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Implementing the WHONET Program for Surveillance of Antimicrobial Resistance in One Hospital in Makkah, Saudi Arabia

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Abstract: Resistance to antimicrobial agents is a major health problem. Continuous surveillance of local antimicrobial susceptibility patterns is necessary for combating antimicrobial resistance. Implementing the computerized system (WHONET program) for surveillance of antimicrobial resistance in one in Hospital in Makkah, Saudi Arabia was studied. This study was based on WHONET software for surveillance study of antimicrobial resistance1012 clinical specimens were submitted or bacterial culture. The collected and analyzed, clinical samples included: urine, blood stream, sputum, wound and abscess and others. Among the 1012 collected samples,733 isolates were detected. The most prevalent microorganism were *Klebsiella pneumonia* (123 /16.8%), *Pseudomonas aeruginosa* (121/16.5%) followed by *Acinetobacter baumannii* (87/ 11.9 %), *Proteus mirabilis* (82 / 11.2%), *E-coli* (76 /6.8 %) and *Staphylococcus aureus* (50/ 6.8%). From the obtained results, it be concluded that WHONET was an effective computerized microbiology laboratory data management and analysis program that can provide guidance for drug-policy decisions and preventive measures and can be used to investigate the impact of interventions.

Key words: WHONET · Antimicrobial Resistance · Surveillance · Infection · Resistance Mechanisms

INTRODUCTION

The burden of antimicrobial resistance worldwide is substantial and is likely to grow [1]. Many factors play into the emergence of resistance; from poor utilization of antimicrobial agents, to transmission of resistant bacteria from patient to patient and from Health-care workers (HCWs) to patients and vice versa, to lack of guidelines for appropriate use of antimicrobial agents, to lack of easy-to-use auditing tools for restriction. In addition, there is clear misuse of antimicrobial in animal industry leaves antibiotics residues in food, those are the same agents used in humans. All these factors together led to the inevitable rise and emergence of resistance [2].

Bacteria develop antimicrobial resistance through many mechanisms including mutations in penicillin binding proteins, efflux mechanisms, alterations in outer membrane proteins and the production of hydrolyzing enzymes such as extended spectrum β lactamase (ESBL) and carbapenemases [3]. Many, if not most, of the Gulf Corporation Council (GCC) countries do not have clear guidelines for antimicrobial use and lack policies for restricting and auditing antimicrobial prescriptions. There are no guidelines for the use of antimicrobials in the animal industries either.Thus, it is not surprising that antimicrobial resistance has emerged in these countries [4].

Emergence of resistance to multiple antimicrobial agents in pathogenic bacteria has become a significant public health threat as there are fewer, or even sometimes no effective antimicrobial agents available for infections caused by these bacteria. Gram-positive and Gram-negative are both affected by emergence and rise of antimicrobial resistance [5]. The problem of increasing

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antimicrobial resistance is even more threatening when considering the very limited number of new antimicrobial agents that are in development [6].

The world Health Organization (WHO) has established and implemented a surveillance tool for antimicrobial resistance known as WHONET. This is a software program designed to meet the need of surveillance and tackle the problem of antimicrobial resistance. It requires accurate and easily accessible data on antimicrobial resistance to support decision making and to take action from local and global level. Susceptibility test measurements of any kind and all other information about each isolates may be entered directly into WHONET's universal file format. It has user- friendly analytical programs that enable workers at any medical centre to analyze their own isolates in many ways easily [7].

This study was conducted to implement the WHONET program for surveillance of antimicrobial resistance in one hospital in Makkah, Saudi Arabia.

MATERIALS AND METHODS

We initiated a prospective laboratory based surveillance study of antimicrobial resistance in one hospital in Makkah, Saudi Arabia.

The study was conducted over one year. The main prerequisite for compilation of data was a PC installed with WHONET software. It has three main parts, a laboratory configuration file which can be used to customize it to the particular laboratory, an interface for data entry and a part for analysis and reporting of resistance data [8].

The study was planned to include 1000 clinicalspecimens submitted for bacterial culture at the microbiology laboratories of selected hospitals. Both hospitalized and non-hospitalized infections will be included. Samples were collected and analyzed, clinical samples included: urine, blood stream, sputum, wound and abscess and others. Urine sample collection included urine from mid-stream urine and catheter, or suprapubic aspiration. A wound infection was identified by the presence of purulent discharge from the incision with erythematous cellulitis, induration or pain, Aspirates were obtained by preparing the wound and abscess area with alcohol, inserting a sterile needle through the healing incision and aspirating fluid into a sterile syringe. Drawn blood samples from the patients were cultured on blood agar media and incubated at 35°Cfor18–24h.

Bacteria recovered from clinical specimens were identified by standard biochemical methods. The samples were cultured on nutrient agar, MacConkey agar, Blood agar and Eosin Methylene Blue (EMB) agar. The plates were incubated at35°C for 24hand the pure isolates will be characterized and identified according to Gram stains and biochemical tests such as catalase, oxidative, indole production, citrate utilization, triple iron sugar utilization, urea test, Oxidative-fermentative test with glucose, ONPG test and methylred-Voges Proskauer as described in standard bacteriological methods[9].

Antibiotic Susceptibility Test: Antibiotic sensitivity pattern of isolates to common antibiotics used in the hospital were determined by the Kirby Bauer's disc diffusion method on Mueller-Hinton agar. All isolates were tested against beta-lactam agents and also they tested against non-beta-lactam agents including gentamicin, amikacin, nalidixic acid, nitrofurantoin, trimethoprim/sulfamethoxazole and ciprofloxacin [10]. (Antibiotics were selected according to WHO model list of essential drugs.

The MIC Results: Results, categorized as being susceptible (S), intermediate (I) and resistant (R) were compared and analyzed by WHONET 5 software [11].

