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Research Article

A DESCRIPTIVE, RETROSPECTIVE CROSS-SECTIONAL STUDY ON THE AGE WISE DISTRIBUTION AND ANTIMICROBIAL RESISTANCE PATTERNS OF CLINICAL BACTERIAL ISOLATES IN A HOSPITAL IN AL-HILLA CITY 2024-2025

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Abstract

Antimicrobial resistance (AMR) has become a global public health concern, with increasing prevalence across all age groups. This study aimed to evaluate the distribution and resistance patterns of bacterial pathogens isolated from patients of different age groups in a hospital in Al_ Hilla during the years 2024 _ 2025. A retrospective analysis was conducted using laboratory data from bacterial cultures and antibiotic sensitivity tests. The results showed that multidrug-resistant organisms (MDR) were most prevalent among elderly patients, while younger age groups exhibited higher susceptibility to commonly used antibiotics. Escherichia coli and p. aeruginosa were the most frequently isolated organisms. The findings highlight the need for age-specific antibiotic stewardship strategies and continuous surveillance to combat the rise of drug-resistant infections.

Keywords: Wiskott-Aldrich, Auto-immune, Optic atrophy, Case report.

INTRODUCTION

Bacterial pathogens are major contributor to global morbidity and mortality due to their capacity to cause serious infectious disease and evade antimicrobial treatment (1,2) . A key driver of this challenge is antimicrobial resistance (AMR), which arises when bacteria develop mechanism to survive exposure to antibiotics (3,4). These resistance mechanisms are complex and may include natural (intrinsic) resistance, such as structural barriers that prevent drug access. For instance, gram negative bacteria are naturally resistance to vancomycin due to the drug's inability to cross their outer membrane (5,6). In contrast, acquired resistance involves genetic change through mutation in bacterial chromosome or the acquisition of resistance gene from external sources via plasmids, transport, and integrons (5,7) these genes can spread horizontally through processes such as conjugation, transformation, and transduction. Resistance may also lead to cross - resistance, where resistance to one antibiotic confers resistance to others, even across unrelated drug lasses (7,8).

The most concerning categories of AMR include:

Multidrug Resistance (MDR): resistance to at least three classes of antibiotics.

Extensive Drug Resistance (XDR): resistance to nearly all available antibiotics.

Pan Drug Resistance (PDR): resistance to all known antibiotics, including last resort drugs such as colistin and tigecycline (6,9)

Historically, antibiotic resistant emerged soon after the clinical use of penicillin, discovered by Alexander Fleming in 1928 (10, 11) . By 1972, methicillin Resistance staphylococcus aureus (MRSA) had been reported in the UK,US, and other regions(12) . The blaNDM_1 gene, conferring resistance to beta _ lactams, was first identified in Klebsiella pneumoniae in 2008 (13), while the mcr _1 gene, conferring resistance to polymyxin, was found in pig _ associated Enterobacteriaceae in 2015 in chin (14). In response to the rising AMR threat, the World health organization (WHO) released its first list of critical priority pathogens in 2017. This list includes carbapenem _ resistance Acinetobacter baumannii, Pseudomonas aeruginosa, and ESBL - producing Enterobacteriaceae such as Klebsiella, E.coli, serratia, and proteus (15) . These organisms are known for their resistance to multiple antibiotic classes and their capacity to cause severe and hard to treat infections. Despite the extensive global research on antimicrobial resistance (AMR), there is limited data regarding how bacterial prevalence and resistance patterns vary across different age groups within specific local population, particularly in low-and middle-income countries such Iraq. Most existing studies focus on isolated pathogens or single age cohorts without integrating demographic factors such as age and gender in a comprehensive analysis. Therefore, this study aims to investigate the distribution of bacterial isolates and their antimicrobial resistance profiles across five distinct age groups in a clinical setting in Al Hilla,Iraq. By identifying age related trends in resistance, the study seeks to inform more targeted antibiotic stewardship programs and age-appropriate treatment guidelines.

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METHODOLOGY

- Study Design and Data Source

This research was designed as a cross-sectional analytical study based on retrospective laboratory data collected from one of the major hospitals in Al-Hilla city, Iraq, during the period January 2024 to April 2025. The study focused on evaluating the distribution and antimicrobial resistance patterns of bacterial pathogens across different age groups, using microbiological records obtained from the hospital's diagnostic laboratory.

- Nature and Structure of the Data

The dataset included the following variables for each patient:

• Age and gender
• Identified bacterial species
• Antibiotic susceptibility test (AST)

- Age Group Classification and Data Handling

Patients were stratified into five epidemiologically relevant age groups

The data were categorized and analyzed to determine:

• The frequency and types of bacterial isolates within each age group.
• The antimicrobial resistance profiles for the most frequently used antibiotics, including: • Ampicillin (AMP)• Amikacin (AMK)• Vancomycin (VAN) (used for comparison; not typically effective against Gram-negative bacteria)

- Ethical Considerations

Official authorization to use and analyze the data was obtained from the hospital administration as the data were pre-existing and fully anonymized, no direct patient interaction occurred, and individual informed consent was not required.

