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Antimicrobial Susceptibility Pattern of Multi Drug Resistant (MDR) *Pseudomonas aeruginosa* in a Tertiary Care Hospital from Central India

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Abstract: ***Background*: Antimicrobial resistance bacteria are the source of a threat to the community and hospital settings. There are many drug resistant human pathogenic bacteria are reported from all over world. Extended spectrum of β lactamases producing organism are increasing and causing more severe infection due to mutation leads to Multi Drug Resistances (MDR) which make treatment difficult. *Aims*: The study focus was undertaken to detect the prevalence and susceptibility of Multi drug resistant (MDR) Pseudomonas aeruginosa strains isolated from clinical specimens in a tertiary care hospital. *Materials & Methods*: Total 110 samples collected from clinical specimen's urine, blood, pus, sputum of different hospitals and clinics and isolates MDR strains of Pseudomonas aeruginosa. ESBLs detection by phenotypic double disk synergy method and antimicrobial susceptibility is done by broth dilution method Minimum inhibitory concentration (MICs) breakpoints using AST instrument VITEK 2 machine recommended by CLSI were used to determine the results. *Result*: Out of 110 isolates n=45 (40.90%) were found to be MDR positive P. aeruginosa strains, majority MDR P. aeruginosa were isolated from pus sample n= 19 (42.22%) followed by urine sample n=12 (26.66%), Blood sample n=09 (20.0%) and sputum sample n=05 (11.11%). The study concluded majority MDR P. aeruginosa were isolated from Pus sample and show highest drug susceptibility against MDR P. aeruginosa are Colistin (MICs≤0.5 µg/ml) & Tigecycline (MICs≤0.5 µg/ml) with lowest MICs values as an efficient choice of treatment among all the tested antibiotics. Urine sample show highest drug susceptibility against MDR P. aeruginosa are Fosfomycin (MICs ≤16 mg/ml), Tigecycline (MICs≤1µg/ml) as an more efficient treatment pattern followed by Piperacillin/ tazobactam (≤4µg/ml), Nitrofurantoin (≤16µg/ml), Cefaperazone/ sulbactam (≤8µg/ml), Colistin (≤0.5µg/ml). Blood sample more efficient choice of antibiotic are Piperacillin/ tazobactam (MICs≤4ug/l), Cefoperazone/ sulbactam (MICs≤8µg/ml) Tigecycline (MICs≤0.5µg/ml) followed by Levofloxacin (≤2µg/ml), Colistin (≤1µg/ml). In the Sputum sample choice of treatment Colistin (≤1.0µg/ml), Tigecycline (≤0.5µg/ml), Piperacillin /tazobactam (≤4ug/l), Meropenem (≤0.25µ/ml) Levofloxacin (≤2µg/ml), Cefoperazonesulbactam (≤8µg/ml) against MDR P. aeruginosa. Colistin, Fosfomycin, Piperacillin/tazobactam, Tigecycline can be suggested as the drugs of choice in our study.***

Keywords: Multi drug resistant (MDR); Extended - spectrum beta lactamases (ESBLs); *Pseudomonas aeruginosa*; Antimicrobial drug Susceptibility; Minimum inhibitory Concentration (MICs)

1. Introduction

Antimicrobial resistance is today a serious and terror for public health by producing multidrug resistant (MDR) bacteria. The emergence of multidrug resistant bacterial strains in community and Hospitals leads to problem of infection caused by *Pseudomonas* species particularly *Pseudomonas aeruginosa*. This pathogen takes immediate advantage with latent resistance to many antimicrobial agents such as Penicillin's, Ceftazidime, Carbapenems, and Aminoglycosides [1]. Pseudomonas *aeruginosa* pathogens causes severe airway infections in humans. This infection are usually difficult to treat and cause high mortality rates. *P. aeruginosa* organism is able to grow versatile as a saprophyte in different types of environments including drains, sinks, respirators, humidifiers and disinfectant solutions. Infection due to *Pseudomonas* species slowly acquired in healthy people and cause serious infections in hospitalized patients [2].

Prevalence of Extended spectrum beta lactamase (ESBLs) is an important cause of resistance in gram negative bacteria. The most commonly used antimicrobial agents all over the world in treating gram positive and gram negative infection are the beta lactam antibiotics [3]. The most common mechanism of bacterial resistance to these antibiotics is the production of beta lactamases enzyme are plasmid mediated and capable of hydrolyzing the beta lactam ring and inactivating a wide variety of beta lactam antibiotics and also shows resistance to other classes of antibiotics carbapenem which leads to Multi drug resistance (MDR). The ability of MDR bacteria to resist different classes of antibiotics (three or more than three classes of antibiotics) which are structurally different and have different molecular targets [4]. Antibiotics resistance is a result of antibiotic use. The greater the volume of antibiotics used, the greater will be the chances of arising antibiotic resistance population of bacteria [5].