All data was entered into the program manually on a weekly basis and analyzed for each ward and presented separately and accumulatively to acquire information about resistance % (R %) to the local laboratory antibiotics panel. Also we use WHONET to analyze resistance as scatterplot which is analysis type correlate resistance of different antibiotic classes. In addition, results obtained can be analyzed as resistance profile which study used to reflect the multiresistant pattern of the isolates to the most antibiotic prescribed.

RESULTS

In our study 1012 samples were examined from 449 (74.8%) males and 151 (25.2%) females hospitalized patients, most cases were from the ICU and Medical ward (42.7 % and 33.9% respectively).

The current study revealed that the major isolates were recovered from the respiratory specimens (39.7 %) followed by wound infection (26.5 %) and urine specimens (20.8%) while blood samples represented only (8.5%).

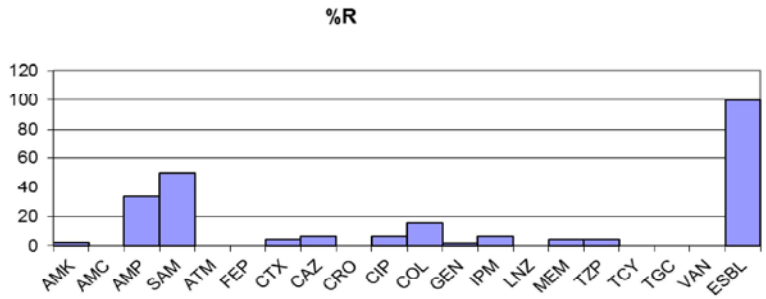

Fig. 1: Resistance (%) of *Klebsiella pneumonia*

Table 1: Antibiotic resistance amongst *Klebsiella pneumonia* (N =123)

Antibiotic Panel tested		*Klebsiella pneumoniae* = 123 isolates				
Code	Antibiotic name	NO.	%R	%I	%S	%R95 %C.I.
AMK_NM	Amikacin	94	2.1	18.1	79.8	0.4-8.2
AMC_NM	Amoxicillin/Clavulanic acid	12	0	8.3	91.7	0.0-30.1
AMP_NM	Ampicillin	15	33.3	13.3	53.3	13.0-61.3
SAM_NM	Ampicillin/Sulbactam	2	50	0	50	2.7-97.3
ATM_NM	Aztreonam	29	0	6.9	93.1	0.0-14.6
FEP_NM	Cefepime	38	0	5.3	94.7	0.0-11.4
CTX_NM	Cefotaxime	25	4	4	92	0.2-22.3
CAZ_NM	Ceftazidime	31	6.5	3.2	90.3	1.1-22.9
CRO_NM	Ceftriaxone	18	0	16.7	83.3	0.0-21.9
CIP_NM	Ciprofloxacin	30	6.7	0	93.3	1.2-23.6
COL_NM	Colistin	77	15.6	0	84.4	8.7- 26.1
GEN_NM	Gentamicin	59	1.7	1.7	96.6	0.1-10.3
IPM_NM	Imipenem	65	6.2	0	93.8	2.0-15.8
LNZ_NM	Linezolid	2	0	0	100	0.0-80.2
MEM_NM	Meropenem	44	4.5	2.3	93.2	0.8-16.6
TZP_NM	Piperacillin/Tazobactam	50	4	6	90	0.7-14.9
TCY_NM	Tetracycline	2	0	50	50	0.0-80.2
TGC_NM	Tigecycline	13	0	46.2	53.8	0.0-28.3
VAN_NM	Vancomycin	2	0	0	100	0.0-80.2
ESBL	ESBL	19	100		0	

Among the 1012 collected samples, 733 isolates were detected, while the rest showed insignificant growth. The following tables and figures shows the susceptibility profiles of the most commonly isolated pathogens.

Table 1 and Figure 1 show that *Klebsiella pneumonia* was resistant 100% to the Extended-spectrum beta-lactamases (ESBL) and was resistant 33.3% to Ampicillin but no resistance was seen against Vancomycin and Linezolid.

Table 2 and Figure 2 show that *Pseudomonas aeruginosa* was resistant 100% to Ampicillin/Sulbactam (SAM) and Oxacillin (OXA) with %R 95 %CI (5.5-100) and was resistant 66.7 to Tigecycline (TGC) with %R 95 %CI (12.5-98.2), but no resistance was seen against Amoxicillin/Clavulanic acid, Ampicillin, Cefotaxime, Ceftriaxone, Clidamycin, Erythromycin, Linezolid and Vancomycin.

Table 3 and Figure 3 show that *Acinetobacter baumannii* has no resistance to all antibiotics that were used while was sensitive 100% to Ciprofloxacin, Colistin and Tetracycline.

Table 4 and Figure 4 show that *E-coli* was resistant 100 % to Beta-lactamase and ESBL while showed 18.4% &16.7 % resistance for Ciprofloxacin and Ampicillin/ Sulbactam, respectively

Table 5 and Figure 5 clear that *Proteus mirabilis* was resistant 100% to Nitrofurantoin (NIT) and the Extended-spectrum beta-lactamases (ESBL) with %R 95 %CI (5.5-100) but no resistance was seen against antibiotic class Amikacin, Aminoglycosides Ampicillin/ Sulbactam, Cephems. Penems, Beta-lactam+ Inhibitors and Tetracyclines.

