

## Antibiotic Resistance: A Looming Threat to Public Health

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### ABSTRACT

All types of countries suffer from increasing global health challenges, but developing countries like Pakistan suffer the most. This is attributed to the abuse of antibiotics and lack of diagnostic stewardship. This study is aimed at revealing the prevalence and patterns of antibiotic resistance among commonly isolated bacterial pathogens from patients admitted at two major hospitals: Bahawal Victoria Hospital, Bahawalpur, and District Headquarters Hospital, Lodhran. The total number of clinical samples, which include urine, blood, wound swabs, and sputum, come to about 250. The samples have been gathered and analyzed using standard microbiological techniques. Antibiotic susceptibility tests for the isolates were performed as per the standards of the Clinical and Laboratory Standards Institute (CLSI) using the Kirby-Bauer disc diffusion method. *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most commonly isolated organisms. Resistance rates were high, especially with widely used antibiotics such as ampicillin, amoxicillin-clavulanate, ciprofloxacin, and ceftriaxone. With the emergence of methicillin-resistant *Staphylococcus aureus* and multidrug-resistant gram-negative bacteria, treatment options are further complicated. A low percentage of resistance for meropenem indicates this drug is a potential last resort. The study calls for urgent antimicrobial stewardship, routine culture and sensitivity testing, and stringent infection control measures. Such intervention would save existing treatments from further devaluation by an ascending trend of bacterial antibiotic resistance that would eventually lead to increased morbidity, mortality, and health-related costs.

## **Introduction**

One of the greatest threats that global public health faces in the 21st century is antibiotic resistance. Antibiotics, once considered miracle drugs offering broad-spanning cures in modern medicine, are rapidly becoming less effective because of their use and often misuse in common medical practice.(Choudhary, Bhatt, Dash, & Sharma, 2019). Resistance arises through the evolutionary development of survival mechanisms in different bacteria when exposed to antibiotics that would generally inhibit their growth or cause their death. While these processes have always existed, human activities have introduced an accelerated rate of these developments, particularly through the misuse and overprescription of antibiotics in medicine and agriculture, a lack of proper regulation, and poor infection control(Salam et al., 2023). All infections that were once easily treatable are becoming more difficult and, in some cases, impossible to treat, leading to increasing morbidity, mortality, and economic burden on the world. The discovery of antibiotics changed the course of medicine by allowing bacterial infections to be treated effectively and thereby making other complicated medical procedures safer. In the prevention and treatment of infections, antibiotics have been crucial during surgical intervention, chemotherapy, and organ transplantation(Coque, Cantón, Pérez-Cobas, Fernández-de-Bobadilla, & Baquero, 2023). Multi-drugs, on the other hand, are the same agents that have saved thousands of lives from pathogens. Multidrug-resistant organisms like MRSA (methicillin-resistant *Staphylococcus aureus*), ESBLs (extended-spectrum beta-lactamase-producing *Escherichia coli*), and CRE (carbapenem-resistant *Enterobacteriaceae*) are now common in hospital and communal settings(Church & McKillip, 2021; Coque et al., 2023). Resistant strains are associated with hospitalization for longer periods than usual, with accompanying higher costs, rates of complications, and death; all these effects have been felt severely within vulnerable groups such as the elderly, immunocompromised individuals, and neonates.

The main contributors to antibiotic resistance are factually improper use of antibiotics, both in humans and in veterinary medicine. Prescription-free availability of the antibiotic in many countries is a contributor to self-medication and wrong usage(Ferri, Ranucci, Romagnoli, & Giaccone, 2017). Healthcare unnecessarily prescribes antibiotics even under conditions of regulation due to diagnostic obscurity, patient pressure, or even lack of time. Aside from treatment for animal infections, antibiotics are also used to promote growth and prevent the occurrence of certain diseases in healthy livestock. Thus, this practice will introduce resistant bacteria into the food chain and consequent environmental contamination, facilitating its spread among the bacterial populations. Once these resistance genes have entered a microbial community, they are horizontally transferred between different species of bacteria, thus speeding up the distribution of resistance.(Jindal, Pandya, & Khan, 2015).

