RESEARCH PAPER

Antibiotic Resistance Patterns of Bacterial Pathogens in Community-Acquired Pneumonia

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ABSTRACT

Among the most common infectious diseases and fatal illnesses globally, community-acquired pneumonia (CAP) continues to rank high. However, the expanding issue of antimicrobial resistance (AMR) exacerbates the situation. Finding out how many CAP patients in Iraq have discovered bacteria resistant to antibacterial treatments is the main goal of this investigation. A cross-sectional study that lasted from May 2023 to June 2024 involved 122 people with CAP who had been clinically and radiologically verified at Al-Yarmouk Teaching Hospital in Baghdad. Sputum samples were microscopically examined, cultured, and subjected to sensitivity testing with the VITEK® 2 system. 36.1% of the 122 patients' bacterial cultures came back positive. 18.2% of all infections were caused by Staphylococcus pneumoniae, Staphylococcus sanguinis, Staphylococcus aureus, and Pseudomonas aeruginosa. Pseudomonas aeruginosa made up 11.4% of the total, whereas Staphylococcus pneumoniae and Staphylococcus sanguinis were completely resistant to ciprofloxacin, clindamycin, and azithromycin. For vancomycin, 60% of the bacteria were resistant, whereas for linezolid, 20% were. Acinetobacter baumannii's near-total resistance provided cause for alarm. This research uses state-of-the-art automated diagnostics to provide the first comprehensive resistance profile for CAP infections in Iraq. Antibiotic resistance, especially pan-resistant bacteria, is rampant, according to the results. The already dire situation of antibiotic resistance in CAP in Iraq has been made worse by the emergence of bacteria that are pan-resistant. At this time, there is a need for nationwide antibiotic stewardship programs in Iraq, as well as stringent action to prevent the free distribution of antibiotics.

Keywords: Community-acquired pneumonia, Bacterial pathogens, Antibiotic sensitivity, antimicrobial resistance, Respiratory infection.

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I.INTRODUCTION

Community-acquired pneumonia is a respiratory illness that can cause significant morbidity and even death and affects people of all ages. However, severe cases and consequences are more likely to affect older people and those with existing medical conditions [1]. India's disease burden will continue to be high due to environmental factors like air pollution and the use of biomass fuels for cooking, as well as delays in diagnosis and treatment and limited access to healthcare [2]. The majority of pneumonia that occurs in the community is brought on by bacteria. Because incorrect or delayed antibiotic treatment will result in an increase in morbidity, hospitalization length, and cost, it is essential to identify the causing organism. However, due to overlapping clinical symptoms and the lack of always-available microbiological identification, identifying the culprit organism is often a difficulty [3].

Among all bacterial pneumonias, it is the most frequent on a global scale. Other Gram-negative organisms, like Haemophilus influenzae and Staphylococcus aureus, are common pathogens [4]. Age, vaccination rates, and the presence of other diseases may influence the relative frequency of these microorganisms. The rise of drug-resistant bacteria and other microbes has made it harder to choose a successful empirical treatment in recent years [5].

The problem of antibiotic resistance is getting worse. The misuse and abuse of antimicrobials in both outpatient and inpatient settings has led to the evolution of resistance, which includes resistance to commonly prescribed antimicrobial treatment methods such as macrolides, fluoroquinolones, and third-generation cephalosporins. To advance antimicrobial

stewardship, enhance patient care in general, and inform treatment decisions, regular assessments of local patterns of antibiotic susceptibility are necessary [6,7]. According to the data, patterns of infection transmission and resistance may differ between hospitals and regions in India. As a first line of defense, physicians choose antibiotics with the best chance of success based on local microbiological surveillance before test data are available. Because delaying treatment lowers the likelihood of a positive outcome, this is of the utmost importance when funds are limited.. Consequently, it is intriguing to investigate the antibiotic sensitivity pattern and bacteriological profile of patients admitted to an Indian tertiary care hospital with community-acquired pneumonia.

