Original Research Article

EVALUATING THE ANTIMICROBIAL RESISTANCE PATTERNS AMONG MAJOR BACTERIAL PATHOGENS ISOLATED FROM CLINICAL SPECIMENS TAKEN FROM PATIENTS IN 2 TERTIARY'S HOSPITAL, FOR ONE YEAR PERIOD IN SANA'A, YEMEN

ABSTRACT

Background and objectives: Nowadays, antimicrobial resistance (AMR) is a major public health threat, with antimicrobial resistance bacteria increasing exponentially. This study evaluates the epidemiological profiles and antimicrobial resistance of Gram-negative bacteria (GNB) and Gram-positive bacteria (GPB) isolated from clinical samples among patients admitted to two tertiary hospitals in Sana'a city for one year (2019). **Methods:** This was a retrospective study of clinical samples of patients collected from January 2019 until the end of December 2019. All samples were evaluated to determine presence of infectious agents using standard methods for isolation and identification of bacteria and yeasts from clinical samples of patients admitted to Al-Jumhouri University Hospital and Al-Kuwait University Hospital in Sana'a city. Antibiotic resistance was determined using Kirby–Bauer disk diffusion methods. Antibiotic sensitivity results were interpreted according to CLSI. **Results:** 2,931 different pathogenic bacteria were detected from 24,690 different clinical specimens. The samples had an overall detection rate of 11.9% (2931/24,690). Among the bacterial pathogens isolated from clinical samples, 52.4% (n = 1536) had GPB and 415% (n = 1207) had GNB. The predominant GNB isolates were *E.coli* (646), *Klebsiella* spp (177), *Pseudomonas aeruginosa* (121), *Acinetobacter baumannii* (43), *Enterobacter* spp. (32), *Citrobacter* spp. (34), respectively. Among the GPB, *S.aureus* was the most common (772), Coagulase-negative *Staphylococcus* (238), Non-hemolytic *Streptococcus* (266), Other alpha-hemolytic *Streptococcus* (115), *Streptococcus pyogenes* (55), and *Streptococcus pneumoniae* (13). A high rate of antibiotic resistance was recorded for sulfamethoxazole/trimethoprim (85.5%), ceftazidime (81.07%), ampicillin (70.4%), cefuroxime (66.4%). **Conclusions:** Our findings revealed that the rate of resistance between GNB and GPB is associated with the incidence of different infections in patients attending two major tertiary hospitals in Sana'a city is very high. These results indicate ongoing screening and follow-up programs to detect antibiotic resistance, and also suggest the development of antimicrobial stewardship programs in Sana'a, Yemen.

KEYWORDS: antimicrobial resistance , Gram-negative bacteria, Gram-positive bacteria, bacterial, infection , Yemen

INTRODUCTION

Global antimicrobial resistance is increasing due to increased prescription and dispensing in developing countries and indiscriminate use. It is estimated that 700,000 to several million deaths occur annually and remain a major public health threat worldwide [1]. Each year in the United States, at least 2.8 million people become infected with antibiotic-resistant bacteria, at least 35,000 people die, and US$55 billion in health care costs and lost productivity increase[2,3]. According to estimates by the World Health Organization (WHO), three hundred and fifty million deaths due to antimicrobial resistance could occur by 2050. By that time, the annual death toll will be ten million, according to a United Nations report [4,5]. Nowadays, antimicrobial resistance (AMR) is a major public health threat,[6,7] and antimicrobial resistance bacteria in different hospital departments are increasing dramatically all over the world and in Yemen this problem is more extensive and complex[8-20]. It has been predicted that if appropriate control and prevention measures are not taken, antimicrobial resistance will become one of the leading causes of death among hospitalized or non-hospitalized patients in developing and developed countries. Proper use and administration of antibiotics is essential to treat bacterial infections[21]. Consequently, inappropriate prescription and abuse of antibiotics can be a factor to the emergence of pathogenic bacteria that are resistant to antibiotics, restriction of treatment options, increased hospitalization time, higher treatment costs and, finally, higher mortality[22].

According to the WHO Global Action Plan on Antimicrobial Resistance, it is important to raise awareness of antimicrobial resistance through monitoring and research programs in different parts of the world. Monitoring antimicrobial resistance is critical and has many benefits including: 1) providing data on the rate of bacterial resistance, 2) helping to select appropriate antibiotics and thus reducing the rate of antimicrobial resistance, 3) lowering hospitalization rate and treatment costs, and 4) Low mortality

rate [21]. Therefore, the current study evaluates the epidemiological profiles and antimicrobial resistance of Gram-negative bacteria (GNB) and Gram-positive bacteria (GPB) isolated from clinical samples among patients admitted to two tertiary hospitals in Sana'a city for one period year (2019).