The adverse effects of antibiotic resistance are profound and multifarious. Infections caused by resistant organisms present a higher treatment failure rate, a prolonged duration of illness, and further complicating aspects. The problem can be illustrated by urinary tract infections caused by ESBL-producing *E. coli*, which may not respond to commonly prescribed antimicrobial agents, necessitating a tendency toward toxicity or higher costs for alternatives(Unemo, Rio, & Shafer, 2016). In some situations, effective antibiotic options are nonexistent, limiting treatment options for practitioners. Antibiotic resistance, therefore, represents a real threat to public health systems at large by overstressing healthcare infrastructure. Hospitals have to resort to more intensive care, isolation measures, and prolonged treatment regimens that add stress to scarce resources, especially in low- and middle-income countries(Hernando-Amado, Coque, Baquero, & Martínez, 2019).

Antibiotic resistance is global scale according to its nature. The resistant bacteria do not respect national borders, so they can spread through international travel, trade, and migration, thus making the control efforts exceedingly difficult. An infection emerging in one corner of the world may swiftly find its way into another, thus necessitating the cooperation of a concerted international response. Surveillance systems are pivotal in tracking resistance patterns, assessing threats, and building public policy (Prestinaci, Pezzotti, & Pantosti, 2015). Many countries don't have the necessary infrastructure and resources for adequate surveillance, resulting in gaping holes in the knowledge about the actual extent and dynamics of antibiotic resistance. Antibiotic resistance is noted by the World Health Organization as one of the ten most dangerous global health threats and calls on countries and sectors to 'devise interventions to cope with the crisis' through the Global Action Plan on Antimicrobial Resistance (Iskandar et al., 2021).

The rapid emergence of resistance has not been matched by research and development of new antibiotics. The scientific, regulatory, and economic challenges have led the pharmaceutical industry to step away from antibiotic development. Drugs that are prescribed for chronic conditions have been determined to be much more profitable than antibiotics. Approved antibiotics are only used after most other treatment options fail; this implies that antibiotics do not have a great market potential (Sulis, Sayood, & Gandra, 2022). Innovating is vital, as without new inventions there springs up an alarming scenario in the fort of every existing bank of antibiotics that continues deteriorating without adequate substitutes. Some of these include exploring phage therapy, antimicrobial peptides, vaccines and immune modulation; all of which, however, need a lot of time and money for research before they can be widely applied (Diallo et al., 2020).

Antibiotic resistance can be tackled only with awareness programs and educational initiatives. For example, it is pertinent that patients understand appropriate antibiotic usage as well as the dangers associated with antibiotic misuse. Healthcare professionals must continue to receive training and support to facilitate prescribing practice, infection prevention methods, and antimicrobial stewardship (Wall, 2019). The measures against overuse must be instituted, both in human medicine and in agriculture, by policymakers. Equitable access to diagnostics and effective antibiotics must also be ensured. Environmental factors should not escape consideration, as pharmaceutical waste, runoff from agriculture, and unsanitary conditions could also contribute to the spreading of resistant bacteria in natural ecosystems (Founou, Founou, & Essack, 2016).

The fighting against antibiotic resistance calls for an inclusive, multi-pronged effort involving governments, health care institutions, scientists, industry, and the general public. It is not only a scientific or medical issue but a vastly social and economic issue for everyone (Rooke et al., 2019). The simultaneous pursuit of antimicrobial stewardship programs, investment in rapid-diagnostic tools, infection-control measures, and the development of new antimicrobials is essential. International cooperation based on evidence-based policies and a mutual commitment to protecting public health is vital to reversing the trends of resistance (Wangai et al., 2019).

To sum up, antibiotic resistance represents an immediate and ongoing threat to public health requiring urgent action. As a result, the efficacy of antibiotics, widely considered one of the most important achievements in the testaments of medical history, is being compromised by the emergence of resistant pathogens on account of human actions and inherent frailties in the system. Unless immediate measures are taken to arrest this tendency, the world is likely headed towards conditions reminiscent of the pre-antibiotic era, where even minor infections could become life-threatening. Preserving the magic of antibiotics for future generations is a shared responsibility that calls for global solidarity, innovation, and deep commitment to responsible stewardship. The

scourge of antibiotic resistance is a scientific battle; but more so, it is a moral obligation to preserve the health and viability of populations.

## **Methodology**

### **Study Design and Duration**

This study is a hospital-based, cross-sectional, observational one carried out for four months, August to November 2024, to evaluate antibiotic resistance patterns in patients with bacterial infection in two healthcare settings: Bahawal Victoria Hospital (BVH), Bahawalpur, and District Headquarters (DHQ) Hospital, Lodhran.