The aim of present study was to determine the choice of drugs in the treatment of Multi drug resistance (MDR) producing organism among the clinical isolates of *Pseudomonas aeruginosa* and their susceptibility to antimicrobials.

2. Methods

The cross - sectional study was carried out in the Institute of Biological Science Sage University Indore during the period of January 2021 to June2021. Total 110 samples were isolates of *Pseudomonas aeruginosa* collected from different clinical specimen's urine, blood, pus, sputum in pathology &

microbiology labs from inpatients and out patients of different hospitals and clinics.

2.1 Bacterial Isolates

One hundred& ten isolates of *Pseudomonas aeruginosa* were recovered from various specimens. Out of 110 isolates n=45 (40.90%) were found to be MDR positive *P. aeruginosa* strains followed by 19 isolates from Pus, 12 isolates from Urine, 09 isolates from Blood and 05 isolates from sputum. All the specimens were quickly sent to microbiology laboratory to be processed with Standard methods for isolation and identification of these bacteria.

Isolation of organisms from urine, blood, pus and sputum sample inoculated on Blood agar media, Mac - Conkey agar and incubated overnight at 37ºc. Identification of *Pseudomonas aeruginosa* organism is done on automated ID/AST instrument VITEK 2 machine.

2.2 Phenotypic detection and Antimicrobial Susceptibility testing (MICs)

Phenotypic confirmatory test (Double - Disc synergy test): In this test third generation cephalosporin i. e. Ceftazidime (30µg) alone and in combination with Clavulanic acid (10µg) were used. Ceftazidime discs is placed on side and combine with Clavulanic acid discs is placed on other side and incubate at 37ºc diameter of zone of inhibition was measured. The diameter of zone of inhibition in combination with clavulanic acid shows 5mm or more increases in diameter of zone inhibition then alone discs [6] **Antimicrobial susceptibility** is done by broth dilution method and susceptibility done by Minimum inhibitory concentration (MICs) using AST instrument VITEK 2 machine recommended by Clinical and laboratory standards institute (CLSI). After isolation of *Pseudomonas aeruginosa* organism should handle with simple standardized inoculum 0.5 McFarland suspension. The inoculum suspension is placed into Vitek 2 cassette which are linked by barcode. Once the cassette is loaded, the instrument handles all subsequently steps for incubation and reading. Results at a glance after incubation of 5 to 8 hrs. The type of antimicrobial susceptibility card (AST) N 281 is used in the testing instrument. Following antibiotics in panel 281 are Ticarcillin/Clavulanic Acid, Piperacillin / Tazobactam, Ceftazidime, Cefopaerazone/ Sulbactam, Cefepime, Aztreonam, Doripenem, Imipenem, Meropenem, Amikacin, Gentamicin Ciprofloxacin, Levofloxacin, Minocycline, Tigecycline, Colistin, Trimethoprim/ Sulfamethoxazole are used for susceptibility.

3. Results

Pseudomonas aeruginosa were isolated from clinical specimens. A total of one hundred tens bacterial isolates were analyzed from various Clinical specimens. Out of 110 isolates n=45 (40.90%) were found to be MDR positive *P. aeruginosa* strains (Table 1). ATCC *P. aeruginosa* 27853 was used as positive control. The maximum number of MDR *P. aeruginosa* were isolated from pus sample n= 19 (42.22%) followed by urine sample n=12 (26.66%), Blood sample n=09 (20.0%) and sputum sample n=05 (11.11%) as represented in **Table 1.**

Table 1: Prevalence of MDR *P. aeruginosa* in various clinical specimens

S. No.	Clinical Samples	No. of Isolates (n=45)	Frequency %
1	Pus Sample	19	42.22 %
2	Urine Sample	12	26.66 %
3	Blood Sample	09	20.00 %
4	Sputum Sample	05	11.11 %