MATERIALS AND METHODS

Study design and identification of microorganisms: This was a retrospective study of clinical samples of patients collected over a one-year period from January 2019 through the end of December 2019 at the Microbiology Department of the National Center for Public Health Laboratories (NCPHL) Sana'a, Yemen. Samples were provided by two major hospitals in Sana'a: Al-Jumhouri University Hospital and Al-Kuwait University Hospital. This research used microbiological laboratory data for 24690 different clinical samples (Table 1) collected from different inpatient hospital wards and from different clinics of the same hospitals. Clinical samples were cultured in an appropriate medium according to standard methods for isolation and identification of bacteria for different samples[23]. Isolation and identification of different bacterial strains from positive cultures were performed using conventional biochemical assays including IMVIC assay (Indole, Methyl red, Voges proskauer and Citrate), catalase and oxidase assay, growth on triglyceride Agar and Kligler Iron Agar, and Bile esculin agar, SH_2 production, motility test, growth on 6% NaCl and DNase assay[23].

Antibiotic susceptibility testing: The antibiotic resistance of isolates was determined using the Kirby–Bauer disk diffusion method (DDM)[24]. Then the results of the DDM method were interpreted according to the criteria of the Clinical and Laboratory Standards Institute (CLSI). Antibiotic disks and media powders used in NCPHL are usually Sigma-Aldrich sources. Gram-positive and negative bacterial isolates including *Escherichia coli* (ATCC 25922), *Pseudomonas aeruginosa* (ATCC 27853) and *Staphylococcus aureus* subsp. *Aureus* ATCC 25923 was used as quality control for the DDM test. Antimicrobial susceptibility to Gram-positive bacteria and GNB was determined using the antibiotic disks mentioned in Table 3. The research results were documented as either sensitive (S), intermediate (I) or resistant (R).

RESULTS

Number and distribution of specimens and positive cultures: During this year period, a total of 24690 different clinical cultures were collected from January 2019 until the end of December 2019. Among them, 2931 (11.9%) positive cultures were isolated from different types of bacteria. Among the GPB, about 52.4% and 41.2% of the total GNB cultures were positive and the remaining positive were *Candida albicans* (6.4%). The frequency of different clinical samples from which bacterial strains were isolated is shown in Table 1. The most common positive samples were as follows: urine (n = 1043; 35.6%), pus (n = 680; 23.2%), semen (337, 11.5). %), sputum (n = 203; 6.9%) and ear swab (n = 163; 5.6%) (Table 1).

Pathogen distribution: GNB and GPB comprised 41.2% (n = 1207) and 52.4% (n = 1536) of the total bacteria, respectively. The most prevalent isolated GPB were *Staphylococcus aureus* (n=772; 26.3%), non-hemolytic *streptococcus* (n=266; 9.1%), coagulasenegative *staphylococcus* (n=238; 8.1%) and alpha-hemolytic *streptococcus* (n=115 ; 3.9%) (Table 2). The most prevalent isolated GNB were *Escherichia coli* (n = 646; 22.04%), *Pseudomonas aeruginosa* (n = 209; 7.1%), *Klebsiella* spp (n = 177; 6.03%) *Acinetobacter* spp (n = 43; 1.46%) and *Citrobacter*. spp (n = 34; 1.16%) (Table 2).

Antimicrobial susceptibility: The resistance rates of isolated bacteria to commonly used antimicrobials are shown in Table 3. In bacteria isolated from different samples, the highest rates of resistance belonged to Sulphamethoxazole/Trimethoprime (n = 900; 85.5%), Ceftazidime (n = 1114; 81.07%), ampicillin (n = 1055; 70.4%), ceftoroxime (n = 886; 66.4%), and cefotaxime (n = 597; 32.6%).