A. Common Pathogens and Shifting Etiology

Although the exact bacteria that cause chronic obstructive pulmonary disease (CAP) varies from one area to another, the most common culprits are Streptococcus pneumoniae, Haemophilus influenzae, Klebsiella pneumoniae, and Moraxella catarrhalis [8]. Isolation of gram-negative bacilli and atypical pathogens including Legionella pneumophila and Mycoplasma pneumoniae has grown in recent years, according to monitoring data [9]. Importantly, there has been a rise in the number of CAP patients with co-infections, which may make it more difficult to diagnose and select a treatment plan due to the presence of numerous pathogens. The elderly, immunocompromised, and chronically ill are just a few of the subpopulations in which atypical presentations or the presence of resistant organisms are more prevalent [10]. Modern diagnostic techniques like multiplex PCR [11] have made it easier to identify pathogens and increase the variety of microbes in CAP. Nevertheless, some infections may be underreported or reported inconsistently due to geographical variations in diagnostic availability. There is evidence that CAP's etiology is influenced by the seasons and climate, occurring more frequently during the colder months and in temperate regions [12]. Consequently, the pathogen profile is influenced by numerous environmental, demographic, and healthcare-related variables, which should be taken into consideration when evaluating empirical treatment options.

B. Mechanisms of Antimicrobial Resistance in CAP Pathogens

CAP pathogen resistance development is influenced by a variety of biochemical and genetic pathways. Streptococcus pneumoniae is one example of a bacterium that may develop resistance to betalactam by altering its penicillin-binding proteins [13]. Beta-lactamases, such as the TEM-type enzymes produced by Haemophilus influenzae and Moraxella catarrhalis, render medications like ampicillin inactive. Active efflux via the mefA gene or methylation of ribosome sites via the ermB gene is one common way that S. pneumoniae gains resistance to macrolides [14].

C. Objectives

- To discover the most prevalent bacterial infections that cause CAP
- To investigate patterns of these diseases' antibiotic resistance For the following reasons:
- To find out how well antibiotics work
- To propose methods for enhancing the use of antibiotics

II.MATERIAL & METHOD

A. Study setting

The STROBE guidelines for cross-sectional research were followed throughout the execution and publication of this study [25]. One hundred twenty-two patients diagnosed with CAP between May 2023 and June 2024 (by clinical and radiological means) were included in this cross-sectional research. Patients were sourced from AL Yarmouk Teaching Hospital's medical ward, emergency department, and outpatient clinic.

B. Patients and Data Collection

All cases of pneumonia were sent for bacterial culture and sensitivity testing after the sputum was carefully examined under a microscope to find the necessary specimen characteristics—at least 10 epithelial cells per low power field and more than 25 leukocytes. This conclusion was based on the treating physician's notes and the radiologist's validation of the matching images. All patient specimens were quickly received by the laboratory department, which analyzed them using the VITEK® 2 technology to identify CAP-causing bacteria and establish medication susceptibility.

Patients with active cancers on chemo, rheumatological diseases on biologics or disease-modifying drugs, advanced systemic illnesses cared for in a hospital or nursing home, active or latent tuberculosis in the lungs, acute pulmonary edema, or recent pulmonary embolism were all part of the exclusion criteria.

C. Identification of CAP Isolates

As soon as sputum samples met the microbiology lab's quality standards—defined as having more than 25 leukocytes and fewer than 10 epithelial cells per low-power field—they were processed. A number of popular culture media were used for bacterial growth, including chocolate agar, MacConkey agar, blood agar, and others. After that, they were incubated for 24-48 hours either aerobically or with 5% CO2. To describe bacterial colonies, we made use of VITEK 2 Compact. Here, bacteriochemical characterization is used. In addition, VITEK 2 Compact was subjected to concurrent antibiotic sensitivity tests. The CLSI scale was used to assess the susceptibility of S.

18 out of 124 sputum samples were deemed unfit for inclusion due to their poor quality, but only those that met our microscopy requirements were included. We introduced the VITEK 2 system and the CLSI M100 guidelines, 30th edition (2020) to decipher resistance. All of the agents analyzed, including the more modern

medications moxifloxacin and linezolid, had their breakpoints determined using the criteria.

