Anti-biotype of Different Bacteria Isolated from Different Clinical Sources

Rebwar Muhammed Hama Salih[1], Khadija Khalil Mustafa[2],
Zirak Faqe Ahmed Abdulrahman[3]

[1]Asst. Lecturer, [2,3]Asst. Professor
[1, 2, 3]Department of Biology, College of Education, University of Salahaddin, Erbil, Iraq

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Abstract: A present study were confirmed on antibiotic resistance against some pathogenic bacterial genera (n = 1178) which include Escherichia coli (n=417), Staphylococcus aureus (n=377), Klebsiella pneumoniae (n=212), Pseudomonas aeruginosa (n=145) and Streptococcus spp (n=27) isolates from clinical sources like; urine (n=641), swab (n=483), wound (n=29) and blood (n=25) was carried out in Internal Lab from Teaching Hospital in Erbil city, in September, 15th 2012 to June, 20th 2013. Susceptibility was determined by the disc diffusion method recommended by the Clinical and Laboratory Standard Institute (CLSI). The following antimicrobials were tested: AMC 20μg, AK (30μg), AM (30μg), AZM (15μg), ATM (30μg), CAR (100μg), CF (30μg), CEC (30μg), CFZ (15μg), CD (5μg), CFM (30μg), CPO (30μg), CP (75μg), FOX (30μg), CPR (30μg), CXM (30μg), KF (30μg), C (30μg), CN (100μg), CIP (5μg), CLM (15μg), DA (2μg), CT (10μg), E (15μg), G (10μg), GIP (5μg), IPM (10μg), DP (5μg), NAF (1μg), NF (30μg), F (300μg), NOR (10μg), OX (1μg), PG (10μg), PIP (100μg), RA (5μg), TE (30μg), TC (75μg), TOB (10μg), SXT (1.25/23.75μg), and VA (30μg). The resistances percent of all bacterial isolates show different range of resistant which start from 0.00% and reach to 100%.

Keywords: Disc diffusion method of Antibiotic Susceptibility, E. coli, K. pneumoniae, P. aeruginosa, S. aureus, and Streptococcus spp.

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1. Introduction

Antibiotics are specific chemical compounds derived from or produced by microorganisms that even in small amounts can selectively inhibit the growth of the life processes or growth of other microorganisms [1]. Antibiotic resistance and reduction in the effectiveness of antibiotics to treat certain bacterial infections in humans has been a growing concern internationally. There has always been consensus that the development of resistance is associated with continued use of antibiotics [2]. Antimicrobial drug resistance is one of the major threats due to widespread use of antimicrobial drugs in general population. Also, it is known that the common infecting organism and pattern of resistance changes over time (changing trends). It can arise from the selection of resistant strains among naturally susceptible species or from the ingress of new strains of naturally resistant species. The extent of use of particular agents in a given environment dictates the rate at which resistance arises among microbial populations [3].

E. coli is the most common cause of infections by gram negative bacilli and it is a frequent cause of outpatient urinary tract infections in women worldwide, septicemia, diarrhea and meningitis. Resistance to recommended first and second line agents, such as penicillin, cephalosporin, sulfa drugs and fluoroquinolones [4,5,6], and is high in many countries and is commonly associated with treatment failure [7,8]. S. aureus has emerged as one of the most important human pathogens and has over the past several decades, been a leading cause of hospital and community acquired infections. One of the reasons for the success of this human pathogen is its great variability, occurring at different periods and places with diverse clonal types and antibiotic resistance patterns within regions and countries. Although infections caused by antibiotic- resistant S. aureus bring about serious problems in the general population, such infections can be particularly devastating for the very young, the elderly and the immunocompromised [9, 10]. Development of resistance to antimicrobial agents by S. aureus is a major concern primarily because they are still frequently associated with hospital and community – acquired infections. The organisms exhibit remarkable versatility in their behavior towards antibiotics, with some strains having overcome most commonly used drugs. Exposure to new antibiotics often results in further selection of homologous resistant strains, a phenomenon particularly favored by irrational antibiotic administration [2].