- Statistical Analysis Data were analyzed using IBM SPSS Statistics version 26.

RESULTS

Table 1. Gender-wise Distribution of Patients with Bacterial Infections

Gender	Count	Percentage
Male	215	43.17%
Female	283	56.83%
Total	498	100%

Table 2. Age group distribution and predominant bacterial isolate among infected patients

Age Group (years)	Frequency	Percentage (%)	Most common bacteria
Less than 5	49	9.84%	Escherichia coli
5–20	62	12.45%	Escherichia coli
21–30	104	20.88%	Escherichia coli
31–60	182	36.55%	Escherichia coli
More than 60	101	20.28%	Escherichia coli
Total	498	100%	

Table 3. Distribution of common bacterial isolates by age group

Age Group (years)	Most common bacteria	Count	Percentage (%)
Less than 5 (49)	Escherichia coli	18	36.73%
	Pseudomonas aeruginosa	15	30.61%
	Acinetobacter baumannii	5	10.20%
	Klebsiella spp.	3	6.12%
	Citrobacter spp.	2	4.08%
	Enterobacter aerogenes	2	4.08%
	Acinetobacter spp.	1	2.04%
	Enterococcus faecalis	1	2.04%
	Klebsiella pneumoniae	1	2.04%
	Norcardia spp.	1	2.04%
5–20 (62)	Escherichia coli	21	33.88%
	Pseudomonas aeruginosa	16	25.82%
	Klebsiella pneumoniae	9	14.51%
	Acinetobacter baumanni	4	6.45%
	Klebsiella spp.	4	6.45%
	Citrobacter spp.	3	4.84%
	Norcardia spp.	2	3.22%
	Enterococcus spp.	1	1.61%
	Enterococcus faecalis	1	1.61%
	Enterobacter cloacae	1	1.61%
21–30 (104)	Escherichia coli	39	37.5%
	Pseudomonas aeruginosa	23	22.11%
	Acinetobacter baumannii	11	10.57%
	Citrobacter spp.	8	7.69%
	Klebsiella pneumoniae	7	6.73%
	Klebsiella spp.	5	4.8%
	Nocardia spp.	4	3.84%
	Enterobacter spp.	2	1.92%
	Enterobacter cloacae	2	1.92%
	Enterococcus faecalis	1	0.96%
	Klebsiella oxytoca	1	0.96%
	Acinetobacter spp.	1	0.96%
31–60 (182)	Escherichia coli	58	31.78%
	Pseudomonas aeruginosa	52	28.9%
	Citrobacter spp.	20	10.9%
	Klebsiella pneumoniae	18	9.89%
	Nocardia spp.	9	4.95%
	Acinetobacter baumanni	9	4.75%
	Enterobacter cloacae	6	3.28%
	Others	10	5.48%
More than 60 (101)	Escherichia coli	39	38.7%
	Pseudomonas aeruginosa	35	34.7%
	Klebsiella spp.	13	12.9%
	Acinetobacter baumanni	5	5.0%
	Klebsiella pneumoniae	5	5.0%
	Acinetobacter spp.	2	1.9%
	Citrobacter spp.	1	0.9%
	Enterococcus spp.	1	0.9%

Table 4. Antibiotic susceptibility profiles of selected bacterial isolates

Bacterial Species	Antibiotic	Sensitive (n, %)	Resistant (n, %)	Total (n)
Escherichia coli	Vancomycin	4 (66.7%)	2 (33.3%)	6
	Ampicillin	20 (17.9%)	92 (82.1%)	112
	Amikacin	77 (79.4%)	20 (20.6%)	97
Pseudomonas aeruginosa	Vancomycin	2 (4.5%)	42 (95.5%)	44
	Ampicillin	3 (3.4%)	85 (96.6%)	88
	Amikacin	28 (43.1%)	37 (56.9%)	65
Acinetobacter baumannii	Vancomycin	7 (50.0%)	7 (50.0%)	14
	Ampicillin	1 (8.3%)	11 (91.7%)	12
	Amikacin	4 (44.4%)	5 (55.6%)	9
Klebsiella spp.	Vancomycin	4 (18.2%)	18 (81.8%)	22
	Ampicillin	1 (4.8%)	20 (95.2%)	21
	Amikacin	10 (45.5%)	12 (54.5%)	22

DISCUSSION

This study include 498 participant distributed across five age group key finding

Gender - infectious diseaselink

This study indicate that female exhibited a greater incidence of bacterial infections than males this is due to many factors:

➢ Anatomical susceptibility in females:

Females are. More prone to certain infections (especially urinary tract infectious) due to their shorter urethra and its proximity to the anus and vaginal introitus. This facilitates easier migration of pathogens such as E- coli, the most commonly isolated bacterium in this study, from the GIT to the urinary system(16).

➢ Hormonal and physiological factors

Hormonal fluctuation particularly during menstruation, pregnancy, and menopause, can alter the normal vaginal microbiota and immune response, increasing susceptibility to infections(17). Estrogen deficiency post -menopause has been linked to reduced vaginal lactobacilli and increase risk of urogenital infections (18)

➢ Behavioral and sociocultural factors

In many culture females may be more likely to seek medical attention or undergo diagnostic testing, leading to higher rates of detection and reporting of infections(19) . Furthermore, increased healthcare exposure during pregnancy and childbirth may heighten risk for hospital acquired infections.

