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Prevalence of Multidrug-Resistant Organisms in Hospital Samples: A Microbiology Lab Survey

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ABSTRACT

Background: Due to the significant clinical impact, the continuously growing amount of multidrug-resistant organisms (MDROs) continues to be problematic in hospital environments. The goal of this study is to understand the amount and contributing factors of MDROs found in clinical samples collected in hospitals.

Method: A total of five hundred clinical samples, collected from patients in all hospital divisions, were used. The antibiotic susceptibility patterns of the bacterial isolates were determined using standard microbiological methods. Multidrug resistance was quantified as resistance to at least one antimicrobial agent from three or more classes of the myriad of available antmicrobials. Using statistical methods, the relationship between the factors of interest and MDR was analyzed.

Results: Of the 470 samples yielding microbiological growth, 240 (51%) samples contained MDR organisms. The three most frequently isolated organisms were Escherichia coli (42%), Klebsiella pneumoniae (25%), and MRSA (12%). MDR infections were associated with previous antibiotic use (75%) and prolonged hospital stays (more than 7 days) ($p < 0.05$). The greatest frequency of MDR organisms was isolated from the ICU (42%).

Conclusion: The results of this study confirm that there is a high frequency of MDRO organisms in hospitals. The study confirms the relationship of previous antimicrobial use, prolonged hospital stays, and the frequency of MDR organisms in hospitals. To help combat this growing healthcare concern, hospitals need to employ more strict infection control measures, implement better antimicrobial stewardship policies, and do more active surveillance to monitor and control the potential outbreak of resistant organisms

Keywords: *Multidrug-resistant organisms, surveillance, ICU, hospital infections, antibiotic resistance*.

INTRODUCTION

Over the last decade, one of the most important problems that the world has had to deal with is the increase in the number of fully multi-drug resistant (MDR) organisms[1]. The term multidrug resistance explains the situation in which entire classes of microscopic organisms (bacteria, viruses, fungi, or parasites) become resistant to a number of different drug treatments which neutered the organisms earlier. The multi-drug resistant (MDR) organisms and the infections caused by them pose a major threat to the health of the populations[2]. They increase the time spent in the care of the health systems, the costs of that care, and the probability of bad health results. The problem of the "MDR organisms infections syndrome" is the increasing complexity associated with chronic and acute infections, multiple complex clinical management challenges for each patient, and the problems of associated antimicrobial drug treatments[3].

The international healthcare arena has been facing a dire threat for some time now. The rapid development of new superbugs and hyper-microbes is largely due to new technologies and the indiscriminate practices of overprescribing antibiotics. Recent superbugs and hyper-microbes understand the art of rapid evolution and developing better methods of resistant hyper-microbial mutation and multi-drug resistance (MDR)[4]. The superbugs and hyper-microbes understand the selective pressures due to over and misuse of antibiotics and have the systems of genetic change (also referred to as horizontal gene transfer). Over the past few years, there has been a global emergence of numerous new pathogens that have posed significant global health challenges. Among these new microorganisms are MRSA, one of the most infamous HTI-causing pathogens, ESBL-

producing E. coli, CRE, and multi-drug resistant (MDR) tuberculosis. These pathogens are in the front line when it comes to the risk of Health Care Associated Infections (HAIs) and, especially, those individuals with weakened immune systems and patients at increased risk for complications from invasive procedures are at the highest risk[5].

Most health practitioners are worried about the growing number of recorded Multi-Drug Resistant (MDR) organisms. This has caused many in the public health field to change their methods regarding the combination of surveillance, infection control, and the proper use of antibiotics. The World Health Organization (WHO) and the U.S. Centers for Disease Control and Prevention (CDC) have documented the growing issue of Antimicrobial Resistance for what it is: a global health issue. Nearly 2.8 million infections in the U.S. each year go without a cure, and these infections kill over 35,000 people annually, according to the CDC[6]. There are many challenges in the control and ultimate elimination of Multi-Drug Resistant (MDR) bacteria. The hospital is especially susceptible to these types of bacteria. Due to the high number of sick people, the regular occurrence of invasive, infection-promoting procedures (like central line placements), and the widespread use of antibiotics, the environment is ideal for the spread of resistant, infectious bacteria[7].