K. pneumoniae is clinically the most important member of the Klebsiella genus of Enterobacteriaceae [11]. K. pneumoniae is resistant to a number of antibiotics mainly extended-spectrum cephalosporin's and penicillin's due to

acquisition of plasmid that encode for the production of extended spectrum beta lactamases (ESBL) especially TEM and SHV enzymes have been described worldwide [12].

P. aeruginosa is commonly associated with hospital-acquired infection, most notably in immunocompromised individuals [13, 14] and accounts for 10% of all hospital-acquired infections. Specifically, the second most frequently recovered pathogen from intensive care unit (ICU) patients, those with neutropenia (low white blood cell count) [15]. P. aeruginosa is intrinsically resistant to narrow-spectrum penicillins, first- and second-generation cephalosporins, trimethoprim, and sulfonamides. The antipseudomonal agents include extended-spectrum penicillins, such as ticarcillin and piperacillin; extended-spectrum cephalosporins, such as ceftazidime and cefepime; carbapenems; aminoglycosides; and fluoroquinolones [16].

Streptococcus is a very heterogeneous group of bacteria; some members are a part of human normal flora while others are potent pathogens. The primary pathogens are S. pyogenes and S. pneumoniae but other species can be opportunistic. For example, S. agalactiae can produce severe neonatal disease including meningitis, pneumonia and bacteremia in infants. S. mutans is an important contributor to dental caries. Nonpneumococcal streptococci are classified into two groups according to their ability to hemolyze sheep red blood cells. Those isolates that completely lyse or hemolyze red blood cells are called beta-hemolytic streptococci. Based upon antigenic characteristics of the C carbohydrate located in their cell wall the beta-hemolytic streptococci are further classified into groups A, B, C, D, F and G. Those species that only partially hemolyze red blood cells are called viridans group streptococci. There are at least 20 species of viridans streptococci. The viridans streptococci are members of the normal flora of the gastrointestinal and respiratory tracts of humans. Common species include S. constellatus, Streptococcus intermedius, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus salivarius and Streptococcus sanguis [17].

2. Materials and Methods

One thousand, one hundred and seventy eight isolates of bacteria which were E. coli, S. aureus, K. pneumoniae, P. aeruginosa and Streptococcus spp were isolated from different clinical sources like; urine, swab, wound and blood taken from patients who admitted to Internal Lab of Teaching Hospital in Erbil city and all bacterial species were identified according to morphological, cultural and biochemical tests, during the periods of September 15th, 2012 to June 20th, 2013 as shown in table (1). In addition to the biochemical tests and different culture media such as Nutrient, Mannitol Salt, Blood, MacConkey, Kligler Iron and Eosin Methylene Blue agar, also different API identification system (bioMèrieux, France) was performed to support and complete the diagnosis and identification.

Nutrient broth was prepared for each bacterial species which containing approximately $1.5 * 10^8$ CFU per millimeter.
Susceptibility studies: The antibiotic susceptibility test was conducted for all genera and isolates against forty one antibiotics which were Amoxiclave (AMC 20μg), Amikacin (AK 30μg), Amoxicillin (30μg), Azithromycin (AZM 15μg), Aztreonam ATM 30μg), Carbenicillin (CAR 100μg), Cefaclor (CF 30μg), Cefotaxime (CEC 30μg), Cefazolin (CFZ 15μg), Cefdinir (CD 5μg), Cefixime (CFM 30μg), Cefonicid (CPO 30μg), Cefoperazone (CP 75μg), Cefoxitin (FOX 30μg), Cefprozil (CPR 30μg), Cefuroxime (CXM 30μg), Cephalothin (KF 30μg), Chloramphenicol (C 30μg), Cinoxacin (CN 100μg), Ciprofloxacin (CIP 5μg), Clarithromycin (CLM 15μg), Clindamycin (DA 2μg), Colistin (CT 10μg), Erythromycin (E 15μg), Gentamycin (G 10μg), Grepafloxacin (GIP 5μg), Imipenem (IPM 10μg), Methicillin (DP 5μg), Nafcillin (NAF 1μg), Nalidixic acid (NF 30μg), Nitrofurantoin (F 300μg), Norfloxacin (NOR 10μg), Oxacillin (OX 1μg), Penicillin G (PG 10μg), Pipercillin (PIP 100μg), Rifampin (RA 5μg), Tetracycline (TE 30μg), Ticarcillin (TC 75μg), Tobramycin (TOB 10μg), Trimethoprim–sulfamethoxazole (SXT 23.75μg), and Vancomycin (VA 30μg), were determined according to National Committee for Clinical Laboratory Standards (**NCCLS**) [18].