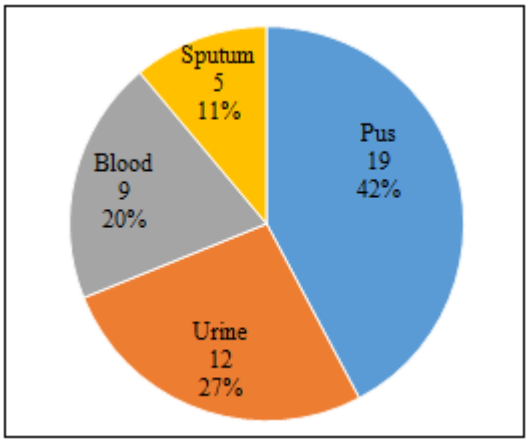

Figure 1: Distribution of MDR. *Pseudomonas aeruginosa* in clinical samples

3.1 Antibiogram of P. aeruginosa in Pus Sample

The highest resistance of antimicrobial agents in pus sample was observed against Cephalosporin group Ceftazidme 100%. which was supported by Wang et al., exhibited 100% resistance to this 3rd generation antibiotics [7]. Study reported by Hanza et al., also explained Pseudomonas aeruginosa with 100% resistance to the same group, Sulfa group Trimethoprim/ sulfamethoxazole 100% followed by Ticarcillin/ Clavulanic acid 84.21%, Carbapenem group meropenem 78.94%, fluoroquinolones group Levofloxacin 73.68%, aminoglycosides Amikacin 68.42% groupof antibiotics. While 68.42% of the isolates were sensitive to Colistin with lowest MICs <=0.5 µg/ml followed by Tigecycline 52.63 % with lowest MICs <=0.5 µg/ml (**Table 2) (Figure 2**).

Table 2: Antibiogram of MDR *P. aeruginosa* in Pus Sample with Minimum inhibitory concentration value

Antimicrobial agents	No. of MDR *P. aeruginosa*isolates					MICs Break Points µg /ml	Percentage% resistance of MDR *P. aeruginosa*
	Sensitive % MICs n=19 µ g/ml			Resistant MICs n=19 µg/ml			
Ticarcillin/Clavulanic acid	3	15.78%	< = 8	16	>=128	≤16 - ≥128	84.21 %
Piperacillin/Tazobactam	8	42.10%	< = 4	11	>=64	≤16 - ≥128	57.89 %
Ceftazidime	0	0 %	< = 1	19	>=64	≤4 - ≥16	100.0 %

Cefoperazone/Sulbactam	7	36.84%	< = 8	12	>=64	≤16 - ≥64	63.15 %
Cefepime	1	5.26 %	< = 1	18	>=16	≤2 - ≥16	94.73 %
Aztreonam	1	5.26 %	< = 2	18	>=32	≤4 - ≥16	94.73 %
Doripenem	3	15.78%	< = 0.5	16	>=16	≤1 - ≥4	84.21 %
Imipenem	1	5.26 %	< = 1	18	>=8	≤1 - ≥4	94.73 %
Meropenem	4	21.05%	<=0.25	15	>=4	≤1 - ≥4	78.94 %
Amikacin	6	31.57%	< = 2	13	>=64	≤16 - ≥64	68.42 %
Gentamicin	1	5.26 %	< = 2	18	>=64	≤4 - ≥16	94.73 %
Ciprofloxacin	0	0 %	0	19	>=4	≤1 - ≥4	100 %
Levofloxacin	5	26.31%	< = 2	14	>=8	≤2 - ≥8	73.68 %
Minocycline	1	5.26 %	< = 0.5	18	>=32	≤4 - ≥16	94.73 %
Tigecycline	**10**	**52.63%**	**< = 0.5**	**09**	**>=16**	**≤2 - ≥8**	**47.36 %**
Colistin	**13**	**68.42%**	**< = 0.5**	**6**	**>=32**	**≤2 - ≥4**	**31.57 %**
Trimethoprim/sulfamethox.	0	0 %	0	19	>=320	≤40 - ≥80	100 %