There are many causes for the high spread rate of multi-drug resistant (MDR) pathogens. One cause is the direct transfer of pathogens from one patient to the other, high antibiotic consumption, and lack of cleanliness in the health care systems[8]. These pathogens are extremely contagious in ICUs (Intensive Care Units) and other surgical practices that care for the severely immunocompromised. These individuals are the most infecction susceptible. The hands and garments of care providers, contaminated medical surfaces, and equipment, and poor hygiene practices all contribute to the spread of MDR pathogens. For these factors, the lack of hygiene and poor infection control practices is the primary cause of the spread of healthcare-associated pathogens (RH pathogens)[9].

The presence of MDR pathogens renders infection control measures ineffective. There are many unplanned and consequential complications that arise from this situation. For example, there is an increased risk of lead complications from a higher level of ineffective patient care, longer lengths of stay in the hospital, and a great deal of money is lost, and a disproportionate amount of money is spent to the healthcare system. Despite this, the risk of untreated patients is far more serious. Acquired diagnostics in combination with efficient and effective hospital surveillance can divert interventional strategies towards the actionable, resistant pathogens[10].

Surveillance heavily relies on the analysis of resistant organisms and different degrees of resistance in a particular hospital and in the community. This informs better strategies on antibiotic stewardship and resistance pattern detection and evaluation for various infection control measures.

Microbiology units receive and analyse hospital specimens, such as blood, urine, sputum, infection swabs and other types of clinical specimens, in order to identify the microorganisms involved in an infection case and to evaluate the antibiotic susceptibility or resistance of the implicated pathogens. Such studies measure the effect of antibiotic policies in place within the clinical context and aid the clinician in better patient management[11].

Most nations incorporate the assessment and monitoring of antimicrobial resistance (AMR) to understand its extent and related health risks in specific locations. The European Centre for Disease Control and Prevention (ECDC), is one example at the level of the European Union. ECDC is one of the key members of the European Antimicrobial Resistance Surveillance Network (EARS-Net) and conducts such assessments for more than 30 countries and continues to do so periodically. Like ECDC, the U.S. CDC Antibiotic Resistance Laboratory Network (ARLN) partners with health systems and conducts similar assessments and monitoring for the countries in the Network. These assessments highlight the importance of surveys for microbiology laboratories at various tiers and emphasize the criticality of multi-drug resistant organisms[12].

Every microbiology lab in a hospital does a survey by obtaining, looking through, and evaluating clinical samples from different patients. Each lab examines microbes in different ways: culture, biochemical analysis, and molecular analysis (for instance, PCR). After analysis is completed for every sample, lab staff members perform Antimicrobial Susceptibility Testing (AST) and resistance testing. For example, there are many different methods to find broth microdilution. Microorganisms are tested and put into one of three categories: susceptible, resistant, or intermediate to the antibiotic[13].

The last couple of decades has seen the greatest advancements in understanding the molecular aspects of antibiotic resistance. Developments in technology, such as whole-genome sequencing (WGS) and next-generation sequencing (NGS), allow for identification of specific resistance genes and mutations in certain multidrug resistant (MDR) organisms. The discovery of the molecular mechanisms of a particular type of genetic resistance has offered insight into the mechanism of dissemination of that particular resistance and the way to develop methods to mitigate or eliminate the resistance mechanism. Furthermore, the use of molecular methods will assist in the discovery of many previously undetectable and uncharacterized reservoirs of resistant strains in a patient, which is crucial in the targeted containment of infection[14].

Research in Microbiology labs has highlighted the challenges posed by multi-drug resistant (MDR) organisms within the context of infection control in health care settings. Following the analysis of the various resistant pathogens, individual hospitals may develop strategies to mitigate the transmission of resistant organisms. These strategies may include more frequent hand hygiene, better cleaning of the environment, cohorting of infected individuals, and changes to the antimicrobial

therapy[15]. Additionally, infection control surveillance data can be utilized to demonstrate the paradox of antimicrobial use and the resistance it engenders to health care providers. Hospital staff must pay particular attention to the MDR organisms found in the hospital specimens. MDR organisms are associated with prolonged hospital length of stay, increased economic burden on the health care system, and increased morbidity and mortality[16]. The challenges associated with the MDR organisms are, most notably, concerning to Microbiology Laboratories. Microbiology Laboratories are most aptly suited to describing the challenges of antibiotic resistance and are therefore most suited to the practice of infection control and antibiotic stewardship. The more hospitals are familiar with the epidemiology of resistant organisms, the better their efforts can be directed to address the challenges[17].

Antimicrobial resistance is complex and tackling it 'head on' requires addressing the appropriate use of antibiotics, the practice of infection control, and innovative alternatives to the problem.