3. Results and Discussion

Collection of bacterial genera isolates: Four hundred and seventeen isolates of E. coli, three hundred and seventy seven isolates of S. aureus, two hundred and twelve isolates of K. pneumoniae, one hundred and forty five isolates of P. aeruginosa and twenty seven isolates of Streptococcus spp were isolated and identified depending on morphological, cultural and biochemical tests including different system of API strips as shown in table (2).

Distribution and percent rates of the bacterial genera isolates according to their source of infection; One thousand, one hundred and seventy eight isolates of bacterial genera isolates include; E. coli, S. aureus, K. pneumoniae, P. aeruginosa and Streptococcus spp which classified according to their source of infection, table (1) shown that urine isolates were the most frequent by forming 54.5 %, while swab formed 41.02 %, then each of wound, and blood were 2.24%, however the samples were taken irregularly, but were dependent on the patients who admitted into these hospital.

Table 1: Distribution and percent rates of all bacterial isolates among specimens

Source of isolation	No. of Samples	% of sample isolates	No. (%) of isolated				
			E. coli	S. aureus	K. pneumoniae	P. aeruginosa	Streptococcus spp
Urine	641	54.5	350 (54.63)	132 (20.61)	106 (16.49)	40 (6.185)	13 (2.06)
Swab	483	41.02	67 (13.698)	204 (42.465)	99 (20.547)	99 (20.547)	14 (2.739)
Wound	29	2.24	0 (0.00)	29 (100)	0 (0.00)	0 (0.00)	0 (0.00)
Blood	25	2.24	0 (0.00)	12 (50)	7 (25)	6 (25)	0 (0.00)
Total	1178	100%	417 (35.393)	377 (32.022)	212 (17.977)	145 (12.359)	27 (2.247)

Table 2: Results of Morphological features, Cultural characteristics and Biochemical test for all bacteria genera

No.	Bacterial Genera	Colonies Feature on Culture media	Biomedical Tests	Motility test	Capsule possessing	Endospore forming bacteria	The profile code number in API 20E)
1	E. coli	Dark center with greenish metallic sheen colonies on EMB agar (selective media) Red or shiny pink dry colonies with rapid lactose fermenting on MC	Indole positive Methyl red positive Voges – Proskauer negative Citrate utilization negative Oxidase negative Urease negative	Motile	Non – capsulated bacteria	Non spore forming bacteria	5 144 552 5 144 572
2	S. aureus	Creamy/buff colored colonies surrounded by a zone of complete B hemolysis Shiny yellow colonies and change the pink color of MSA to yellow	Catalase positive Voges – Proskauer positive Coagulase positive DNase positive Gelatinase positive Oxidase negative Indole negative Methyl red negative	Non – Motile	Non – capsulated bacteria	Non spore forming bacteria	
3	K. pneumoniae	Large, mucoid, brownish on EMB Pink, large, glistening and mucoid colonies with rapid lactose fermenting on MC	Indole negative Methyl red negative Voges – Proskauer positive Citrate utilization positive Gelatinase negative Oxidase negative Urease positive	Non – Motile	Capsulated bacteria	Non spore forming bacteria	2 004 343 1 214 773
4	P. aeruginosa	Translucent, colorless to gold on EMB Transparent, colorless on MC Secrete pyocyanin pigment on nutrient agar and change the pale red color of medium to green color	Oxidase positive Citrate utilization positive Urease positive DNase negative	Motile	Non – capsulated bacteria	Non spore forming bacteria	2 200 026 2 206 004
5	Streptococcus spp	Shown different types of hemolysis on Blood agar	Catalase negative	Non – Motile	Non – capsulated bacteria	Non spore forming bacteria	