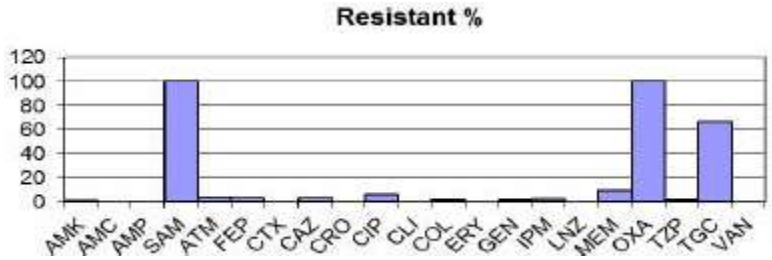

Fig. 2: Resistance (%) against *Pseudomonas aeruginosa*

Table 2: Antibiotic resistance amongst *Pseudomonas aeruginosa* (N= 121)

Antibiotic Panel tested		*Pseudomonas aeruginosa* = 121 isolates				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
AMK_NM		91	1.1	3.3	95.6	0.1-6.8
AMC_NM	Amoxicillin/Clavulanic acid	3	0	0	100	0.0-69.0
AMP_NM	Ampicillin	3	0	0	100	0.0-69.0
SAM_NM	Ampicillin/Sulbactam	1	100	0	0	5.5-100
ATM_NM	Aztreonam	53	3.8	13.2	83	0.7-14.1
FEP_NM	Cefepime	59	3.4	8.5	88.1	0.6-12.8
CTX_NM	Cefotaxime	5	0	0	100	0.0-53.7
CAZ_NM	Ceftazidime	61	3.3	3.3	93.4	0.6-12.4
CRO_NM	Ceftriaxone	1	0	0	100	0.0-94.5
CIP_NM	Ciprofloxacin	68	5.9	5.9	88.2	1.9-15.2
CLI_NM	Clindamycin	1	0	0	100	0.0-94.5
COL_NM	Colistin	109	1.8	2.8	95.4	0.3-7.1
ERY_NM	Erythromycin	1	0	0	100	0.0-94.5
GEN_NM	Gentamicin	61	1.6	1.6	96.7	0.1-9.9
IPM_NM	Imipenem	77	2.6	1.3	96.1	0.5-9.9
LNZ_NM	Linezolid	1	0	0	100	0.0-94.5
MEM_NM	Meropenem	43	9.3	9.3	81.4	3.0-23.1
OXA_NM	Oxacillin	1	100	0	0	5.5-100
TZP_NM	Piperacillin/Tazobactam	71	1.4	2.8	95.8	0.1-8.6
TGC_NM	Tigecycline	3	66.7	33.3	0	12.5-98.2
VAN_NM	Vancomycin	1	0	0	100	0.0-94.5

Table 3: Antibiotic resistance amongst *Acinetobacter baumannii* (N = 87)

Antibiotic Panel tested		*Acinetobacter baumannii* = 87 isolates				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
AMK_NM	Amikacin	21	0	14.3	85.7	0.0-19.2
AMP_NM	Ampicillin	3	0	33.3	66.7	0.0-69.0
ATM_NM	Aztreonam	7	0	42.9	57.1	0.0-43.9
FEP_NM	Cefepime	10	0	10	90	0.0-34.5
CTX_NM	Cefotaxime	7	0	14.3	85.7	0.0-43.9
CAZ_NM	Ceftazidime	9	0	22.2	77.8	0.0-37.1
CRO_NM	Ceftriaxone	8	0	37.5	62.5	0.0-40.2
CIP_NM	Ciprofloxacin	7	0	0	100	0.0-43.9
COL_NM	Colistin	86	0	0	100	0.0-5.3
GEN_NM	Gentamicin	16	0	6.2	93.8	0.0-24.1
IPM_NM	Imipenem	19	0	10.5	89.5	0.0-20.9
MEM_NM	Meropenem	11	0	0	100	0.0-32.1
TZP_NM	Piperacillin/Tazobactam	14	0	14.3	85.7	0.0-26.8
TCY_NM	Tetracycline	1	0	0	100	0.0-94.5
TGC_NM	Tigecycline	2	0	100	0	0.0-80.2

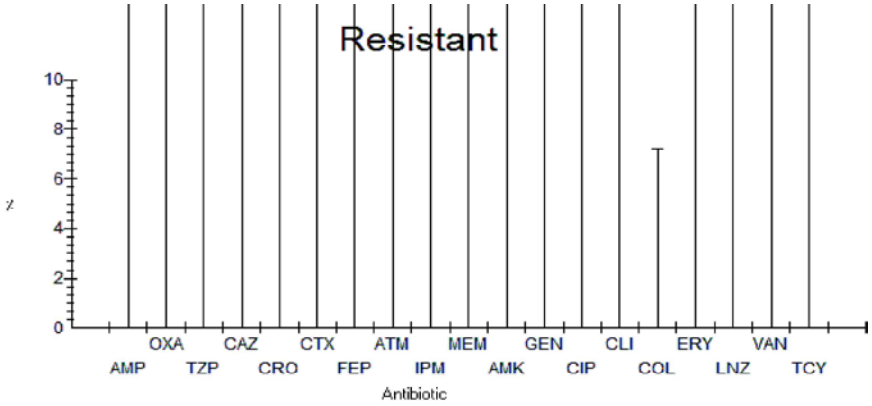

Fig. 3: Resistance (%) of *Acinetobacter baumanni*

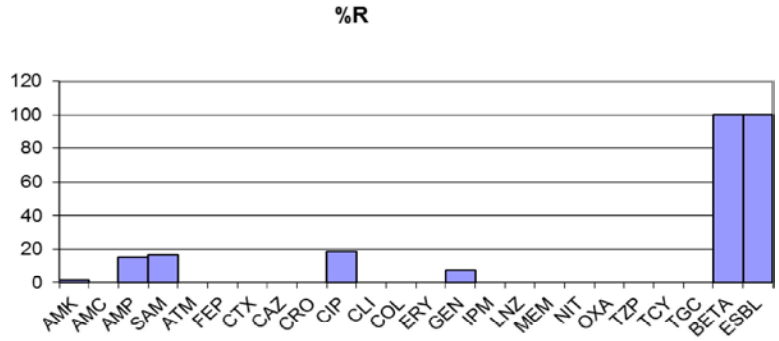

Fig. 4: Resistance (%) of *E-coli*

Table 4: Antibiotic resistance amongst *E-coli* (N= 76)