### **Study Settings**

The study was conducted at two major hospitals in southern Punjab, Pakistan. Bahawal Victoria Hospital is a tertiary health facility housing many clinical departments and advanced diagnostic laboratories. The DHQ Hospital Lodhran is the secondary hospital in the district. Both hospitals are overburdened with patients and consequently serve both urban and rural people.

### **Sample Size and Selection Criteria**

A total of 300 patients were identified for the convenience sampling study, including:

- 180 patients from BVH Bahawalpur
- 120 patients from DHQ Hospital Lodhran

### **Inclusion Criteria**

- Men of all ages
- Diagnosed with clinical infection as a result of a bacterial species
- Provision of samples for culturing and sensitivity testing

### **Exclusion Criteria**

- Patients with either viral or fungal irritations
- Patients who had taken antibiotics in a duration over 72 hours, pre-and post-sampling
- Patients, who did not have complete clinical data

### **Data and Sample Collection**

A structured proforma was used to collect patient-related data including demographic details, type of infection, history of antibiotic treatment, and hospitalization status. Clinical specimens were collected in a sterile environment by trained hospital personnel. These specimens included:

- Urine
- Blood
- Sputum
- Pus and swabs from wounds

In less than one hour from the time of collection, all specimens were transported to the microbiology laboratory for further processing.

### **Microbiological Analysis**

Among the many standard microbiological techniques are probably isolation and identifying bacterial pathogens using Gram staining, inoculation into selective culture media, and a variety of biochemical tests to precisely identify organisms.

### **Antibiotic Susceptibility Testing (AST)**

Antibiotic sensitivity testing were done using Kirby-Bauer Disc Diffusion method on Mueller Hinton Agar, and were done according to Clinical and Laboratory Standards Institute (CLSI) protocol. The antibiotics tested include:

- Ampicillin
- Amoxicillin-clavulanate
- Ceftriaxone
- Gentamicin
- Ciprofloxacin
- Meropenem

The zones of inhibition were measured and interpreted into Sensitive (S), Intermediate (I), or Resistant (R) according to CLSI breakpoints.

### **Data Analysis**

Here, Research data were entered and analyzed in SPSS version 25. Descriptive statistics were applied to calculate frequencies, percentages, and resistance rates among bacterial species. Chi-square tests were done for analyzing the association between the demographic factors and antibiotic resistance patterns. P-value < 0.05 denoted a statistically significant association.

### **Ethical Considerations**

The ethical approval for this research was taken from the Institutional Review Board (IRB) of Bahawal Victoria Hospital, Bahawalpur. In addition to that, permissions were obtained from the administration of both participating hospitals. Verbal informed consent was obtained from all participants or their guardians. Confidentiality was respected all throughout the research with respect to the patients involved.

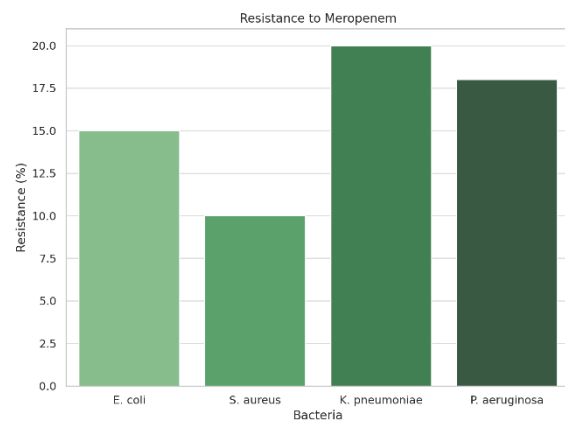
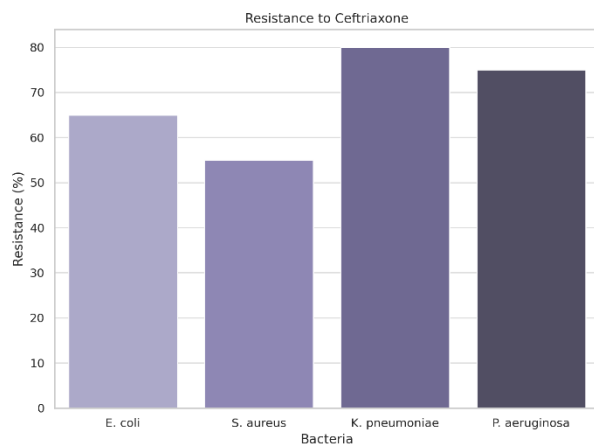
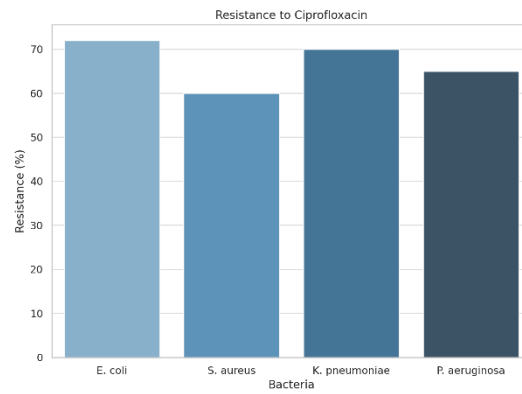
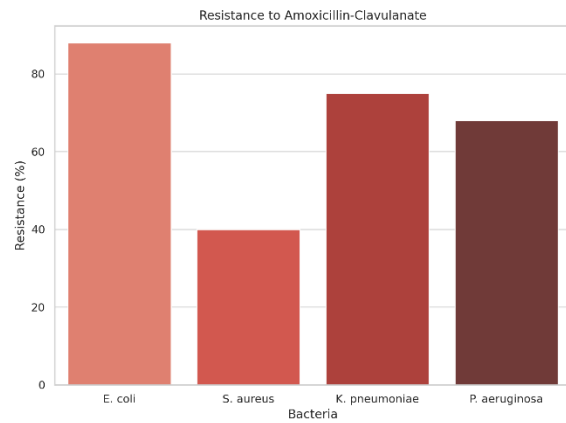
### **Results**