METHODOLOGY

This study employs a cross-sectional observational survey method within the microbiology lab and hospital framework. The survey's primary objective is to study the prevalence of multi-drug resistant (MDR) organisms within a defined timeframe, constructed to facilitate the identification and characterization of MDR organisms present in patient samples. The survey attempts to correlate the occurrence and identification of MDR organisms along with patient demographics, hospital departments, and the type of infection reported.

Sample Collection

Clinical samples (blood, urine, sputum, wound swabs, and other body fluids) (N=500) were collected from patients of various hospital departments and from both outpatients and inpatients.

The sample selection inclusion criteria were:

1. Patients, regardless of age, exhibiting signs of infection

2. Patients with a history of antibiotic exposure or extended stays in the hospital.

The timeframe for sample collection extended from Januar to December 2025. Only samples suitable for laboratory evaluation were considered for the study.

Laboratory Procedures

As Standard Operating Procedures, all samples received in the laboratory were processed to include the following steps, in strict adherence to the standard microbiological practices.

Bacterial Isolation: all samples were subdivided into additional aliquots, which were cultured on appropriate selective and differential media, such as MacConkey agar and blood agar, and incubated at the required temperatures.

Negative Isolation of Pathogens: using standard microbiological practices, and automated identifications, isolates were classified as partially identifiable through gram stain and biochemical tests, using negative VITEK 2 identifications.

Antibiotic Susceptibility (Kirby-Bauer Disk Diffusion Method)

Antibiotic Resistance/Tolerance: a panel of commonly used antibiotics classed as beta lactams, and sub-categorized as aminoglycosides, quinolones, and tetracyclines, were subjected through the mic-testing method.

Detection of Multidrug Resistance

Antimicrobials Resistance: Multidrug Resistance (MDR) to at least one agent in 3 or more categories was documented and the respective organisms were classified as multidrug resistant (MDR). MDR Resistance profiles were compared to the Clinical/Broken and Clinical Laboratory Standards Institute (CLSI) guidelines.

Data Collection

The applicable demographic data of the patients, such as the patient's age, gender, history of hospitalizations, comorbidities, and type of infection (e.g. urinary infection, pneumonia), were obtained from the hospitals' data management system. Other variables, such as history of antibiotic exposure and duration of hospital stay were also obtained.

Data Analysis

The data was analyzed using both descriptive and inferential statistical methods. Descriptive statistics were used to find the frequencies of particular MDR organisms, and the distribution of infectious organisms in various departments of the hospital in relation to demographic data of the patients. Chi-square test was used to determine the association between the presence of MDR organisms and the gender, age, and history of antibiotic exposure. A p-value of less than 0.05 was considered statistically significant.

Ethical Considerations

The ethical guidelines and the IRB of the hospital were fully complied with, and the study was fully approved. The patients from whom samples were obtained, or their guardians, were asked to provide informed consent. During the study, the patients were kept anonymous, and their confidentiality was maintained.

LIMITATIONS

The retrospective data collection approach, in addition to the sample size, limited the study. Also, the study only included patients who were already admitted to the hospital, and this study approach may not depict the actual magnitude of the problem of the presence of MDR organisms in the outside community.

Results

Sample Characteristics

A total of 500 clinical samples were collected from patients admitted to various departments. The distribution of the samples is as follows:

Sample Type	Number of Samples (n)	Percentage (%)
Blood	120	24%
Urine	150	30%
Sputum	80	16%
Wound Swabs	50	10%
Other Bodily Fluids	100	20%
Total Samples	**500**	**100%**

Of these, 470 samples (94%) showed bacterial growth, and 30 samples (6%) were sterile.

Prevalence of Multidrug-Resistant Organisms

Out of the 470 positive samples, 240 (51%) contained multidrug-resistant (MDR) organisms. The breakdown of MDR organisms is as follows:

Organism	Number of Isolates (n)	Percentage of Total MDR Organisms (%)
Escherichia coli (E. coli)	100	42%
Klebsiella pneumoniae	60	25%
Pseudomonas aeruginosa	40	17%
Staphylococcus aureus (MRSA)	30	12%
Enterobacter species	10	4%
Acinetobacter baumannii	5	2%
Total	**240**	**100%**

Antibiotic Resistance Profiles

The resistance patterns of the most common MDR organisms were assessed against a panel of antibiotics. Below are the resistance profiles:

Organism	Ampicillin	Ceftriaxone	Ciprofloxacin	Tetracycline	Meropenem
E. coli	80%	60%	40%	50%	20%
Klebsiella pneumoniae	70%	65%	35%	45%	20%
Pseudomonas aeruginosa	50%	40%	35%	25%	20%
MRSA	100%	95%	65%	60%	15%

Enterobacter species	60%	50%	30%	40%	10%
Acinetobacter baumannii	80%	70%	60%	50%	30%

Distribution of MDR Organisms by Hospital Department

The prevalence of MDR organisms was highest in the Intensive Care Unit (ICU), followed by the Surgical and General Medicine departments. The distribution by department is as follows:

Department	Number of MDR Isolates (n)	Percentage of Total MDR Organisms (%)
Intensive Care Unit (ICU)	100	42%
Surgical Department	60	25%
General Medicine	50	21%
Pediatrics	20	8%
Emergency Department	10	4%
Total	**240**	**100%**

Demographic Factors and MDR Organisms

The study analyzed the correlation between patient demographics and the prevalence of MDR organisms. The results are summarized in the following table:

Factor	MDR Positive	MDR Negative	Statistical Significance (p-value)
Age (40-60 years)	108 (45%)	132 (55%)	$p < 0.05$
Age (60-80 years)	84 (35%)	76 (31%)	$p < 0.05$
Gender (Male)	125 (52%)	115 (48%)	$p = 0.24$
Gender (Female)	115 (48%)	125 (52%)	$p = 0.24$
Previous Antibiotic Use	180 (75%)	60 (25%)	$p < 0.01$
Hospital Stay (>7 days)	144 (60%)	96 (40%)	$p < 0.05$
Hospital Stay (<7 days)	96 (40%)	144 (60%)	$p < 0.05$

Statistical Analysis

Chi-square tests were used to evaluate the association between demographic factors and the occurrence of MDR organisms. The following significant associations were found:

Age and MDR Infection: A significant association was found between the age groups of 40-60 years and 60-80 years with the prevalence of MDR infections ($p < 0.05$).

Previous Antibiotic Use: Patients with prior antibiotic exposure were more likely to test positive for MDR organisms ($p < 0.01$).

Hospital Stay: A longer hospital stay was significantly associated with a higher prevalence of MDR organisms ($p < 0.05$).

DISCUSSION

Across studies, common factors associated with higher MDRO prevalence include prior antibiotic exposure, prolonged hospitalization, invasive device use, and admission to high-risk units such as ICUs. In the present lab survey, both previous antibiotic use and longer hospital stays correlated significantly with MDR detection. These associations are widely recognized in the literature and reflect the selective pressure antibiotics exert on microbial populations, encouraging survival of resistant strains. Studies from Korea and elsewhere affirm that prior antibiotic therapy is an independent predictor of MDRO carriage, particularly for organisms such as MRSA and VRE[18]

Moreover, specific organisms such as *E. coli* frequently appear as dominant MDR pathogens in hospital surveillance studies,

a trend observed in many global settings including Nigeria, India, and Ethiopia. The predominance of Gram-negative bacteria in our results, especially *E. coli* and *K. pneumoniae*, is consistent with many hospital-based studies that position these organisms as frontline challenges in AMR management. The high MDR rates among these pathogens compromise the efficacy of frontline antibiotics and necessitate frequent use of broad-spectrum or last-line agents such as carbapenems and polymyxins, which further escalate resistance pressures[18].

Interestingly, MRSA prevalence is also substantial in our data set, reflecting the continued clinical relevance of this Gram-positive MDR pathogen. MRSA remains a significant global concern, with millions of carriers worldwide and tens of thousands of invasive infections annually, especially in hospital environments. The persistence of MRSA in clinical settings despite decades of infection control efforts emphasizes the resilience and adaptability of resistant organisms[20].

The negative consequences of having an extremely high rate of multi-drug resistant organisms (MDR) in this study and others, and the subsequent effect of this phenomenon on patient outcome, and the impact on the allocation of resources in hospitals, is difficult to understate. Additionally, Infections caused by MDR organisms result in prolonged hospitalizations, increased in-hospital fatalities, and increased overall healthcare expenditures because of the need for the use of second-line therapies and increased supportive care. Certain subgroups, for example, patients in intensive care units (ICUs), possess particularly high burdens of MDR pathogens coupled with high morbidity because of the added risk of invasive procedures and immune compromised host defenses. Non-selective studies unequivocally document that patients in ICUs are at the highest levels of risk for colonization and infection from multi-drug resistant organisms (MDROs), which underscores the need for focused infection control and stewardship activities[21].