D. Laboratory Procedures and Quality Control

To ensure that all sputum specimens could be treated within 30 minutes of collection, they were all carried in sterile, leak-proof containers. The stringent standards of Biosafety Level 2 were followed in all microbiological operations. Bacteria were identified and their antibiotic susceptibility was determined using the VITEK® 2 Compact system. For Gram-positive organisms, the AST-P580 card was used, and for Gram-negative isolates, the AST-N255 card. To ensure that our quality control procedures adhered to CLSI guidelines, we double-checked our results each week by comparing them to the reference strains of E. coli, Staphylococcus aureus, and Pseudomonas aeruginosa. Automatic application of internal system controls was also carried out during each run. For bacteria to meet the requirements of the ECDC and CDC's multidrug resistance (MDR) program, they must be resistant to at least three distinct antibiotic classes. Patients who were able to provide their own sputum samples for analysis were present in every hospitalization for community-acquired cases, despite the fact that the investigation employed a sequential sampling strategy. Consequently, there was a wide range of examples. Patients who were unable to supply their own sputum samples were frequently excluded from the study, despite the repeated sampling technique used to reduce selection bias.

E. Statistical Analysis

In order to code and enter all of the data that was acquired, Based in Chicago, Illinois, USA, we used IBM SPSS Statistics version 29. Means, standard deviations, ranges, percentages, and frequencies could be summarized using descriptive statistics. The discovery of potential risk factors for multidrug resistance (MDR) was the goal of logistic regression analysis. The model also produced exact p-values and 95% confidence intervals (CIs), in addition to odds ratios (ORs). Due to the exploratory nature of this study, multiple comparisons were not officially taken into account. Due to the descriptive nature of the investigation, power estimate was unnecessary. We were unable to account for potential confounding variables including comorbidities and prior antibiotic exposure due to unreliability of the data in the patient records. This constraint is well-known towards us. For a number of bacterial families, three or four isolates were discovered.

The Pearson chi-square test was used to specifically examine the significance of the category values. However, when the anticipated count was small (less than 5), either Yates continuity correction or Fisher's exact test were used. A significance level of 0.05 was used to determine the research's importance.

F. Ethical Approval

The research was approved by the Institutional Review Board (IRB) No. 22 on April 3, 2023, after receiving approval from the medical departments of Mustansiriyah University and Al-Yarmouk Teaching Hospital. Ethical guidelines established by the institution and the principles stated in the 1975 Declaration of Helsinki, as updated in 2024, were followed consistently throughout the investigation. All participants or their legal guardians were asked to sign an informed consent form after being briefed on the study's purpose, methodology, potential hazards, and advantages. To ensure privacy and avoid identifying patients, all of their data was anonymised.

III.RESULTS

A. Section A: Patient Features

Out of 122 patients who took part, 36.1% had positive sputum culture results, whereas 63.9% had no bacterial growth at all (Fig. 1).

21 (47.7% of the total) of the 44 people had positive sputum cultures, while 23 (52.3% of the total) were male. There was a wide range of ages represented among the 44 patients, with 24 (54.5%) being 55 and over.

11 (or 25%) of the 44 patients surveyed had a history of smoking, while 33 (or 75% of the total) did not (Table 1).

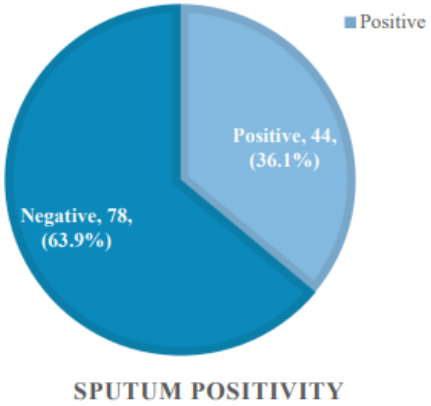

Fig. (1). Visual representation of the CAP cohort's sputum culture positive flowchart.

