# Molecular Epidemiology of Antimicrobial Resistance in Saudi Arabia for Public Health Implications: A Review Study on Laboratory Based Surveillance and Future Directions

Mansour Saeed Mohammed Alawaji[1], Nasser Shabab Alharbi[1*], Abdullah Saad Ali Alharbi[1], Marwan Ataullah Abdulrahman Alahmadi[1], Sami Hudayban Alamri[1], Nashmi Shalwah S Alalawi[1], Hamzah Awadh Alsaedi[1], Hatem Hommaid Almalki[1], Jamilah Oudah Aljohani[1], Abdullah Saeed Abdulrahman Alamri[1], Hind Hamidi Hamdan Alhubaishi[1], Tareq Abdulhafiz A. Mohammed[2]

[1]Madinah Health Cluster, IAA-7011, POBox 4102, Madinah 42325, Saudi Arabia
[2]King Salman Bin Abdulaziz Medical City, Mahzur, Madinah 42319, Saudi Arabia
Email: shabab101@hotmail.com

## Abstract

This is a worldwide, major issue in public health due to the clinical cost and strategic effects on public health practice. The focus of this research will be based on the laboratory analysis on molecular epidemiology in antimicrobial resistance cases in Saudi Arabia. Most prominent patterns and mechanisms were seen and explained along with the contributing factors of such resistance patterns. Major Findings Inappropriate use of antibiotics Development of multi-drug resistance organisms and effects of carbapenem-resistant Enterobacteriaceae on health care settings. The use of advanced molecular techniques such as whole genome sequencing and antimicrobial susceptibility testing to monitor resistance mechanisms will inform public health interventions. Control of antimicrobial resistance relies on surveillance systems, antimicrobial stewardship programs, and public awareness campaigns. Future work will take the form of increasing the scope of research on mechanisms of resistance, further strengthening one-health approaches and international cooperation to be better placed to reduce AMR burden in Saudi Arabia.

**Keywords:** Antimicrobial resistance, Molecular epidemiology, Multidrug-resistant organisms, Antimicrobial stewardship, Carbapenem-resistant Enterobacteriaceae, Surveillance systems, Public health interventions, Resistance mechanisms.

## 1. Introduction

Antimicrobial resistance is the process whereby microorganisms, such as bacteria, viruses, fungi, and parasites, develop resistance to drugs that previously cured them. This has emerged as an

important global health issue considering its implications on public health, healthcare costs, and effectiveness of treatment for medical conditions. As stated by the World Health Organization, antimicrobial resistance (AMR) has become the major threat to global public health among the top ten threats. The anticipated cumulative projection, some 10 million people dying annually due to AMR by 2050, can be avoided through effective intervention (Garau & Bassetti, 2018). The main driver of AMR is the uncontrolled use of antimicrobials in both human medicine and agriculture. An increasing relation exists between antibiotic misuse, that being its excessive use, such as for viral infections where there is no use of this antibiotic, and the antibiotic-resistant strains rate (Silva et al., 2022). Misuse leads to emerging resistant strains but also raises hospital and medical treatment duration, raises expenditures, and enhances mortality ratios (Cassini et al., 2019). For example, it has been estimated that AMR caused about 1.27 million deaths globally in recent years, which shows the need for effective antimicrobial stewardship programs (Ungureanu, 2023).

The economic burden of AMR is also high. For instance, in the United States, the infections that result from antibiotic-resistant pathogens are estimated to amount to between $21 billion and $34 billion per year and lead to more than 8 million extra hospital days (Spellberg et al., 2011). It has so far been evident that there is an urgent need to have surveillance and monitoring of such trends in AMR to inform public health strategies and interventions for controlling immediate financial impact. Surveillance has been essential in the understanding of the epidemiology of AMR, which identifies resistant strains and monitors them across different populations and geographical locations (Perovic et al., 2018; Baron et al., 2017). Surveillance efforts give in in the understanding of AMR epidemiology since resistant organisms can be identified as well as traced through different populations and geographical space (Baron et al., 2017).