DISCUSSION

In the current study, the highest rates of resistance occurred to Sulphamethoxazole/Trimethoprime (85.5%), Ceftazidime (81.07%), Ampicillin (70.4%), Cefturixime (66.4%), Cefotaxime (32.6%) (Table 3). This generally high rate of resistance can be explained by the fact that the rise in drug resistance is mainly caused by the use of antimicrobials in humans and other animals, and the prevalence of resistant strains between the two. Increased resistance has also been linked to the release of inadequately treated effluents from the pharmaceutical industry, especially in countries where bulk pharmaceuticals are manufactured. Antibiotics increase the selective pressure in bacterial populations, causing the susceptible bacteria to die; this increases the percentage of resistant bacteria that continue to grow. Even at very low levels of antibiotics, resistant bacteria can have the advantage of growing and growing faster than weak bacteria. As antibiotic resistance becomes more common, so does the need for alternative

treatments. There have been calls for new antibiotic treatments, but new drug development is becoming scarce[25, 26].

This study examined the prevalence of antibiotic resistance among major pathogenic bacteria isolated from inpatient and outpatient settings in two tertiary's hospitals, in Sana'a city, Yemen. Given that these antibiotic resistance to GNB and GPB can cause severe infections in hospitalized patients, especially in immunocompromised patients, the elderly, neonates and children, the presence and distribution of these agents is one of the main concerns of clinicians[19, 20, 27]. The application of several classes of antibiotics is not permitted in neonates and children and because there are different patterns of antimicrobial resistance in different areas, selection and prescribing of appropriate antibiotics to treat different infections in immunocompromised, elderly, neonates and children is difficult. Moreover, knowing the patterns of antimicrobial resistance can help clinicians and policy makers to find solutions to resistance problems in their countries [28]. The lack of public surveillance programs for antimicrobial resistance in development such as Yemen and many developed countries will lead to inappropriate use among patients and health care personnel[29]. Therefore, investigation of antimicrobial resistance patterns is critical and important, especially in developing countries such as Yemen, where there are no systematic guidelines for antibiotic use. On the other hand, it is necessary to investigate the antibiotic resistance patterns of GPB and GNB in hospitals and clinics in Sana'a city, during 2019, which could be a valuable model for both clinicians and policy makers in applying experimental treatment.

The result of our study revealed that among 24,690 different clinical samples from patients, 2931 (11.9%) cultures were positive from which various bacteria were isolated. The minimal rate of positive culture in the current study could be due to several reasons: 1) our study used different types of clinical specimens such as cerebrospinal fluid, pleural fluid, dialysis fluid and luminal fluid as the rate of pathogens varies in these specimens, 2) effective training for correct administration of antibiotics , 3) better management and control of infection, and 4) pre-hospitalization antibiotic use.

In the current study, the most prevalent isolated GPB were *Staphylococcus aureus* (26.3%), non-hemolytic *streptococci* (9.1%), coagulase-negative *staphylococci* (8.1%) and alpha-hemolytic *streptococcus* (3.9%). In addition, the most common GNB isolated were *Escherichia coli* (22.04%), *Pseudomonas aeruginosa* (7.1%), *Klebsiella* spp (6.03%) *Acinetobacter* spp (1.46%) and *Citrobacter* spp (1.16%) (Table 2), which is in agreement with two different studies conducted in Tehran, Iran[22,30]. Though, in investigations previously conducted in Yemen[19,20], Saudi Arabia[32] and Iran by Ibrahim Saray *et al.*[33] and Alam *et al.*[31], *Acinetobacter* spp. GNB was most common in positive culture samples. The result of a published studies[18,34] revealed that *E. coli* was the most frequent Gram-negative pathogen in positive cultures of the specimens as in our study (22.04%) (Table 2). The detected differences in proportions of GNB and GPB could be due to the diversity of specimen type, specimen size and applied detecting methods. The results also showed that CoNS isolated from clinical samples may have been considered a common contaminant. Therefore, more effective measures such as hygiene of the hands of health care workers, regular disinfection of medical devices, and disinfection of the sampling site during sampling should be taken. However, although rare, CoNS can cause many infections including infections of the skin and soft tissues, and therefore should not be considered as contaminants at all times[20,35]. Persistent CoNS infection is likely to be associated with various serious complications such as embolic complications, metastatic seeding and septic thrombophlebitis[36]. For that reason, the evaluation the medical association of CoNS is a challenging problem. In medical diagnostic laboratories, the main diagnostic challenge is to assess whether the expected CoNS isolate represents: 1) common colonization of the skin, soft tissues, or mucous membranes, 2) sample contamination during sample collection, handling, and handling, or 3) clinically significant infection[16,19,20,37]. In the case of co-infection of CoNS with other bacterial infections (multimicrobial infections by CoNS), different bacteria isolates showed different patterns of sensitivity and resistance, this difficult diagnostic situation becomes more complex [36,37]. Close cooperation between physicians and diagnostic laboratory specialists can solve this medical and diagnostic problem. In the case of false positive CoNS cases, patients are treated with several antibiotics, and it is expected that in addition to the additional costs, excessive antibiotic selection pressures occur that can lead to the emergence of antibiotic resistance[38]. Consequently, it is essential to answer the question that CoNS isolated from a clinical sample is a true infection or just a common cutaneous colonization. Some of the key factors useful in predicting true infection are: 1) isolating similar strains repeatedly during infection after isolating a strain in pure culture from the infected site, 2) in bloodstream infection, patients must have clinical evidence of infection with a single positive blood culture or Only two positive blood cultures were in CoNS within 5 days, and 3) if CoNS was isolated from the skin or soft tissue bacterial culture of a suspected infectious