Table 1. Specifics regarding the participants

Classification	Heading	Quantity (n)	Ratio (%)
Age (Years)	<30	–	–
	30–40	–	–
	40–55	–	–
	≥55	–	–
	Mean ± SD	–	50.0 ± 18.2
	Range	17–88	–
Gender	Male	23	52.3
	Female	21	47.7
	Total	44	100
Tobacco Use Status	Smoker	11	25.0
	Non-Smoker	33	75.0

	Total	44	100

B. Bacteria Causing Capilloperitoneal Pneumonia

Pseudomonas aeruginosa and Staphylococcus aureus were the next most common bacteria, followed by Streptococcus sanguinis (18.2%) and Streptococcus pneumoniae (11.4%), respectively, among the participants. Staphylococcus epidermidis and Streptococcus mitis both made 9.1%. One example of an uncommon microbe is Acinetobacter baumannii, but other examples include Pseudomonas aeruginosa and Klebsiella spp. (oxytoca/pneumonia).

Table 2. The findings of sputum culture and the frequency of bacteria the cause of CAP.

S. No.	Bacterial Type	Quantity (n)	Percentage (%)
1	Streptococcus pneumoniae	7	17.2
2	Streptococcus sanguinis	7	17.2
3	Streptococcus mitis	3	8.1
4	Streptococcus gordonii	2	3.3
5	Staphylococcus aureus	6	13.4
6	Staphylococcus epidermidis	7	11.1
7	Pseudomonas aeruginosa	5	3.8
8	Acinetobacter baumannii	4	7.8
9	Klebsiella spp. (oxytoca/pneumoniae)	2	5.8
10	Enterococcus spp. (avium/gallinarum)	2	5.8
11	Escherichia coli	2	3.3
12	Aeromonas hydrophila	2	3.3

C. The Rate of Resistance to Antibiotics

Streptococcus pneumoniae exhibited a high prevalence of antibiotic resistance within the streptococcus group: 100% for azithromycin, clindamycin, and ciprofloxacin; 88% for doxycycline; 88% for ceftriaxone; 75% for levofloxacin; 63% for vancomycin; 50% for moxifloxacin, indicating intermediate resistance; and 12% for linezolid, indicating a good sus It seems that Streptococcus mitis is resistant to moxifloxacin (75%), doxycycline (100%), ciprofloxacin (100%), levofloxacin (75%), and clindamycin (100%).

One hundred percent resistance to azithromycin, clindamycin, and ciprofloxacin was found in Streptococcus sanguinis, with doxycycline, ceftriaxone, levofloxacin, and moxifloxacin following closely behind at one hundred percent and sixty-three percent, respectively.

All five cases of staphylococcus aureus are resistant to ceftriaxone; for anti-staph antibiotics, the rate of resistance to vancomycin is 60%, and only one case is resistant to linezolid (20%). Doxycycline, clindamycin, azithromycin, ciprofloxacin, levofloxacin, and moxifloxacin have resistance rates of 40%, 40%, and 20%, respectively. There were no cases of Staphylococcus epidermidis found, with the exception of doxycycline (50%) and ceftriaxone (100%). All four of these cases exhibited resistance to ciprofloxacin, clindamycin (75%), azithromycin, moxifloxacin, and levofloxacin (50%). The percentage of cases resistant to vancomycin was 25%, while linezolid resistance was discovered in another instance. Only three instances were associated with the Pseudomonas species. The following antibiotics were effective in two cases (66% of the time): moxifloxacin, levofloxacin, ciprofloxacin, doxycycline, ceftriaxone, meropenem, and azithromycin; however, piperacillin-tazobactam, ceftazidime, cefepime, and imipenem did not.