Resistance rates of antibiotics for bacterial genera; Table (3) showed the resistance percent of forty one antibiotics which tested against five genera of bacterial isolates. The resistance rates were occurred between 0.00% and 100.00%., which the high resistance percent record in AZM, CD, CPR, E, and VA against E. coli, AZM, NA, NOR, PIP, and TOB against S. aureus, OX against K. pneumoniae, AK, CEC, CD, and TE against Streptococcus spp were 100%, while the highest percent in P. aeruginosa 90.91% was recorded for SXT, while the lowest resistance percent was 0.00% recorded in CEC, KF, NOR, and TC for E. coli, CN, DP, OX, and PG, to S. aureus, CEC, CFM, CPO, CP, FOX, and DP to K. pneumoniae, CXM, KF, CN, CLM, CT, and E to P. aeruginosa, and AM, ATM, FOX, DA, NA, and TC in Streptococcus spp. The other antibiotics were shown different range of resistance to all bacterial isolates.

Toroglu and Keskin [12] demonstrated that resistance rate of 22 isolates of K. pneumoniae which collected from urine, vaginal fluid, wound, cerebrospinal fluid and blood against eleven antibiotics were 95% to PG, 82% to AM, 77% to CFZ, 59% to CPR and TC, 46% to G, 332% to F, 27% to FOX and OF, 23% to ST and 19% to C. Desai and Malek [19] used eight antibiotics for susceptibility against 140 isolates of K. pneumoniae (n=66), S. aureus (n=35), E. coli (n=15),

and P. aeruginosa (n=6) and the percent of resistance were 100% in K. pneumoniae and P. aeruginosa while 96% in E. coli against AM. However, the resistance percent against these bacteria were G (76.3, 83.4 and 69.2%), PIP (2.1, 1.42 and 2.3%), CP (3.45, 3.12 and 3.76%), CTX (40.4, 45 and 48.2%), CIP (68.4, 76.4 and 74.7%) and CEF (28.7, 32.5 and 20.3%) for K. pneumoniae, E. coli and P. aeruginosa respectively. While for S. aureus, the resistance rates were AM 85.56%, E 49.12%, KF 34.3%, G 45%, VA 0.00%, CIP 42.41%, and AK15.23%. Egbebia and Famurewa [20] they studies on 970 samples which collected from urine, high vaginal swab, blood, ear, sputum, pus, cerebrospinal fluid, semen, stool and nasal fluids. Among of all samples they detected 544 isolates of K. pneumoniae (56.1%), when 120 isolates (96%) resist to CFM, 117 (93.6%) to ATM, 109 (87.2%) to CTX, and 106 (84.4%) to CXM. Also Younis [21] reported that 397 samples (13.8%) are positive growths of bacterial genera among 2872 patients were admitted with clinical diagnosis of neonatal sepsis. E. coli comprise with 48 (12.1%), K. pneumoniae 40 (10%), S. aureus 29 (7.3%), P. aeruginosa 14 (3.5%) and Streptococcus spp 9 (2.3%) among all of 2872 samples. He reported that the resistance percent of AMP were 73, 93, 90, 86 and 56%, G 64.5, 62, 60, 71 and 66%, AK 19, 21, 22.5, 29 and 22%, CEF 37.5, 31, 45, 43 and 33%, CFT 42, 41, 55, 86 and 22%, CTX 29, 31, 32.5, 43 and 22%, IP 0, 10, 2.5, 28.5 and 11% for E. coli, S. aureus, K. pneumoniae, P. aeruginosa and Streptococcus spp and the rates of resistances of VA 3.4 and 0% for S. aureus and Streptococcus spp, while the rates of CIP were 42, 32 and 36% for E. coli, K. pneumoniae and P. aeruginosa.

