The Prevalence of Antibiotic Resistance of Non-Fermenting Gram-Negative Bacilli in Sputum Culture among Hospitalized Patients in Duhok City-Iraq

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ABSTRACT

Non-fermenting Gram-Negative Bacilli (NFGNB) are a varied collection of aerobic, non-spore-forming organisms devoid of the capacity to ferment carbohydrates to provide energy for cellular needs. This research aimed to identify the medication resistance pattern among the isolates of NFGNB generating respiratory tract infections (RTIs). This work exposes several NFGNB isolated and identified by Vitek2 Compact System that cause respiratory tract infection (RTI). With a rate of 65.2%, *A. baumanii* was the most often isolated; *P. aeruginosa*, with a rate of 28.3%, followed by other NFGNB, particularly in immunocompromised patients. For NFGNB, Colistin had the most sensitive and antibiotic choice with a rate of sensitivity above 80%. Particularly the Cephalosporin group—which comprises Ceftazidime, Cefepime, Cefotaxime and Ceftriaxone—a significant resistance rate of it about (100%) was recorded. With resistance rate Aminoglycosides (Amikacin and Gentamicin) (93.33%), Tobramycin (83.33%) for *A. baumanii* and Resistance to Aminoglycosides for *Pseudomonas aeruginosa* is low to moderate according to our data (Amikacin 53.84%, Gentamicin 46.15%, and Tobramycin 38.46%). Based on our findings, *Serratia marcescens* demonstrate 100% sensitivity to Aminoglycosides (Amikacin, Gentamicin and Tobramycin). Furthermore, observed were distinct resistotyping patterns (Fifteen, Ten, Three) for (*A. baumanii*, *P. aeruginosa*, and *S. marcescens*)consequently. At last, it is essential to find NFGNB and track their susceptibility pattern to direct the doctor for improved patient management and treatment.

Introduction:

The varied group of aerobic, non-spore-forming organisms known as non-fermenting gram-negative Bacilli (NFGNB) cannot ferment carbohydrates to produce energy for cellular actions (Bansal, Soni, and Tiwari 2019). Although NFGNB are ubiquitous saprophytes in the surroundings and are sometimes regarded as contaminants of clinical samples, their clinical relationship with a variety of disorders thoroughly proves their possible harmful significance (C. et al. 2024). Often correlated with nosocomial infections and immunocompromised patients include bacteria including *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Stenotrophomonas maltophilia* (Buzilă et al. 2021; Sharma, Pujari, and Kumar Sharma 2020a). From a clinical microbiology lab, NFGNB are well-known to account for 16% to 21% of all bacterial isolates (Juyal et al. 2013; Somily et al. 2021). The Centers for Disease Control and Prevention classify *P. aeruginosa and A. baumannii* as urgent/severe risks due to possible resistance to a high number of antibiotics; they are also featured on the list of critical priority infections published by the World Health Organization (Magiorakos et al. 2012; Vicente et al. 2006). Most of which are simultaneously multidrug-resistant (MDR, non-

susceptible to at least one agent in more than three antimicrobial categories), or extensively drug-resistant (XDR, non-susceptible to at least one agent in all but two or less). These bacteria are often intrinsically resistant to various antibiotic groups, including macrolides and penicillin and are particularly problematic; carbapenem-resistant *P. aeruginosa* (CRPA) and *A. baumannii* (CRAB) (Abdullah 2022; Asokan et al. 2019; Kadri 2020; Ménard, Clain, and Ariey 2018).

Outer-membrane impermeability, change of antibiotic target sites, expression of efflux system, hydrolyzing enzyme synthesis, plasmid, or transposon-mediated resistance facilitate the several resistance mechanisms of NFGNB (Higgins et al. 2001; McGowan 2006).

Antimicrobial medication resistance often complicates treatment, raises mortality rates, and drives healthcare costs (Ménard, Clain, and Ariey 2018). The broad use of antibiotics that stimulates the selection pressure in bacteria and increases the drug resistance phenomena in various surroundings causes changes in the patterns of antibiotic sensitivity throughout time (Karam et al. 2016). In the intensive care unit (ICU), *P. aeruginosa* and *A. baumannii* are the most often derived NFGNB-causing nosocomial infections (Abdullah 2022; Aly, Al-Mousa, and Al Asar 2008). About 10.6% of deaths in cases of hospital-acquired infections are brought on by multidrug-resistant *Acinetobacter species* (Abdullah 2022; Perez et al. 2007).