The presence of the Klebsiella species was detected in only three cases. Two of the three cases were resistant to moxifloxacin, levofloxacin, doxycycline, ceftriaxone, and azithromycin; one case was resistant to ciprofloxacin, piperacillin-tazobactam, ceftazidime, cefepime, imipenem, and meropenem. Except for one patient who showed sensitivity to ciprofloxacin, none of the three patients whose Acinetobacter baumannii cultures were responsive to treatment. The medications azithromycin, levofloxacin, and doxycycline were totally ineffective against all four cases of enterococci. The rates of resistance for ceftriaxone, ceftazidime, cefepime, piperacillin-tazobactam, imipenem, meropenem, and aminoglycoside were 75% and 50%, respectively, according to Tables 3-5. Bacterial type revealed that Gram-positive organisms constituted the majority of the multidrug resistant (MDR) isolates (Fig. 2).

D. Multivariate Analysis of Risk Factors for MDR Infection

A binomial logistic regression was used to look into possible factors that could lead to multidrug resistance with MDR status as the dependent variable. Gender, smoking status, and bacterial group served as our categorical variables, while age served as a continuous variable. There were no statistically significant relationships between any of the covariates and MDR ($p > 0.05$), however the model did indicate a good fit (McFadden's $R2 = 0.299$).

Table 3. The trend of antibiotic resistance among gram-positive bacteria in CAP.

S. No.	Bacterial Species	n	Moxin (%)	Levon (%)	Cipron (%)	Doxyn (%)	Linzn (%)	Vann (%)	Clindn (%)	Ceftrn (%)	Azithromycin n (%)
1	Streptococcus pneu	6	3	4	6	5	1	3	8	7	6

	monia e										
2	Streptococcus mitis	4	3	4	4	4	2	2	4	2	4
3	Streptococcus sanguinis	8	5	7	8	8	1	2	8	8	8
4	Streptococcus gordonii	1	1	1	1	1	0	0	1	1	1
5	Staphylococcus aureus	5	1	2	2	4	1	3	3	5	4
6	Staphylococcus epidermidis	4	2	2	3	3	0	1	3	4	2

Table 4. Investigation on the antibiotic resistance pattern of gram-negative bacterial strains.

S.No.	Bacterial Species	n	Mox in (%)	Lev on (%)	Cip ron (%)	Dox yn (%)	Cef trn (%)	Pip ern (%)	Cef tzn (%)	Cef epn (%)	Imi pn (%)	Mer on (%)	Azithro mycin n (%)
1	Pseudomonas spp.	3	2	2	2	2	2	0	0	0	0	2	2
2	Klebsiella spp.	3	2	2	1	2	2	1	1	1	1	1	2

Table 5. Species of Enterococcus and Acinetobacter baumannii and their antibiotic resistance profiles.

S.	Bact	n	Mo	Le	Ci	Do	Ce	Pi	Ce	Ce	Im	Me	Azith	Am

No.	erial Species		xin (%)	von (%)	pron (%)	xyn (%)	ftrn (%)	pern (%)	ftzn (%)	fepn (%)	ipn (%)	ron (%)	romycinn (%)	gn (%)
1	Acinetobacter baumannii	3	3 (100%)	2 (66%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)
2	Enterococci spp.	4	4 (100%)	4 (100%)	2 (50%)	4 (100%)	3 (75%)	3 (75%)	3 (75%)	3 (75%)	3 (75%)	3 (75%)	4 (100%)	3 (75%)