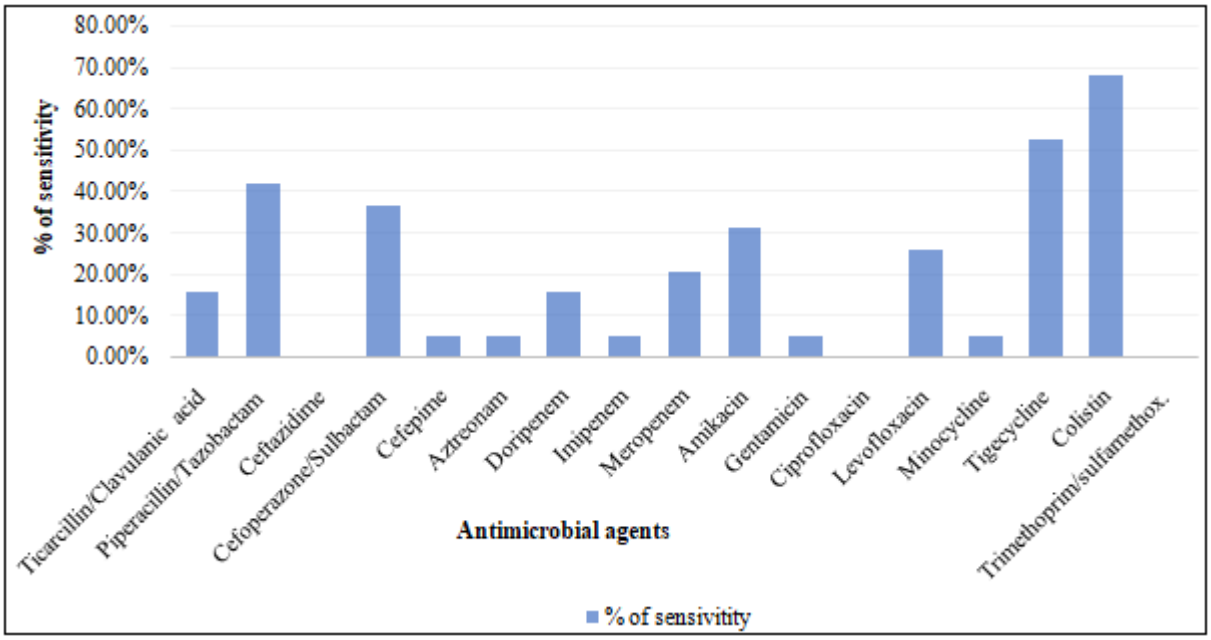

Figure 2: Antimicrobial sensitivity pattern of MDR *P. aeruginosa* in Pus sample

3.2Antibiogram of MDR *P. aeruginosa* in Urine Sample

The highest resistance of antimicrobial agents in Urine sample was observed against Cephalosporin group Ceftazidme 100% which was supported by Wang et al., exhibited 100% resistance to this 3rd generation antibiotics [7]. Study reported by Hanza et al. also explained Pseudomonas aeruginosa with 100% resistance to the same group [8]. The study shows 75.00% of the isolates were sensitive to Fosfomycin with lowest MICs <=16µg/ml followed by Piperacillin/ Tazobactam 66.66% MICs <=4 µg/ml, Nitrofurantoin 66.66% MICs<=16 µg/ml, Amikacin 66.66% MICs <=2 µg/ml, Cefoperazone/ Sulbactam 58.35% MICs <=8 µg/ml, Colistin and Levofloxacin is 50% MICs<=0.5, MICs<=2 respectively. The antimicrobial agents sensitivity & resistance patterns of MDR *P. aeruginosa* in Urine sample (n=12) are presented in **Table 3 Figure 3**. In urine sample antibiotics AST panel N 235 is used.

Table 3: Antibiogram of MDR *P. aeruginosa* in UrineSample Minimum inhibitory concentration

Antimicrobial agents	No. of MDR *P. aeruginosa*isolates					MICs Break Pointsµg	Percentage% resistance of MDR *P. aeruginosa*
	Sensitive % MICs n=12 µ g/ml			Resistant MICs n=12			
Ticarcillin/Clavulanic acid	4	33.33%	< = 8	8	>=128	≤16 - ≥128	66.66 %
Piperacillin/Tazobactam	**8**	**66.66%**	**< = 4**	**4**	**>=64**	**≤16 - ≥128**	**33.33 %**
Ceftazidime	0	0%	0	12	>=64	≤4 - ≥16	100.0 %
Cefoperazone/Sulbactam	**7**	**58.33%**	**< = 8**	**5**	**>=64**	**≤16 - ≥64**	**41.66 %**
Cefepime	0	0%	0	12	>=16	≤2 - ≥16	100.0 %
Aztreonam	0	0%	0	12	>=32	≤4 - ≥16	100.0 %
Fosfomycin	**9**	**75.00%**	**< = 16**	**3**	**>=256**	**≤64 - ≥256**	**25.0 %**
Nitrofurantoin	**8**	**66.66%**	**< = 16**	**4**	**>=128**	**≤32 - ≥128**	**33.33 %**
Meropenem	3	25.00%	<=0.25	9	>=4	≤1 - ≥4	75.00 %
Amikacin	**8**	**66.66%**	**< = 2**	**4**	**>=64**	**≤16 - ≥64**	**33.33 %**
Gentamicin	2	16.66%	< = 4	10	>=64	≤4 - ≥16	83.33 %
Ciprofloxacin	0	0%	0	12	>=4	≤1 - ≥4	100 %
Levofloxacin	**6**	**50.00%**	**< = 2**	**6**	**>=8**	**≤2 - ≥8**	**50.0 %**