Therefore, the objectives of this research are to:

-Using biochemical and Vitek 2 compact, find the rate of NFGNB in sputum infections.

-To identify the resistance profiles of isolated NFGNB strains against a therapeutically relevant antibiotic panel.

Materials and Methods:

Following approval from our institute's research and ethical committee, this was a cross- sectional study using descriptive techniques in analyzing Non-Fermenting Gram-Negative Bacilli (NFGNB) like *Pseudomonas aeruginosa, Acinetobacter baumannii* and *Serratia marcescens*

In 200 Sputum samples collected from Hospitalized Patients from September 2024 to December 2024 at Duhok Hospitals including: Azadi Teaching Hospital, Vin Hospital and Shiryan Hospital. Specimens were taken from hospitalized adult patients, and the majority of them were in the ICU department.

The greatest NFGNB pneumonial isolates and the frequency of multidrug-resistant (MDR) isolates among Hospitalized Patients and ICU patients were ascertained using such a research strategy. The study variables were thus investigated using a mix of frequency tabulations and percentages.

Sample processing and NFGNB identification:

Following sample confirmation to be representative of lower respiratory tract secretion samples, all the samples were processed as per standard technique and stained by Gram stain and cultured on MacConkey Agar, Blood Agar and Chocolate Agar plates and incubated aerobically at 37°C for 18–24 hours and then examined for bacterial growth. Separated from all the sequential samples, single or mixed growth (two or more than two isolates per specimen) was identified up to species level and their antimicrobial susceptibilities were identified manually and automatically. **Manually** using biochemical tests (catalase and oxidase) and then the Antimicrobial Susceptibility Test (AST) was done by the Kirby-Bauer technique, which was carried out on Muller-Hinton Agar by inoculation of Muller-Hinton Agar with bacteria and antibiotic disks placed on this plate. After that, this plate was incubated at 37°C for 18 to 24 hours. The diameter of the inhibitory zone was then determined, and the findings of susceptibility testing were

handled in compliance with CLSI recommendations (Weinstein 2019), the manual AST was done for the antibiotic selected for research, but not found in the Vitek 2 paper. **Automated** by using Vitek 2 compact (Bio Mérieux, France).

Results:

NFGNB isolates identification:

Of the 46 individuals who were infected by NFGNB, 25 were male and 21 female individuals tested positive for NFGNB, as shown in Table 1. Isolate distribution indicated all isolates were obtained from adult patients, and all of the isolates were obtained from inpatients, mostly in the ICU department. NFGNB bacterial isolates from sputum include: 30 *Acinetobacter baumannii*, 13 *Pseudomonas aeruginosa* and 3 *Serratia marcescens* as shown in Table 2**.**

Gender	No. of Patients	Percentages of Patients (%)
Male	25	54.35%
Female	21	45.65%
Total	46	100%

Table 1: Sex distribution of patients

NFGNB	No. of isolates	Percentages of isolates (%)
A. baumannii	30	65.2%
P. aeruginosa	13	28.3%
S. marcescens	3	6.5%
Total	46	100 %

Table 2: Number and percentage rates of NFGNB isolates from sputum

Antibiotic resistance patterns:

The antibiotic resistance rate is explained in Table 3. Generally, as it showed in this table, the total resistance average of *A. baumannii*, *P. aeruginosa* and *S. marcescens* isolates to the antibiotics were (85.62%, 72.07%, 26.32%) respectively while the total sensitivity rate were (12.80%, 23.48%, 70.17%) respectively. *A. baumanii* had shown maximum sensitivity to colistin followed by tigecycline while most of them were found to be resistant to carbapenems (Imipenem, Meropenem), Aminoglycosides (Amikacin, Gentamicin and Tobramycin) and Cephalosporins (Ceftazidime, Cefepime, Cefotaxime and Ceftriaxone). *P. aeruginosa* was most sensitive to colistin with moderate sensitivity to Tobramycin. *S. marcescens* had shown 100% sensitivity to Aminoglycosides, Sulfonamides and Penicillins.