Antibiotic Panel tested		*Escherichia coli* = 76 isolates				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
AMK_NM	Amikacin	65	1.5	0	98.5	0.1-9.3
AMC_NM	Amoxicillin/Clavulanic acid	14	0	7.1	92.9	0.0-26.8
AMP_NM	Ampicillin	20	15	15	70	4.0-38.9
SAM_NM	Ampicillin/Sulbactam	6	16.7	16.7	66.7	0.9-63.5
ATM_NM	Aztreonam	22	0	0	100	0.0-18.5
FEP_NM	Cefepime	27	0	3.7	96.3	0.0-15.5
CTX_NM	Cefotaxime	46	0	6.5	93.5	0.0-9.6
CAZ_NM	Ceftazidime	27	0	0	100	0.0-15.5
CRO_NM	Ceftriaxone	23	0	4.3	95.7	0.0-17.8
CIP_NM	Ciprofloxacin	38	18.4	7.9	73.7	8.3-34.9
CLI_NM	Clindamycin	1	0	0	100	0.0-94.5
COL_NM	Colistin	65	0	1.5	98.5	0.0-7.0
ERY_NM	Erythromycin	2	0	0	100	0.0-80.2
GEN_NM	Gentamicin	39	7.7	0	92.3	2.0-22.0
IPM_NM	Imipenem	68	0	2.9	97.1	0.0-6.7
LNZ_NM	Linezolid	1	0	0	100	0.0-94.5
MEM_NM	Meropenem	56	0	0	100	0.0-8.0
NIT_NM	Nitrofurantoin	10	0	0	100	0.0-34.5
OXA_NM	Oxacillin	1	0	0	100	0.0-94.5
TZP_NM	Piperacillin/Tazobactam	68	0	7.4	92.6	0.0-6.7
TCY_NM	Tetracycline	1	0	0	100	0.0-94.5
TGC_NM	Tigecycline	8	0	12.5	87.5	0.0-40.2
BETA_LACT	Beta-lactamase	1	100		0	
ESBL	ESBL	28	100		0	

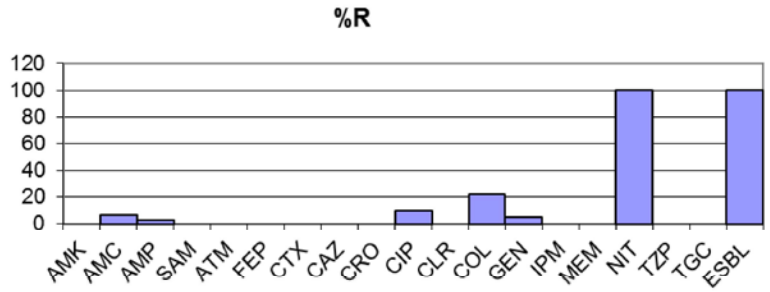

Fig. 5: Resistance (%) of *Proteus mirabilis*

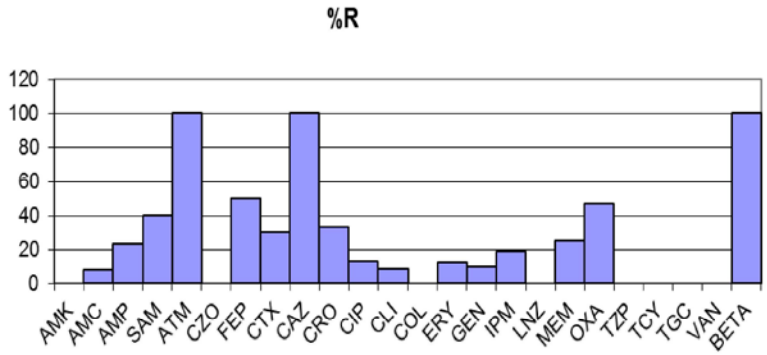

Fig. 6: Resistance (%) of *Staphylococcus aureus*

Table 5: Antibiotic resistance amongst *Proteus mirabilis* (N=82)

Antibiotic Panel tested		*Proteus mirabilis* =82 isolates				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
AMK	Amikacin	60	0	13.3	86.7	0.0-7.5
AMC	Amoxicillin/Clavulanic acid	15	6.7	6.7	86.7	0.4-34.0
AMP	Ampicillin	40	2.5	17.5	80	0.1-14.7
SAM	Ampicillin/Sulbactam	1	0	0	100	0.0-94.5
ATM	Aztreonam	45	0	11.1	88.9	0.0-9.8
FEP	Cefepime	33	0	6.1	93.9	0.0-13.0
CTX	Cefotaxime	47	0	8.5	91.5	0.0-9.4
CAZ	Ceftazidime	30	0	0	100	0.0-14.1
CRO	Ceftriaxone	19	0	0	100	0.0-20.9
CIP	Ciprofloxacin	30	10	13.3	76.7	2.6-27.7
CLR	Clarithromycin	1	0	0	100	0.0-94.5
COL	Colistin	27	22.2	3.7	74.1	9.4-42.7
GEN	Gentamicin	20	5	0	95	0.3-26.9
IPM	Imipenem	77	0	2.6	97.4	0.0- 5.9
MEM	Meropenem	49	0	2	98	0.0-9.1
NIT	Nitrofurantoin	1	100	0	0	5.5-100
TZP	Piperacillin/Tazobactam	70	0	4.3	95.7	0.0-6.5
TGC	Tigecycline	2	0	100	0	0.0-80.2
ESBL	Extended-spectrum beta-lactamases	1	100		0	

Table 6 and Figure 6 show that the *Staphylococcus aureus* was resistant 100% to the Monobactams (ATM), Cephems (CAZ) and Beta-lactamases (BETA) with %R 95 %CI (5.5-100) and was resistant 50% to Cephems (FEP)with %R 95 % CI (2.7-97), but no resistance was seen against Amikan Colistin Cfazolin, Linezolid, Piperacillin/ Tazobactam, Tigecycline and Vancomycin.