➢ Genital and Reproductive healthcare exposure

Frequent medical intervention such as urinary catheterization, gynecological exam, and childbirth - related procedures increase opportunities for pathogen transmission in women(20)

Age infectious disease link

As observed in this study incidence of bacterial infections is highest in the 31 - 60 age group most important reasons are.

➢ Peak exposure during working and socially active years

This age group typically represents the most professionally and socially active population, often exposed to diverse environments such as work places, public transport, and crowded setting all of which increase the risk of pathogen transmission (21) furthermore, occupational stress and irregular routines may negatively affect immunity(22)

➢ Higher prevalence of chronic disease

Adults in this age rangemore likely to develop or manage non - communicable diseases (e.g, diabetes, hypertension, COPD), which compromise the immune system and predispose to recurrent infections, especially with resistant organisms(23). For example, diabetes mellitus is a well-documented risk factor for urinary tract and soft tissue infections due to impaired leukocyte function and vascular insufficiency (24). Increase use of medical interventions many individuals between 31-60 undergo elective surgeries, regular checkups, dentalwork, or minor procedures. These interventions often involve antibiotics or medical devices, contributing to both infection risk and antimicrobial resistance development (25) .

➢ Reduced innate immunity over time

Although still within the adult range, immune function begins to decline gradually after the third decade of life, particularly in individuals with unhealthy lifestyle (e.g, smoking, poor diet) increasing vulnerability to infections(26) . Greater likelihood of self-medication and antibiotic misuse in low and middle-income countries, this age group often has autonomy over healthcare decisions and may engage in unsupervised antibiotic use, which can lead to colonization by resistant strains and higher infection burdens (27) .

Bacterial prevalence by age group

➢ Age less than 5

E.coli predominant in this age group because its associated with UTI due to anatomical vulnerability (e.g short urethra) and incomplete toilet training(28),And GIT infections due to immature immunity and fecal oral transmission in children(29) P.aerugenosa, linked to respiratory infection (cystic fibrosis) and hospital - acquired infections in neonate(30) .

➢ Age 5_20

This group showed E.coli (33.9%) as most common, followed by p . aeruginosa (25.8%) and pneumonia(14.5%)

Eccoli : related to UTI (common in sexually active adolescent) and community acquired infections (31).P.areuginosa : linked to trauma, IV drug use, or hospitalization.

➢ Age 21-30: Persistence of EColi , Rise in resistance

In this young adult population, E.coli remained dominant, but there was a notable presence of P.areugenosa and A.baumannii. This reflects the high prevalence of UTIs in sexually active females.as well as increased occupational exposure to contaminated surfaces or medical settings (32,33). A.bumanni, frequently isolated in this group, is Known for colonizing patients in hospital or military settings, suggesting increased exposure to invasive care or community _ onset multidrug _ resistance strains (34).

➢ 31_60 years

E_coli decline vs p.aeruginosa rise

Comorbidities (DM, COPD) increase susceptibility to P.aeruginosa (e.g, ventilator _ associated pneumoniae)

Citrobacter spp. Thrives in immunocompromised or hospitalized (35) .

➢ More than 60 years

E.coli and P.aeruginosa

Weakened immunity, catheters, and UTIs drive E.coli infections (36) .

P.aeruginosa exploits chronic lung diseases, wounds, and medical devices (37).

Klbsiellaspp : common in pneumonia and UTIs in the elderly with comorbidities (38). P.areuginosa : associated with wound, burns, or contaminated water exposure in this active age group 30 .

Antimicrobial resistance profile

Resistance data showed a worrying trend of multi-drug resistance (MDR) among common pathogens:

- E. coli: 82.1% resistance to ampicillin, but retained 79.4% sensitivity to amikacin. These figures align with WHO global AMR surveillance findings.
- P. aeruginosa: Exhibited >95% resistance to ampicillin and vancomycin, and 56.9% resistance to amikacin, indicating high intrinsic and acquired resistance mechanisms(39).
- A. baumannii: Displayed alarming resistance rates, especially to β-lactams and aminoglycosides, consistent with its classification as a critical priority pathogen by WHO.
- Klebsiella spp.: Showed >95% resistance to ampicillin and >80% to vancomycin, echoing global concerns about extended-spectrum beta-lactamase (ESBL) production

Conclusion

This study highlights the significant variation in bacterial prevalence and antimicrobial resistance patterns across different age groups in a clinical population from A-Hilla city. Escherichia coli and pseudomonas aeruginosa emerged as the most commonly isolated pathogens, with notability high rate of multi-drug resistance (MDR), particularly in adult aged 31-60 and the elderly population. the finding underscores the critical need for age – specific stewardship policies and enhanced infection control strategies, especially in resource limited-setting.moreover, the observed patterns suggest that demographic factor such as age and gender play avital role epidemiology of bacterial infections and resistance. future research should expand on these finding by incorporating larger, multicenter datasets and molecular analyses to track resistance gene transmission and evolution.

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