lesion, the isolated organism should be suggested as the pathogen and appropriate treatment should be started[39-41].

Among the antibiotics tested differently, the results of our study showed that the rate of resistance to linezolid was very low [0.42% (Table 3)] making it highly effective antibiotics against *S. aureus* and *Enterococcus* spp, which it was in agreement with the rates previously reported by Al-Safani *et al.* [20], by Azimi *et al*. in Iran [30], Dharmapalan *et al*. from India[42], He *et al*. from China [43], Li Tian *et al.* from China [44] and Al-Naqshbandi and others from Iraq[45]. However, the results of several studies were inconsistent with our research and it has been reported that the resistance to linezolid is high [46, 47]. In current vancomycin resistance in *Enterococcus* spp. was much higher (7/32); 21.8% of *Enterococcus* spp. were resistant to vancomycin. Although the identification of *Enterococcus* spp. not performed at the species level, we suggested that most vancomycin-resistant isolates were likely *Enterococcus faecium.* According to several published studies and reports, effective measures have been taken to reduce the risk of VRSA in many countries such as the USA, and some guidelines have been developed to control infections caused by these pathogenic microorganisms[48]. Thus, we suggest similar guidelines and programs designed for patients in Sana'a, Yemen. Our study also revealed that colistin (3.45% resistant rate), in comparison with ciprofloxacin (15.8% resistant rate). These finding were similar with the results of Mahmoudi *et al*. from Iran[22] and Dharmapalan *et al*. from India [42], but different from that reported by Azimi et al in which colistin has a higher rate of resistance than ciprofloxacin[30].

Overall, the results of the current study showed that sulfamethoxazole/trimethoprim, ceftazidime, ampicillin, ceftoreximе and cefotaximе are ineffective antibiotics against GPB or GNB. It is worth mentioning that these antibiotics in different hospitals in Sana'a are often used to control various infections especially sepsis and septicemia. It is well understood that resistance to these antibiotics is increasing daily, which is the result of the selective pressure that is secreted by bystander selection and the misuse or overuse of antibiotics [49].

Consistent with the high antibiotic resistance among bacteria, in an attempt to prevent the undesirable effects of sepsis and septicemia, as well as with the purpose of reduce the mortality rate due to these infections, accurate detection and use of effective antibiotics for effective treatment is critical[50-53]. Thus, awareness of antibiotic resistance patterns among common pathogens, holding workshops to correct prescribing for empirical therapy, and changes in antimicrobial use are necessary and highly recommended. Finally, the results of the DDM are of great importance, and individuals' free access to access to antibiotics should be prevented. In this study, we revealed that GNB and GPB are resistant to different groups of antibiotics. However, it should be noted that these bacteria have two types of antibiotic resistance: acquired resistance and endogenous resistance. For example, according to EUCAST guidelines, most GNB (*Enterobacteriaceae*, *Pseudomonas* spp.) are self-resistant to various antibiotics including penicillin G, oxacillin, macrolides (eg, azithromycin, erythromycin, tylosin), lincosamides (eg lincomycin), streptogramins (eg, Virginiamycin), glycopeptides (eg, vancomycin) and bacitracin. Moreover, based on these guidelines, most GPB are intrinsically resistant to polymyxins and quinolones/fluoroquinolones (eg, enrofloxacin, ciprofloxacin, difloxacin, marbofloxacin)[54]. Therefore,

these resistances should be known by clinicians in order to avoid unsuitable and ineffective therapy.