Minocycline	4	33.33%	< = 0.5	8	>=32	≤4 - ≥16	66.66 %
Tigecycline	**9**	**75.00%**	**< = 1**	**3**	**>=16**	**≤2 - ≥8**	**25.00 %**
Colistin	**6**	**50.00%**	**< = 0.5**	**6**	**>=32**	**≤2 - ≥4**	**50.00 %**
Trimethoprim/sulfa	0	0%	0	12	>=320	≤40 - ≥80	100 %

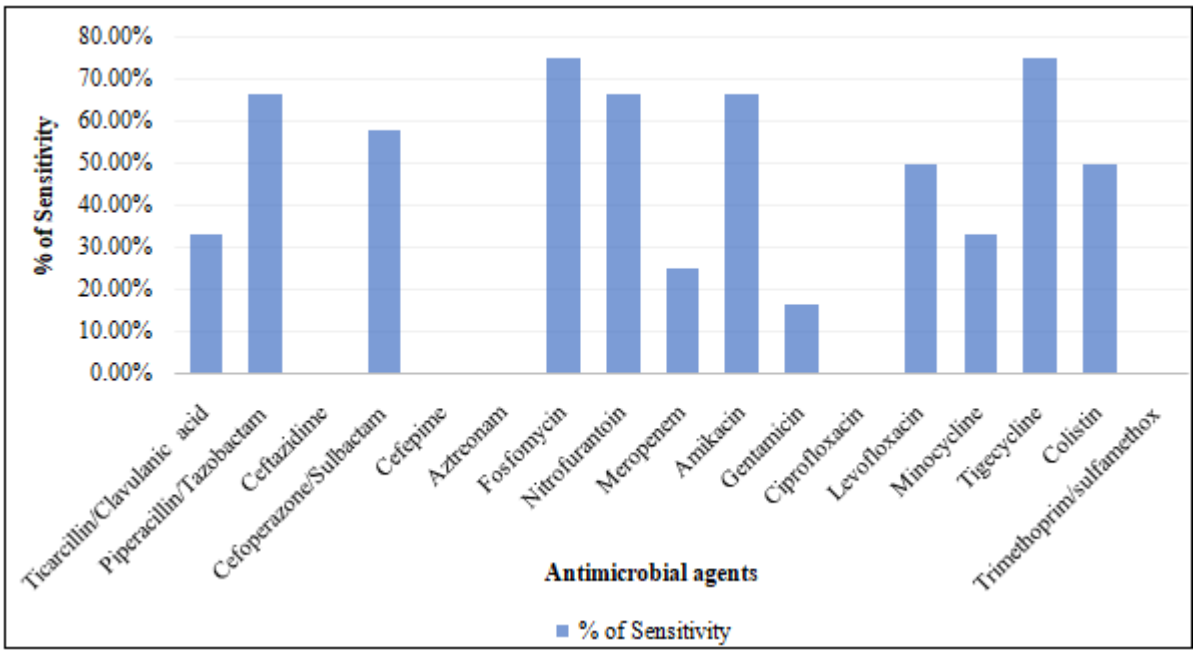

Figure 3: Antimicrobial sensitivity pattern of MDR *P. aeruginosa* in Urine sample

3.3Antibiogram of MDR *P. Aeruginosa* in Blood Sample

The highest resistance of antimicrobial agents in Blood sample was observed against Cephalosporin group Ceftazidme, cefepime 100%, Sulfagroup Trimethoprim/ sulfamethoxazole100% monobactam Aztreonam 100% followed by Gentamicin, Ciprofloxacin 100% respectively. While 88.88% of the isolates were sensitive to Piperacillin/ tazobactam with lowest MICs <=4µg/ml followed by Tigecycline 77.77% with lowest MICs <= 0.5µg/ml, Meropenem, Levofloxacin, Colistin 55.55% respectively The antimicrobial agents sensitivity & resistance patterns of MDR *P. aeruginosa* in Blood sample (n=9) are presented in **Table 4 figure 4**.

Table 4: Antibiogram of MDR *P. aeruginosa* in Blood Sample with Minimum inhibitory concentration

