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Bacteriological Profile of Non-Fermenting Gram Negative Bacilli and its Antibiogram in Tertiary Care Hospital, Calicut, India

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A B S T R A C T

Non-fermenting Gram-negative bacilli (NFGNB) have emerged as a major cause of healthcare-associated infections and are innately resistant to many antibiotics. High intrinsic resistance of NFGNB to antimicrobial compounds makes the treatment caused by them difficult and expensive. To identify and determine the antibiogram of Nonfermenting gram negative bacilli isolated in clinical samples and to compare the its pattern over a period of 2 years. This ambidirectional study was done at our Department of Microbiology Aster MIMS, Calicut. NFGNB were isolated from a variety of clinical specimens, plated on blood agar and MacConkey agar and incubated at 37°C for 18–24 h under aerobic conditions. Appropriate biochemical tests were done to identify the organisms isolated. Antibiotic susceptibility test was performed using the modified Kirby–Bauer disc diffusion method using commercially available discs on Mueller–Hinton agar. Blood culture was done by automated blood culture system, (BacT/Alert 3 D) and identification and antibiotic susceptibility of non-fermenting gram-negative bacilli was done by VITEK 2 Compact System**.** Out of 28162 clinical samples, 2148 (1109 in year 2023 and 1038 in year 2024) (7.6%) yielded NFGNB. *Acinetobacter baumanni* was the most common NFGNB, isolated in 965/2148 (44.9%) samples which were susceptibile to colistin (100%) and tigecycline (66.9%) , followed by Pseudomonas aeruginosa in 700/2148 (32.5%) susceptible to colistin (98.2%) and amikacin (75.7%) and a total of 965/2148 (44.9%) carbapenem-resistant *Acinetobacter baumannii* (CRAB) and 700/2148 (32.5%) carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) was detected in the study. This study revealed a significantly high prevalence of non-fermenting Gram-negative bacilli (NFGNB), with *Acinetobacter baumannii* and *Pseudomonas aeruginosa* being the most frequently isolated species. The high rates of. multidrug-resistant *A. baumannii* and *P. aeruginosa* underscore a growing concern regarding the rapid emergence and spread of antimicrobial resistance in the region. These findings reflect the rising threat of multidrug resistance among NFGNB and emphasize the urgent need for enhanced antimicrobial stewardship, infection control, and routine resistance surveillance to contain their spread and preserve treatment efficacy.

Introduction

Non-fermentative gram-negative bacilli (NFGNB) are a group of aerobic, non–spore-forming rod-shaped bacteria that do not relay on carbohydrates for energy through fermentation, instead relying on alternative metabolic pathways. These organisms are able to induce a wide variety of infections, ranging from mild surface infections to severe, deep-seated, and systemic infections. They primarily affect those with impaired immunity, including those with neutropenia, cystic fibrosis, patients on mechanical ventilation, those with indwelling medical devices, and individuals undergoing invasive diagnostic procedures. [1-2]

NFGNB were previously considered as non-pathogenic or contaminant but in past few years they have become serious threat to the society as a result of their common occurrence and drug resistance.

In recent years, initiation of antibiotic therapy based on clinical presentation, combined with a lack of robust, evidence-based data has contributed to the rise of NFGNB as significant pathogens in clinical settings. These organisms now represent approximately 12–15% of bacterial isolates identified from clinical specimens.

Their natural resistance to many commonly used disinfectants and they can adhere to and persist on various surfaces have played a major role in their emergence as prominent hospital-acquired pathogens. Although typically regarded as saprophytes and generally harmless commensals, NFGNB are increasingly being recognized for their clinical importance [3]

In 2017, the CDC recorded 32,600 instances of multidrug-resistant *Pseudomonas aeruginosa* infections among admitted individuals in the U.S., resulting in 2,700 fatalities [4].

Likewise, when *Acinetobacter baumannii* becomes resistant to carbapenems, it typically develops resistance to the majority of other antibiotics as well, significantly limiting available treatment options [5]

Recent reviews of the literature indicate that these pathogens are increasingly connected to serious, life-threatening infections, including septicemia, pneumonia, urinary tract infections, meningitis, wound infections, ventilator-associated pneumonia (VAP), surgical site infections, and osteomyelitis [6].

This group includes four primary bacterial species: *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, and *Burkholderia cepacia* [7]. In the past, infections caused by ria NFGNB were managed using carbapenems as the treatment of last resort. However, cases of carbapenem-resistant NFGNB have recently been documented in multiple regions around the world [8]. Owing to their exceptional ability to adapt and their wide range of both intrinsic and acquired resistance mechanisms, these bacteria frequently show resistance to several major classes of antibiotics, significantly restricting treatment options [7]. As a result, they pose a serious global health threat by increasing patient morbidity and mortality rates, prolonging hospital stays, and driving up healthcare costs.

While colistin and polymyxin B continue to play an essential role as salvage treatments or when alternative therapies are lacking, several new antimicrobial agents have recently emerged or are anticipated to be introduced soon that are likely to supplant traditional polymyxins as the preferred first-line options for managing infections caused by carbapenem-resistant non-fermenting Gram-negative bacteria.[9]

Extended hospitalization, use of range of antibiotics, and underlying patient conditions are key factors influencing clinical outcomes.

Widespread antibiotic use has led to resistance in many of these organisms, rendering commonly prescribed antibiotics ineffective and leading to treatment failures..

This study aims to recover and characterize NFGNB and assess their antibiotic susceptibility patterns in a tertiary care teaching hospital. Additionally, the study examines the trends in bacteriological profiles and antimicrobial resistance of NFGNB over a two-year period.

Materials and Methods

Specimen

Blood
Urine
Respiratory samples (Sputum, Bronchial wash, BAL, ET Aspirate)
Body fluids
Pus samples (Aspirated pus, Pus swab)
Tissue

Specimen Processing

Samples were collected in appropriate specimen containers using standard precautions, properly labeled and transported to the Microbiology laboratory.

Specimens are inoculated in to suitable culture media and incubated at 37°C for 48 hours.

For blood and body fluids BACT/ALERT 3D was used for incubation.

Bacterial identification is carried out by standard microbiological techniques.

The isolates which were Non lactose fermenting were further processed.

VITEK 2 System is employed in identification and susceptibility testing of isolates.

Bacterial isolates were also subjected to antibiotic susceptibility testing by employing the Kirby Bauer disc diffusion technique according to Clinical and Laboratory Standards Institute (CLSI) Guidelines M100 34thedition**.**

Results and Discussion

A total of 28,162 clinical specimens were received by the Microbiology Laboratory over a two-year period 13,927 in 2023 and 14,235 in 2024. In 2023, 1,109 NFGNB isolates were obtained, yielding an isolation rate of 8.0%, while in 2024, 1,038 isolates were recovered, corresponding to a slightly lower rate of 7.3%

In 2023, of the 1,038 NFGNB isolates, respiratory samples represented 478 (43.1%) of the cases, followed by pus samples at 220 (19.8%), urine cultures at 200 (18.0%), blood cultures at 183 (16.5%), and body fluids at 29 (2.6%). In 2024, among the 1,038 NFGNB isolates, respiratory samples accounted for 366 (35.3%), pus samples were 210 (20.2%), urine cultures were 209 (20.1%), blood cultures were 220 (21.2%), and body fluids 34 (3.3%).

From the graph *Acinetobacter baumannii* was isolated in 535 samples (48.24%) and from 430 samples (41.4%) followed by *Pseudomonas aeruginosa* in 362 samples (32.64%) and from 338 samples (32.5%), *Elizabethkingia meningoseptica* in 44 samples (3.97%) and from 17 samples (1.6%) *Burkholderia cepacia* in 40 samples (3.61%) and 89 samples in 2024 (8.6%) , *Chryseobacterium indologens* in 35 samples (3.16%) and 45 samples (4.3%), *Stenotrophomonas maltophilia* in 27 samples (2.4%) and 29 samples (2.8%), *Burkholderia pseudomallei* in 12 samples (1.08%) and 11 samples (1.1%). *Sphingomonas paucimobilis* in 10 samples (0.90%) and 14 samples (1.3%) in 2023 and 2024 respectively. Other NFGNB obtained were (*Acinetobacter lwoffii, Achromobacter xylosoxidans, Ochromobacter anthropic, Pseudomonas fluorescens, Ralstonia mannitolilytica, Pseudomonas putida, Pseudomonas oryzihabitans, Acinetobacter ursingii, Brevundimonas diminuta, Pandoraea species, Acinetobacter junii, Ralstonia insidiosa, Myroides species, Shewanella putrefaciens, Rhizobium radiobacter, Roseomonas gilardii, Chryseobacterium gleum, Pseudomonas mendocina, Ralstonia pickettii, Cupriavidus pauculus, Delftia acidovorans*)

Location Wise Data of NFGNB 2023&2024

The above data shows the most common location of isolation of NFGNB was from IP (61.8%) followed by MDICU (27.3%).