Table 7 and Figure 7 show that *Candida albicans* was resistant 100% to the Oxacillin, Clindamycin and Erythromycin, but was sensitive for most antibiotics which used.

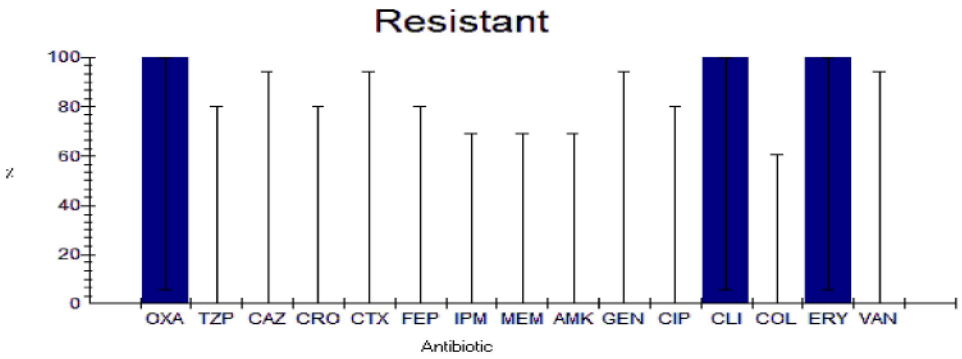

Fig. 7: Resistance (%) of *Candida albicans*

Table 6: Antibiotic resistance amongst *Staphylococcus aureus* (N=50)

Antibiotic Panel tested		*Staphylococcus aureus* =50				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
AMK	Amikacin	2	0	0	100	0.0-80.2
AMC	Amoxicillin/Clavulanic acid	12	8.3	0	91.7	0.4-40.2
AMP	Ampicillin	13	23.1	0	76.9	6.2-54.0
SAM	Ampicillin/Sulbactam	5	40	0	60	7.3-83.0
ATM	Aztreonam	1	100	0	0	5.5-100
CZO	Cefazolin	1	0	0	100	0.0-94.5
FEP	Cefepime	2	50	0	50	2.7-97.3
CTX	Cefotaxime	33	30.3	0	69.7	16.2-48.9
CAZ	Ceftazidime	1	100	0	0	5.5-100
CRO	Ceftriaxone	3	33.3	0	66.7	1.8-87.5
CIP	Ciprofloxacin	22	13.6	0	86.4	3.6-35.9
CLI	Clindamycin	33	9.1	0	90.9	2.4-25.5
COL	Colistin	1	0	0	100	0.0-94.5
ERY	Erythromycin	31	12.9	0	87.1	4.2-30.8
GEN	Gentamicin	29	10.3	6.9	82.8	2.7-28.4
IPM	Imipenem	21	19	0	81	6.3-42.5
LNZ	Linezolid	32	0	0	100	0.0-13.3
MEM	Meropenem	4	25	0	75	1.3-78.1
OXA	Oxacillin	32	46.9	0	53.1	29.5-65.0
TZP	Piperacillin/Tazobactam	1	0	0	100	0.0-94.5
TCY	Tetracycline	2	0	0	100	0.0-80.2
TGC	Tigecycline	3	0	33.3	66.7	0.0-69.0
VAN	Vancomycin	42	0	0	100	0.0-10.4
BETA	Beta-lactamase	1	100		0	

Table 7: Antibiotic resistance amongst *Candida albicans* (N=40)

Antibiotic Panel tested		*Candida albicans* (N=40)				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
OXA_NM	Oxacillin	1	100	0	0	5.5-100
TZP_NM	Piperacillin/Tazobactam	2	0	0	100	0.0-80.2
CAZ_NM	Ceftazidime	1	0	0	100	0.0-94.5
CRO_NM	Ceftriaxone	2	0	0	100	0.0-80.2
CTX_NM	Cefotaxime	1	0	0	100	0.0-94.5
FEP_NM	Cefepime	2	0	0	100	0.0-80.2
IPM_NM	Imipenem	3	0	0	100	0.0-69.0
MEM_NM	Meropenem	3	0	0	100	0.0-69.0
AMK_NM	Amikacin	3	0	0	100	0.0-69.0
GEN_NM	Gentamicin	1	0	0	100	0.0-94.5
CIP_NM	Ciprofloxacin	2	0	50	50	0.0-80.2
CLI_NM	Clindamycin	1	100	0	0	5.5-100
COL_NM	Colistin	4	0	0	100	0.0-60.4
ERY_NM	Erythromycin	1	100	0	0	5.5-100
VAN_NM	Vancomycin	1	00	100	0.0-	94.5

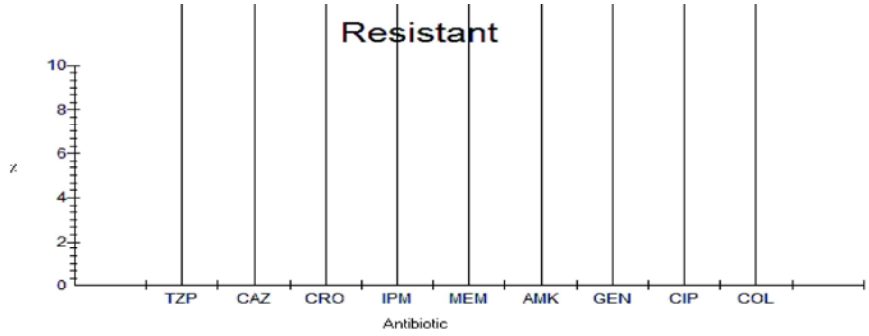

Fig. 8: Resistance (%) of *Acinetobacter calcoaceticus*

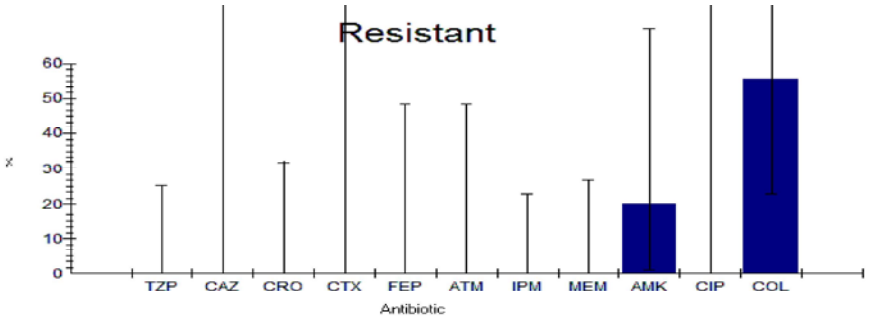

Fig. 9: Resistance (%) of *Providencia stuarti*

Table 8: Antibiotic resistance amongst *Acinetobacter calcoaceticus* (N=10)

