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Antimicrobial Characteristics of Bacteria Obtained from Various Body Site Infections in Patients Located in Al-Bayda City

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Abstract

This retrospective study (2020–2021) in Al-Bayda, Libya, analyzed 177 bacterial isolates from various body site infections. Predominant bacteria included *Staphylococci* (61), *Streptococci* (46), and *Escherichia coli* (36). Most isolates were multidrug-resistant (MDR). *Staphylococci* were susceptible only to amikacin, meropenem, and tetracycline but resistant to 16 antibiotics. *Streptococci* were susceptible to doxycycline and meropenem but resistant to 17 antibiotics. E. coli showed susceptibility to doxycycline, meropenem, and tetracycline but high resistance to 16 antibiotics. Other Gram-negative bacteria (*Klebsiella*, Proteus, *Neisseria*) also exhibited high MDR rates, with Proteus resistant to 18 antibiotics. The findings highlight severe antibacterial resistance in the region,and this is limiting treatment options.

Keywords: Antibacterial profile, Antibiotic resistant, Site of infections, Bacterial infections, Multidrug resistant.

INTRODUCTION

Antimicrobial resistance (AMR) limits available treatment options and has emerged as a pressing global concern. Consequently, it adversely affects community health, healthcare expenditures, and overall economic performance. The incidence of infections caused by resistant microorganisms is increasing worldwide (Naylor et al., 2018). According to the 2014 report by the World Health Organization (WHO), AMR stands out as one of the principal global challenges within the realm of infectious diseases. Evidence from around the globe indicates a decline in the effectiveness of existing antibiotics and a surge in bacterial resistance to both first-line and last-resort antibiotic treatments. The ramifications of antibiotic resistance are clinical, economic, and societal. Patients in hospitals often acquire infections during their stay in inpatient wards and intensive care units (Aftab, 2016). The implications of AMR are profound; as new strains of bacteria emerge, there will be repercussions that diminish consumer income, employment stability, healthcare accessibility, and gross domestic product (GDP) (Mazel & Mobashery, 2012).

Infections caused by drug-resistant pathogens pose a significant threat not only to public health but also to the economic integrity of communities. It is estimated that microbial diseases account for at least 25% of the 60 million deaths occurring annually worldwide. Despite advancements in infection control methods, clinical infections resulting from drug-resistant pathogens continue to be substantial contributors to morbidity and mortality, affecting both hospitalized patients and the general population in developed nations, middle-income countries, and sub-Saharan Africa (Celi et al., 2017). Commonly isolated pathogens in clinical and community settings include *Escherichia coli* (*E. coli*), *Staphylococcus aureus (S. aureus), Klebsiella pneumoniae (K. pneumoniae), Pseudomonas aeruginosa (P. aeruginosa), Streptococcus pneumoniae (S. pneumoniae),* and *Salmonella* spp. These organisms represent the most significant antibiotic-resistant threats currently (Schiavetti et al., 2018).

MATERIALS AND METHODS

Study Site

This research was conducted in the city of Al-Bayda, situated in Libya.

Data Collection

This retrospective study utilized data from the ALBORJ laboratory, which generated reports on all isolated organisms over a two-year period from January 2020 to December 2021. The microbiology department of the laboratory received various specimens from both inpatient and outpatient departments for bacteriological evaluation, totaling 177 specimens (including urine, stool, vaginal swabs, sputum, and wound swabs). The bacteriological assessment included culturing specimens on suitable growth media following national standard operating procedures and Clinical Laboratory Standards Institute (CLSI) guidelines. The isolated organisms underwent additional identification tests. Furthermore, antibiotic susceptibility testing (AST) was carried out using the Kirby-Bauer disc diffusion technique on the isolated/identified organisms.

Inclusion and Exclusion Criteria

All specimen records containing patient age, specimen source, specimen type, isolated organisms, and performed ASTs were included in this investigation. Records lacking any of the specified information or specimens with an unknown type or source, and/or those without identified organisms, were excluded from the study. Additionally, organisms with fewer than three entries were not considered in the analysis.

Data Analysis

The AST results were evaluated using Microsoft Excel 2010 and IBM SPSS Statistics version 20 software. The susceptibility rates for each antibiotic were calculated for every bacterial isolate. The mean susceptibility percentages for each isolate against all tested antibiotics were determined by calculating the number of resistant strains out of the total strains tested with a specific antibiotic in a specimen.

RESULTS

A total of 200 specimens were analyzed, and only 177 met the inclusion criteria for this study. Specimens were collected from different body sites (urine, stool, wound swabs, vaginal discharge, and sputum). The commonest bacteria isolated from these specimens were *Staphylococci, Streptococci, Escherichia coli, Klebsiella, Proteus, and Nisseria. The* number of isolates for each was (61, 46, 36, 26, 5, 3), respectively, as shown in the figure 1 below.