CONCLUSION

There have been increasing public calls for global collective action to address the threat, including a proposal for international treaty on antimicrobial resistance. Further detail and attention is still needed in order to recognize and measure trends in resistance on the international level; the idea of a global tracking system has been suggested but implementation has yet to occur. A system of this nature would provide insight to areas of high resistance as well as information necessary for evaluating programs and other changes made to fight or reverse antibiotic resistance. Moreover, based on the fact that we did not have full access to patients' information such as treatment outcomes, mortality rate, etc., no specific analysis was carried out, so this information should be provided and an additional study should be carried out to clarify the picture of this problem. According to this data, choosing the right antibiotic is important and vital in treating bacterial infections. Therefore, awareness of antibiotic resistance patterns in pathogenic bacteria can be helpful in making the right therapeutic choice.

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CONFLICT OF INTEREST

No conflict of interest associated with this work.

AUTHOR CONTRIBUTIONS

All authors contributed to data analysis, drafting and revising the paper, gave final approval of the version to be published and agree to be accountable for all aspects of the work. Huda Al-Shami has first authorship.

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Table 1 : Types of specimens collected from inpatients and outpatients in the two hospitals in Sana'a city for culture and sensitivity examination

Type of specimens	Inpatients		Outpatients		Total No (%)
	Al-jmhori hospital	Al-Kuwait hospital	Al-jmhori hospital	Al-Kuwait hospital	
Body fluid	3	0	20	5	28 (0.95)
Breast discharge	0	0	1	7	8(0.27)
CSF	3	0	30	2	35(1.2)
Ear swab	39	8	25	91	163(5.6)
Eye	1	0	3	0	4 (0.14)
Mouth swab	0	0	2	0	2 (0.07)
Nasal swab	1	1	7	2	11 (0.38)
Pus	113	41	231	295	680 (23.2)
Sputum	27	5	56	115	203 (6.9)
Stool	4	0	10	0	14 (0.48)
Throat swab	2	0	30	28	60 (2)
Tongue swab	0	0	0	6	6 (0.02)
Urethral discharge	1	0	5	1	7 (0.03)
Urine	104	65	793	81	1043 (35.6)
Prostatic discharge	0	0	3	0	3 (0.01)
Seminal fluid	10	0	292	35	337 (11.5)
Cervical swab	1	2	110	0	113 (3.9)
High vaginal swab	0	1	23	0	24 (0.81)
Vaginal swab	37	9	100	44	190 (6.5)
Total	346	132	1741	712	2931

Table 2 : First Common isolated pathogens from inpatients and outpatients in the two hospitals in Sana'a city for culture and sensitivity examination		
Name of isolated pathogens	**Frequency**	**Percent %**
Gram positive bacteria		
Staphylococcus aureus	**772**	**26.3**
Staphylococcus saprophyticus	**8**	**0.3**
Other Alpha hemolytic Streptococcus	**115**	**3.9**
Other Beta hemolytic Streptococcus	**19**	**0.6**
Streptococcus pneumonia	**13**	**0.5**
Streptococcus pyogenes	**55**	**1.9**
Non hemolytic Streptococcus	**266**	**9.1**
Streptococcus viridians	**18**	**0.6**
Enterococcous spp	**32**	**1.1**
Coagulasenegative Staphylococcus	**238**	**8.1**
Total	**1536**	**52.4**
Gram Negative Bacteria		
Neisseria gonorrhea	**5**	**0.17**
Neisseria meningitidis	**1**	**0.03**
Haemophilus influenzae	**9**	**0.31**
Escherichia coli	**646**	**22.04**
Klebsiella spp	**177**	**6.03**
Citrobacter spp	**34**	**1.16**
Enterobacter spp	**32**	**1.09**
Proteus mirabilis	**26**	**0.88**
Proteus vulgaris	**15**	**0.5**
Acinetobacter spp	**43**	**1.46**
Pseudomonas aeruginosa	**209**	**7.1**
Salmonella spp	**7**	**0.2**
Salmonella paratyphi	**1**	**0.03**
Salmonella typhi	**1**	**0.03**
Vibrio cholerae	**1**	**0.03**
Total	**1207**	**41.2**
Fungi		
Candida albicans	**188**	**.6.4**
Total	**2931**	**100.0**

Table 3 : Antibiotics resistant percentages average ranges for the first common isolated pathogens number one from inpatients and outpatients in the two hospitals in Sana'a city for culture and sensitivity examination