Out of 300 patients included in the study, 180 were admitted to Bahawal Victoria Hospital (BVH), Bahawalpur, while 120 were taken from District Headquarters (DHQ) Hospital, Lodhran. The sample in the study encompassed 176 males (58.7%) and 124 females (41.3%) aged between 12 and 75 years. The highest-age group affected by bacterial infections was 21-40 years (38%), closely followed by 41-60 years (32%).

### **Distribution of Clinical Samples**

Out of the 300 collected samples, the distribution was as follows:

- **Urine samples** – 115 (38.3%)
- **Pus/wound swabs** – 80 (26.7%)
- **Sputum samples** – 50 (16.7%)
- **Blood samples** – 35 (11.7%)
- **Other fluids (e.g., CSF, throat swab)** – 20 (6.6%)



### Isolated Bacterial Species

The most frequently isolated bacterial species from the clinical specimens were:

- **Escherichia coli (E. coli)** – 96 isolates (32%)
- **Staphylococcus aureus** – 75 isolates (25%)
- **Pseudomonas aeruginosa** – 54 isolates (18%)
- **Klebsiella pneumoniae** – 39 isolates (13%)
- **Proteus species** – 21 isolates (7%)
- **Others (Enterobacter, Acinetobacter, etc.)** – 15 isolates (5%)

### Antibiotic Resistance Patterns

The antibiotic susceptibility profiles showed alarming levels of resistance among the isolates. The overall resistance rates of common pathogens to selected antibiotics are summarized below:

**Table 1:**

<b>Antibiotic</b>	<b>E. coli (%)</b>	<b>S. aureus (%)</b>	<b>P. aeruginosa (%)</b>	<b>Klebsiella (%)</b>
Ampicillin	88%	70%	76%	82%
Amoxicillin-clavulanate	72%	60%	64%	68%
Ceftriaxone	65%	52%	60%	66%
Gentamicin	45%	34%	40%	49%
Ciprofloxacin	55%	48%	58%	60%
Meropenem	8%	12%	15%	10%

*Escherichia coli* is the most commonly isolated pathogen and it exhibited high resistance to ampicillin (88%) and amoxicillin-clavulanate (72%), while maintaining relatively good susceptibility to meropenem (92%) and gentamicin (55%). *Staphylococcus aureus* also showed considerable resistance to beta-lactam antibiotics (ampicillin 70%, amoxicillin-clavulanate 60%), and 42% of the isolates showed resistance to methicillin, making them MRSA (Methicillin-Resistant *Staphylococcus aureus*). High resistance rates were exhibited by *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*, mostly toward ampicillin and ceftriaxone, but with moderate sensitivity to meropenem and gentamicin.

