A study of the antibiotic resistance trajectory of clinical bacterial infections obtained from patients in Govt hospital

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ABSTRACT:

Objective: This research emphasizes on analyzing resistance pattern in bacteria, all samples are taken at the District Health Quarter in Hyderabad and the Rural Health Center in Mirpur Khas.

Methodology: All the results related to antibiotic susceptibility and microbiological cultures from different patients samples submitted to the EPHI laboratory between September 2015 and August 2019 were analyzed through a retrospective cross-sectional study. Microbial isolates were isolated and identified by using state of the art microbiological machines and after that characterization of all samples done by using standard bacteriological methods. Information on the type of clinical specimen cultured, the bacterial species identified, the antibiotics employed for susceptibility testing, and the corresponding susceptibility outcomes were all extracted from the records of 840 patients.

Results: The bacterial isolates and patterns of antibiotic resistance were explained using statistical techniques. Eight categories of clinical samples were analyzed for the presence of bacterial isolates with blood specimens being the most thoroughly examined. Thirteen distinct bacterial genera were found by culturing. Almost 80% of the isolates belonged to the Gram-negative group of bacteria., but three gram-positive species (Enterococcus, Staphylococcus aureus, and MRSA) were identified. Antimicrobial susceptibility testing of seventy isolates showed higher resistance in Escherichia coli than in other species.

Conclusion: This study revealed worrying rates of multidrug resistance. antibiotic resistance surveillance must be strengthened nationally, and antibiotic sensitivity testing in community-level diagnostic centers is highly recommended.

Key words: Sensitivity pattern, Antibiotic resistance, Clinical bacterial infections, Govt Hospital

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Introduction:

The development of antimicrobial agents against pathogenic microorganisms stands among the greatest achievements of modern medicine; however, after more than seven decades of extensive use, their therapeutic efficacy has gradually diminished.[1] Antibiotic resistance, a phenomenon that has seen tremendous uncontrolled growth in the entire world over the last two decades, is widely regarded today as one of the key concerns of public health at the global level. [2] However, additional factors are mostly responsible for the growth in its occurrence. This issue is closely linked to factors such as poor public hygiene, inadequate infection control in healthcare settings, excessive environmental exposure to antibiotics, and their extensive use in livestock and food production industries.[3] The antibiotics existence in the surrounding, improper use in agriculture, and weak infection prevention measures in hospitals and clinics have all contributed to the growing problem of antimicrobial resistance.[3]

Globally, this has become a critical concern, especially with the increasing prevalence of MDR, XDR, and PDR microorganisms.[4] XDR refers to bacterial strains that remain susceptible to only one or two classes of antibiotics, whereas PDR describes pathogens that show full resistance to above mentioned antibacterial agents. MDR is characterized by resistance to one or more agents across a minimum of three antimicrobial categories. [5] MDR bacteria are mostly related to hospital-acquired infections, already several have also emerged as major causative agents of community-acquired diseases.[6] Gram-negative (GN) microorganisms are responsible for significant mortality rates among infections caused by MDR agents. [7] Despite continued study into antibiotic resistance, there is no evidence of improvement, and effective AMR control requires a clear understanding of the current situation to guide when, how, and where to act. [8]

Objective:

The objective of this study was to give descriptive information on infections and antibiotic resistance patterns in bacterial pathogens at Govt Hospital, District Health Quarter, Hyderabad, and Rural Health Center Mirpur Khas.

Methodology:

This particular study of diverse clinical specimens examined for bacterial isolation and subsequent antimicrobial susceptibility testing between October and December 2024. at a government hospital. District Health Quarter in Hyderabad and the Rural Health Center in Mirpur Khas are among the study venues. All of the locations are in Sindh province, Pakistan. For data extraction, 70 complete records were selected. Patient demographics (age and gender), the type of cultured clinical specimen, the bacterial