AMR is one of the most important determinants of public health and clinical outcomes in Saudi Arabia, with a trend that also reflects global concerns. The increasingly emerging multidrug-resistant pathogens, especially in the healthcare sector, may present important challenges to treatment and patient safety. Carbapenem-resistant Enterobacteriaceae has been reported to increase very highly in Saudi Arabia, and alarming rates have been reported in major cities like Riyadh (Bandy & Tantry, 2021). This is a serious issue because the organisms resistant to carbapenem are usually linked with very high morbidity and mortality rates that further complicate the treatment options for ordinary infections (Aldawsari et al., 2020).

Misuse and overprescription of antibiotics are the leading contributors to the increasing AMR rate in Saudi Arabia. Medical literature has reported inappropriate use through broad-spectrum antibiotic prescribing without proper indication with increasing resistance rates in typical pathogens (Alasmary, 2021). As such, for instance, research into one study found that antibiotic prescriptions in emergency departments showed that a significant proportion was found to be above the threshold established by the World Health Organization; there was an urgent need for improving stewardship (Balkhi et al., 2018). Such inappropriate usage fuels resistant strains but also brings hospital stay and healthcare costs into increasing folds, which increases the load on the healthcare sector (Almutairi, 2023). Other than the clinical importance, AMR has effects on public efforts to curb infectious diseases. Resistance has been seen in the forms of VREs and extensive multi-resistant strains of Acinetobacter spp. that have found their way into hospitals

within Saudi. Such resistance has led to rising rates of healthcare-associated infections (Shorman & Al-Tawfiq, 2013; Al-Ghamdi, 2024). Resistant infections complicate treatment regimens requiring the use of more expensive, less effective alternatives, which in turn impinges on patient outcomes and the health-care budget (Bazaid et al., 2021).

The most critical component for dealing with the issue is public awareness and education concerning AMR. It is an observation that much recent educational intervention tends to raise awareness of AMR issues among healthcare providers and the public alike. According to Almutairi (2023), status, knowledge among physicians is still deficient in terms of antimicrobial stewardship practices because most of the doctors do not know the term which makes it indicate the need for a complete training session as well as the implementation of policies in practice (Almutiri et al., 2020). It forms the basis of the comprehension of AMR patterns since it provides insights into genetic and epidemiological characteristics of resistant pathogens. Molecular epidemiology represents an important field that combines techniques in molecular biology with conventional methods of epidemiology for tracing resistance genes and for defining the clonal relationships among strains of bacteria. By using advanced molecular typing techniques, including MLST and WGS, the researchers may identify the transmission dynamics of resistant strains in relation to certain resistance mechanisms (Harris et al., 2018) Warner et al., 2016).

One of the important applications of molecular epidemiology is for the surveillance of AMR, to identify high-risk transmission networks and monitor the changes in resistance pattern over time. For instance, genomic surveys are now rolling out a project that aims to track multidrug-resistant clones of Neisseria gonorrhoeae within Europe, demonstrating the association between specific lineages and some resistance to frequently used antibiotics (Harris et al., 2018). Such data can inform public health intervention activities though increasing testing, screening, and provision of customized treatments to populations at risk (Wi et al., 2017).

In addition, molecular epidemiology helps in elucidating the development and transmission of resistance determinants. For instance, MGEs have been found to be significantly involved in the spread of AMR genes among enterococci, and thus there is a continuous need for research on the molecular mechanisms of resistance (Hegstad et al., 2010). That understanding will enable scientists to characterize the genetic content of these elements and, thus, improve the acquisition and diffusion of resistance traits among bacterial populations, which is essential for developing effective control measures (Jiang & Chen, 2020). In addition to tracking resistance patterns, molecular epidemiology has helped in the identification of specific resistance mechanisms. For instance, characterization of A. baumannii isolates from hospital outbreaks has revealed specific genetic profiles that are associated with different resistance phenotypes. This has enhanced our understanding of factors that result in the emergence of MDR strains (Warner et al., 2016; Ou et al., 2015). This information is important not just for guiding treatment practice but also for deriving new therapeutic strategies aimed at combating resistant infections.

More importantly, it combines molecular epidemiology with clinical data to be able to come up with more profound insights into public health impacts of AMR. Linking molecular data to patient demographics and clinical outcomes helps in identifying actual risk factors for AMR, which then enables the development of targeted interventions to mitigate such factors (Dai et al.

2019). This one stops at the multiple challenges presented in multiple healthcare avenues with regards to AMR.