In the other hand, Ghafourian et al., [22] isolated and identified 113 isolates of K. pneumoniae which taken from respiratory tract infections (RTIs), 67 isolates of them produce extended spectrum beta lactamase (ESBL) and 46 isolates not produce extended spectrum beta lactamase (non-ESBL). They found that 19 isolates (28.3%) resist to AK, 67 (100%) to ATM, 62 (92.5%) to CFT, 46 (68.6%) to CTX, 11 (16.4%) to CIP, 62 (92.5%) to CEF and 0.00% to IP. Chinwe and Ezeronye [9] worked on susceptibility tests on 80 isolates of S. aureus and used nine antibiotics for this purpose, and the their results shown 80 isolates (100%) resist to PG, 77 (96.3%) to AM, 27 (33.8%) to OX, 24 (30%) to CFT, 23 (28.8%) to CFM, 14 (17.5%) to E, 31 (38.5%) to G, 56 (70%) to TE and 30 (37.5%) to C. Schito et al,. [23] reported in their research that among 2315 isolates of E. coli, 48.3% show resistance to AMP, 3.8% to AM, 2.4% to CXM, 8.6% to NA, 8.1% to CIP, 29.4% to SXT and 1.6% to F.

Table 3: Antimicrobial sensitivity pattern (Resistant number (No.) and percent (%) of 1178 bacterial genera isolated from different clinical sources

No.	Antibiotics	Number (No.) and Percent rate (%) of resistant isolates									
		E. coli (n=417) (%)		S. aureus (n=377) (%)		K. pneumoniae (n=212) (%)		P. aeruginosa (n=145) (%)		Streptococcus spp (n=27) (%)	
		R**	S**	R	S	R	S	R	S	R	S
1	AMC*	22 5.27	395 94.73	120 31.83	257 68.17	20 9.43	192 90.57	7 4.82	138 95.18	16.2 60	10.8 40
2	AK	307 73.62	110 26.38	302 80.1	75 19.9	178 83.96	34 16.04	119 82.06	26 17.94	27 100	0 0
3	AM	31 7.43	386 92.57	132 35.01	245 64.99	159 75	53 25	….	….	0 0	27 100
4	AZM	417 100	0 0	377 100	0 0	….	….	….	….	….	….
5	ATM	199 47.72	218 52.28	21 5.57	356 94.43	23 10.84	189 89.16	95 65.51	50 34.49	0 0	27 100
6	CAR	195 46.77	222 53.23	140 37.13	237 62.87	96 45.28	116 54.72	103 71.03	42 28.97	….	….
7	CF	224 53.71	193 46.29	194 51.45	183 48.55	71 33.49	141 66.51	64 44.13	81 55.87	….	….
8	CEC	0 0	417 100	168 44.56	209 55.44	0 0	212 100	37 25.51	108 74.49	27 100	0 0
9	CFZ	46 11.03	371 88.97	67 17.77	310 82.23	….	….	….	….	….	….
10	CD	417 100	0 0	139 36.87	238 63.13	….	….	….	….	27 100	0 0
11	CFM	89 21.34	328 78.66	47 12.46	330 87.54	0 0	212 100	18 12.41	127 87.59	….	….
12	CPO	130 31.25	287 68.75	308 81.69	69 18.31	0 0	212 100	….	….	….	….
13	CP	334 80.09	83 19.91	54 14.32	323 85.68	0 0	212 100	74 51.03	71 48.97	….	….
14	FOX	139 33.33	278 66.67	215 57.02	162 42.98	0 0	212 100	74 51.03	71 48.97	0 0	27 100