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species isolated, the antibiotics employed for sensitivity testing, and the corresponding sensitivity results observed in the lab reports were all collected from the District Health Quarter in Hyderabad and the Rural Health Centre in Mirpur Khas. The District Health Quarter in Hyderabad and the Rural Health Centre in Mirpur Khas received clinical specimens that were collected, preserved, and transferred in accordance with standard operating procedures (SOPs). Following standard procedures, the gathered microbiological specimens were submitted to the laboratory for processing. Urine, blood, sputum, wound swabs, pus, cerebrospinal fluid, and other body fluids were among the clinical samples that were cultured. Standard microbiological culture methods were applied to every clinical sample. As per the standard procedure, samples were streaked onto appropriate microbiological culture media and incubated at 35 -37 °C. Following CLSI guidelines, the bacterial isolates were isolated to antibiotic susceptibility testing across various drug classes using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar. Amoxycillin, gentamycin, ciprofloxacin, norfloxacin, cefuroxime, imipenem, meropenem, chloramphenicol, azithromycin, tetracycline, cotrimoxazole, and piperacillin-tazobactam antimicrobial discs were utilized. Bacterial species were considered as resistant, intermediate, or sensitive to each antibiotic according to the given standards by the CLSI. The reference was E. coli strain ATCC 25922. MAR index for every sample was estimated by using the formula MAR index = a/b, where “a” represents the number of specimens was resistant, and “b” denotes the amount of antibiotics used . MDR means ineffectiveness against 2 or 3 groups of antibiotics, while extensively drug-resistant (XDR) isolates were characterized by resistance to all but one or two antimicrobial categories.

Bacterial pathogens were divided as sensitive, intermediate, or resistant according to the (CLSI) standards, based on their antibiotic susceptibility profiles. Descriptive statistics such as relative abundance, category proportions, and frequency distributions were calculated to interpret the data. The chi-square test was applied to establish differences in the existence of isolates across various patient samples.

Results:

Prevalence of bacterial agents in clinical samples:

In this study, total observed microbial growth was 70 clinical specimens; almost all bacterial isolates taken from blood (45.7%) followed by wound swabs (22.9%) and after that urine (11.4%), pus (8.6%), culture specimens (5.7%), sputum (2.8%), and cerebrospinal fluid (1.4%). All samples that are collected it includes 43 females (61%) and 27 males (39%) (Table 1). on culture report there are 13 bacterial genera as well.. Most of the isolates were Gram-negative, while only four species—Citrobacter, Enterococcus, Staphylococcus aureus, and MRSA—were identified as Gram-positive.

Trends in antibiotic resistance of bacterial isolates

Trends in Antibiotic Resistance of Bacterial Isolates

Total of 13 bacterial strains analyzed and observed over the period of three months and that is from October 2024 to December 2024.after the analysis it showed there is high pattern of resistance developed among bacteria against notable antibiotics that shows alarming situation and increasing trend in the persistence and spread of resistant bacterial infections Escherichia coli strains showed resistance to Trimethoprim/sulfamethoxazole (SXT), Levofloxacin (LEV), Cephalosporin (CFM), Gentamicin (CN), Ceftriaxone (CRO), Ceftazidime-avibactam (CZA),

Table No 1: Demographic Profile, Clinical Sample Distribution, Microbial Classification, and Prevalence of Bacterial Isolates.

Profile	Frequency	Percent
Gender		
Male	27	39%
Female	43	61%
Clinical samples		
Blood	32	45.70%
Urine	8	11.40%
Sputum	2	2.80%
Pus	6	8.60%
Wound swab	16	22.90%
Culture specimen	4	5.70%
Cerebrospinal fluid	1	1.40%
Body fluid	1	1.40%
Type of organism		
Gram negative	9	69.20%
Gram positive	4	30.80%
Bacterial strains		
Klebsiella pneumoniae	6	8.50%
MRSA	17	24.30%
Escherichia coli	13	18.60%
Pseudomonas burkholderia cepacia	1	1.40%
Salmonella	1	1.40%
Acinetobacter	8	11.40%
Staphylococcus aureus	3	4.30%
Pseudomonas aureus	8	11.40%
Enterococcus	1	1.40%
Proteus mirabilis	4	5.70%
Enterobacter	2	2.80%
Pseudomonas aeruginosa	3	4.30%
Citrobacter	3	4.30%

Moxifloxacin (MXF), Augmentin (AUG), nitrofurantoin (F), Tigecycline (TGC), Fosfomycin Tromethamine (FOS), Intraperitoneal (IP), Ciprofloxacin (CIP), Innovative Medicine. Klebsiella pneumoniae strains demonstrated resistance to CN, MRP, LEV, CZA, SXT, AVG, CFM, CRO, CIP, TZP, CNF, FOS, MA, TGC, AUG, MRP, and IMI. The MRSA isolates showed insensitive to a vast number of antibiotics, including FOX, TGC, AZM, TE, TEC, SXT, FC, CN, C, CF, CP, AZP, CD, VA, CPT, and CX. Pseudomonas burkholderia cepacia strains were found to be resistant to LEV, MRP, IMI, TZP, CIP, CAZ, CZA, and ATM. Similarly, Acinetobacter isolates exhibited resistance to CN, CRO, SXT, TZP, AUG, CFM, IMI, MRP, AZM, CIP, LEV, TGC, CTX, FE, AMP, ATM, and CAZ. In addition, Staphylococcus