Antibiotic Panel tested		*Acinetobacter calcoaceticus* (N = 10)				
Code	Antibiotic name	NO.	%R	%I	%S	%R 95 %C.I.
TZP_NM	Piperacillin/Tazobactam	1	0	100	0	0.0-94.5
CAZ_NM	Ceftazidime	1	0	100	0	0.0-94.5
CRO_NM	Ceftriaxone	1	0	100	0	0.0-94.5
IPM_NM	Imipenem	2	0	0	100	0.0-80.2
MEM_NM	Meropenem	1	0	0	100	0.0-94.5
AMK_NM	Amikacin	3	0	33.3	66.7	0.0-69.0
GEN_NM	Gentamicin	2	0	100	0	0.0-80.2
CIP_NM	Ciprofloxacin	2	0	0	100	0.0-80.2
COL_NM	Colistin	10	0	0	100	0.0-34.5

Table 9: Antibiotic resistance amongst *Providencia stuartii* (N=21)

Antibiotic Panel tested		*Providencia stuartii* (N=21)				
Code	Antibiotic name	No.	%R	%I	%S	%R 95 %C.I.
TZP_NM	Piperacillin/Tazobactam	15	0	0	100	0.0-25.3
CAZ_NM	Ceftazidime	1	0	100	0	0.0-94.5
CRO_NM	Ceftriaxone	11	0	45.5	54.5	0.0-32.1
CTX_NM	Cefotaxime	2	0	0	100	0.0-80.2
FEP_NM	Cefepime	6	0	0	100	0.0-48.3
ATM_NM	Aztreonam	6	0	50	50	0.0-48.3
IPM_NM	Imipenem	17	0	5.9	94.1	0.0-22.9
MEM_NM	Meropenem	14	0	7.1	92.9	0.0-26.8
AMK_NM	Amikacin	5	20	40	40	1.1-70.1
CIP_NM	Ciprofloxacin	1	0	0	100	0.0-94.5
COL_NM	Colistin	9	55.6	22.2	22.2	22.7-84.7

Table 8 and Figure 8 clear that *Acinetobacter calcoaceticus* had no resistance against antibiotics which.

Table 9 and Figure 9 show that *Providencia stuartii* was resistant 55.6% to Colistin and 20 % to Amikacin.

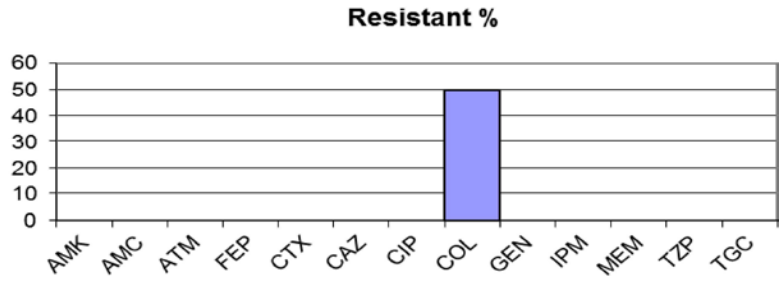

Fig. 10: Resistance (%) of *Stenotrophomonas maltophilia*

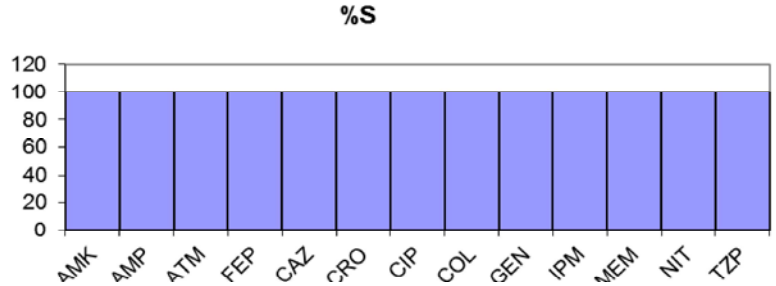

Fig. 11: Sensitive (%) of *Enterobacter aerogenes*

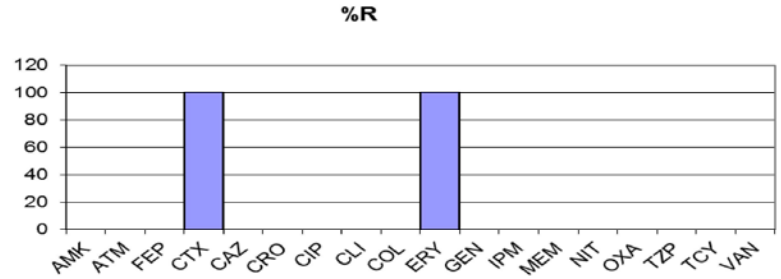

Fig. 12: Resistance (%) of *Enterobacter cloacae*

Table 10: Antibiotic resistance amongst *Stenotrophomonas maltophilia* (N = 5)