15	CPR	417 100	0 0	162 42.97	215 57.03	148 69.81	64 30.19	74 51.03	71 48.97	9 33.33	18 66.67
16	CXM	60 14.38	357 85.62	110 29.17	267 70.83	141 66.5	71 33.5	0 0	145 100	….	….
17	KF	0 0	417 100	113 29.97	264 70.03	106 50	106 50	0 0	145 100	….	….
18	C	289 69.3	128 30.7	203 53.84	174 46.16	47 22.16	165 77.84	53 36.55	92 63.45	….	….
19	CN	125 29.97	292 70.03	0 0	377 100	212 100	0 0	0 0	145 100	….	….
20	CIP	192 46.04	225 54.05	157 41.64	220 58.36	120 56.6	92 43.4	42 28.96	103 71.04	18 66.66	10.8 33.34
21	CLM	83 19.9	334 80.1	189 50.13	188 49.87	71 33.49	141 66.51	0 0	145 100	….	….
22	DA	….	417	287 76.12	90 23.88	….	….	….		0 0	27 100
23	CT	….	….	….	….	….	….	0 0	145 100	….	….
24	E	417 100	0 0	170 45.09	207 54.91	….	….	0 0	145 100	13 48.14	14 51.86
25	G	182 43.64	235 56.36	242 64.19	135 35.81	148 69.81	64 30.19	16 11.03	129 88.97	….	….
26	GIP	….	….	283 75.06	94 24.94	….	….	145 100	0 0	….	….
27	IPM	382 91.6	35 8.4	308 81.69	69 18.31	199 93.86	13 6.14	118 81.37	27 18.63	13 48.14	14 51.86

Table 3: Antimicrobial sensitivity pattern (Resistant number (No.) and percent (%)) of 1178 bacterial genera isolated from different clinical sources (Continued…)

No.	Antibiotics	E. coli (n=417) (%)		S. aureus (n=377) (%)		K. pneumoniae (n=212) (%)		P. aeruginosa (n=145) (%)		Streptococcus spp (n=27) (%)	
		R**	S**	R	S	R	S	R	S	R	S
28	DP	….	….	0 0	377 100	0 0	212 100	….	….	….	….
29	NAF	….	….	226 59.94	151 40.06	….	….	….	….	….	….
30	NA	245 58.75	172 41.25	377 100	0 0	85 40.09	127 59.91	42 28.96	103 71.04	0 0	27 100
31	F	397 95.2	20 4.8	168 44.56	209 55.44	56 26.41	156 73.59	110 75.86	35 24.14	….	….
32	NOR	0 0	417 100	377 100	0 0	13 6.13	199 93.87	95 65.51	50 34.49	….	….
33	OX	209 50.11	208 49.89	0 0	377 100	212 100	0 0	….	….	20 74.07	7 25.93
34	PG	….	….	0 0	377 100	148 69.81	64 30.19	114 78.62	31 21.38		….
35	PIP	….	….	377 100	0 0	164 77.35	48 22.65	37 25.51	108 74.49	14 51.85	13 48.15
36	RA	192 46.04	225 53.96	316 83.81	61 16.19	42 19.81	170 80.19	67 46.2	78 53.8	….	….
37	TE	79 18.94	338 81.06	118 31.29	259 68.71	186 87.73	26 12.27	59 40.68	86 59.32	27 100	0 0
38	TC	0 0	417 100	63 16.71	314 83.29	82 38.67	130 61.33	….	….	0 0	27 100
39	TOB	156 37.41	261 62.59	377 100	0 0	83 39.15	129 60.85	13 8.96	132 91.04	….	….
40	SXT	56 13.42	361 86.58	203 53.84	174 46.16	201 94.81	11 5.19	134 92.41	11 7.59	9 33.33	18 66.67
41	VA	417 100	0 0	362 96.02	15 3.98	170 80.18	42 19.82	60 41.37	85 58.63	….	….