Table No 2. Distribution of Bacterial Isolates Across Various Clinical Specimen

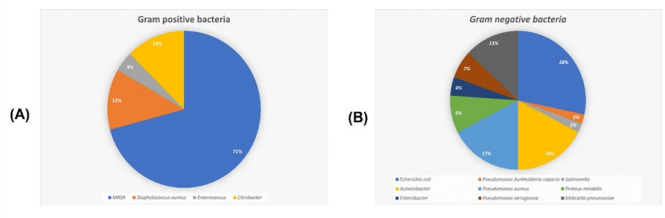
Bacterial Species	Sample Type																
	Blood		Urine		Wound swab		Pus		Culture specimen		CSF		body fluid		sputum		Total
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	
Klebsiella pneumoniae	4	57.1	1	14.3	1	14.3	0	0	0	0	0	0	0	0	1	14.30	7
MRSA	11	68.8	0	0	2	12.5	3	18.8	1	7.7	0	0	0	0	0	0	16
Escherichia coli	4	30.8	4	30.8	1	7.70	2	15.4	0	0	0	0	1	7.70	0	0	13
Pseudomonas burkholderia cepacia	0	0	0	0	1	100	0	0	0	0	0	0	0	0	0	0	1
Salmonella	1	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Acinetobacter	7	77.8	0	0	1	11.1	0	0	0	0	1	11.1	0	0	0	0	9
Staphylococcus aureus	1	100	0	0	1	33.3	0	0	1	33.3	0	0	0	0	0	0	3
Pseudomonas aureus	1	100	2	25	4	50	0	0	1	12.5	0	0	0	0	0	0	8
Enterococcus	0	0	1	100	0	0	0	0	0	0	0	0	0	0	0	0	1
Proteus mirabilis	0	0	0	0	1	25	1	25	1	25	0	0	0	0	1	25	4
Enterobacter	1	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Pseudomonas aeruginosa	0	0	0	0	3	100	0	0	0	0	0	0	0	0	0	0	3
Citrobacter	2	66.7	0	0	1	33.3	0	0	0	0	0	0	0	0	0	0	3

aureus strains demonstrated resistance to FC, SXT, C, FOX, CD, AZM, CPT, FG, TE, and CDC. Pseudomonas aureus strains exhibited resistance to CIP, CFM, TZP, AUG, CZA, IMI, LEV, MRP, CRO, SXT, and CAZ. Proteus mirabilis strains were resistant to TZP, CFM, CRO, CN, IMI, MRP, AUG, CP, LEV, CZA, SXT, and CIP. Enterobacter bacteria demonstrated resistance to CN, CZA, IMI, CFM, AUG, CRO, TZP, MRP, and SXT. Pseudomonas aeruginosa strains were resistant to CZA, CAZ, TZP, MRP, CIP, LEV, IMI, MXF, and ATM. Citrobacter strains demonstrated resistance to TZP, AUG, CFM, CZA, IMI, CRO, CN, SXT, CIP, LEV, and MRP.

Trends of multidrug resistance (MDR) among bacterial strains.

MDR percentages for each bacterium were obtained using 70 isolates. Overall, 84.3% (n=59) were MDR (resistance to three or more antibiotic classes), while 32.75% (n=339) did not have an MDR profile. While 12.9% (n=9) were XDR (a resistance to all but one or two antimicrobial classes, with susceptibility retained in only one or two drug class.), 2.9% (n=2) were PDR (total resistance to all antimicrobial agents) Figure 1.

Fig No 1: Gram Positive Bacteria.



Gram-negative bacterial isolates is shown in the pie chart. Proteus mirabilis (9%), Acinetobacter (18%), Pseudomonas aureus (7%), Pseudomonas aeruginosa (4%), Pseudomonas burkholderia cepacia (2%), Salmonella (2%), and Escherichia coli (28%) are the most prevalent bacteria. A visual summary of the diversity and frequency of bacterial pathogens in the clinical specimens under analysis is given by these charts.