The highest number of cases was observed in the age group above 61 years, followed by the group aged 51-60 years.

Sensitivity Pattern NFGNB 2023 and 2024

The data shows the sensitivity pattern of *Acinetobacter baumanni* , which shows 100% sensitivity to colistin in 2023 and 99.6% in 2024, followed by tigecycline (61.8% in 2023 and 66.9% in 2024),minocycline (56.8% in 2023 and 60.6% in 2024) and shows reduced sensitivity to gentamicin (37.4%), cefoperazone-sulbactam combination (36.2%), amikacin (36.5%), ciprofloxacin (35.5%), and imipenem (26.9%)

This graph shows the antibiotic sensitivity pattern of *Pseudomonas aeruginosa* which shows 99.4% sensitivity to colistin in 2023 and 98.2% in 2024 followed by amikacin (72.4% and 75.7%) cefepime (66.0% and 69.2%) piperacillin-tazobactum (63% to 69.2%), ceftazidime (66.0% and 67.8%), imipenem (63.8% to 67.2%), ciprofloxacin (62.7% to 67.5%), and gentamicin (63.5% to 57.4%) in 2023 and 2024 respectively.

The graph shows the antibiotic susceptibility pattern of *Burkholderia cepacia* were it shows 92.5% and 94.4%

sensitivity to meropenem , followed by ceftazidime (95% and 93.3%), cotrimoxazole (90% and 93.3%) in 2023 and 2024 respectively, also shows a decreased sensitivity to chloramphenicol. The graph shows sensitivity pattern of *Burkholderia pseudomallei* were it is 100% to cotrimoxazole and meropenem in 2023 and 2024 respectively. Here it shows a decreased sensitivity towards imipenem, ceftazidime, and doxycycline.

The graph represents the sensitivity pattern of *Stentrophomonas maltophilia* were it shows 96.3% and 82.8% sensitivity to Minocycline followed by cotrimoxazole (96.3% and 79.3%) levofloxacin (92.6% and 75.9%) in 2023 and 2024 respectively. A decreased pattern of sensitivity was observed in all the antibiotics.

This graph shows the sensitivity pattern of *Elizabethkingia meningoseptica* were it shows 100% sensitivity towards minocycline in both the years followed by cotrimoxazole (93.2%), levofloxacin (68.2%) in 2023 whereas in 2024 a decreasing pattern of sensitivity was shown by cotrimoxazole (52.9%).

The graph shows 100% sensitivity of *Chryseobacterium indologenes* to minocycline in 2023 and 93.3% 2024, followed by cotrimoxazole 81.8% and 100%, levofloxacin 65.7% in 2023 and 2024 respectively.

This graph shows the sensitivity pattern of *Sphingomonas paucimobilis* were it shows 100% sensitivity towards amikacin followed by gentamicin (90% and 100%), cotrimoxazole (60% and 100%), a decreased sensitivity seen in meropenem (100% and 71.4%).

In 2023, among 362 *Pseudomonas aeruginosa* isolates, 114 (31.4%) were identified as carbapenem-resistant. In 2024, 100 out of 338 *P. aeruginosa* isolates (29.6%) were classified as CRPA. Colistin exhibited complete effectiveness against all CRPA isolates.

Regarding *Acinetobacter baumannii*, 535 isolates were recorded in 2023, of which 372 (69.5%) were found to be carbapenem-resistant. In 2024, 287 out of 430 isolates (66.7%) were reported as CRAB.

This study was conducted to evaluate the incidence of non-fermenting gram negative bacilli in hospitalized patients and to know their antibiotic sensitivity pattern.
In the present study Respiratory samples accounted for the largest proportion of NFGNB isolates 43.1% in 2023 and 35.3% in 2024 followed by pus samples (19.8% and 20.2%, respectively). These findings are in line with the study by Santhosh Kumar Yadav *et al.,* which reported the highest isolation from lower respiratory tract samples (43.0%), followed by pus samples (24.6%). [(10)] Notably, a significant decrease in the proportion of isolates from respiratory samples was observed in 2024 compared to the previous year.

Over a two-year period, the Microbiology Laboratory received a total of 28,162 clinical specimens 13,927 in 2023 and 14,235 in 2024. In 2023, 1,109 NFGNB isolates were obtained, resulting in an occurrence rate of 8.0%. In contrast, 1,038 isolates were recovered in 2024, reflecting a modest decrease in the isolation rate to 7.3%. These findings are consistent with previous studies by Abhishek Mehta *et al.,* Rajesh Bansal *et al.,* and Shushitha T. S. *et al.,* which reported isolation rates of 8.2%, 7.84%, and 7.14%, respectively [(11–12) (14).]

The current analysis reveals, a decline of 0.7% in the isolation rate was observed in 2024 compared to 2023. In contrast, studies conducted by Benachinmardi *et al.,* and Malini *et al.,* reported significantly lower NFGNB positivity rates of 3.5% and 4.5%, respectively [(13) (3)]. Such variations in the prevalence of NFGNBs across different studies are likely influenced by local epidemiological factors, infection control practices, patient demographics, and antimicrobial usage patterns.

The commonest isolated strains in this study were *Acinetobacter baumannii* (48.2% and 41.4%), followed by *Pseudomonas aeruginosa* (32.6% and 32.5%) in 2023 and 2024 respectively, correlates with the data published Mandira sarkar et al and Ranjan Kumar et al where the commonest isolates where *Acinetobacter baumannii* (51.34% and 48.78%) and *Pseudomonas aeruginosa* (42.09 % and 37.71 %) respectively. [(15-16)]

In this research, the incidence of *Elizabethkingia meningoseptica* decreased from 4% in 2023 to 1.6% in 2024. The occurrence of *Burkholderia cepacia* rose from 3.6% in 2023 to 8.6% in 2024, while *Chryseobacterium indologens* varied from 3.2% in 2023 to 4.3% in 2024. *Stenotrophomonas maltophilia* was observed at 2.4% in 2023 and 2.8% in 2024, and *Burkholderia pseudomallei* was isolated at 1.1% in both years. These non-fermenters, though rare, remain significant in clinical samples.

Table.1 Clinical sources of various NFGNB isolates

NFGNB Isolated from Clinical Samples 2023 - 2024				
	2023		2024	
		%		%
Respiratory samples	478	43.1	366	35.3
Pus samples	220	19.8	210	20.2
Urine	200	18.0	209	20.1
Blood	183	16.5	220	21.2
Body fluids	29	2.6	34	3.3
NFGNB isolated	1109	100	1038	100

Table.2 Total number of NFGNB isolated from inpatients 2023 & 2024

Name of Organisms	2023N	2023%	2024 N	2024%
Acinetobacter baumannii	535	48.2	430	41.4
Pseudomonas aeruginosa	362	32.6	338	32.5
Elizabethkingia meningoseptica	44	4.0	17	1.6
Burkholderia cepacia	40	3.6	89	8.6
Chryseobacterium indologens	35	3.2	45	4.3
Stenotrophomonas maltophilia	27	2.4	29	2.8
Burkholderia pseudomallei	12	1.1	11	1.1
Sphingomonas paucimobilis	10	0.9	14	1.3
Acinetobacter lwoffii	7	0.6	7	0.7
Achromobacter xylosoxidans	5	0.5	12	1.2
Ochromobacter anthropi	5	0.5	9	0.9
Pseudomonas fluorescens	4	0.4	0	0.0
Ralstonia mannitolilytica	4	0.4	9	0.9
Pseudomonas putida	3	0.3	5	0.5
Pseudomonas oryzihabitans	2	0.2	0	0.0
Acinetobacter ursingii	2	0.2	7	0.7
Brevundimonas diminuta	2	0.2	1	0.1
Pandoraea species	2	0.2	0	0.0
Acinetobacter junii	2	0.2	1	0.1
Ralstonia insidiosa	2	0.2	1	0.1
Myroides species	1	0.1	0	0.0
Shewanella putrefaciens	1	0.1	0	0.0
Rhizobium radiobacter	1	0.1	5	0.5
Roseomonas gilardii	1	0.1	3	0.3
Chryseobacterium gleum	0	0.0	2	0.2
Pseudomonas mendocina	0	0.0	1	0.1
Ralstonia pickettii	0	0.0	1	0.1
Cupriavidus pauculus	0	0.0	1	0.1
Delftia acidovorans	0	0.0	1	0.1