Laboratory-based studies play an important role in the AMR context mainly based on the ability to provide timely and accurate data on resistance patterns, hence guiding clinical decision-making and informing public health policy. These studies involve various methodologies, including AST, which characterizes the resistance profiles of bacterial isolates to understand the dynamics of AMR in different settings. Laboratory-based research is one of the main functions that supplement conventional antimicrobial susceptibility testing, which is the most essential part of monitoring resistance trends and emerging resistance patterns. Such testing is the foundation for effective practice and policy formulation by which AMR should be controlled Mubita et al. (2021). Such studies confirming the susceptibility of the bacteria to available antibiotics ensure that clinicians make informed decisions regarding treatment options, thus improving patient outcomes and minimizing the risk of treatment failure.

Furthermore, studies conducted in the laboratory complement the surveillance of AMR. They provide real-time prevalence data of resistant strains. The importance of electronic laboratory-based surveillance systems in monitoring community outbreaks of pathogens such as Shigella spp was highlighted by Viñas et al. (Viñas et al., 2013). Such systems ensure that the response from healthcare providers and public health officials is prompt towards an emerging threat. It further enhances the general effectiveness of control measures against AMR. Apart from routine testing, the use of whole-genome sequencing, among others, is increasingly being implemented during laboratory research to acquire detailed insight into the genetics involved in resistance. McDermott et al. demonstrated the potential of using WGS for identifying resistance genes directly for isolates of bacteria, a very important approach towards tracking the spread of resistance and mechanisms (McDermott et al., 2016). This genomic approach will not only increase the sensitivity and specificity of detecting resistance but will also help identify outbreaks and guide targeted interventions.

Additionally, laboratory-based studies are important in revealing the impact of antimicrobial stewardship programs. As put by Cardoso et al., microbiology laboratories form part of such programs whose aim is to ensure that the use of antimicrobials is optimum and the emergence of resistance is minimized (Cardoso et al., 2019). Laboratories help the clinicians in coming up with accurate susceptibility data, which ensures the use of appropriate therapies and eliminates the use of broad-spectrum antibiotics that fuel resistance. Laboratory-based studies also enable the investigation of environmental factors contributing to AMR. In this regard, Fouz et al. demonstrated that wastewater and environmental reservoirs are key in the dissemination of resistant pathogens, requiring an all-encompassing surveillance approach that incorporates samples from the environment (Fouz et al., 2020). This can be a way to realize an all-encompassing approach in understanding the general ecological dynamics of AMR and for implementing control measures that work effectively.

## 2. Overview of Antimicrobial Resistance in Saudi Arabia

The presence of antimicrobial-resistant pathogens in Saudi Arabia remains a significant public health challenge, which is the consequence of the complex interplay of antibiotic misuse, hospital practice, and the peculiar healthcare environment in the region. Several studies have isolated relevant resistant pathogens that are unmanageable and not readily controlled in infections.

*Staphylococcus haemolyticus and staphylococcus aureus:* Methicillin-resistant Staphylococcus aureus (MRSA) is still a great concern in Saudi hospitals. Around 32% of the isolates of S. aureus were reported to show methicillin resistance, and these need strict surveillance and infection control measures (Aldawsari et al. 2020). A third strain, Staphylococcus haemolyticus, mostly overlooked, has appeared in the form of a nosocomial pathogen displaying multidrug resistance that further includes bacteremia and urinary tract infections (UTIs) (Alahmadi et al., 2021). The highly resistant strains are present in the hospital environments, thus making them call for a high alert as they easily adapt to clinical environments.

*Enterobacteriaceae:* Uropathogens with the highest percentage of being identified and that are resistant among Gram-negative bacteria include Escherichia coli and Klebsiella pneumoniae. A study established early resistance rates of E. coli to be 33.7% while that of K. pneumoniae was 15.21% to urinary tract infections (Alasmary, 2021). Extended-spectrum beta-lactamase (ESBL) production is a common mechanism of resistance observed in these pathogens, with studies showing that a significant percentage of uropathogens were ESBL-positive (Alasmary, 2021; Alyamani et al., 2017).