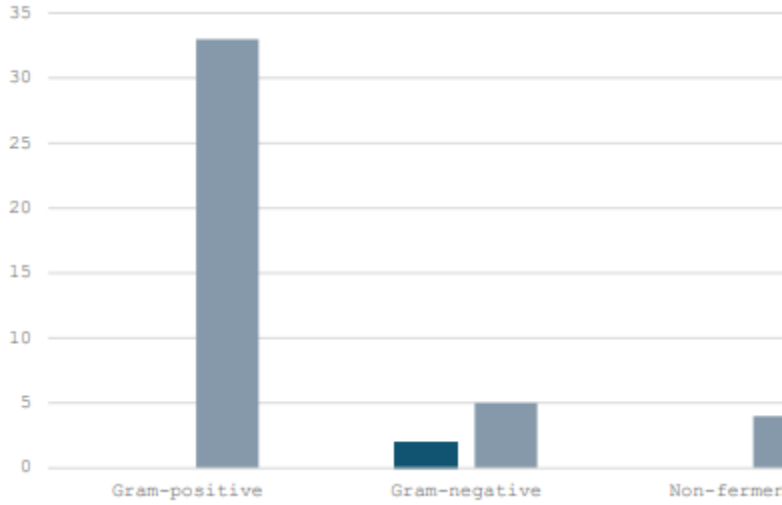

Fig. (2). The frequency of drug-resistant gram-positive, gram-negative, and non-fermenter bacteria.

IV.DISCUSSION

When it comes to treating pneumonia, especially CAP, the unappreciated but pervasive problem of antibiotic resistance is becoming more and more of a problem. There is no consensus among scientific groups about the use of empirical antibiotic therapy for CAP patients since antibiotic sensitivity and resistance vary greatly between countries. Here, we use the VITEK 2 auto-

analysis system. Iraq has never before been found to have pan-resistant Acinetobacter baumanii or highly resistant streptococci from the viridans group (S. sanguinis and S. mitis). The current analysis incorporates updated data from 2023 and beyond because to the fast-paced changes in antibiotic availability in the region.

In this investigation, sputum culture only detected bacteria in 44 out of 122 patients; however, the majority of CAP cases tested negative for bacterial sputum [4]. This is pretty much in line with the usual findings everywhere. Streptococci were the most frequently detected bacterium in 21 out of 44 sputum cultures, which is in line with the global average for bacterial isolation in pneumonia patients [26]. Antibiotic resistance is prevalent in Streptococcus pneumonia cases. This is mainly because the drugs azithromycin and ceftriaxone are commonly prescribed for suspected cases of CAP and because these antibiotics are available over the counter in Iraq. Moxifloxacin and linezolid, two relatively new antibiotics that rarely appear on over-the-counter prescriptions, still cause some sensitivity. Similar to Streptococcus pneumoniae, additional Streptococcus species exhibit strong resistance to azithromycin, cephalosporins, fluoroquinolones, and doxycycline. Linezolid, on the other hand, has excellent sensitivity, which may be why it is prescribed so little.

A leading cause of community-acquired pneumonia (CAP) and Staphylococcus pneumoniae (Pneumococcal infection) is the development of antibiotic-resistant strains of the bacteria. Among the many types of Staphylococcus aureus, the two most common types that cause infections are methicillin-resistant and vancomycin-resistant. The development of the VRSA strain is greatly impacted by the fact that there is a 60% incidence of resistance to vancomycin, when taking the resistance pattern into account. Because of its newer-generation anti-staphylococcal status and its low prescription rate relative to vancomycin, linezolid nevertheless shows high effectiveness. Although meropenem exhibited 2 resistant instances, anti-pseudomonal medicines generally have high sensitivity against Pseudomonas species.

In keeping with global trends, this study emphasizes the crucial clinical significance of Acinetobacter baumannii pan-resistance. Bacteroides fragilis, A class of bacteria noted for their resistance to typical antibiotics includes Staphylococcus aureus, Klebsiella pneumoniae, Enterococcus faecium, Pseudomonas aeruginosa, and Enterobacter. Escherichia baumannii is one such microbe. These germs pose a serious threat to pharmaceutical treatments due to their rapid development of resistance to numerous medications. World Health Organization (WHO) research objectives for antibiotic development include carbapenem-resistant Acinetobacter baumannii (CRAB), one of the most concerning microorganisms. This ranking has persisted since 2018. Because it is frequently associated with co-resistance to numerous other kinds of antibiotics, carbapenem resistance is frequently referred to as broad resistance. A disturbing trend has emerged in Iraqi local epidemiology about antimicrobial resistance: an upsurge in the incidence of multidrug resistance among the infectious microbes. Awayid et al. discovered that in 2022, more than 90% of MRSA strains found in Iraqi hospitals would be resistant to penicillin and erythromycin. SCCmec III was also the most common subtype in that region. In particular, ST239 was the most prevalent clone. This indicates that MRSA acquired in hospitals is endemic, in addition to the genetic diversity of the clones. A concerningly high resistance rate of 95%+ for broad-spectrum β-lactam medicines ampicillin, amoxicillin, and cefixime was found in P. aeruginosa isolated from Kirkuk, as noted by Hasan et al. (2020) [16]. It exhibited some susceptibility to gentamicin and imipenem. As a consequence of this, the therapeutic medications that are currently available in the Iraqi environment are limited. While CRAB rates vary by location, the Levant (Syria, Jordan, Lebanon, Iraq, and the Palestinian territories) and other Arab League nations have seen an increase. Recent years have seen a surge in research into new antimicrobial medicines and creative treatment approaches in response to the alarming spread of these highly resistant bacteria.