Table.3 Location wise data of NFGNB 2023 and 2024

Location	N	%
IP	1328	61.8
MDICU	587	27.3
NSICU	78	3.6
PCICU	39	1.8
PICU	37	1.7
MOTICU	29	1.4
NICU	25	1.2
CICU	18	0.8
CSICU	7	0.3

Table.4 Sensitivity pattern of *Acinetobacter baumanni*

Antibiotics	2023 (%)S	2024 (%)S
Amikacin	34.9	36.5
Cefepime	29.6	26.5
Cefepime Tazobactum	26.7	20.2
Cefoperazone Sulbactum	38.3	36.2
Cefriaxone	7.6	5.8
Ciprofloxacin	37.3	35.5
Cotrimoxazole	41.4	38.8
Gentamicin	34.9	37.4
Imipenem	30.2	26.9
Levofloxacin	36.8	40.2
Meropenem	30.6	29.7
Piperacillin Tazobactum	31.9	29.0
Doxycycline	35.3	29.5
Minocycline	56.8	60.6
Colistin	100.0	99.6
Tigecycline	61.8	66.9

Table.5 Sensitivity pattern of *Pseudomonas aeruginosa*

Antibiotics	2023 (%)S	2024 (%)S
Amikacin	72.4	75.7
Aztreonam	64.4	58.6
Cefepime	66.0	69.2
Cefepime+Tazobactam	65.4	69.4
Cefoperazone+Sulbactam	59.4	67.5
Ciprofloxacin	62.7	67.5
Gentamicin	63.5	57.4
Imipenem	63.8	67.2
Levofloxacin	61.9	67.2
Meropenem	64.9	69.2
Piperacillin+Tazobactam	63.0	69.2
Ceftazidime	66.0	67.8
COLISTIN	99.4	98.2

Table.6 Sensitivity pattern of *Burkholderia cepacia*

Antibiotics	2023 (%)S	2024 (%)S
Meropenem	92.5	94.4
Levofloxacin	72.5	71.9
Cotrimoxazole	90	93.3
Minocycline	77.5	80.9
Ceftazidime	95	93.3
Chloramphenicol	70	22.5

Table.7 Sensitivity pattern of *Burkholderia pseudomallei*

Antibiotics	2024 (%) S	2024 (%) S
Ceftazidime	100	90.9
Cotrimoxazole	100	100
Imipenem	91.6	81.8
Meropenem	100	100
Doxycycline	100	90.9
Amoxycillin + clavulanic acid	83.3	90.9

Table.8 Sensitivity pattern of *Stenotrophomonas maltophilia*

Antibiotics	2023 % S	2024 %S
Levofloxacin	92.6	75.9
Cotrimoxazole	96.3	79.3
Minocycline	96.3	82.8
Ceftazidime	51.9	10.3
Chloramphenicol	40.7	24.1

Table.9 Sensitivity pattern of *Elizabethkingia meningoseptica*

Antibiotics	2023 (%) S	2024 (%) S
Ciprofloxacin	45.5	17.6
Cotrimoxazole	93.2	52.9
Levofloxacin	68.2	82.4
Minocycline	100	100
Piperacillin+tazobactam	59.1	29.4

Table.10 Sensitivity pattern of *Chryseobacterium indologenes*

Antibiotics	2023 %S	2024 %S
Amikacin	14.3	14.3
Aztreonam	5.7	8.6
Cefepime	51.4	31.4
Cefepime+tazobactam	65.7	45.7
Cefoperazone+sulbactam	57.1	57.1
Ceftriaxone	5.7	5.7
Ciprofloxacin	42.9	48.6
Cotrimoxazole	97.1	84.4
Gentamicin	28.6	20.0
Imipenem	17.1	20.0
Levofloxacin	65.7	65.7
Meropenem	25.7	22.9
Piperacillin+tazobactam	68.6	51.4
Doxycycline	57.1	65.7
Minocycline	100	93.3
Tigecycline	37.1	20.0
Ceftazidime	40.0	17.8

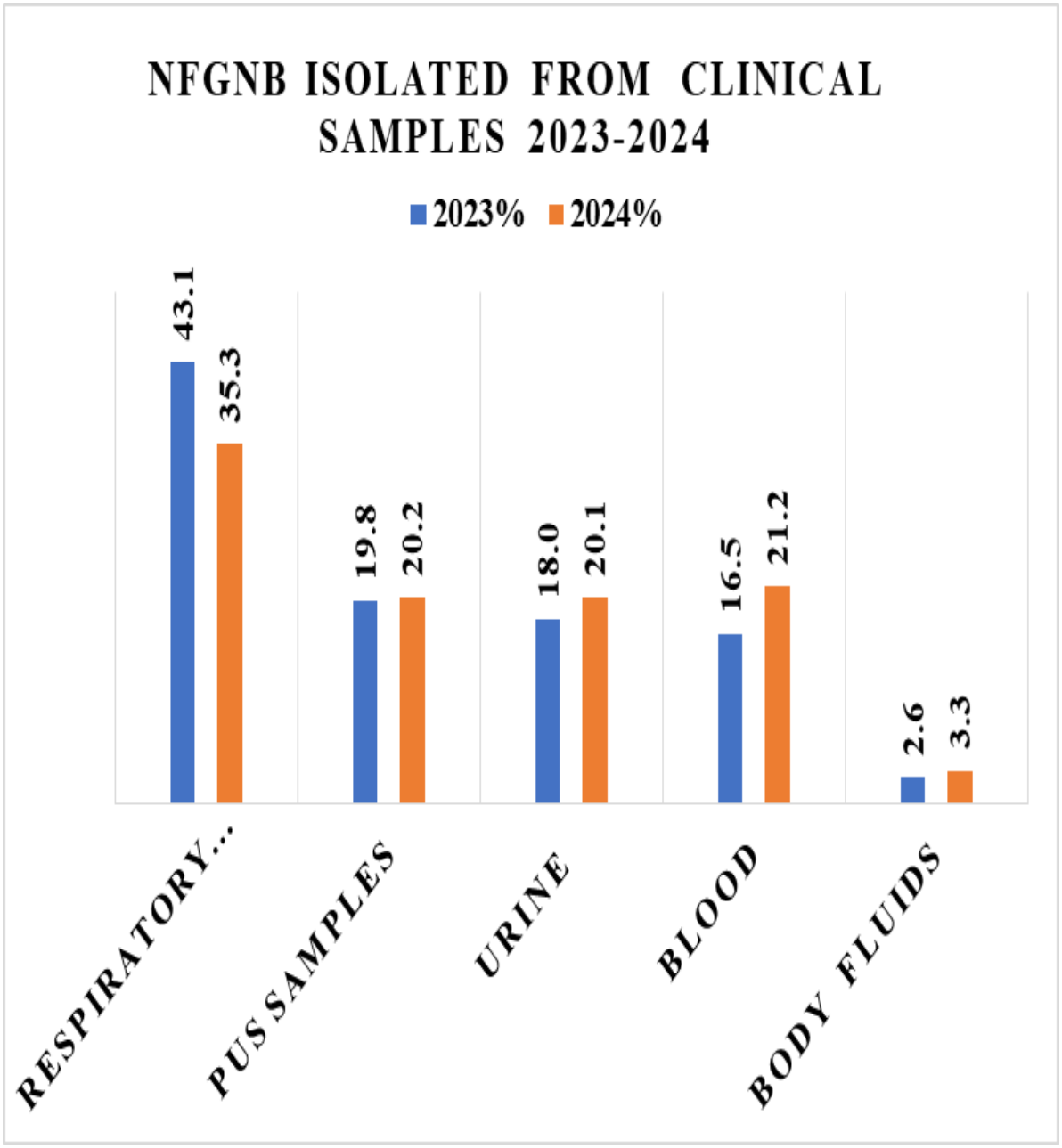
Table.11 Sensitivity pattern of *Sphingomonas paucimobilis*

Antibiotics	2023 (%) S	2024 (%) S
Amikacin	100	100
Aztreonam	10	14.3
Cefepime	60	50
Cefriaxone	60	14.3
Cefoperazone+sulbactam	80	92.9
Ciprofloxacin	50	85.7
Gentamicin	90	100
Imipenem	100	64.3
Levofloxacin	80	85.7
Meropenem	100	71.4
Piperacillin+tazobactam	90	64.3
Ceftazidime	40	64.3
Cotrimoxazole	60	100
Minocycline	40	85.7