*Acinetobacter baumannii:* This organism has become notorious due to its multidrug resistance, especially in hospital-acquired infections. The results show an increasing trend of carbapenem resistance among Acinetobacter baumannii in Saudi Arabia, with significant resistance rates against fluoroquinolones and aminoglycosides (Al-Ghamdi, 2024; Almaghrabi et al., 2018). The inherited resistance genes such as bla OXA-51-like add to the complexity of treatment options (Al-Ghamdi, 2024).

*Pseudomonas aeruginosa:* This organism is yet another major contributor to the AMR scenario of Saudi Arabia. And then, various studies had reported multidrug resistance profiles ranging from resistance to carbapenems to clinical isolates with high level multidrug resistance as stated by Abdalla et al. The increase in P. aeruginosa ESBL-producing strains has made infections by this organism very difficult to treat (Aldawsari et al., 2020). (2023) and Bandy & Tantry in 2021.

*Salmonella spp.:* Antimicrobial-resistant Salmonella strains have also been recorded in Saudi Arabia with especial significance of third generation cephalosporin-resistance. A research survey shows the high prevalence level of resistance to nalidixic acid and ampicillin among isolated Salmonella. Therefore, the therapy and management of salmonellosis seem to be threatening within this region (Kraiem et al., 2019; El-Tayeb et al., 2017).

*Vancomycin Resistant Enterococcus (VRE):* Though it is being reported less frequently, the emergence of vancomycin-resistant Enterococcus species has been noted for the most part in hospitals. The trend of increasing multi-drug-resistant Enterococcus species is another challenge against infection control and its treatment (Abdalla et al., 2023). Most common antimicrobial

resistance mechanisms among popular pathogens in Saudi Arabia are diverse genetic modifications and biochemical processes making the bacteria live in the presence of antibiotics. The understanding of these mechanisms is important to help identify the problems offending the treatment of infections through antimicrobial resistance and developing relevant treatment strategies.

*Production of Beta-Lactamase:* All Gram-negative bacteria, among the most common mechanisms of resistance is the production of extended spectrum beta-lactamases (ESBLs) in organisms such as Escherichia coli and Klebsiella pneumoniae. According to Mboowa et al. (2020), these enzymes break down a vast array of beta-lactam antibiotics to a level that makes them useless. A few plasmid-mediated beta-lactamases, for example bla_CTX-M and bla_TEM, have enviably been implicated in resistance in strains causing uropathogenic infection (Mboowa et al., 2020).

*Efflux Pumps:* These pumps are utilized by several pathogens like Pseudomonas aeruginosa and Acinetobacter baumannii to expel antibiotics from inside their cells, thereby reducing the concentration of the drug in the intracellular medium and lowering its efficacy (Faria, 2023; Si et al., 2020). This mechanism is particularly scary because it develops multidrug resistance due to its ability of conferring resistance against multiple classes of antibiotics at a time, thereby further complicating the treatment options.

*Target Site Modification:* Other mechanisms of resistance acquisition also include mutations in the antibiotic targets' encoding genes. An example is mutation of gyrA and parC of E. coli, resulting in fluoroquinolone resistance through modification of fluoroquinolone targets sites (Bao et al., 2012). Methicillin resistance in Staphylococcus aureus is imparted through the mecA gene and the expression of a penicillin-binding protein of low affinity for beta-lactams (Chon et al., 2020). One important mechanism of antibiotic resistance in certain microorganisms is the alteration of the permeability of the outer membrane such that the antibiotic is unable to penetrate to its active site. For example, Acinetobacter baumannii and Pseudomonas aeruginosa become such mutants with porin channels in such a way that there is a dramatic decrease in the uptake of hydrophilic antibiotics thereafter, which is an important contribution of these species towards the multidrug-resistant character of these bacteria (Faria, 2023; Si et al. 2020).

*Biofilms Formation:* In terms of their importance as a resistance mechanism, biofilm formation is also an attribute of many pathogenic bacterial species such as Staphylococcus epidermidis or Pseudomonas aeruginosa. With them, entire colonies of bacteria are present under protection against host defenses, antimicrobials, or both. It makes it difficult to eradicate an entire infection (Faria, 2023). This biofilm-related issue is especially great in chronic infections and all implanted medical devices.

