCA TGC CGG GTG AAA TTC T-3’ | 660 bp |
| blaKPC | Reverse primer | 5’ATG CTG GCC TTG GGG AAC G-3’ | 400 bp |

Internal control
at 94°C for 2 min, followed by 30 amplifications cycles of 94°C for 1 min, 55°C for 1 min, and 72°C for 1 min 30 sec, with final extension step of 72°C for 5 min. The cycling parameters for the bla\textsubscript{IMP, VIM, NDM, OXA} genes were as follows: initial denaturation: 94°C for 3 min, denaturation: 94°C for 1 min, annealing: 58°C for 1 min 35 cycles, extension: 72°C for 1 min, final extension: 72°C for 5 min. After screening for the MBL, the positive PCR products were sequenced. Sequencing the amplified products, the BLAST results were analyzed.

**Results**

The nonfermenters isolated from ICU were found to be notorious as there were possibilities of drug-resistant strains being horizontally spread among the patients. In our study, a total of 195 isolates of NFGNB were obtained from various ICUs. Among them, 61 (31.2%) were *Pseudomonas* spp and 134 (68.8) were *Acinetobacter* spp. Among the 84 isolates of NFGNB, 32 (38%) were *P. aeruginosa* and 61.9% *A. baumannii* were isolated from surgical ICU. Distribution of NFGNB – *P. aeruginosa* and *A. baumannii* in different ICUs is shown in Table 3. Among 61 *P. aeruginosa* from ICU patients, 19 (31.1%) were from males and 42 (68.8%) were from females. Distribution of *P. aeruginosa* from ICU among different sexes is shown in Chart 1. Among 134 *A. baumannii* from ICU patients, 89 (66.4%) were from males and 45 (33.5%) were from females [Chart 2].

Among 195 NFGNB isolates from ICU, 89 (45.6%) were drug resistant. Out of these, 26 (13.33%) were *P. aeruginosa* and 63 (32.3%) were *A. baumannii*. Overall, the MDR isolates from ICU were 33.33%. The MBL producers from ICU were 49 (25.12%) [Table 4]. Of these MBL producers, 16 (26.22%) were *P. aeruginosa* and 33 (24.62%) were *A. baumannii* [Table 5 and Chart 3].

The maximum numbers of MBL producers were in surgical ICU followed by general ICU. Among ICUs, 6.1% of isolates were from pediatric ICU and one isolate of *P. aeruginosa* was MBL producer [Table 6]. Among the MBL producers in ICU, *P. aeruginosa* was obtained from

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**Table 3: Distribution of *P. aeruginosa* and *A. baumannii* in different ICUs**

| Source       | No of isolates | *P. aeruginosa (%) | *A. baumannii (%) |
|--------------|----------------|--------------------|-------------------|
| Surgical ICU | 84             | 32 (38)            | 52 (61.9)         |
| General ICU  | 57             | 17 (29.8)          | 40 (70.1)         |
| Paediatric ICU | 12         | 9 (75)             | 3 (25)            |
| Neuro ICU    | 35             | 1 (2.8)            | 34 (97.2)         |
| Neonatal ICU | 7              | 2 (28.5)           | 5 (71.4)          |
| Total ICU    | 195            | 61                 | 134               |

**Table 4: Drug resistance in ICU isolates**

| Isolates from ICU (n) | Drug resistant isolates | Multidrug resistant isolates | Metallo beta lactamase producers |
|-----------------------|-------------------------|-----------------------------|---------------------------------|
| *P. aeruginosa* (61)  | 26                      | 23                          | 16                              |
| *A. baumannii* (134)  | 63                      | 42                          | 33                              |
| Total (195)           | 89                      | 65                          | 49                              |

**Table 5: Showing MBL positive by Estrip method**

| Method (E strip–MIC E strip) | *P. aeruginosa* (n=61) | *A. baumannii* (n=63) |
|------------------------------|------------------------|------------------------|
| CDT - Imp, Imp + EDTA        | 16                     | 33                     |

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![Chart 1](image1.png)

*Chart 1:* Distribution of *Pseudomonas aeruginosa* from Intensive Care Unit among different sexes

![Chart 2](image2.png)

*Chart 2:* Distribution of *Acinetobacter baumannii* from Intensive Care Unit among different sexes
11 males and 5 females and *A. baumannii* was isolated from 13 males and 20 females.

MDR and MBL producers were more from general ICU and surgical ICU. Among the 63 drug-resistant *A. baumannii*, 42 (66.6%) were multidrug resistant and 33 (52.3%) were MBL producer.