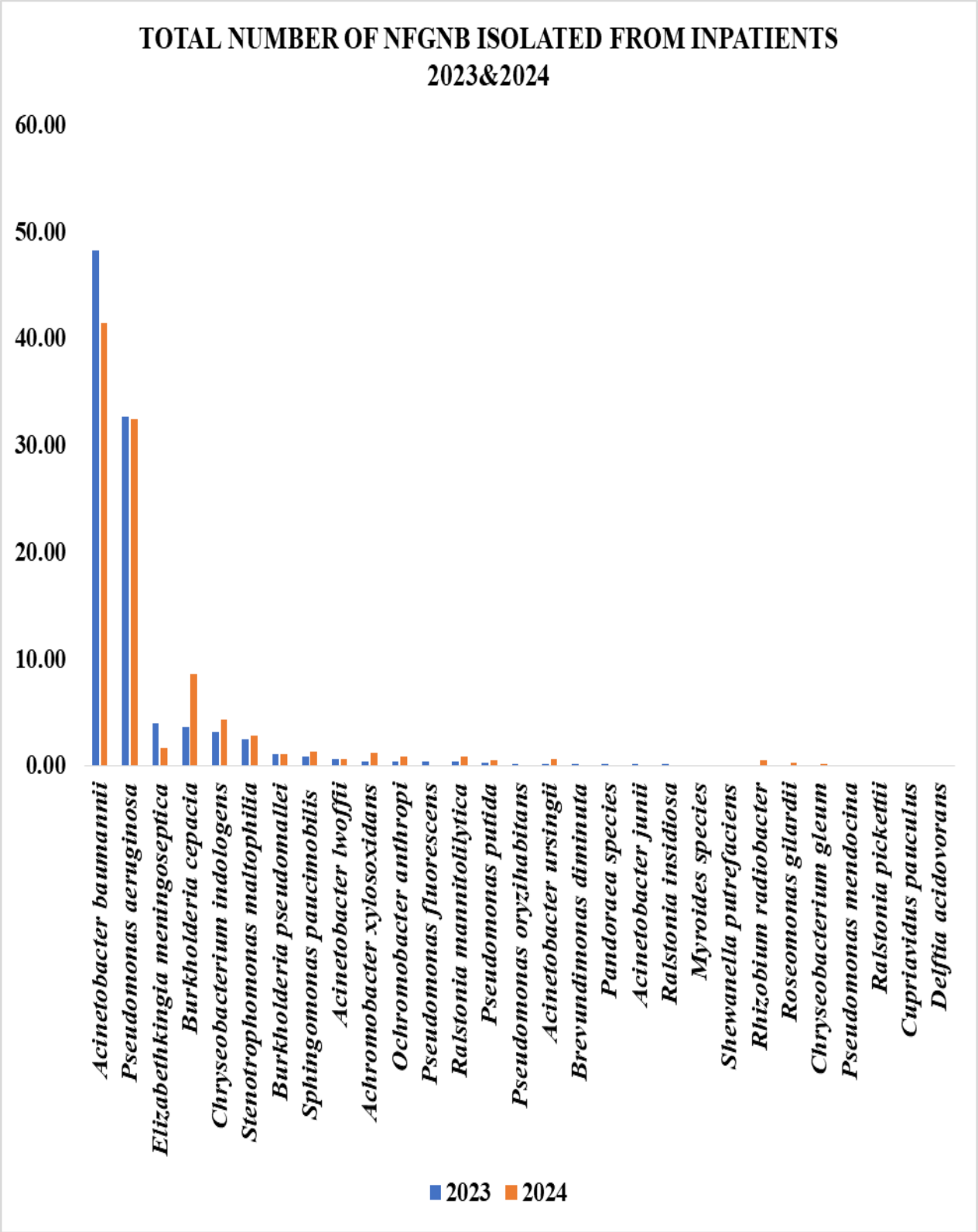
Table.12 Total multidrug resistant organisms 2023 & 2024

Total Multi Drug Resistant Organisms 2023-2024			
Carbapenem resistant Acinetobacter		**Carbapenem resistant Pseudomonas**	
2023 (N=535)	**2024 (N=430)**	**2023 (N=362)**	**2024 (N=338)**
372	287	114	100
69.50%	66.70%	31.40%	29.60%

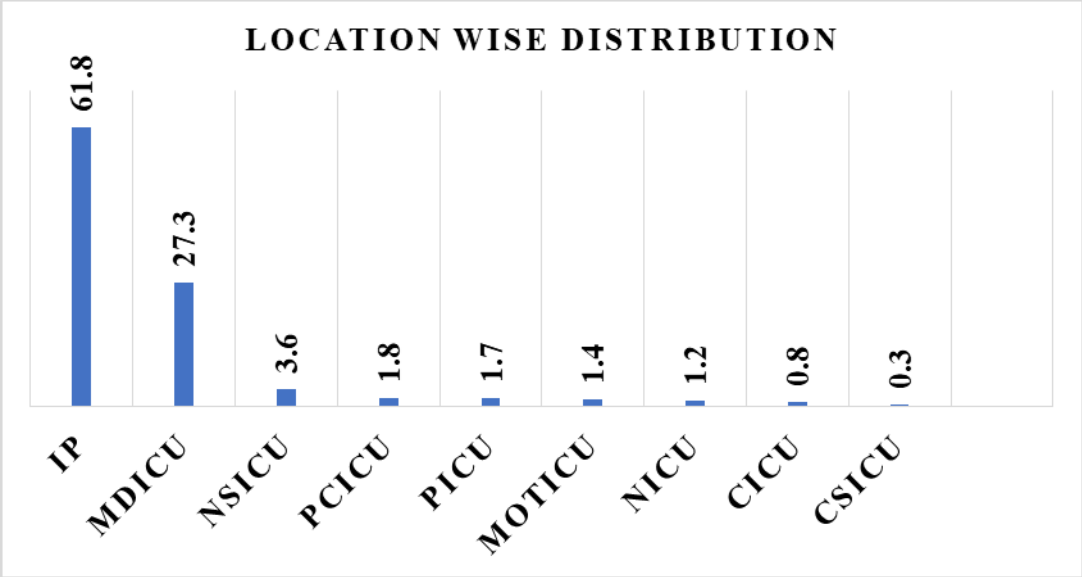
Graph.1 NFGNB Isolated from clinical samples 2023 and 2024



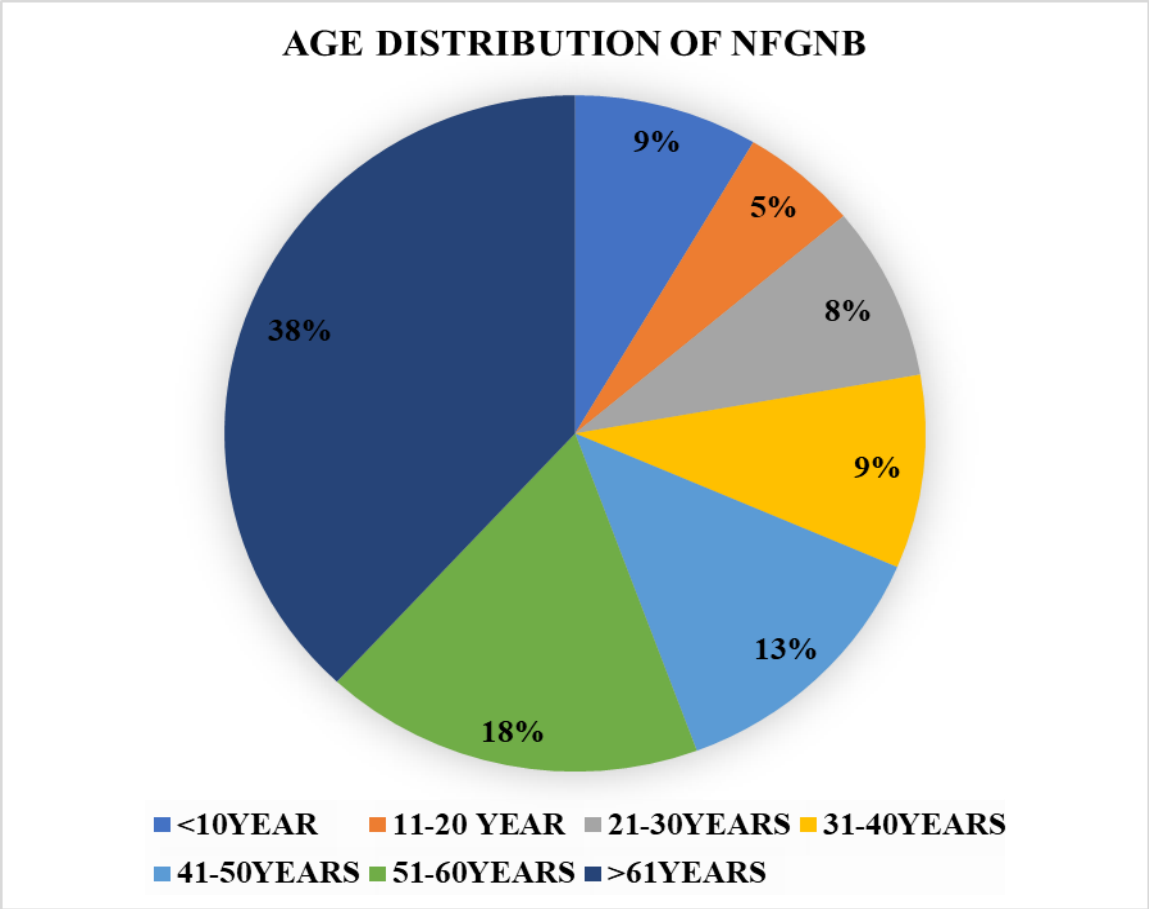
Graph.2 Total number of NFGNB isolated from inpatients 2023&2024