*Horizontal Gene Transfer:* This is facilitated through several mechanisms including transformation, transduction, and conjugation and helps the bacteria to spread their resistance genes among the different bacterial populations. Plasmids such as the IncA/C plasmids are known for carrying more than one resistance gene allowing rapid transfer of resistance characteristics between various species of bacteria (Aperce et al., 2016; Fernández-Alarcón et

al., 2011). This is particularly worrisome in the case of foodborne pathogens, where resistance genes can be transferred from commensal to pathogenic strains.

*Alteration of Antibiotic Targets:* Some bacteria can directly alter the antibiotic targets. For instance, Enterococcus faecalis alters its membrane phospholipids by the action of the mprF gene, which confers resistance against cationic antimicrobial peptides (Bao et al., 2012). This alteration allows the bacteria to avoid the host immune defense.

**Table 1:** Key Antimicrobial-Resistant Pathogens in Saudi Arabia

| Pathogen | Resistance Mechanism | Prevalence in Saudi Arabia | Clinical Significance |
|---|---|---|---|
| Methicillin-resistant Staphylococcus aureus (MRSA) | mecA gene encoding low-affinity penicillin-binding protein | 32% methicillin resistance among isolates in hospitals | High morbidity and mortality; challenges treatment of common bacterial infections. |
| Klebsiella pneumoniae | ESBL production (e.g., bla_CTX-M, bla_TEM) | 15.21% ESBL-producing isolates in urinary tract infections | Complicated treatment; necessitates carbapenems, increasing treatment costs. |
| Acinetobacter baumannii | Carbapenem resistance via bla_OXA-51-like genes | High prevalence in hospital-acquired infections | Linked to multidrug resistance; severely limits treatment options in ICUs. |
| Pseudomonas aeruginosa | Efflux pumps and ESBL production | Increasing multidrug-resistant strains reported | Compromises treatment efficacy; leads to prolonged hospital stays and poor patient outcomes. |
| Vancomycin-resistant Enterococcus (VRE) | Alteration of cell wall target sites | Rare but emerging in hospital environments | Increases risk of hospital-associated infections; limited therapeutic options. |

## 3. Laboratory-Based Surveillance

In Saudi Arabia, different approaches are used in the laboratory for the detection of antimicrobial resistance (AMR). This includes the traditional culture-based methods up to the modern molecular approach. Each of these contributes to the understanding and management of AMR in clinical practice. Some of the commonly used methods are as follows.

*Antimicrobial Susceptibility Testing (AST):* Traditional culture-based methods remain the cornerstone of AMR detection. The techniques applied in the laboratory for determining MICs include disk diffusion and broth microdilution. BMD is more reliable for determining the MIC of antibiotics against bacterial isolates and is therefore a gold standard in the validation of automated AST systems (Thabit, 2023). For all its apparent simplicity, the disk diffusion technique hardly qualifies to be called a stand-alone method; rather, it is semiquantitative regarding its susceptibility measure. It is, however, the most popularly used and widely applied in routine diagnostic settings.

*Polymerase chain reaction:* PCR has been widely employed as a molecular technique for the identification of already known genes of resistance in bacterial strains and within the category.

It generally opens out much-known-mechanisms of resistance as the presence of the bla_CTX-M genes for ESBL resistance or methicillin resistance in Staphylococcus aureus strains harboring mecA (Aldawsari et al., 2020). The sensitivity and specificity of PCR therefore make the method an invaluable tool for diagnostics concerning resistance profiles in situations where the classical approaches may not allow definitive diagnosis.

*Enzymatic amplification of DNA:* PCR is the most used molecular method for the identification of known resistance genes in bacterial strains. Rapidly, it can also be used to detect well-established mechanisms of resistance, e.g. bla_CTX-M for ESBL or mecA for methicillin resistance in Staphylococcus aureus (Aldawsari et al., 2020). The sensitivity and specificity of PCR and of all its improvements make it a fundamental diagnostic tool as far as resistance profiles are concerned, particularly in cases where classical approaches were unable to provide a definitive diagnosis.

*Whole Genome Sequencing (WGS):* Whole genome sequencing is now being adopted as one of the major techniques of complete analysis of bacterial genomes of Saudi laboratories. It yields abundant information on resistance genes and plasmids with details of their genetic backgrounds. According to Sherry et al. (2023) WGS allows identification of new resistance determinants tracing transmission pathways of resistant strain and serves as an informative tool for epidemiologists dealing with outbreak investigations.