Antibiotic Panel tested		*Stenotrophomonas maltophilia* =5 isolates				
Code	Antibiotic name	Number	%R	%I	%S	%R 95 %C.I.
AMK_NM	Amikacin	3	0	0	100	0.0-69.0
AMC_NM	Amoxicillin/Clavulanic acid	2	0	0	100	0.0-80.2
ATM_NM	Aztreonam	1	0	0	100	0.0-94.5
FEP_NM	Cefepime	1	0	0	100	0.0-94.5
CTX_NM	Cefotaxime	1	0	0	100	0.0-94.5
CAZ_NM	Ceftazidime	2	0	50	50	0.0-80.2
CIP_NM	Ciprofloxacin	2	0	0	100	0.0-80.2
COL_NM	Colistin	4	50	0	50	9.2-90.8
GEN_NM	Gentamicin	3	0	0	100	0.0-69.0
IPM_NM	Imipenem	3	0	0	100	0.0-69.0
MEM_NM	Meropenem	3	0	0	100	0.0-69.0
TZP_NM	Piperacillin/Tazobactam	2	0	0	100	0.0-80.2
TGC_NM	Tigecycline	1	0	100	0	0.0-94.5

Table 10 and Figure 10 show that *Stenotrophomonas maltophilia* was resistant by 50% to Colistin (Lipopeptides) (with %R 95 %CI (9.2-90.8).

Table 11 and Figure 11 show that *Enterobacter aerogenes* was sensitive to all used antibiotics.

Table 12 and Figure 12 showthat *Enterobacter cloacae* was resistant by 100% to Cefotaxime and Erythromycin

Table 13 and Figure 13 show that *Enterobacter faecalis* was resistant by 100% to Cefotaxime, Ceftriaxone, Clindamycin, Erythromycin, and Oxacillin.

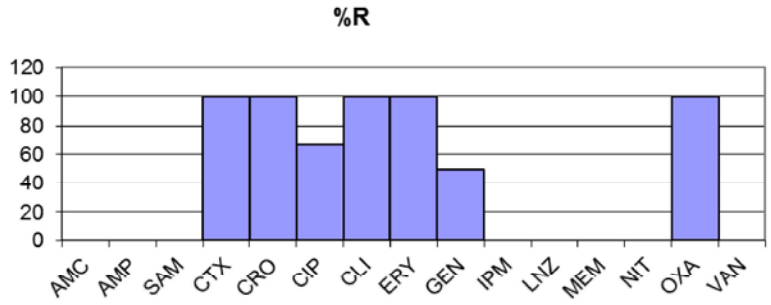

Fig. 13: Resistance (%) of *Enterobacter faecali*s

Table 11: Antibiotic resistance amongst *Enterobacter aerogenes* (N = 7)

Antibiotic Panel tested		*Enterobacter aerogenes*-Number of isolates=7				
Code	Antibiotic name	No.	%R	%I	%S	% R 95 %C.I.
AMK_NM	Amikacin	6	0	0	100	0.0-48.3
AMP_NM	Ampicillin	1	0	0	100	0.0-94.5
ATM_NM	Aztreonam	4	0	0	100	0.0-60.4
FEP_NM	Cefepime	4	0	0	100	0.0-60.4
CAZ_NM	Ceftazidime	3	0	0	100	0.0-69.0
CRO_NM	Ceftriaxone	3	0	0	100	0.0-69.0
CIP_NM	Ciprofloxacin	2	0	0	100	0.0-80.2
COL_NM	Colistin	3	0	0	100	0.0-69.0
GEN_NM	Gentamicin	3	0	0	100	0.0-69.0
IPM_NM	Imipenem	6	0	0	100	0.0-48.3
MEM_NM	Meropenem	5	0	0	100	0.0-53.7
NIT_NM	Nitrofurantoin	1	0	0	100	0.0-94.5
TZP_NM	Piperacillin/Tazobactam	5	0	0	100	0.0-53.7

Table 12: Antibiotic resistance amongst *Enterobacter cloacae* (N = 7)

Antibiotic Panel tested		*Enterobacter cloacae* (N= 7)				
Code	Antibiotic name	No.	%R	%I	%S	%R 95 %C.I.
AMK_NM	Amikacin	5	0	0	100	0.0-53.7
ATM_NM	Aztreonam	4	0	0	100	0.0-60.4
FEP_NM	Cefepime	5	0	0	100	0.0-53.7
CTX_NM	Cefotaxime	1	100	0	0	5.5-100
CAZ_NM	Ceftazidime	5	0	20	80	0.0-53.7
CRO_NM	Ceftriaxone	5	0	0	100	0.0-53.7
CIP_NM	Ciprofloxacin	5	0	20	80	0.0-53.7
CLI_NM	Clindamycin	1	0	0	100	0.0-94.5
COL_NM	Colistin	4	0	0	100	0.0-60.4
ERY_NM	Erythromycin	1	100	0	0	5.5-100
GEN_NM	Gentamicin	3	0	0	100	0.0-69.0
IPM_NM	Imipenem	6	0	0	100	0.0-48.3
MEM_NM	Meropenem	6	0	0	100	0.0-48.3
NIT_NM	Nitrofurantoin	1	0	0	100	0.0-94.5
OXA_NM	Oxacillin	1	0	0	100	0.0-94.5
TZP_NM	Piperacillin/Tazobactam	4	0	0	100	0.0-60.4
TCY_NM	Tetracycline	1	0	0	100	0.0-94.5
VAN_NM	Vancomycin	1	0	0	100	0.0-94.5

Table 13: Antibiotic resistance amongst *Enterobacter faecalis* (N = 7)