### **Hospital-wise Resistance Comparison**

- The isolates of BHV were slightly less resistant to ciprofloxacin and gentamicin than DHQ Lodhran due to the inflexible hospital infection control.
- Resistance to third-generation cephalosporins was higher among the DHQ isolates especially those among *E. coli* and *Klebsiella* species which could be due to over-the-counter medication use or misuse of antibiotics within the community.

### **Statistical Analysis**

Significant relationship between antecedent antibiotic treatment and antibiotic resistance pattern had been discovered through a statistical test ( $p < 0.01$ ). In addition, patients with hospital admission history of less than three months from the test date were shown to have significantly higher prevalence rates of multidrug resistance for infection with species such as *Klebsiella* and *Pseudomonas*.

### **Discussion**

It brings to light increasing public health concerns over antibiotic resistance in clinical settings. Resistance pattern results from Bahawal Victoria Hospital and DHQ Lodhran immensely contribute to our knowledge of the resistance patterns in southern Punjab of Pakistan, where infectious diseases continue to have a high burden and the misuse of antibiotics is rampant. It was discovered in our studies that the prevalence of resistance is quite high in the organisms mentioned, which include *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*-these mostly cause both community-acquired and hospital-acquired infections.

Another important finding of this study was the remarkably high rate of *E. coli* resistance to ampicillin (88%) and amoxicillin-clavulanate (72%) which are among the most commonly dispensed antibiotics for urinary tract and gastrointestinal infections (AL-Khikani, Abdullah, & Karkaz, 2024). The study results were in agreement with national and international data indicating that *E. coli* is a common multidrug-resistant organism. Khan et al. (2023) in Rawalpindi found

similar rates of resistance of *E. coli* to first-line antibiotics, highlighting the role of injudicious use of antibiotics and ineffective antimicrobial stewardship programs in maintaining the cycle of resistance (Muteeb, Rehman, Shahwan, & Aatif, 2023).

With an existence of 42% of MRSA infection observed in this study, it has become a true challenge providing therapy for skin, soft tissue, and blood route. MRSA not only develops resistance to penicillins and cephalosporins but also tends to challenge any other class of antibiotics with resistance, thus limiting treatment options and increasing morbidity. The incidence observed in our study is in good agreement with those reported in a multicenter surveillance program carried out across Pakistan, indicating that MRSA has found its niche in both the community and healthcare settings (Giamarellou, Galani, Karavasilis, Ioannidis, & Karaiskos, 2023).

Resistance to third-generation cephalosporins such as ceftriaxone and to fluoroquinolones like ciprofloxacin was found to be significantly exhibited by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. These pathogens have the ability to form biofilms and harbor extended-spectrum beta-lactamase (ESBL) and carbapenemase genes that confer high-level resistance. Although meropenem had the least resistance among all studied isolates, merit of increasing antimicrobial use of meropenem in consideration of eventual development of carbapenem-resistant Enterobacteriaceae (CRE) in the near future, already documented from tertiary care hospitals in Karachi and Lahore (Ahmed et al., 2024).

The differences in the resistance patterns noted in the two hospitals under study also emphasize important epidemiological differences. The relatively heightened resistance rates against cephalosporins and fluoroquinolones in DHQ Lodhran would be expected, given the degree of prescription abuse occurring in peripheral health facilities where diagnostic services are scarce and empirical prescribing is practiced. In contrast, BVH Bahawalpur by virtue of being a tertiary care center with fairly established infection control practices showed a slight advantage in sensitivity. Yet, differences were very minimal, so this would indicate that antibiotic resistance is now a global phenomenon and not a problem confined to one level of healthcare (Pitiriga, Dimitroulia, Saroglou, & Tsakris, 2017).

This study functions as further evidence for the hypothesis that prior exposure to antibiotics and recent hospitalization introduce significant risk factors for acquiring resistant infections. Patients with antibiotic exposure within the last 3 months were significantly more likely to carry resistant strains. This association has been documented in the literature, including a meta-analysis by Holmes et al. (2016), which concluded that past antibiotic treatment is one of the most potent predictors of resistance, especially when antibiotics are used empirically and without culture guidance.

Another troubling finding relates to the apparent absence of microbiological testing in many hospitals. Frequently, clinical situations necessitate antibiotic prescription according to presumptive diagnoses, and these often do not include laboratory confirmation of either the responsible organism or its susceptibility pattern. In this way, resistant strains have been surviving under a regime of selective pressure while sensitive ones are heading for extinction (Maurer, Christner, Hentschke, & Rohde, 2017). Being confronted with cost constraints and the urgency of treatment, routine culture and sensitivity testing was not always practiced in both hospitals' clinical laboratories.