Antimicrobial agents	No. of MDR *P. aeruginosa*isolates					MICs Break Points µg /ml	Percentage% resistance of MDR *P. aeruginosa*
	Sensitive % MICs n= 9 µ g/ml			Resistant MICs n= 9 µg/ml			
Ticarcillin/Clavulanic acid	2	22.22%	< = 8	7	>=128	≤16 - ≥128	77.77 %
Piperacillin/Tazobactam	**8**	**88.88%**	**< = 4**	**1**	**>=64**	**≤16 - ≥128**	**11.11 %**
Ceftazidime	0	0 %	0	9	>=64	≤4 - ≥16	100.00 %
Cefoperazone/Sulbactam	**7**	**77.77%**	**< = 8**	**2**	**>=64**	**≤16 - ≥64**	**22.22%**
Cefepime	0	0 %	0	9	>=16	≤2 - ≥16	100.00 %
Aztreonam	0	0 %	0	9	>=32	≤4 - ≥16	100.00 %
Doripenem	1	11.11%	< = 0.5	8	>=16	≤1 - ≥4	88.88 %
Imipenem	1	11.11%	< = 1	8	>=8	≤1 - ≥4	88.88 %
Meropenem	**5**	**55.55%**	**<=0.25**	**4**	**>=4**	**≤1 - ≥4**	**44.44 %**
Amikacin	4	44.44%	< = 2	5	>=64	≤16 - ≥64	55.55 %
Gentamicin	0	0%	0	9	>=64	≤4 - ≥16	100.00 %
Ciprofloxacin	0	0%	0	9	>=4	≤1 - ≥4	100.00 %
Levofloxacin	**5**	**55.55%**	**< = 2**	**4**	**>=8**	**≤2 - ≥8**	**44.44%**
Minocycline	3	33.33%	< = 0.5	6	>=32	≤4 - ≥16	66.66 %
Tigecycline	**7**	**77.77%**	**< = 0.5**	**2**	**>=16**	**≤2 - ≥8**	**22.22 %**
Colistin	**5**	**55.55%**	**< = 1**	**4**	**>=32**	**≤2 - ≥4**	**44.44 %**
Trimethoprim/sulfa	0	0%	0	9	>=320	≤40 - ≥80	100 %

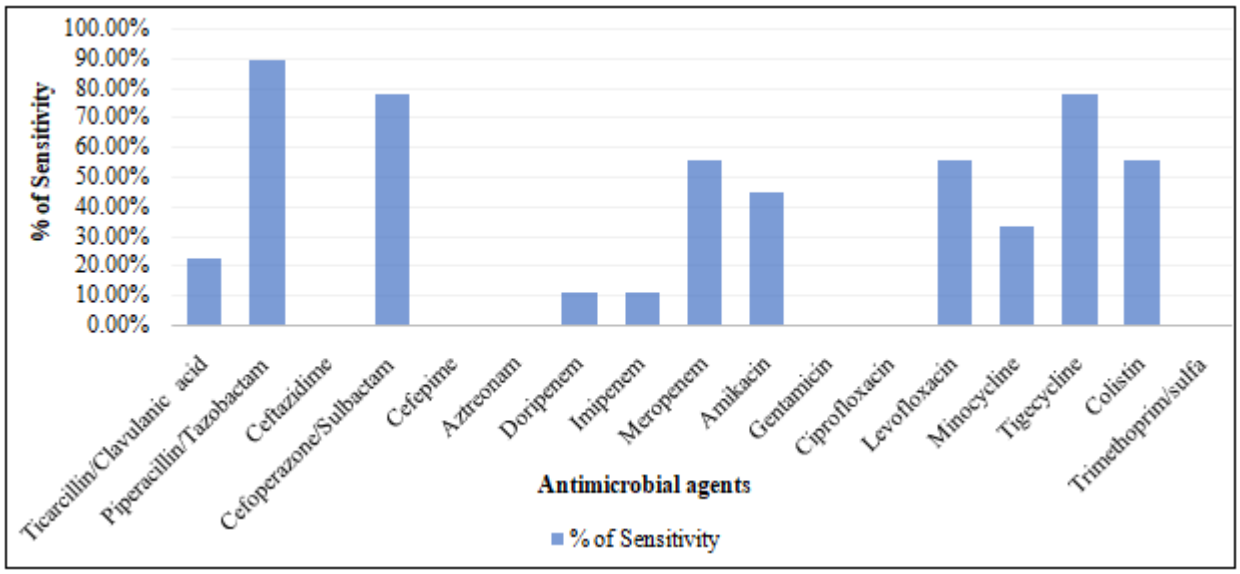

Figure 4: Antimicrobial sensitivity pattern of MDR *P. aeruginosa* in Blood sample

3.4 Antibiogram of MDR *P. aeruginosa*in Sputum

The highest resistance of antimicrobial agents in Blood sample was observed against Cephalosporin group Ceftazidme, cefepime100%, Sulfagroup Trimethoprim/ sulfamethoxazole 100% monobactam Aztreonam 100%followed by Gentamicin, Ciprofloxacin 100% respectively. While 100.0% of the isolates were sensitive to Colistin with lowest MICs <=0.5µgfollowed by Piperacillin/ tazobactam 80% with lowest MICs <=4µg/ml, Cefoperazone/ sulbactam 80% MICs <=8 µg/ml, Meropenem 80% MICs <=0.25, Levofloxacin 80% MICs <=2. The antimicrobial agents sensitivity & resistance patterns of MDR *P. aeruginosa* in Sputum sample (n=5) are presented in Table 5.