NO.	Antibiotics	Acronym	*Acinetobacter baumannii*			*Pseudomonas aeruginosa*			*Serratia marcescens*		
			S No. (%)	I No. (%)	R No. (%)	S No. (%)	I No. (%)	R No. (%)	S No. (%)	I No. (%)	R No. (%)
1	Piperacillin/ Tazobactam	PTZ	1(3.33)	0(0)	29(96.66)	2(15.38)	0(0)	11(84.61)	0(0)	0(0)	3(100)
2	Ceftazidime	CAZ	1(3.33)	0(0)	29(96.66)	3(23.07)	1(7.69)	9(69.23)	2(66.66)	0(0)	1(33.33
3	Cefepime	FEP	1(3.33)	0(0)	29(96.66)	3(23.07)	2(15.38)	8(61.53)	2(66.66)	0(0)	1(33.33)
4	Imipenem	IPM	1(3.33)	0(0)	29(96.66)	3(23.07)	0(0)	10(76.92)	0(0)	0(0)	3(100)
5	Meropenem	MEM	1(3.33)	0(0)	29(96.66)	3(23.07)	0(0)	10(76.92)	1(33.33)	0(0)	2(66.66)
6	Amikacin	AK	2(6.66)	0(0)	28(93.33)	5(38.46)	1(7.69)	7(53.84)	3(100)	0(0)	0(0)
7	Ciprofloxacin	CIP	1(3.33)	0(0)	29(96.66)	4(30.76)	0(0)	9(69.23)	1(33.33)	1(33.33)	1(33.33)
8	Tigecycline	TIG	24(80)	2(6.66)	4(13.33)	1(7.69)	0(0)	12(92.30)	3(100)	0(0)	0(0)
9	Trimethoprim/Sulfamethoxazole	TMP-SMX	5(16.66)	0(0)	25(83.33)	2(15.38)	2(15.38)	9(69.23)	3(100)	0(0)	0(0)
10	Cefotaxime	CTX	0(0)	0(0)	30(100)	0(0)	0(0)	13(100)	0(0)	0(0)	3(100)
11	Gentamicin	GN	1(3.33)	1(3.33)	28(93.33)	6(46.15)	1(7.69)	6(46.15)	3(100)	0(0)	0(0)
12	Colistin	COL	24(80)	4(13.33)	2(6.66)	11(84.61)	1(7.69)	1(7.69)	3(100)	0(0)	0(0)
13	Pipracillin	PIP	0(0)	0(0)	30(100)	2(15.38)	1(7.69)	10(76.92)	1(33.33)	1(33.33)	1(33.33)
14	Tobramycin	TOB	5(16.66)	0(0)	25(83.33)	8(61.53)	0(0)	5(38.46)	3(100)	0(0)	0(0)
15	Levofloxacin	LEV	4(13.33)	2(6.66)	24(80)	2(15.38)	2(15.38)	9(69.23)	3(100)	0(0)	0(0)
16	Tetracycline	TET	1(3.33)	0(0)	29(96.66)	0(0)	0(0)	13(100)	3(100)	0(0)	0(0)
17	Ticarcillin	TIC	0(0)	0(0)	30(100)	1(7.69)	0(0)	12(92.30)	3(100)	0(0)	0(0)
18	Ticarcillin/ ClavulanicAcid	TIC/ C LA	1(3.33)	0(0)	29(96.66)	2(15.38)	0(0)	11(84.61)	3(100)	0(0)	0(0)
19	Ceftriaxone	CRO	0(0)	0(0)	30(100)	0(0)	0(0)	13(100)	3(100)	0(0)	0(0)
Total Rate			12.80%	1.58%	85.62%	23.48%	4.45%	72.07%	70.17%	3.51%	26.32%

Table 3: Antibiotic Susceptibility Pattern for NFGNB Isolates

Resistotyping patterns:

The following Tables (4, 5 and 6) show the resistotyping patterns of the isolates to commonly used antibiotics. Every isolate turned out to be multiple resistant, which meant that each one of them was resistant to several kinds of antibiotics.