Nineteen types of antibiotics were used for antibiotic susceptibility testing on both Gram-positive and Gram-negative isolated bacteria. The collected data is shown in the tables below. Isolated *Staphylococci* were susceptible to amikacin, meropenem, and tetracycline but had resistance to sixteen types of antibiotics at high rates. The majority of isolates were resistant to one or more antimicrobials tested. In general, *Staphylococci* were multidrug resistant (MDR). Whereas isolated *Streptococci* were susceptible to doxicyclin and meropenem but had resistance to 17 types of antibiotics at high rates. The majority of isolates were resistant to one or more antimicrobials tested. *Streptococci* were multidrug resistant (MDR). Isolated *E.coli* was susceptible to doxicyclin, meropenem, and tetracycline but had resistance to 16 types of antibiotics at a high rate. The majority of isolates were resistant to one or more antimicrobials tested. *Staphylococci* were multidrug resistant (MDR). On the other hand, the Gram-negative isolated bacteria were tested and showed multi-drug resistance, also with high rates. *Klebsiella* were susceptible to doxicyclin, cephatexine, and tetracycline but had resistance to 16 types of antibiotics at a high rate. *Proteus* in this study was susceptible to tetracycline only, but had resistance to 18 types of antibiotics at high rates, and it had MDR at a high rate. *Niesseria* was susceptible to Amikacin, Doxicyclin, Azithromycin, Clindamycin, Gentamycin, Tetracycline, Erythromycin, and Chloramphenicol. *Niesseria* had resistance to 11 types of antibiotics and MDR at high rates.

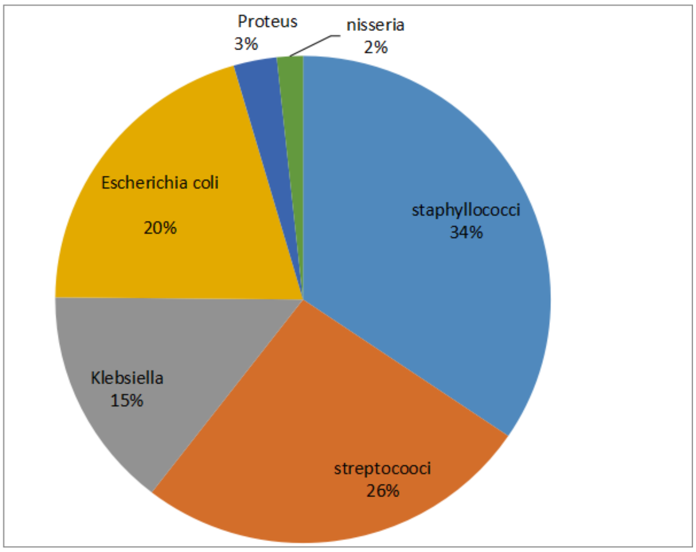

Figure (1): The percentage of isolated bacteria from specimens

Table (1). Antibacterial profiles of Gram-positive bacteria isolated from different body site infections among patients in Al-Bayda city in Libya

	Staph.		*Strept.*	
Antibiotics	T	R	T	R
Amikacin	61	0	46	3
Augmantin	61	32	46	17
Azithromycin	61	35	46	23
Cefotaxime	61	40	46	30
Cefotrexone	61	34	46	29
Clindamycin	61	23	46	14
Doxycyclin	61	2	46	0
Gentamycin	61	9	46	4
Cephatexin	61	1	46	1
Meropenem	61	0	46	0
Tetracycline	61	0	46	1
Erythromycin	61	9	46	4
choloramphenichol	61	6	46	2
Cefazid	61	3	46	2
Streptomyacin	61	17	46	11
Septrin	61	36	46	17
Ciprofloxacin	61	16	46	10
Nitrofloxacin	61	15	46	7
Levofloxacin	61	7	46	7

Table (2). Antibacterial profiles of Gram-negative bacteria isolated from different body site infections among patients in Al-Bayda city in Libya

	Kleb		*Proteus*		*Niess*		*E.coli*	
AB	T	R	T	R	T	R	T	R
AMK	26	7	5	1	3	0	36	6
AUG	26	16	5	2	3	2	36	23
AZT	26	14	5	2	3	0	36	5
CFXM	26	13	5	3	3	2	36	12
CFRX	26	15	5	2	3	1	36	32
CLN	26	13	5	3	3	0	36	21
DOX	26	0	5	1	3	0	36	0
GNT	26	9	5	3	3	0	36	5
CPHX	26	0	5	1	3	1	36	4
MER	26	1	5	1	3	1	36	0
TET	26	0	5	0	3	0	36	0
ERY	26	4	5	3	3	0	36	13
CHOL	26	5	5	1	3	0	36	10
CFZ	26	1	5	1	3	1	36	2
STR	26	6	5	/	3	/	36	3
SPT	26	7	5	1	3	1	36	8
CIP	26	11	5	2	3	1	36	10
NTRF	26	7	5	/	3	/	36	2
LEVO	26	5	5	1	3	3	36	4

Table (3): Multi-drug resistance profiles among bacterial isolates at Al-Bayda city in Libya

	R0	R1	R2	R3	R4	R5
Staph.	1	2	2	4	4	7
Strep.	6	4	1	3	4	6
E.coli	0	2	3	4	3	3
Klebs.	1	1	0	0	0	1
Protues	0	1	0	0	0	0
Niesseria	0	0	1	0	1	0

DISCUSSION

The rise of antibiotic resistance stemming from excessive antibiotic use poses an increasing threat to public health. In the city of Al-Bayda, geographical, cultural, and other unique differences impact this issue. Without comprehensive monitoring of antibiotic resistance and consumption, significant findings can be overlooked in this distinct region. This study aimed to enhance the understanding of trends related to antibiotic resistance and usage within Al-Bayda city.