Antibiotic name	Antibiotics /classes	Resistant		Moderate		Sensitive		Total (n)
		No.	%	No.	%	No.	%	
Ampicillin	**Penicillin/amino-penicillin**	1055	**70.4**	19	1.2	359	23.9	1498
Ceftazidime	**3rd Cephalosporins B-lactam**	1114	**81.07**	26	1.8	415	30.2	1374
Cefdroxil	**4th Cephalosporins B-lactam**	173	**6.49**	4	0.15	92	3.45	2662
Cefepime	**4th Cephalosporins B-lactam**	36	**1.25**	2	0.06	15	0.52	2878
Cefurixime	**2nd Cephalosporins B-lactam**	886	**66.4**	26	1.9	685	51.3	1333
Ceftizoxime	**3rd Cephalosporins B-lactam**	46	**1.62**	0	0	58	2.05	2827
Cefaxime	**4th Cephalosporins B-lactam**	483	**21.4**	7	0.3	193	8.58	2247
Cefotaxime	**3rd Cephalosporins B-lactam**	597	**32.6**	34	1.8	468	25.5	1831
Cefoxtine	**2nd Cephalosporins B-lactam**	141	**5.47**	1	0.03	213	8.26	2576
Cefazoline	**1st Cephalosporins B-lactam**	50	**1.75**	0	0	34	1.19	2847
Cefatrixone	**3rd Cephalosporins B-lactam**	210	**8.33**	6	0.23	197	7.82	2518
Nitrofuranatoin	**Nitrofurans**	41	**1.48**	6	0.21	115	4.15	2769
Ciprofloxacin	**Fluoroquinolones**	307	**15.8**	31	1.2	652	33.3	1941
Ofloxacin	**Fluoroquinolones**	132	**5.20**	12	0.4	251	9.89	2536
Norfloxacin	**Fluoroquinolones**	353	**15.5**	18	0.7	282	12.3	2276
Sulphamethoxazole/Trimethoprime	**Folate pathway inhibitors**	900	**85.5**	29	2.7	949	90.2	1052
Azithromycin	**Macroloides**	409	**18.5**	19	0.8	299	13.5	2204
Doxycyclin	**Tetracycline**	356	**20.3**	60	3.4	762	43.4	1753
Tetracycline-	**Tetracycline**	273	**11.6**	25	1.06	294	12.5	2338
Ampicillin/Sulbactam	**B-lactamase inhibitor combinations**	188	**7.02**	1	0.03	65	2.42	2677
Amoxicillin-Clavulanic Acid	**B-lactamase inhibitor combinations**	646	**35.4**	35	1.9	426	23.3	1824
Piperacillin/Tazobactam	**B-lactamase inhibitor combinations**	28	**0.99**	4	0.1	77	2.72	2822
Fosfomycin	**Fosfomycin**	5	**0.17**	1	0.03	35	1.21	2890
Gentamicin	**Aminogylcosides**	121	**4.86**	10	0.4	312	12.5	2488
Amikacin	**Aminogylcosides**	203	**9.26**	29	1.3	509	23.2	2190
Chloramphenicol	**Phenicols**	50	**1.82**	3	0.1	143	5.23	2734
Imipenem	**Carbapenems**	54	**2.08**	7	0.2	277	10.6	2593
Piperacillin	**Ureido- penicillin**	40	**1.39**	3	0.1	27	0.94	2861
Aztroneome	**Monobactams**	102	**3.77**	7	0.2	117	4.32	2705
Mezlocillin	**Ureido-penicillin**	83	**2.96**	5	0.1	44	1.57	2799
Colistin Sulphate	**Poly-peptide**	96	**3.45**	0	0	54	1.94	2781
Nalidixic Acid	**Quinolones**	273	**10.8**	7	0.2	135	5.36	2516
Methicillin	**Penicillin–stable penicillin**	105	**3.93**	1	0.03	155	5.81	2666
Oxacillin	**Penicillin -stable penicillin**	462	**20.3**	5	0.2	192	8.45	2271
Cloxacillin	**Penicillin -stable penicillin**	171	**6.40**	8	0.2	82	3.07	2669
Erythromycin	**Macroloides**	476	**23.5**	26	1.28	402	19.8	2025
Penicillin-	**Penicillin**	511	**22.6**	5	0.2	154	6.81	2259
Clindamycin-	**Lincosamides**	77	**2.75**	0	0	62	2.22	2792
Vancomycin	**Glycopeptides**	132	**7.80**	24	1.4	1081	63.8	1692
Linzolid	**Oxazolidinones**	12	**0.42**	0	0	98	3.47	2821
Rifampicin	**Ansamycins**	1	**0.03**	0	0	6	0.20	2924