The obtained results of resistotyping patterns (resistant profiles) showed that 46 NFGNB isolated include 30 *A. baumannii*, 13 *P. aeruginosa, and* 3 *S. marcescens,* which were multiple drug-resistant to antibiotics, and different resistotyping patterns (Fifteen, Ten, Three) respectively were found.

Resistotyping patterns	**Resistance Spectrum Phenotype**	**No. of isolates (%)**
Resistotype1	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP- SMX, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	14(46.68)
Resistotype2	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype3	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP- SMX, CTX, GN, PIP, TOB, LEV, TIC, TIC/CLA, CRO	1(3.33)
Resistotype4	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP-SMX, CTX, GN, PIP, TOB, TET, TIC, TIC/CLA, CRO	2(6.68)
Resistotype5	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, TMP-SMX, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype6	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP-SMX, CTX, PIP, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype7	PTZ, CAZ, FEP, IPM, MEM, CIP, TIG, TMP- SMX, CTX, GN, COL, PIP, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype8	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP-SMX, CTX, GN, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype9	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, TMP-SMX, CTX, GN, PIP, TOB, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype10	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	2(6.68)
Resistotype11	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TMP-SMX, CTX, GN, PIP, TET, TIC, TIC/CLA, CRO	1(3.33)

Resistotype12	CAZ, FEP, IPM, MEM, AK, CIP, TMP-SMX, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype13	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, CTX, GN, PIP, LEV, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype14	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, CTX, GN, PIP, TOB, TET, TIC, TIC/CLA, CRO	1(3.33)
Resistotype15	PTZ, CAZ, TMP-SMX, CTX, PIP, TET, TIC, CRO	1(3.33)
Total		**30(100)**

Table 4: Resistotyping patterns of *A. baumannii* isolates

Resistotyping patterns	**Resistance Spectrum Phenotype**	**No. of isolates (%)**
Resistotype1	PTZ, CAZ, FEP, AK, CTX, GN, PIP, TET, TIC, TIC/CLA, CRO	1(7.69)
Resistotype2	PTZ, TIG, TMP-SMX, CTX, PIP, TET, TIC, CRO	1(7.69)
Resistotype3	PTZ, CAZ. IPM, MEM, AK, CIP, TIG, TMP-SMX, CTX, GN, PIP,TOB, LEV, TET, TIC, TIC/CLA, CRO	1(7.69)
Resistotype4	TIG, TMP-SMX, CTX, LEV, TET, CRO	1(7.69)
Resistotype5	IPM, MEM, CIP, TIG, TMP-SMX, CRX, LEV, TET, TIC, TIC/CLA, CRO	1(7.69)
Resistotype6	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, TMP-SMX, CTX, COL, PIP,TOB, LEV, TET, TIC, TIC/CLA, CRO	2(15,39)
Resistotype7	PTZ, IPM,MEM, TIG, TMP-SMX, CTX, LEV, TET, TIC, TIC/CLA, CRO	1(7.69)
Resistotype8	PTZ, CAZ, FEP, IPM, MEM,CIP, TIG, TMP-SMX, CTX, PIP, TET, TIC, TIC/CLA, CRO	2(15,39)
Resistotype9	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, CTX, GN, PIP, TOB, LEV, TET, TIC, TIC/CLA, CRO	2(15,39)
Resistotype10	PTZ, CAZ, FEP, IPM, MEM, AK, CIP, TIG, TMP-SMX, CTX, GN, PIP, LEV, TET, TIC, TIC/CLA, CRO	1(7.69)
Total		**13(100)**

Table 5: Resistotyping patterns of *P. aeruginosa* isolates

Resistotyping patterns	**Resistance Spectrum Phenotype**	**No. of isolates (%)**
Resistotype1	PTZ, CAZ, FEP, IPM, MEM, CTX	1(33.33)
Resistotype2	PTZ, IPM, CTX, PIP	1(33.33)
Resistotype3	PTZ, IPM, MEM, CIP, CTX	1(33.33)
Total		**3(100)**