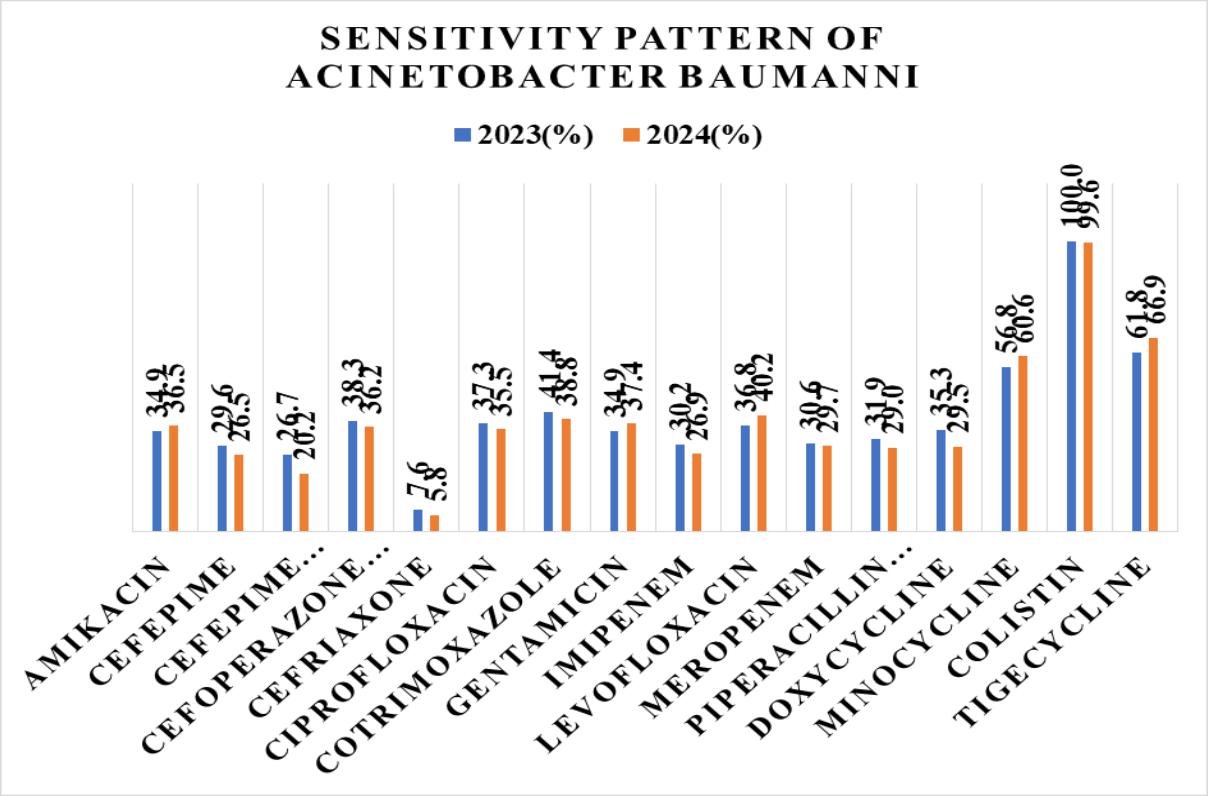
Graph.3 Location wise distribution of NFGNB



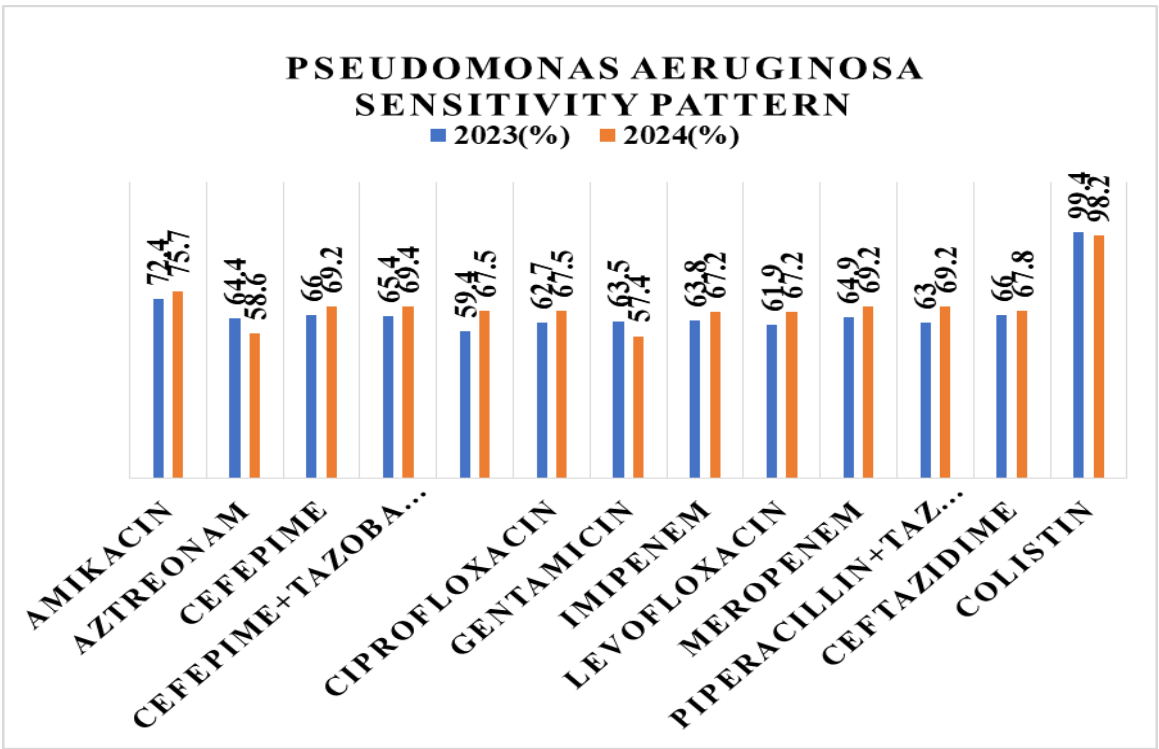
Graph.4 Age group wise distribution of NFGNB



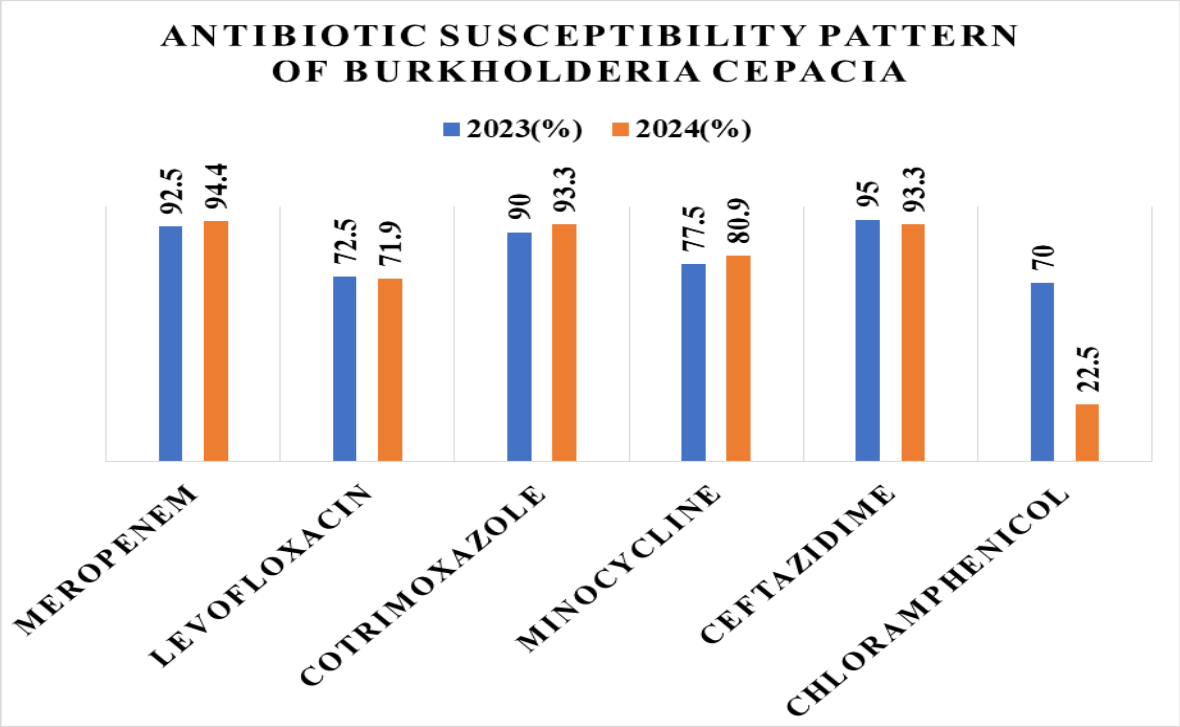
Graph.5 Sensitivity pattern of *Acinetobacter baumanni*