Discussion:

The findings of this study clearly elucidate the patterns of prevalence and drug resistance among bacterial isolates from clinical samples as a very serious public health concern. Bacterial growth in 70 clinical specimens implicates the importance of bacterial infection in health care settings. Most isolates (45.7%) were blood samples, and then wound swabs (22.9%), consistent with relatively high prevalence of bloodstream and wound related infections. Some previous studies show that female patients outnumber males (61% Vs 39%) but further investigations are needed to determine if there are gender predisposition towards bacterial infection.

Bacterial Diversity

The complexity of bacterial infections revealed in a clinical practice is testified by the identification of 13 different bacterial genera, which are mostly Gram negative bacteria. Gram positive species such as Citrobacter, Enterococcus, Staphylococcus aureus and MRSA are isolated along with these pathogens persist in spite of the impact of infection control measures. Additionally, due to the prevalence of Gram-negative pathogens which, in general, are often more difficult to treat because of intrinsic and known acquired resistance mechanisms, there is a clearly a need for targeted antimicrobial strategies.

Antibiotic Resistance Patterns

The resistance profiles obtained in this study are alarming indeed. Among the common pathogens, Escherichia coli was resistant to several antibiotics including the critical ones such as Trimethoprim/sulfamethoxazole (SXT), Ciprofloxacin (CIP) and Ceftriaxone (CRO). While exten-

sive resistance was displayed by Klebsiella pneumoniae strains to Gentamicin (CN), Meropenem (MRP), and Tazobactam (TZP) among others. Notably, MRSA strains with resistance to key antibiotics including TE and [VA] (i.e. strains possessing phenotypes of vancomycin and tetracycline resistance, denoted VAN and [TE] respectively) continue to be prevalent because clinical reliance on these antibiotics exists for the treatment of Gram-positive severe infections.

Resistance patterns also observed with other pathogens such as Acinetobacter, Pseudomonas aeruginosa, and Citrobacter illustrate the prevailing tendency to develop the AMR. This indicates that the clinicians now have fewer treatment options and has led to resistance to critical, final resort of antimicrobials e.g., Tigecycline (TGC) and Ceftazidime avibactam (CZA) are detected.

Antimicrobial Resistance Profiles: MDR, XDR, and PDR Bacteria

Bacterial isolation of 84.3% was indicator of MDR that shows how bad the situation and how AMR problem is emerging and effecting our healthcare system. MDR & XDR strains 12.9% and 2.9% respectively are clear indicator of emerging AMR problems.In upcoming trend, Emergence of PDR strains shows resistance to the entire groups of antibiotics that are available in our social circle.

Clinical and Public Health Implications

The current situation we are facing is very critical and alarming due to high prevalence of XDR & MDR bacteria, this is the real threat to our healthcare system.due to increasing trending of XDR & MDR, diseases, mortality rates and economical burdens are adding towards society.this resistant patterns prolong hospital stays and less effective treatments. PDR is although less common in our region but there presence signals the hidden potential for complete treatment failure in near future and poses serious threats to the human kind. The result shows the urgent implementation of antimicrobial stewardship programs (ASPs) to combat against resistance and to deliver effective treatment with less financial burdens.this system will also reduce antibiotic misuse and prevent the further spread of resistance strains. Preventive measures such as proper hand hygiene, improved environmental sanitation, and continuous monitoring of resistant organisms should also be prioritized.

Future Directions

In future, genetic analysis of bacteria will required to study resistance patterns. NGS, Sanger sequencing can be done to study in detail about genomics variations of bacteria especially the resistance bacteria. Whole-genome sequencing (WGS) data could help and give minute details about resistance genes , their mode of actions , transmissions, variations and disease causing agents in precise and accurate way. All above genomics process can be done under the umbrella of antimicrobial stewardship program and IPCs committee.

Conclusion:

The result of this study raised serious concerns about the resistance pattern and resistance gene of bacteria where MDR, XDR, and PDR bacterial isolates are increasingly prevalent. Addressing this growing threat requires a multifaceted approach that includes the development of new antibiotics, enhanced diagnostic capabilities, and sustained efforts in infection prevention and antimicrobial stewardship. Such measures are essential to improve treatment outcomes and curb the ongoing spread of resistance.

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