More and more enterococci are developing resistance to drugs that were formerly common, including fluoroquinolones, third- and fourth-generation cephalosporines, and others. Consequently, there are less viable therapies for CAP caused by MDR Gram-negative bacteria. Rising healthcare expenditures, longer hospital admissions, and death rates are all associated with this worldwide public health challenge, which also presents a substantial risk of treatment failure [5].

In accordance with previous Iraqi research, our findings emphasize the significant impact that antibiotic resistance has on CAP. Streptococcus pneumoniae (26% of cases), Klebsiella pneumoniae (94.06% resistance in K. pneumoniae), and Streptococcus pneumoniae (71.43% resistance in E. pneumoniae) were found to be the most common infections associated with pneumonia in a cross-sectional study by Jaaffar et al. (2019). By demonstrating the persistence of resistant strains in the community, these resistance patterns support our findings. Only nine percent of antibiotic prescriptions are based on culture results. The findings of our investigation are supported by new data on Iraqi large-scale monitoring. Multidrug-resistant Klebsiella pneumoniae and Staphylococcus aureus were prevalent, particularly in adult patients, according to a review of over 11,000 clinical records from seven provinces by Al-Fahad et al. (2024) [18]. We found that our CAP isolates matched these resistance patterns quite well. There has to be increased public education of prescribers, more regulation of over-the-counter antibiotic sales, and a focus on the effectiveness of community-level AMS models in comparable contexts, as advocated by Lam et al. (2021). The needs of Iraq's healthcare system may be

accommodated by modifying the evidence-based, two-pronged approach to fighting antibiotic-resistant microorganisms. Use of nonsteroidal anti-inflammatory medications (NSAIDs) for fever treatment without proper sensitivity testing contributes to Iraq's high resistance rates. Fever is an adaptive physiological response that boosts the effectiveness of leukocytes and, by extension, of antimicrobial therapy in eliminating germs. When taken early on in an illness, antipyretic medicine might lessen the body's reaction to a fever. A large amount of research suggests that raising core body temperature improves the immune system's ability to fight against microbes.

V.CONCLUSION

The increased usage of antibiotics and Iraq's lackluster drug management may explain why this research found a significant likelihood of antibiotic resistance in CAP patients. A new wave of germs, some of which are almost resistant to all known antibiotics, is emerging. A total prohibition on antibiotic distribution from pharmacies, a push for treating physicians to decrease community-wide antibiotic prescriptions, and an increase in the utilization of culture and sensitivity testing for the administration of particular antibiotics are all measures that we urge Iraq to adopt as part of its antibiotic stewardship initiative.

A. Suggestions / Recommendations

- initiatives for antimicrobial stewardship
- Encourage the use of antibiotics in moderation.
- Maintain consistent hospital-based monitoring
- Quick research on potential new antibiotics
- Make people aware of the misuse of antibiotics.

B. Limitations

- by utilizing secondary sources
- Insufficient comparison to specific regions
- No examination at the molecular level

C. Future Scope

- Multi-center research
- Anticipation of resistance via AI
- Study of particular treatment options
- Molecular diagnostics integration

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