**: R: Resistant, S: Sensitive.

The bacterial isolates (n=1178) were classified and grouped in to 23 groups according to their resistances through antimicrobials which used in this study, as clarified in table (3) and known as Antibiogram groups. This Antibiogram

table of antimicrobial resistance for bacterial isolates demonstrated that the predominant mode which include more resistant isolate represented in mode (1), which was resist to 85.36% of all antimicrobials, except FOX, CPR, PIP, RA, TE and VA, while the resistance Antibiogram pattern of remained groups ranged between 78.04% - 43.9%.

Table 4: Antibiogram groups and resistance percent to antimicrobial agents

Antibiogram Groups		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
No. of Isolates		11	27	102	221	78	63	11	29	45	91	187	23	1	39	79	32	15	26	2	62	18	6	10
No. of Each B. species	E. coli	4	11	38	92	19	28	2	9	6	24	90	3	0	15	27	9	3	8	0	20	6	2	1
	S. aureus	2	3	41	46	28	13	5	15	21	36	56	12	0	9	24	13	8	11	1	21	5	2	5
	K. pneumoniae	3	8	22	28	23	9	3	2	6	19	25	5	0	6	16	8	3	5	0	12	6	1	2
	P. aeruginosa	1	3	1	49	7	11	1	2	12	8	14	3	1	8	9	2	1	2	1	5	1	1	2
	Streptococcus spp	1	2	0	6	1	2	0	1	0	4	2	0	0	1	3	0	0	0	0	4	0	0	0
% of Resistance		85.36	78.04	73.17	65.85	63.41	63.41	63.41	60.97	60.97	56.09	56.09	56.09	56.09	56.09	53.65	53.65	53.65	53.65	53.65	51.21	43.9	43.9	43.9
Antibiotics	AMC	+	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	+	+	+
	AK	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	AM	+	+	+	+	+	-	+	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-
	AZM	+	+	+	+	+	+	-	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	-
	ATM	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	+	-	+	+	+	-	-	+
	CAR	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	-	-
	CF	+	+	+	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	CEC	+	+	+	-	+	-	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	-	+
	CFZ	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+
	CD	+	+	+	+	+	-	-	+	+	-	+	+	+	+	-	+	-	+	+	+	+	+	+
	CFM	+	+	+	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	CPO	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+
	CP	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	-	-	-	-	-
	FOX	-	-	+	-	-	+	+	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+
	CPR	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+
	CXM	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	-	-	-	-
	KF	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

Table 4: Antibiogram groups and resistance percent to antimicrobial agents (Continued…)

C	+	-	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CN	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
CIP	+	+	+	+	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	-	-	-
CLM	+	+	+	-	-	+	+	+	+	-	+	+	-	+	-	-	-	-	-	-	-	-	-
DA	+	+	+	+	-	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-
CT	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	+
E	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
G	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	-	-	-
GIP	+	+	-	+	-	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-
IPM	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	+	+	+	+	+	+
DP	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
NAF	+	+	-	-	-	-	+	+	+	+	+	-	+	-	-	-	-	-	-	-	-	-	-
NA	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+
F	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
NOR	+	+	+	+	+	-	+	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+
OX	+	+	-	-	+	-	-	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-
PG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-
PIP	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RA	-	-	+	-	-	-	-	-	-	+	-	-	-	-	+	+	+	+	-	-	-	-	-
TE	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TC	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+
TOB	+	+	-	-	+	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-
SXT	+	-	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
VA	-	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	+	+	+

Conclusions

This study emphasizes the problems with antimicrobial resistances of bacteria, the increased use, and sometimes misuse, of antibiotic drugs has resulted in bacterial resistance to a large and growing number of these drugs. Although research into newer antibiotics continues, measures can and should be taken to reverse the practices that promote development of antibiotic resistance in bacteria.

Acknowledgements

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