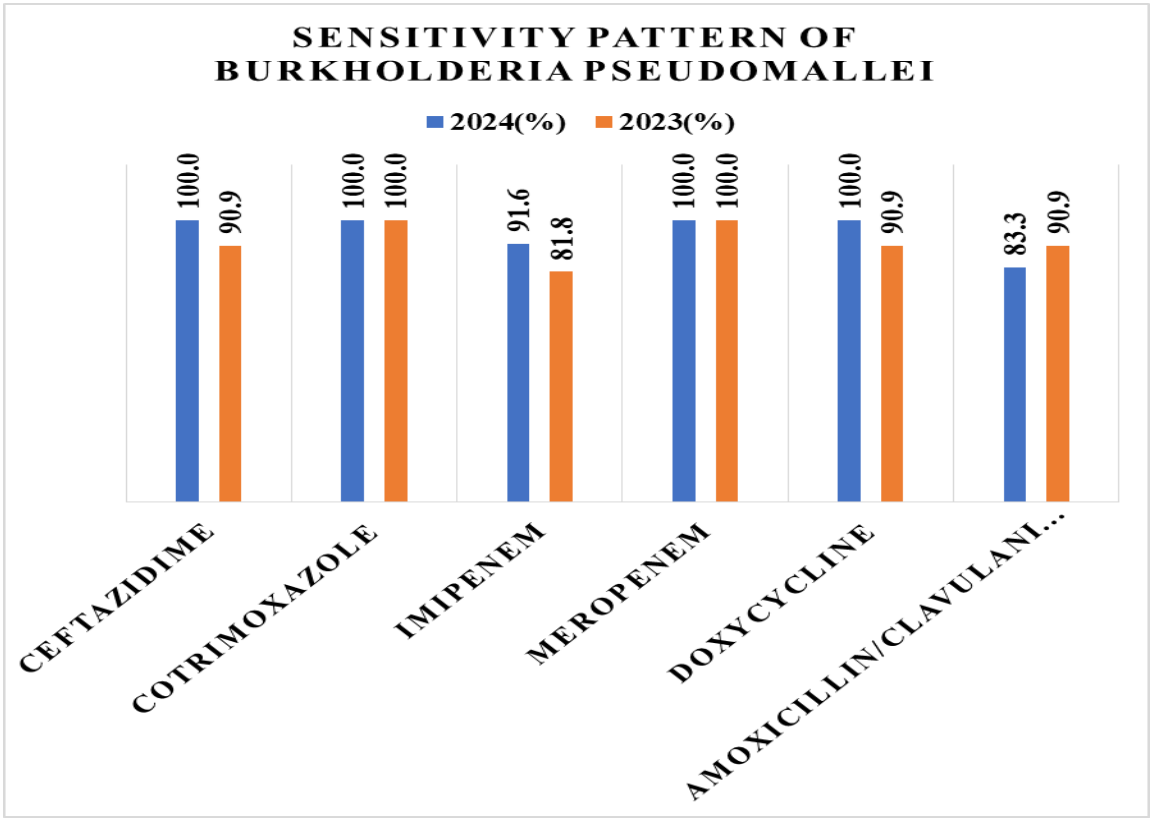
Graph.6 Sensitivity pattern of *Pseudomonas aeruginosa*



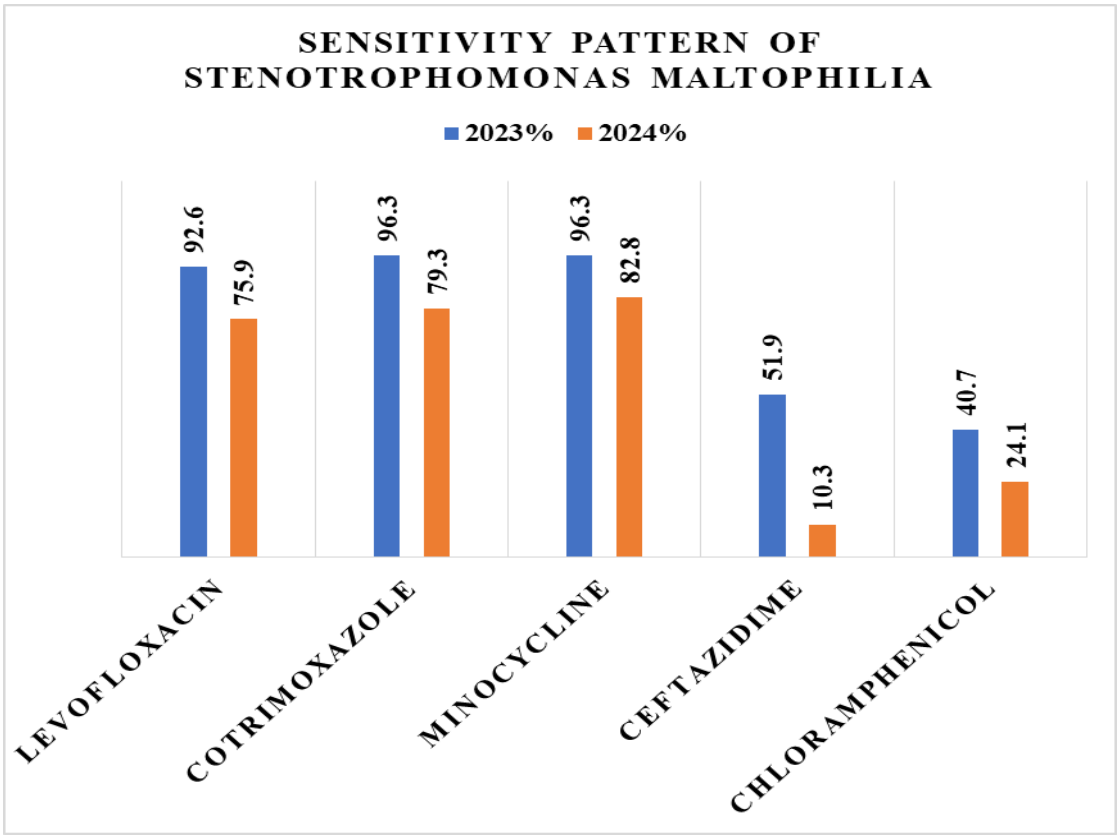
Graph.7 Antibiotic susceptibility pattern of *Burkholderia cepacia*



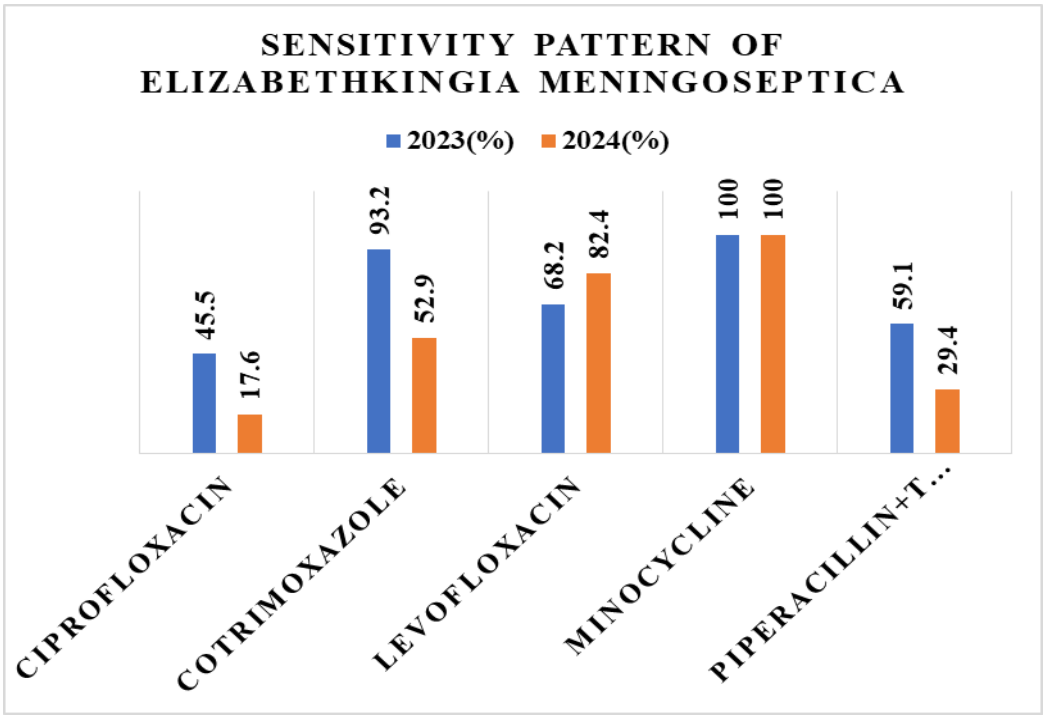
Graph.8 Sensitivity pattern of *Burkholderia pseudomallei*