*MALDI-TOF mass spectrometry:* It has an exciting application since it uses the matrix-assisted laser desorption-ionization time-of-flight mechanism to rapidly identify microbial species that may have resistance characteristics. Although it is an inherently diagnostic technique, MALDI-TOF can sometimes be used to identify several resistance markers depending on the protein profiles characterizing resistance (Kusuma, 2023). Its speed and reliability have made it a new complement to AMR detection methods.

*Metagenomics:* Analysis of the genetic material which could be obtained directly from any environmental sample, such as soil or water samples or even patient samples. As a result, metagenomic analysis can easily unveil the AMR genes circulating in the complex microbial ecosystem that exists within different clinical settings and agriculture (Ma et al., 2022). It is highly advantageous for deciphering the whole ecological aspect of AMR.

*Bioinformatic Tools:* The integration of bioinformatics is growing in importance in AMR detection. Genomic data genomic tools are now being developed and refined in the identification of resistance genes and prediction of phenotypic resistance (Sherry et al. 2022). These will improve interpretation of WGS data and help in discovering novel resistance mechanisms. As stated by Thabit, surveillance networks: Various national and state surveillance systems have emerged to carry out AMR tracking over the years. Trend analysis would generally aggregate data from diverse detection methods to ensure the widest possible scope on resistance patterns among pathogens. In summary, surveillance shall support public health strategies and antibiotic stewardship programs in general. Saudi laboratories at the center of national and international surveillance networks form the backbone of the understanding AMR dynamics, public health policy formulation, and making antimicrobial stewardship programs more effective. These

laboratories are among the most important sites of contributions to surveillance on AMR through:

*Laboratory Capacity Building:* Therefore, Saudi laboratories are part of building laboratory capacity for AMR surveillance through standardized testing protocols and improvements in the laboratory infrastructure. It is according to Seale et al. as a strength in developing the laboratory capacity for the efficient surveillance of drug-resistant infections particularly in low-and middle-income countries Seale et al. (2017). Such capacity building could concern training within a laboratory, provision of tools, and standardization of methodologies in detecting the AMR.

*Execution of One Health Approach:* Under the "One Health" concept, human, animal, and environmental health are considered a continuum in combating AMR. It was noted that a successful monitoring of AMR requires total surveillance across all contributing areas (Amin et al., 2022). To this effect, Saudi labs form part of this approach where they are collaborating with sectors of veterinary and environmental health to monitor how resistance patterns play out in varying ecosystems, giving one a holistic view of dynamics of AMR.

*Data Collection and Reporting:* The laboratories in Saudi Arabia gather data on AMR on a systematic basis that can be used to support the national and international surveillance initiatives. According to Saeed et al., a strong LIS will ensure the gathering, validation, and compilation of resistance information (Saeed et al., 2017). Saudi laboratories become part of the international surveillance network and thus provide complete data to international databases, which makes comparisons and collaborative work across countries even easier.

*International Surveillance:* The Kingdom of Saudi Arabia Membership on the Global Antimicrobial Resistance Surveillance System of the World Health Organization (WHO). The national labs in this regard contribute to the global surveillance of AMR (Thabit, 2023). By coordinating their surveillance activities with protocols of GLASS, Saudi laboratories would contribute to understanding the trends in AMR worldwide and subsequently contribute to the efforts in public health at an international level.

*Research and Development:* The Saudi laboratories also do research that identifies resistance mechanisms and epidemiology of resistant pathogens. Such studies from the laboratories help in determining the trend for emerging resistance patterns and, in the long run, public health responses. In this regard, a latest prevalence study of extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli and Klebsiella pneumoniae has been highly essential in providing the required local trend information (Alnasser et al., 2021; Alyamani et al., 2017).

*Training Programs:* The laboratories in the Kingdom of Saudi Arabia offer training programs. The programs are to raise awareness among health workers about AMR besides raising awareness among the people. Almutairi concludes that there is an education need on health matters. This is because the increased awareness and knowledge of the problem will be raised (Almutairi, 2023). Awareness will further enable responsible use of antibiotics besides fighting the AMR.

*Quality Assurance and External Quality Assessment:* Through the participation in external quality assessments, Saudi labs continued maintaining their high standards of testing for AMR.