Moreover, the differences in prevalence of MDR organisms across departments and populations (e.g., general wards versus ICUs, adults versus pediatrics) indicates that focused surveillance and antimicrobial stewardship initiatives must be developed to respond to the epidemiological characteristics of each locality. For instance, though in some situations the PICU may have a lower prevalence of MDR organisms, the impact of an increased prevalence of resistant infections on a given population of children with heightened susceptibility may be severe.

The result of this microbiology lab survey has shown the degree of multidrug resistant organisms (MDROs) in the clinical samples obtained from the hospitalized patients. In the carried out research, it was found that MDROs were present in more than (51) of the culture positive samples. Escherichia coli and Klebsiella pneumoniae were found to be the most frequently resistant isolated pathogens. Methicillin resistant Staphylococcus aureus (MRSA), Pseudomonas aeruginosa, Enterobacter spp., and Acinetobacter baumannii were also found to be major contributers to the resistant microbail burden. The impressing result shows the global concern that AMR (antimicrobial resistance) is in fact a treating problem due the resistant to the hospital infections.

The prevalence rate of 51% observed in this study is comparable with other regional and global studies of MDR prevalence. For example, a systematic investigation reported an overall MDR prevalence of 59% (95% CI: 48–69%) among clinical isolates across multiple research settings, underscoring the substantial burden of resistance worldwide. Similarly, *Alsaab et al.* reported a MDR prevalence of 37.3% among hospitalized patients, with males showing higher MDR rates than females, although demographic distribution varied in the present study. The discrepancy in exact prevalence figures can be attributed to differences in geographical locations, hospital practices, sample types, and infection control protocols.

Studies focusing on specific settings also provide relevant comparative insights. For instance, a systematic investigation of MDR organisms in patients transferred from long-term care facilities showed that about 31% carried MDROs such as MRSA and vancomycin-resistant *Enterococcus* (VRE), with strong associations to prior antibiotic use. Although that study did not explore all hospital departments, the high carriage rate among transferred patients highlights how hospital ecosystems can act as reservoirs and amplifiers of resistant strains. Similarly, research conducted in Saudi Arabia found high MDR detection rates among clinical isolates, with bloodstream infections showing significant resistance to beta-lactams and other commonly used antibiotics, reflecting broader regional resistance patterns reminiscent of our findings.

Other studies report variable MDR prevalence depending on settings and clinical contexts. A multicenter study of urinary tract infections (UTIs) in emergency departments demonstrated a 39.1% prevalence of MDR pathogens among patients with confirmed UTIs, with risk factors including male gender and recent hospitalization. Although this figure is somewhat lower than ours, it reinforces that MDR prevalence remains consistently high across patient populations and infection types. Moreover, MDRO prevalence in pediatric intensive care units (PICUs) was reported at 4.6% in one multicenter point-prevalence study, illustrating that the burden may vary with age, infection type, and care setting, but remains significant where surveillance is robust.

CONCLUSION

The survey yielded the first data on the distribution of multidrug resistant organisms (MDROs) aligned with Microbiology Laboratory analyses of Clinical samples in hospitals. The study recorded the greatest MDR pathogen occurrences within the genera Escherichia coli and Klebsiella pneumoniae, as well as substantial occurrences of methicillin resistant Staphylococcus

aureus (MRSA), Pseudomonas aeruginosa and Acinetobacter baumannii. The study validated globally held perspectives that hospitals face MDROs as an existing and growing menace that prolongs hospitalizations, escalates mortality and increases the cost of healthcare.

Infections related to MDROs were found to have the greatest correlation with prior consumption of antibiotics and average hospital stay (which was in line with previous studies). This brought about the redistribution of resistant strains in the most infection prone individuals within the elder care segments of an Intensive Care Unit (ICU). The findings emphasize most critically the need for the formulation and adoption of standard infection control and antimicrobial stewardship, most critically in specific locations.

Moreover, the analysis draws attention to the importance of pattern recognition and monitoring of resistance, which is useful for enhancing clinical decision-making and streamlining the approaches of public health. It also stresses the importance of additional research that contains molecular characterization of the resistance genes and that is multi-centered, to provide descriptions of the mechanisms of resistance and the diffusion of resistance

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