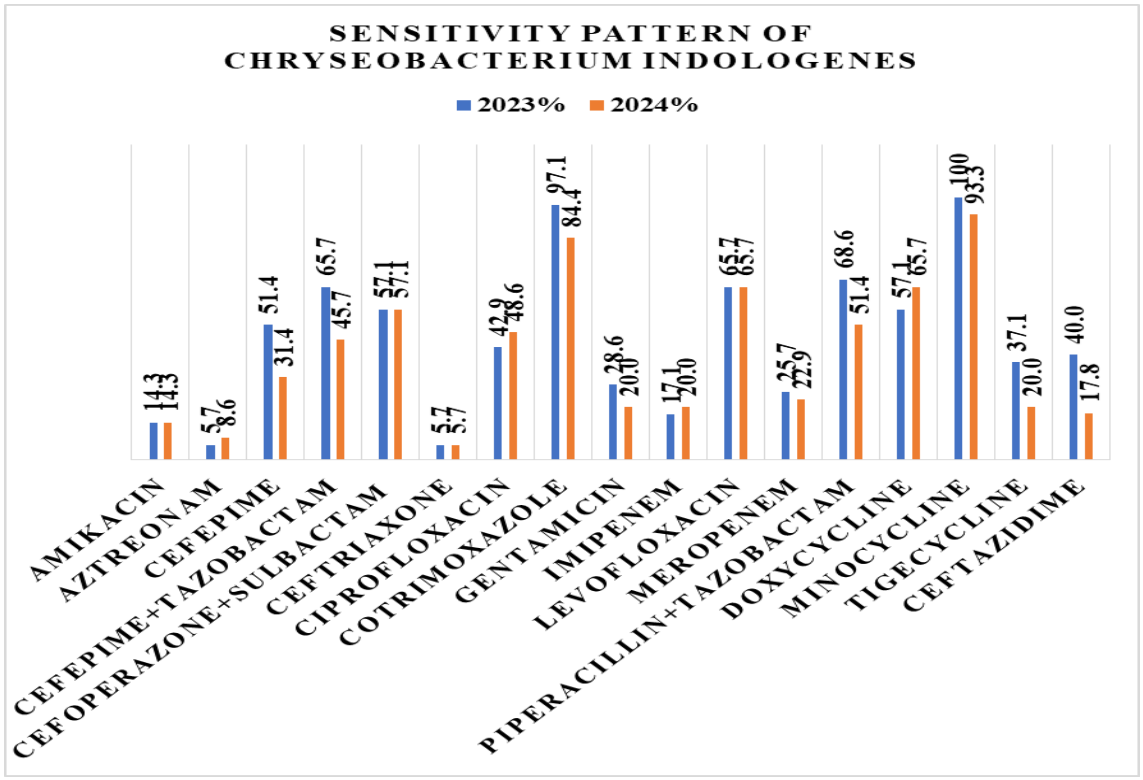
Graph.9 Sensitivity pattern of *Stenotrophomonas maltophilia*



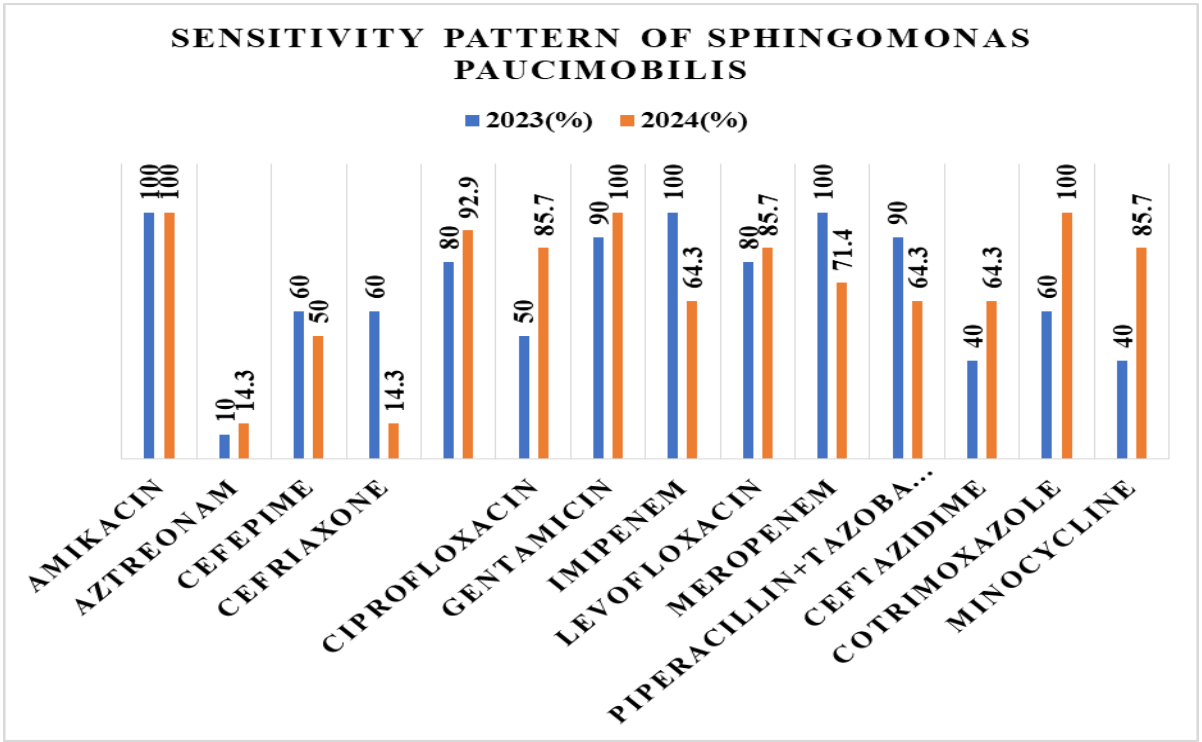
Graph.10 Sensitivity pattern of *Elizabethkingia meningoseptica*



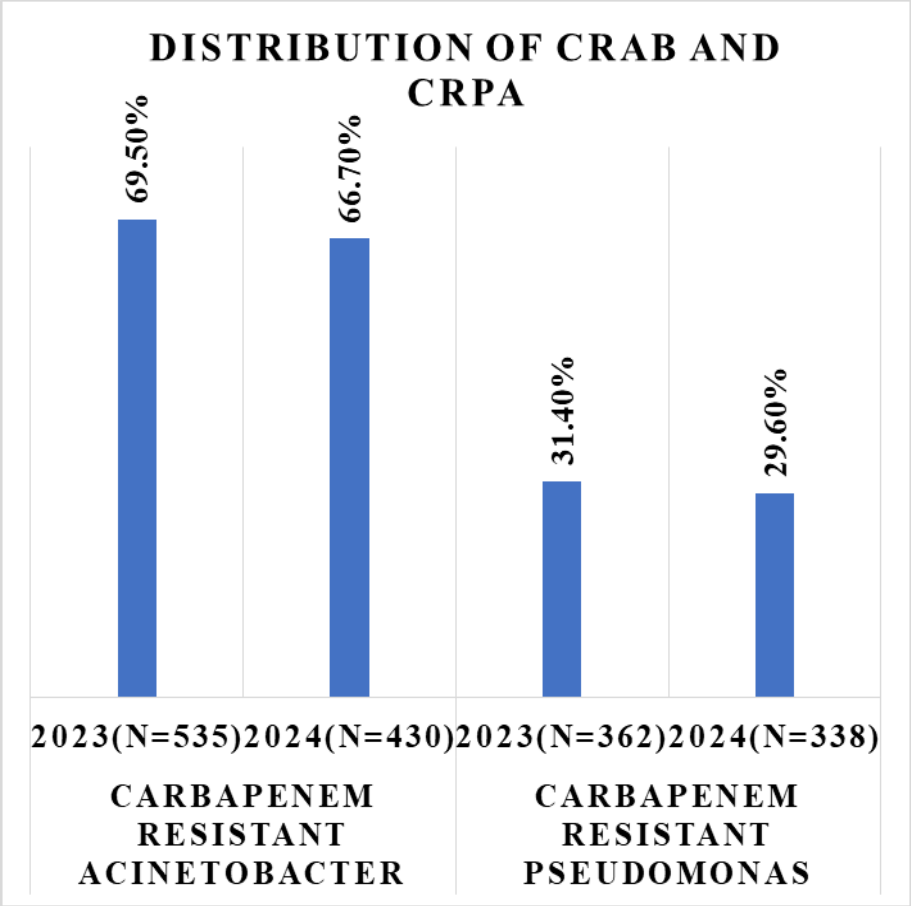
Graph.11 Sensitivity pattern of *Chryseobacterium indologenes*