These are key issues concerning the reliability of the surveillance data and for sustaining the confidence in the outcome reports reverted to national and international institutions. Assessments periodically expose flaws or shortcomings and ensure that the following best practices take place in the identification of AMR (Zongo, 2024).

## 4. Clinical and Public Health Implications

AMR significantly affects clinical outcomes and treatment plans in health care centers throughout Saudi Arabia. The impacts of the problem expose dangers in terms of patient safety, efficiency of treatment, and escalating healthcare cost. Some of the ways this can be understood include.

*Higher Treatment Failures:* The presence of MDROs increases treatment failures, particularly among the infected because they are sensitive to MDROs. As in the case of Aldawsari et al., their report indicated that the requirement of an alternative, often less potent antibiotic in the treatment of drug-resistant bacteria results in suboptimal clinical outcomes (Aldawsari et al., 2020). The situation is even worse when it comes to UTIs due to ESBL-producing Escherichia coli, where resistance rates towards conventional antibiotics are more than 20%, and thus requiring a carbapenem to be used as a first-line treatment (Alqasim et al., 2018).

*Longer Hospital Stay:* Drug-resistant pathogens patients tend to spend more extended periods in hospitals because complications from such poor first-line treatments require further aggressive care. According to Alhumaid et al., HAIs frequency was found to be more common in the ICU settings where AMR is highly burdensome (Alhumaid et al., 2021). This lengthy duration is not only increasing the chances of other secondary complications but also increases healthcare cost highly.

The healthcare costs are the treatment costs are increased due to longer hospital stays with the use of more costly antibiotics and the additional diagnostic tests. Aldawsari et al. opined that ASPs play a crucial role in maximizing therapy, decreasing costs, and enhancing clinical outcomes (Aldawsari et al., 2020). ASPs focus on appropriate use of antibiotics to minimize the economic consequences of AMR on healthcare systems.

*Changing Treatment Guidelines:* Emerging AMR calls for an updating of clinical practice guidelines and treatment guidelines. As observed above, increased resistance levels of first-line antibiotics prompt a treatment suggestion by indicating carbapenems when dealing with specific infections with all isolates of E. coli that is fully sensitive to imipenem (Alqasim et al., 2018). This suggests that the patterns of resistance are always followed to determine changes in the treatment procedures that will be implemented clinically.

*Impact on Surgical Results:* AMR will make surgeries complicated since most patients requiring elective surgery or those who have pre-existing diseases may experience this kind of resistance from their infecting agents. Postoperative infection by resistant organisms increases morbidity and mortality. Alomi et al. emphasized the role of clinical pharmacy services in managing antibiotic use at mass gatherings such as Hajj, when the risk of transmission is high for infection

(Alomi et al., 2017). Prophylactic antibiotics management should, therefore, be efficiently done to avert surgical site infections in such a scenario.

*Public Health Consequences:* AMR is a severe public health concern since resistant infections can be transmitted in communities and health care facilities. Almutairi's investigation into health education interventions has also examined awareness related to AMR impacts on healthcare providers and the public (Almutairi, 2023). This is where education comes in handy to realize responsible use of antibiotics, as well as curtail incidences of resistant infections.

*Demand for Intensive Monitoring:* Monitoring of antimicrobial resistance trends must be strictly and uninterruptedly followed to accommodate treatment approaches and effectively follow the patients. A strict monitoring system in Saudi would enable tracing resistance patterns, and hence surveillance can lead to a correct public health policy (Thabit, 2023). Such preventive measures are most necessary in preventing the repercussions of AMR on health outcomes.

## 5. Antimicrobial Stewardship and Infection Control

Antimicrobial resistance policies and initiatives in Saudi Arabia include interventions against antimicrobial resistance, an upgrade of antimicrobial stewardship, enhancement of surveillance capacity and practices, and promotion and responsible antibiotic use. Therefore, AMR in the healthcare set has been recognized to be rapidly posing a growing threat. Such initiatives include the following.

*The Antimicrobial Stewardship Programs (ASPs):* The implementation of ASP is one of the core points of the national strategy set up against antimicrobial resistance. These interventions aim at optimizing antibiotic use, decreasing inappropriate use, and enhancing patient outcomes. Aldawsari et al. suggested that active antibiotic stewardship guidelines be in place to control irrational antibiotic use in the health care settings of Saudi Arabia (Aldawsari et al., 2020). The national ASP strategy was launched in 2014 and has faced enforcement problems, as noted by Alghamdi et al., where the strategy has been essentially academic without strong enforcement tools (Alghamdi et al., 2019). However, ASPs are necessary for the proper usage of antibiotics.