Antibiotic Panel tested		*Enterococcus faecalis* N = 7				
Code	Antibiotic name	No.	%R	%I	%S	%R 95 %C.I.
AMC_NM	Amoxicillin/Clavulanic acid	2	0	0	100	0.0-80.2
AMP_NM	Ampicillin	5	0	0	100	0.0-53.7
SAM_NM	Ampicillin/Sulbactam	2	0	0	100	0.0-80.2
CTX_NM	Cefotaxime	2	100	0	0	19.8-100
CRO_NM	Ceftriaxone	1	100	0	0	5.5-100
CIP_NM	Ciprofloxacin	3	66.7	0	33.3	12.5-98.2
CLI_NM	Clindamycin	2	100	0	0	19.8-100
ERY_NM	Erythromycin	2	100	0	0	19.8-100
GEN_NM	Gentamicin	2	50	0	50	2.7-97.3
IPM_NM	Imipenem	6	0	0	100	0.0-48.3
LNZ_NM	Linezolid	5	0	0	100	0.0-53.7
MEM_NM	Meropenem	1	0	0	100	0.0-94.5
NIT_NM	Nitrofurantoin	2	0	0	100	0.0-80.2
OXA_NM	Oxacillin	3	100	0	0	31.0-100
VAN_NM	Vancomycin	5	0	0	100	0.0-53.7

DISCUSSION

The emergence of MDR (Multi Drug Resistant) bacteria is an increasing problematic cause of health care associated infections, not only due to increased morbidity and mortality, but also due to increased treatment costs as result of frequent and lengthy hospital stay [12]. Antimicrobial resistance is on increase – threatening our ability to treat some of the infectious diseases that cause most deaths. Antimicrobial resistance is today challenging our ability to treat effectively at least four of these infections: acute respiratory infections, diarrheal disease, malaria and TB.

In our study 1012 samples were examined from 449 (74.8%) males and 151 (25.2%) females hospitalized patients, most cases were from the ICU and Medical ward (42.7 % and 33.9% respectively). The major isolates were recovered from the respiratory specimens (39.7 %) followed by wound infection (26.5 %) and urine specimens (20.8%) while blood samples represented only (8.5%).

From the 733 isolates we found that the major isolated microorganism was gram negative *Klebsiella pneumonia* (123 /16.7%), *Pseudomonas aeruginosa* (121/ 16.5%) followed by *Acinetobacter baumannii* (87 / 11.87%), *E-coli* (76/10.37 %), *Proteus mirabilis* (82/ 11.19%), *Staphylococcus aureus* (50// 6.82%), *Candida albicans* (40/5.46%). Some isolates *like*, *Morganella, Providencia*, *Stenotrophomonas maltophilia*, *Enterobacter faecalis* and *Enterobacter Colace* and *Morganella morganii* represented less than 1% Some national isolates showed high resistance than others.

These results agreed with finding of Saeed *et al*. [13] who reported that the major isolates were Grame-negative microorganisms 83.45 %. However our finding disagreed with Lee *et al.* [15] who found that the incidence of Gram-positive and Gram-negative bacilli was 15% and 85% respectively.

In the present study, *Proteus mirabilis*, *Klebsiella pneumonia*, *Staphylococcus aureus* and *E-coli* were resistant 100 % to Beta-lactamase and ESBL and Nitrofurantoin (NIT) and the Extended-spectrum beta-lactamases (ESBL) with %R 95 %CI (5.5-100).

In addition the current study showed that *Pseudomonas aeruginosa* was resistant 100% to the Ampicillin/Sulbactam (SAM) and Oxacillin (OXA) while *Klebsiella pneumonia* was resistant 50% to Ampicillin/Sulbactam but showed showed 33.3% resistance for Oxacillin for isolates of *E- coli*.

This MRSA rate in our study was similar to that reported by Jones *et al*. and Lee *at al*. [14, 15].

The isolates which show great percent in our study were Gram-negative pathogens; MDR*P. aeruginosa* and ESBL-producing *K. Pneumonia* are of great concern.

According to the human health hazards and the pathogenicity of isolated organisms, *Klebsiella* ranks second to *E. coli* for urinary tract infections in older people. It is also an opportunistic pathogen for patients with chronic pulmonary disease, enteric pathogenicity, nasal mucosa atrophy and rhinoscleroma. New antibiotic-resistant strains of *K. pneumoniae* are appearing [16].

Also, Infections with *Pseudomonas aeruginosa* have become a real concern in hospital-acquired infections, especially in critically ill and immune compromised patients. The major problem leading to high mortality lies in the appearance of drug-resistant strains. Among infections caused by Gram-negative rods, *Pseudomonas aeruginosa* has a leading role [17].

For *Proteus mirabilis* it is a common pathogen responsible for complicated urinary tract infections (UTIs) that sometimes causes bacteremia. Most cases of *P. mirabilisbacteremia* originate from a UTI [18].

On the other hand *Acinetobacter spp*. has recently advanced to one of the most common pathogens isolated from ICUs. Also *Staphylococcus* aureus is well established as an important cause of hospital- and community-acquired infections [19].

Shigidi *et al.,* [20] found that *Staphylococcus* was most prevalent (29%), followed by E. coli (9%) and *Pseudomonas aeruginosa* was the least resistant with only 3% prevalence among dialysis patients.

Recent studies interested by the Extended Spectrum β-Lactamase (ESBLs) which are are enzymes produced by bacteria, mostly *E- coli* and *Klebsiella* species, rendering them resistant to cephalosporins including cefotaxime, cefuroxime and ceftazidime. These enzymes were first reported in the mid-1980s mainly in hospitals. These studies also found that production of ESBL is significantly associated with *E- coli* and *K. pneumoniae* from inpatients compared with outpatients [21, 22].

Extended spectrum β-lactamase (ESBL) producing *Escherichia coli* has tremendously increased worldwide and it is one of the most common causes of morbidity and mortality associated with hospital-acquired infections. This could be attributed to association of multi drug resistance in ESBL producing isolates [22].

CONCLUSION

Application of the WHONET software provides a uniform and a standardized platform for the management and analysis of microbiology data, with a special focus on the analysis of antimicrobial susceptibility test results. It should be used by the laboratory to collect, collate, analyze and share the data at various levels – local, regional and national. This will enable in building a strong antimicrobial resistance surveillance network

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