Graph.12 Sensitivity pattern of *Sphingomonas paucimobilis*



Graph.13 Distribution of CRAB AND CRPA



Similar findings have been reported in other studies conducted in India [3] [10] [17] [18-26]. Although less common, these organisms can cause severe infections in immunocompromised patients. Therefore, identifying and monitoring their susceptibility profiles is crucial for optimal control of these infections, given their unpredictable sensitivity patterns.

In this study most of the NFGNB were from IP (61.8%) followed by MDICU (27.3%), higher isolation rate was seen in Grewal U S et al studies i.e., 75.8% isolates from ICU and 24.16% from other wards [6]. The lower isolation rate in the ICU observed in the current study may reflect improved infection control measures, including better adherence to hand hygiene protocols.

With respect to age, higher isolation rate was seen among patients in age group > 61 years (38 %) followed by the age group between 51-60 years (18%). This indicates that comorbidities that develop with age likely influence the invasiveness of NFGNB and also due to weakened immune system of old age people. Similar results were seen in Berwal A et al study. [27]

Because of the high inherent resistance of various NFGNB to several antimicrobial agents, precise identification and resistance testing are vital in healthcare settings to guide the proper choice of empirical treatment.

Isolates of *Acinetobacter baumanni* were susceptible to colistin (100%) and tigecycline (66.9%) but showed reduced sensitivity to gentamicin (37.4%), cefoperazone-sulbactam combination (36.2%), amikacin (36.5%), ciprofloxacin (35.5%), and imipenem (26.9%). These results are similar to various other studies. [28-30].

The antimicrobial susceptibility pattern of *Pseudomonas aeruginosa* revealed high sensitivity to colistin, with 99.4% in 2023 and 98.2% in 2024. This was followed by amikacin (72.4% in 2023 and 75.7% in 2024), cefepime (66.0% and 69.2%), piperacillin-tazobactam (63.0% and

69.2%), ceftazidime (66.0% and 67.8%), imipenem (63.8% and 67.2%), ciprofloxacin (62.7% and 67.5%), and gentamicin (63.5% in 2023, decreasing to 57.4% in 2024) similar studies of Hafiz T A et al shows highest sensitivity to amikacin (92.6%) [31]

In this study, *Burkholderia cepacia* exhibited high sensitivity to meropenem, with rates of 92.5% in 2023 and 94.4% in 2024. This was followed by ceftazidime (95.0% in 2023 and 93.3% in 2024) and cotrimoxazole (90.0% and 93.3% respectively). Meanwhile, *Burkholderia pseudomallei* demonstrated 100% sensitivity to both meropenem and cotrimoxazole in both 2023 and 2024, indicating consistent susceptibility to these key antibiotics.

In this study Antibiotic susceptibility patterns for *Stenotrophomonas maltophilia*, a notable decline in sensitivity was observed across all tested antibiotics from 2023 to 2024, for Minocycline sensitivity decreased from 96.3% in 2023 to 82.8% in 2024, Cotrimoxazole Sensitivity declined from 96.3% to 79.3%, Levofloxacin: Sensitivity dropped from 92.6% to 75.9%. This downward trend in antibiotic susceptibility highlights the emerging resistance of *S. maltophilia*. studies by Lee Y L et al shows similar values. [32]

In both 2023 and 2024, *Elizabethkingia meningoseptica* exhibited 100% sensitivity to minocycline, making it the most consistently effective antimicrobial agent against this organism. In 2023, sensitivity to cotrimoxazole was high at 93.2%, followed by levofloxacin at 68.2%. However, in 2024, a notable decline in sensitivity to cotrimoxazole was observed, dropping to 52.9%, indicating a potential emerging resistance trend. Similar values were seen in Alhuthil RT et al study. [33]. In this study sensitivity pattern of *Chryseobacterium indologenes* to minocycline is 100% in 2023 and 93.3% 2024, followed by cotrimoxazole 81.8% and 100%, levofloxacin 65.7% in 2023 and 2024 respectively the results of study conducted by Chang J et al shows similarities. [34]

Sphingomonas spp. are found in the environment and are known to cause mostly nosocomial illnesses [48]. The sensitivity pattern of *Sphingomonas paucimobilis* shows 100% sensitivity towards amikacin followed by gentamicin (90% and 100%), cotimoxazole (60% and 100%), a decreased sensitivity seen in meropenem (100% and 71.4%) in 2023 and 2024 respectively similar results observed in Kumar H et al study. [35]

The present study revealed that carbapenem-resistant *Acinetobacter baumannii* (CRAB) was isolated in 69.5% of cases in 2023 and 66.7% in 2024. Similarly, carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) was detected in 31.4% of cases in 2023 and 29.6% in 2024. These findings demonstrate a notable decrease in resistance rates for both CRAB and CRPA in 2024 compared to the previous year. This trend likely reflects the impact of enhanced infection control practices and the implementation of effective antibiotic stewardship programs within the hospital setting.

Due to presence of high level of intrinsic resistance among various NFGNB we need to identify and detect antibiotic sensitivity accurately. Therefore, various international authorities emphasize that every hospital should have antibiotic policy of its own.

In conclusion, this study highlights a significant burden of non-fermenting Gram-negative bacilli (NFGNB), with *Acinetobacter baumannii* and *Pseudomonas aeruginosa* being the most commonly isolated pathogens. *P. aeruginosa* isolates demonstrated good susceptibility to colistin and amikacin, while *A. baumannii* showed favorable susceptibility to colistin and tigecycline.

The detection of carbapenem-resistant *P. aeruginosa* (CRPA) and *A. baumannii* (CRAB) in this research is a cause for concern, reflecting the growing threat of antimicrobial resistance among NFGNB in this region. However, the observed decline in isolation rates over the two-year period suggests a positive impact of the hospital's infection control strategies and antibiotic stewardship program.

Effective management of infections caused by NFGNB requires robust screening protocols, regular monitoring of antimicrobial susceptibility patterns, careful administration of antibiotics to mitigate the development and spread of multidrug-resistant strains.

In conclusion, NFGNB once considered mere contaminants has now become a significant etiological agent of healthcare-associated infections. Their inherently unpredictable susceptibility patterns necessitate continuous surveillance and microbiological evaluation to guide appropriate therapeutic interventions. The prevalence and resistance profiles of these organisms can vary not only between different geographic locations but also within hospitals and among various patient populations.

Therefore, it is essential for clinicians to remain informed about local epidemiological trends and resistance data. Empirical therapy should be guided by local antibiograms, and the implementation of rigorous antimicrobial stewardship and infection control measures remains critical to curbing the emergence and dissemination of drug-resistant NFGNB in healthcare settings.

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Declarations

Conflict of Interest:

"The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper."

Ethical Approval and Informed Consent Statement

Study Involving Identifiable Human Data or Samples - With Consent: "The research involving the use of human data/samples was approved by the Institutional ethics committee of MALABAR INSTITUTE OF MEDICAL SCIENCES LTD (IEC Ref No : 27/24). Informed consent for the use of their data/samples was obtained from all participants."

Author Contributions

Gayathri M. Conceived the original idea and designed the model and Analysed, Investigated and wrote the manuscript. Dr. Reshmi Gopalakrishnan, Validation, Formal Analysis, Project Administration, Supervision. Prof. Savitha M.: Writing - Review & Editing. Swathy Viswanath, Review and Editing. Anjali M P, Created supplementary visual material. Athulya M M,: Rechecked all major findings to validate their accuracy. Irfana, Contributed to data representation in the final manuscript. Vismaya P P.: Review, Contributed to data representation in the final manuscript.

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