Table 6: Resistotyping patterns of *S. marcescens* isolates

Discussions:

Given that the bacteria responsible for infections and their patterns of antibiotic resistance differ across locations and evolve, it is crucial to examine the pathogens and their sensitivity profiles to enhance the treatment of infections (Inam et al. 2023). One main challenge is resistance to antibiotics, especially by the newly discovered pathogens NFGNB, which affects the control of infections, especially in hospitalized patients (Behzadi, Baráth, and Gajdács 2021). One of the most alarming features of NFGNB infections is their both acquired and natural resistance to many different medicines (Behzadi, Baráth, and Gajdács 2021). Often utilized first-line therapies, these bacteria are notorious for their resistance to beta-lactams, aminoglycosides, fluoroquinolones, and other types of antibiotics (Wang et al. 2022). The processes underlying this resistance are several and include the synthesis of carbapenemases, which hydrolyse and deactivate common antibiotics, and extended-spectrum beta-lactamases (ESBLs), which hydrolyse and deactivate other antibiotics (Hussain et al. 2021). Furthermore, these species sometimes show low permeability of their outer membranes, which inhibits the antibiotic access into bacterial cells. Further adding to the resistance of the bacteria are efflux pumps, which actively release antimicrobial chemicals out of the cell (Huang et al. 2022).

These elements make treating infections brought on by NFGNB more difficult since only a few suitable medications are available (Hussain et al. 2021). Major therapeutic problems in recent years have come from carbapenem-resistant strains of *Acinetobacter baumannii* and *Pseudomonas aeruginosa* (Mancuso et al. 2023). These strains, which resist carbapenems, a class of antibiotics usually employed as a last resort, are linked with significant death rates (Giaccari et al. 2021). Often, the presence of such resistant bacteria causes doctors to depend on an older, less-used antibiotic called colistin (El-Sayed Ahmed et al. 2020; Muteeb et al. 2023). But the growing resistance of NFGNB to colistin raises questions regarding the direction of treating these diseases (Baral et al. 2019). Moreover, there are few options for treating extensively drug-resistant (XDR) and multidrug-resistant (MDR) NFGNB infections as well as for new medication development in this field is somewhat slow. Resistance in NFGNB arises not just from their inherent processes (Esther 2017). Particularly in hospitals, the overuse and abuse of antibiotics have generated selected pressures encouraging the growth and dissemination of resistant bacteria (Muteeb et al. 2023). The fact that many of these germs may survive in the hospital environment aggravates this issue and raises more patient transmission risk (Soni et al. 2023). Therefore, our study sought to separate NFGNB in sputum culture in Duhok hospitals and subsequently ascertain their sensitivity for antibiotics to probe the frequency of resistant NFGNB strains in various patient populations, especially in intensive care units and among those with chronic respiratory diseases. This will highlight any developing resistance patterns and help to define the degree of the issue. Understanding how resistance mechanisms vary across different geographical areas will be especially important as local antibiotic use and infection control strategies can greatly affect resistance patterns. This data could be very vital in guiding local treatment plans and improving empirical therapy for respiratory tract infections brought on by NFGNB (Yadav et al. 2020). The findings of our study results, as our isolated NFGNB was 23% of all other pathogens that cause respiratory tract infections. From 200 clinical specimens, 46 are NFGNB and consist of *Acinetobacter baumannii* 30 (65.2%), *Pseudomonas aeruginosa* 13 (28.3%), and *Serratia marcescens* 3(6.5%). According to the present study, *Acinetobacter species* and *Pseudomonas aeruginosa* were discovered to infect 48% of men and 52% of women virtually equally, harming both sexes(Baral et al. 2019).

This is not like a research evaluating the clinical epidemiological characteristics of *Acinetobacter sp.* and *Pseudomonas* infections. Our study observed that the percentage of NFGNB in males was 54.35% and in females 45.65%. Major causes of Ventilator-associated pneumonia (VAP) in the ICU environment in our study seem to be *A. baumanii* and *P. aeruginosa*.