Table 5: Antibiogram of MDR *P. aeruginosa* in Sputum Sample with Minimum inhibitory concentration

Antimicrobial agents	No. of MDR *P. aeruginosa*isolates					MICs	Percentage% resistance of MDR *P. aeruginosa*
	Sensitive [%]MICs n= 5 µ g/ml			Resistant MICs n=5µg/ml		Break Pointsµg	
Ticarcillin/Clavulanic acid	1	20.00%	< = 8	4	>=128	≤16 - ≥128	80.00 %
Piperacillin/Tazobactam	**4**	**80.00%**	**< = 4**	**1**	**>=64**	**≤16 - ≥128**	**20.00 %**
Ceftazidime	0	0%	0	9	>=64	≤4 - ≥16	100.00 %
Cefoperazone/Sulbactam	**4**	**80.00%**	**< = 8**	**1**	**>=64**	**≤16 - ≥64**	**20.00%**
Cefepime	0	0	0	5	>=16	≤2 - ≥16	100.00 %
Aztreonam	0	0	0	5	>=32	≤4 - ≥16	100.00 %
Doripenem	3	60.00%	< = 0.5	2	>=16	≤1 - ≥4	40.00 %
Imipenem	3	60.00%	< = 1	2	>=8	≤1 - ≥4	40.00 %
Meropenem	**4**	**80.00%**	**<=0.25**	**1**	**>=4**	**≤1 - ≥4**	**20.00 %**
Amikacin	2	40.00%	< = 2	3	>=64	≤16 - ≥64	60.00 %
Gentamicin	0	0%	0	9	>=64	≤4 - ≥16	100.00 %
Ciprofloxacin	0	0%	0	9	>=4	≤1 - ≥4	100.00 %
Levofloxacin	**4**	**80.00%**	**< = 2**	**1**	**>=8**	**≤2 - ≥8**	**20.00%**
Minocycline	3	60.00%	< = 0.5	2	>=32	≤4 - ≥16	40.00 %
Tigecycline	**4**	**80.00%**	**< = 0.5**	**1**	**>=16**	**≤2 - ≥8**	**20.00 %**
Colistin	**5**	**100.00%**	**< = 1**	**5**	**>=32**	**≤2 - ≥4**	**0 %**
Trimethoprim/sulfa	0	0%	0	5	>=320	≤40 - ≥80	100 %

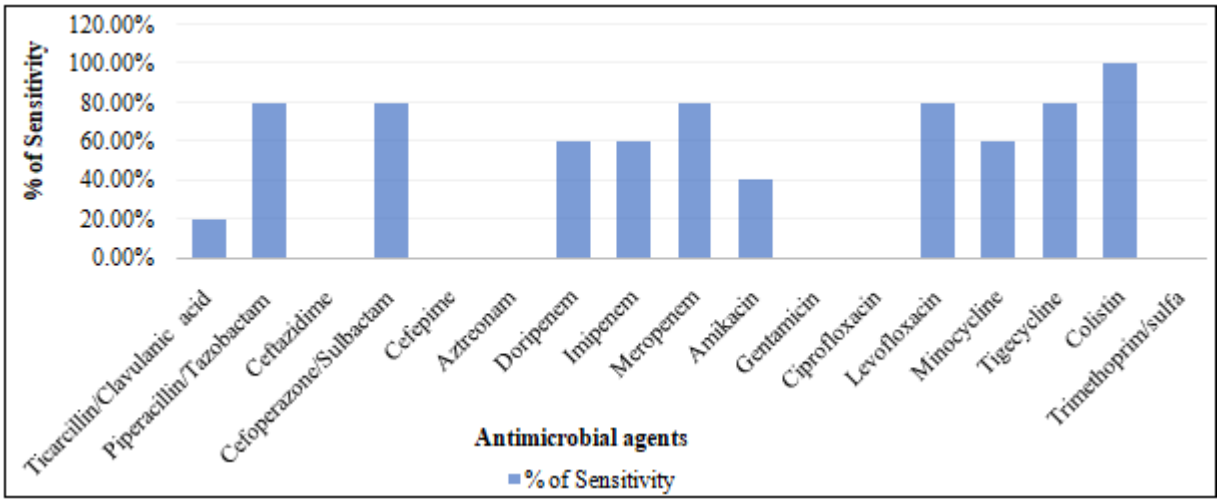

Figure 5: Antimicrobial sensitivity pattern of MDR *P. aeruginosa* in Sputum sample