This research revealed statistically significant increases in resistance among *Staphylococcus, Streptococcus, Escherichia coli, Klebsiella, Proteus,* and *Neisseria* against *Clindamycin,* Doxycycline, Gentamicin, Cephalexin, Meropenem, Tetracycline, Erythromycin, Chloramphenicol, Cefazolin, Streptomycin, Trimethoprim-Sulfamethoxazole, Ciprofloxacin, Nitrofurantoin, Levofloxacin, and Augmentin. The findings highlighted a surge in resistance among both Gram-positive and Gram-negative bacteria to the aforementioned antibiotics prevalent in Al-Bayda city. Notably, the resistance rates of Staphylococcus to antibiotics have been on the rise over the past decade.

A total of 200 samples were examined, of which 177 met the criteria for inclusion in the study. The samples were collected from various body sites (urine, stool, wound swabs, vaginal secretions, and sputum) from 2020 to 2021. In this retrospective analysis, the most frequently isolated bacteria were *Staphylococci, Streptococci, Escherichia coli, Klebsiella, Proteus, and Neisseria,* with respective isolate counts of 61, 46, 36, 26, 5, and 3. A total of 19 different antibiotics were employed for susceptibility testing on both Gram-positive and Gram-negative bacterial isolates.

An intriguing outcome of this thesis is the observed increase in sensitivity of *Staphylococcus aureus* to Ciprofloxacin, Levofloxacin, and Penicillin. Previous studies conducted in the United States have also found heightened sensitivity of *Staphylococcus aureus* to Penicillin (Chaubot, Stephan, Fredericy, Schimmel, & Lariosa, 2015; Canjilal et al, 2017). Due to its notable resistance to Penicillin, clinicians at the study hospital often refrain from prescribing this antibiotic for this particular bacterial species. However, penicillin should be considered for *Staphylococcus aureus* strains that are susceptible to it, given its advantages such as a narrow activity spectrum and lack of association with *Clostridium difficile* infection (Chabot et al., 2015). Although no correlation was found between the consumption of levofloxacin and Staphylococcus aureus, the reduced use of levofloxacin at the hospital may have contributed to the observed increase in sensitivity of *Staphylococcus aureus* to this antibiotic.

Isolates of Staphylococcus aureus exhibited sensitivity to Amikacin, Meropenem, and Tetracycline but showed high resistance rates to 16 different antibiotics, with the majority of isolates being resistant to one or more of the tested antimicrobials. *Staphylococcus* was found to be multidrug-resistant (MDR). The *Streptococci* isolated in this research were sensitive to Doxycycline and Meropenem but resistant to 17 antibiotics at high rates, with most isolates also being resistant to one or more of the antimicrobials tested, indicating they too were multidrug-resistant (MDR).
The two-year study period may be too brief to adequately capture significant trends in emerging antibiotic resistance patterns. Resistance can develop shortly after an antibiotic is introduced, or it may take decades, as seen with Vancomycin-resistant Staphylococcus aureus (Zaman et al., 2017). This underlines the necessity of persistent surveillance for antibiotic resistance to identify new patterns.

Monitoring resistance trends is crucial for effectively managing antibiotic resistance within any healthcare facility. Local public health authorities may also find this data useful, as it offers a snapshot of antibiotic resistance patterns specific to this region. Tracking antibiotic resistance can be performed at the city level since most hospitals generate antibiotic data annually or biannually. Another retrospective study evaluated the antibiotic susceptibility profiles of organisms isolated from routine specimens submitted for bacteriological culture at the microbiology lab of Ndola Teaching Hospital from May 2016 to July 2018. Throughout this study period, it was noted that urine, blood, and wound swab samples were the most frequently analyzed routine specimens, predominantly collected from inpatient departments and patients aged 40 years and older. From these samples, *coliforms, E. coli, S. aureus,* and *Staphylococcus epidermidis* were the most common pathogens identified, and Chloramphenicol and Nitrofurantoin were effective during the study period.

Streptococci were found to be multidrug-resistant (MDR) in 34% of cases. *Escherichia coli* isolates demonstrated sensitivity to Doxycycline, Meropenem, and tetracycline but were resistant to 16 antibiotics at a high rate of 20%, with the majority of isolates resistant to one or more of the tested antimicrobials overall.

CONCLUSION

Infections with bacterial isolates resistant to the majority of antimicrobials are a major issue in the study area.

Most of the isolated bacteria were resistant to the commonly used antimicrobials, and MDR isolates were significantly high.
Therefore, Clinicians should practice rational choice of antimicrobials, and treatment should be guided by antimicrobial susceptibility testing.

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