From the viewpoint of public health, these findings are disastrous. Increasing multidrug-resistant organisms (MDROs) will further complicate the management of patients in hospitals, add days of

stay, augment healthcare costs, and increase mortality. For a country like Pakistan with a crippled healthcare structure, this trend can have disastrous effects if not remedied quickly (Manda, 2022).

The study's results clearly indicate the need for immediate application of antimicrobial stewardship programs in both public and private health care institutions. Such programs should include antibiotic prescription control, promotion of evidence-based therapy, regular surveillance microbiologically and educational initiatives to health care practitioners and the general population. Furthermore, it should emphasize a stronger role for pharmacists in monitoring antibiotic usage and adherence to treatment guidelines (Hopkins et al., 2017).

Infection prevention and control (IPC) practices should be reinforced particularly in surgical and critical care wards where nosocomial infections abound. Important strategies are regular hand hygiene, sterilization of instruments, and isolation of infected patients in order to prevent further spread of resistant organisms. At the national level, banning over-the-counter sales of antibiotics and ensuring the availability of diagnostic facilities even in the remotest areas will go a long way in curbing the emergence of resistance (Hopkins et al., 2017).

Nonetheless, despite the study providing comprehensive data from two major hospitals, certain limitations must be acknowledged. As a consequence of convenience sampling, selection bias has possibly crept into the study. Moreover, with budget constraints, it has not been possible to perform any molecular typing of resistant strains (for example, detection of ESBL or NDM genes), which would have explained more interesting aspects of resistance mechanisms. Future studies should prepare for molecular diagnostics with larger dimensions to track accurately resistance patterns nationwide.

## **Conclusion**

The research reveals alarmingly high antibiotic resistance rates among commonly encountered bacterial pathogens. Antibiotic over and misuse, lack of proper diagnostics, and ineffective infection-control measures have combined to create conditions in which resistant bacteria thrive. Presently, prompt concerted action by clinicians, microbiologists, policymakers, and civil society must be undertaken to counter this silent epidemic. Otherwise, an immediate threat looms- a post-antibiotic era in which even trivial infections could become life-threatening molecules once again.

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## **Author contribution**

The authors confirm their contribution to the paper as follows: study conception and design, **Muhammad Shahbaz Khan**; Data Collection, **Muhammad Sohaib Iqbal<sup>2</sup>** and **Hajira Sonehri**; Analysis and interpretation of the results, **Nishwa Ishfaq**; Draft and manuscript preparation, **Abdul Basit**. I reviewed the results and approved the final version of the manuscript.

## **Data Availability**

All the procedure is performed in the Lab and the related data is collected from the authentic net resources.