A. baumanii was the main etiological agent responsible for 65.2% of NFGNB that caused respiratory tract infections in our study. *A. baumanii* had shown maximum sensitivity to colistin and tigecycline by (80%), and are the most active drugs against *A. baumannii*. This outcome parallels an Egyptian study (Al-Agamy et al. 2014), which revealed that Colistin sensitivity was 95.9% of *A. baumannii* isolates.

Furthermore, included in a Turkish paper were Colistin and Tigecycline as the most often used active medications against *A. baumannii* (Bayram et al. 2015). These bacteria were found to be resistant to carbapenems (Imipenem and Meropenem with (96.66%), Aminoglycosides (Amikacin and Gentamicin with (93.33%), Tobramycin (83.33%). This study also revealed rather strong opposition to the most often used antibiotics, especially the Cephalosporin group, which includes Ceftazidime, Cefepime, Cefotaxime and Ceftriaxone, with the rate of resistance of these antibiotics reaching approximately 100%. Other investigations have recorded this bacterium's great resistance to the Cephalosporins (Tian et al. 2011). When they discuss the extended spectrum class C-lactamases produced by A. baumannii, which do impart resistance against Cephalosporins (Tian et al. 2011). We also discussed resistotyping, a phenotypic technique whereby bacterial strains are tested against a series of arbitrarily selected antibiotics. Our study's results revealed that the (30) isolates of *A. baumannii* belonged to (15) different resistotype patterns. The resistotype number (1) has a much higher frequency rate, comprising 46.68%, followed by Resistotype (4 and 10) with a rate of 6.68%, and other resistotypes with a rate of 3.33%.

Pseudomonas aeruginosa, another often occurring isolate in respiratory tract infections, particularly in cystic fibrosis and ventilator-associated pneumonia. In our study, the rate of isolation of *P. aeruginosa* was found to be 28.3%, whereas 39.1% isolation of *P. aeruginosa* was reported by Sharma (Sharma, Pujari, and Kumar Sharma 2020b). With a rate of resistance of these antibiotics reaching 100%, we found a strong resistance of these isolates against the Cephalosporin group, which comprises Cefotaxime and Ceftriaxone. Resistance to Aminoglycosides is low to moderate according to our data (Amikacin 53.84%, Gentamicin 46.15%, and Tobramycin 38.46%. For *P. aeruginosa*, Fatima et al. observed resistance for piperacillin/tazobactam at 42%, cefepime at 40%, and amikacin at 35% showing a rising resistance (Fatima et al. 2012). Limited usage of ciprofloxacin may explain the declining resistance pattern found by Joseph et al. for ciprofloxacin (49% to 33%), meropenem (35% to 19%), ceftazidime (50% to 33%), and imipenem (28% to 14%), in 2012 in comparison to 2007 (Joseph 2013). Our study showed *P. aeruginosa* was also highly responsive to colistin (84.61%), with intermediate susceptibility to Tobramycin (61.53%). Another observation of *P. aeruginosa* in our study, this bacterium belonged to (10) distinct resistotype patterns. The resistotype number (6,8, and 9) has a much higher frequency rate, comprising 15.39% and other resistotypes with a rate of 7.69%.

The isolation rate of *Serratia marcescens* was 6.5% in our study. Usually affecting individuals with compromised immune systems or those working in hospital environments, it is a very rare cause of pneumonia. Particularly in susceptible groups, it can lead to serious illness; its antibiotic resistance can complicate treatment (Panigrahy 2015). The small sample size for

Serratia marcescens isolates limited this study and may influence the probability of finding antibiotic resistance in these isolates.

Conclusions:

This research shows that Respiratory Tract Infection (RTI) is caused by many NFGNB isolated and identified using the Vitek2 Compact System. *A. baumanii* (65.2%) and *P. aeruginosa* (28.3%) were the most often occurring isolates; other NFGNB, particularly in immunocompromised patients, came next.

Colistin is the most sensitive antibiotic available. But NFGNB showed more resistance to regularly used antibiotics, which resulted in a major public health concern. Furthermore, NFGNB has great chances to survive in a hospital environment; therefore, better antibiotic management and infection control strategies are required to stop the emergence and spread of multidrug-resistant NFGNB in medical environments. Therefore, it is important to find NFGNB and track their sensitivity pattern to direct the doctor for improved patient management and treatment.

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