4. Discussion

P. aeruginosa is a leading cause of infection in hospitalized patients, nosocomial infections including urinary tract infections, pneumonia and bacteremia. The surveillance systems reports (National Nosocomial Infections Surveillance, NNIS), 17% cases of *P. aeruginosa* to be the second most common organism isolated in nosocomial pneumonia, the third 11% of cases were most common organism isolated in both surgical site pus infection and urinary tract infection (UTI) and the fifth 9% of cases were most common organism isolated from all sites of nosocomial infection [9]. The survival of organism in environment cause Nosocomial infection due to some favorable condition that *P. aeruginosa* organisms survive and thrives in moist environments such as soil, water and found in large numbers on fresh fruits and vegetables. This organism required minimal nutritional requirements in a group as pseudomonads and are capable of using a wide variety of environmental sources for nutrition. As a source of carbon and nitrogen *P. aeruginosa* only needs acetate and ammonia in anaerobic conditions and does not carry out fermentation, rather obtaining energy from the oxidation of sugars. This flexible nature of nutritional requirement permits its growth in marginal environments. They are difficult organisms to eradicate from areas that become contaminated, such as operating rooms, hospital rooms, clinics, and medical equipment [10].

In the present study we observed isolates n=45 (40.90%) MDR *P. aeruginosa* from110 different clinical specimens. The maximum number of MDR *P aeruginosa* were isolated from Pus sample n=19 (42.22%) followed by Urine sample n=12 (26.66%), Blood sample n=9 (20.0%) and sputum n=5 (11.11%). The study shows that maximum number of MDR *P aeruginosa* were isolated from Pus sample n=19 (42.22%). The most commonly pus infection is focused on surgical site [11]. *Pseudomonas aeruginosa* is primarily a nosocomial pathogen. Within the hospital, *P. aeruginosa*present in numerous reservoirs respiratory equipment, disinfectants, food, tap, sinks and mops. Likewise a study conducted by Fouzia Khan *et al* 2014The maximum number of MDR *P. aeruginosa* were isolated from pus samples (33.3%), followed by wound swabs (26.6%), bronchial fluid (23.3%), urine (10%) and blood samples (6.6%) [12]. Related study conducted by Basanti Pathi et al 2013 Maximum number of *P aeruginosa* were isolated from pus/wound swab (93) followed by urine (74), sputum (60), blood and body fluids (36) [13].

The ESBLs producing *P. aeruginosa* isolates exhibited co - resistance against most of the antibiotics tested. All ESBL producing *P. aeruginosa* isolates in pus sample were sensitive to Colistin and Tigecycline, urine sample were sensitive to fosfomycin, tigecycline, amikacin, piperacillin/tazobactam and nitrofurantoin, blood sample were sensitive to piperacillin/ tazobactam, Cefoperazone/ sulbactam and tigecycline and sputum sample were sensitive to Colistin, piperacillin/ tazobactam, Cefoperazone/ sulbactam, Meropenem and Tigecycline. This is in harmony with a study is conducted by Farooq L*et al* 2019 [14], similarly conducted by Maria Mustaqul gill *et al*.2013 [15], Banerjee S. *et al*.2017 [16], Laura Puzniak et al.2019 [17] and Pradeep Gamit *et al.* (2016) [18].

The study concluded a great advance for treatment of serious bacterial infections caused by MDR beta lactam resistant bacteria, due to their broad spectrum of activity and stability to hydrolysis by most beta lactamases, combination therapy penicillin and cephalosporin's group with beta lactamases inhibitors (piperacillin/ tazobactam, Cefoperazone/ sulbactam), carbapenems, colistin, fosfomycin and tigecycline have been the drug of choice for treatment of infections caused by cephalosporin - resistant or multi drug resistant gram negative bacilli

5. Conclusion

The present study highlights existing of Multi Drug Resistance will create panic problems in the future due to mutation and lack of therapeutic option. In order to prevent widespread of antimicrobial resistance in MDR producing organism is important to stop misuse & overuse of antibiotics especially broad spectrum antibiotics. Routine survey and monitoring MDR producing organism help in selection of appropriate antibiotics. Colistin, Fosfomycin, Piperacillin/ tazobactam, Tigecycline can be suggested as the drugs of choice against MDR *P. aeruginosa* in different clinical specimens in our study. It is also important to aware community as well as hospitals to monitoring antibiotics

patterns and policies to decrease the spread of MDR &ESBLs producing microorganism.

6. Acknowledgement

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