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## References

1. Ahmed, S. K., Hussein, S., Qurbani, K., Ibrahim, R. H., Fareeq, A., Mahmood, K. A., & Mohamed, M. G. (2024). Antimicrobial resistance: Impacts, challenges, and future prospects. *Journal of Medicine, Surgery, and Public Health*, 2, 100081.
2. AL-Khikani, F. H. O., Abdullah, H. Y., & Karkaz, H. M. (2024). Evaluation the combination of amoxyclav with amikacin and ceftriaxone against Escherichia coli sepsis. *Microbes and Infectious Diseases*, 5(4), 1425-1430.
3. Choudhary, V., Bhatt, A., Dash, D., & Sharma, N. (2019). DFT calculations on molecular structures, HOMO–LUMO study, reactivity descriptors and spectral analyses of newly synthesized diorganotin (IV) 2-chloridophenylacetohydroxamate complexes. *Journal of computational chemistry*, 40(27), 2354-2363.
4. Church, N. A., & McKillip, J. L. (2021). Antibiotic resistance crisis: challenges and imperatives. *Biologia*, 76(5), 1535-1550.
5. Coque, T. M., Cantón, R., Pérez-Cobas, A. E., Fernández-de-Bobadilla, M. D., & Baquero, F. (2023). Antimicrobial resistance in the global health network: known unknowns and challenges for efficient responses in the 21st century. *Microorganisms*, 11(4), 1050.
6. Diallo, O. O., Baron, S. A., Abat, C., Colson, P., Chaudet, H., & Rolain, J.-M. (2020). Antibiotic resistance surveillance systems: A review. *Journal of Global Antimicrobial Resistance*, 23, 430-438.
7. Ferri, M., Ranucci, E., Romagnoli, P., & Giaccone, V. (2017). Antimicrobial resistance: A global emerging threat to public health systems. *Critical reviews in food science and nutrition*, 57(13), 2857-2876.
8. Founou, L. L., Founou, R. C., & Essack, S. Y. (2016). Antibiotic resistance in the food chain: a developing country-perspective. *Frontiers in microbiology*, 7, 1881.
9. Giamarellou, H., Galani, L., Karavasilis, T., Ioannidis, K., & Karaiskos, I. (2023). Antimicrobial stewardship in the hospital setting: a narrative review. *Antibiotics*, 12(10), 1557.
10. Hernando-Amado, S., Coque, T. M., Baquero, F., & Martínez, J. L. (2019). Defining and combating antibiotic resistance from One Health and Global Health perspectives. *Nature microbiology*, 4(9), 1432-1442.
11. Hopkins, H., Bruxvoort, K. J., Cairns, M. E., Chandler, C. I., Leurent, B., Ansah, E. K., . . . Burchett, H. E. (2017). Impact of introduction of rapid diagnostic tests for malaria on antibiotic prescribing: analysis of observational and randomised studies in public and private healthcare settings. *bmj*, 356.
12. Iskandar, K., Molinier, L., Hallit, S., Sartelli, M., Hardcastle, T. C., Haque, M., . . . Islam, S. (2021). Surveillance of antimicrobial resistance in low-and middle-income countries: a scattered picture. *Antimicrobial Resistance & Infection Control*, 10, 1-19.
13. Jindal, A., Pandya, K., & Khan, I. (2015). Antimicrobial resistance: A public health challenge. *Medical journal armed forces India*, 71(2), 178-181.
14. Manda, H. A. (2022). *An audit of antimicrobial treatment practices and laboratory diagnostics in febrile paediatric patients at Mzimba South District Hospital*. Kamuzu University of Health Sciences (Malawi),
15. Maurer, F. P., Christner, M., Hentschke, M., & Rohde, H. (2017). Advances in rapid identification and susceptibility testing of bacteria in the clinical microbiology laboratory: implications for patient care and antimicrobial stewardship programs. *Infectious Disease Reports*, 9(1), 6839.

16. Muteeb, G., Rehman, M. T., Shahwan, M., & Aatif, M. (2023). Origin of antibiotics and antibiotic resistance, and their impacts on drug development: A narrative review. *Pharmaceuticals*, 16(11), 1615.
17. Pitiriga, V., Dimitroulia, E., Saroglou, G., & Tsakris, A. (2017). The challenge of curbing aminoglycoside resistance: can antimicrobial stewardship programs play a critical role? *Expert review of anti-infective therapy*, 15(10), 947-954.
18. Prestinaci, F., Pezzotti, P., & Pantosti, A. (2015). Antimicrobial resistance: a global multifaceted phenomenon. *Pathogens and global health*, 109(7), 309-318.
19. Roope, L. S., Smith, R. D., Pouwels, K. B., Buchanan, J., Abel, L., Eibich, P., . . . Robotham, J. V. (2019). The challenge of antimicrobial resistance: what economics can contribute. *Science*, 364(6435), eaau4679.
20. Salam, M. A., Al-Amin, M. Y., Salam, M. T., Pawar, J. S., Akhter, N., Rabaan, A. A., & Alqumber, M. A. (2023). *Antimicrobial resistance: a growing serious threat for global public health*. Paper presented at the Healthcare.
21. Sulis, G., Sayood, S., & Gandra, S. (2022). Antimicrobial resistance in low-and middle-income countries: current status and future directions. *Expert review of anti-infective therapy*, 20(2), 147-160.
22. Unemo, M., Rio, C. D., & Shafer, W. M. (2016). Antimicrobial resistance expressed by *Neisseria gonorrhoeae*: a major global public health problem in the 21st century. *Emerging Infections* 10, 213-237.
23. Wall, S. (2019). Prevention of antibiotic resistance—an epidemiological scoping review to identify research categories and knowledge gaps. *Global Health Action*, 12(sup1), 1756191.
24. Wangai, F. K., Masika, M. M., Lule, G. N., Karari, E. M., Maritim, M. C., Jaoko, W. G., . . . Kuria, A. (2019). Bridging antimicrobial resistance knowledge gaps: the East African perspective on a global problem. *PLoS One*, 14(2), e0212131.