Clinical sources of the MBL-producing *P. aeruginosa* are shown in Table 7. The subtypes of *bla* VIM-MBL-producing *P. aeruginosa* were 26% and strains of *P. aeruginosa* from ICU were negative for other *bla* KPC, NDM, IMP genes. Distribution of all three subtypes of MBL-producing *P. aeruginosa* was as follows: 13.1% *bla* VIM-4, 9.8% *bla* VIM-5, and 3.2% *bla* VIM-38 strains [Chart 4].

In MBL-positive *A. baumannii*, *bla* VIM gene was demonstrated in 4.4% strains, *bla* OXA gene was seen in 11.9%, and *bla* IMP gene was seen in 5.2%. Thus, the predominant gene coding for MBL activity was found to be OXA. Distribution of genes responsible for MBL activity in *A. baumannii* and its clinical source is shown in Table 8. The resulting sequences were compared with those available in GenBank (www.ncbi.nih.gov/BLAST) and the gene accession numbers were KF975367, KF975372.

### Discussion

There is an increase in infection caused by the MBL-producing NFGNB in the ICUs, along with the significant morbidity and mortality. The incidence of infection in ICUs, especially the nosocomial infections, is a rising trend with a spectrum of clinical conditions. They may be in the range from impaired immunity, lapse in the sterilization, use of various invasive devices, and procedure to indiscriminate use of antibiotics.

A study by Aliskan *et al.*[24] showed that there was a decrease in susceptibility pattern of *A. baumannii* and *P. aeruginosa* isolates from the ICU samples. In our study, maximum *P. aeruginosa* and *A. baumannii* were from tracheal aspirates, followed by wound swab which was in concordance with study of Jaggi *et al.*[25]

In a study by Orrett, 17.3% of *P. aeruginosa* were from ICU.[26] The prevalence of *Acinetobacter species* from various parts of our country was 3%,[27] 4.5%,[28] and 9.6% in West Bengal.[29] In our study, the prevalence of *P. aeruginosa* (31.2%) and *A. baumannii* (68.8%) in ICU was higher when compared with above study. Among the
$A.\ baumannii$ strains isolated from ICU, 65%–70% were resistant and they were not in concordance with our study\cite{33,30,31} which is higher when compared to our study.

The percentage of MDR $A.\ baumannii$ isolates increased from 4% to 55% and 2%–8% in $P.\ aeruginosa$ isolates. According to Yan et al., 56.7% and 58.3% of $P.\ aeruginosa$ were found to be imipenem resistant.\cite{33,32}

Many studies have reported <50% of resistance to imipenem and meropenem in $P.\ aeruginosa$. Imipenem resistance according to Livermore\cite{33} was 77.5% and Lone et al.,\cite{34} was 25.6%. Tan\cite{35} reported that 9.6% carbapenem-resistant $P.\ aeruginosa$ and 27.2% carbapenem-resistant $P.\ aeruginosa$ were from ICU reported by Hsu et al.,\cite{36} In our study, carbapenem-resistant $Acinetobacter\ spp.$ isolated from ICU were 25% and lesser than the resistance pattern (69%) reported by Tan.\cite{33}

A study by Hsu et al.,\cite{36} showed that carbapenem resistance of $Acinetobacter$ was 49.6%. Lagatolla et al.\cite{37} showed that 70% of carbapenem-resistant $P.\ aeruginosa$ were MBL producers. A study by Kabbaj et al.\cite{38} showed that, among 57.4% imipenem-resistant isolates of $Acinetobacter\ baumannii$, 74% were MBL producers and in concordance with our study. An Indian study stated that MBL producers among the $A.\ baumannii$ were 70.9%,\cite{39} and another study reported that 21%\cite{40} of $A.\ baumannii$ were MBL producers.

Tanzinah Nasrin showed the high level of MBL producers isolated from ICU unlike our study. Studies from the Indian subcontinent have shown the $bla_{IMP}$ gene carried by meropenem-resistant isolates.\cite{41} Our study confirmed the presence of $bla$ gene ($bla_{VIM}$ 26% and $bla_{OXA}$ 12%) among the isolates of $P.\ aeruginosa$ and $A.\ baumannii$ from the ICU samples and comparable with the study of Gautam et al.,\cite{30} 25% prevalence of NDM-1 $A.\ baumannii$ in ICU isolates.

**Conclusion**

We have to control the development and dissemination of these superbugs among the ICUs. Insight into the incidence of these superbugs alarms the need of every institution to have the interventional strategies to prevent these infections. The prevalence in ICU emphasizes the need for early detection of beta-lactamas-producing organisms.

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**Conflicts of interest**

There are no conflicts of interest.

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