*Public Surveillance Initiatives:* Saudi Arabia has set up surveillance systems for the monitoring of AMR trends across many pathogens in the kingdom. It works with health facilities to collect and analyze resistance pattern data as a ministry for public health policies and clinical guideline setting. For example, Balkhy et al., indicated a trend of healthcare-associated infections and the effectiveness of infection control interventions over a decade, indicating the necessity for continued surveillance (Balkhy et al. 2020). The information is important for understanding the epidemiology of AMR and informing interventions. While public education remains a very important aspect of national response towards AMR, human health professional education or training will be another important aspect. In this regard, Almutairi observed the dualistic education program of health education targeting both the general population as well as healthcare professionals (Almutairi, 2023). Moreover, the training programs for medical students and pharmacy students also include details on antimicrobial stewardship to be prepared in advance to fight AMR effectively (Ahmed et al., 2019).

One such form of international collaboration is through members of the Kingdom of Saudi Arabia with world health agencies such as the World Health Organization (WHO) to make its AMR strategies in agreement with the international expectations and integrate its country into GLASS, a WHO initiative to collect data on antibiotic resistance patterns and deliver best practices for AMR management. Not only this, but such collaboration also develops the well-refined capacity of the nation to act on AMR at the global level.

*Research and Development:* There is a continued need for research into mechanisms of AMR and the interventions that work. Experiments conducted by research laboratories in Saudi Arabia have allowed better understanding of the emergence of resistance patterns and enabled new strategies to be developed for combating AMR. The research on prevalence of multidrug-resistant pathogens affects the clinical guidelines and determines where interventions are focused.

*Regulatory Steps:* In Saudi Arabia, there are governmental regulations controlling the sale and distribution of antibiotics. It has decreased the availability of antibiotics as over-the-counter drugs. Antibiotics would be available only when prescribed, and people would use it only upon prescription. This step is quite important in stopping the abuse of antibiotics, which, in turn, reduces resistance development (Aldawsari et al., 2020).

*Public Awareness Campaign:* The national strategy includes educating the general population about the risks of AMR and the need for responsible use of antibiotics with public health campaigns. In such campaigns, the people are motivated to consult physicians for antibiotic prescriptions and comply strictly with the treatment regimens ordered by the physician (Almutairi, 2023).

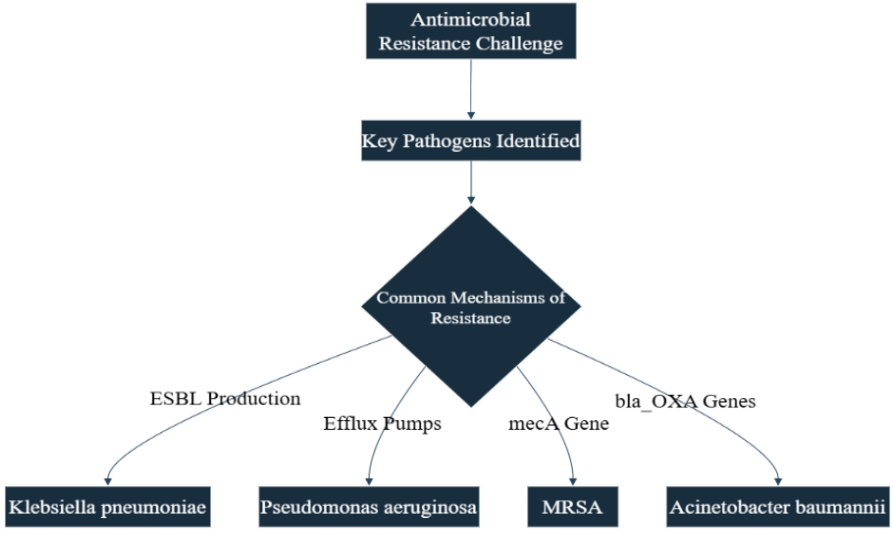


**Figure 1:** This flowchart illustrates the key pathogens associated with antimicrobial resistance (AMR) in Saudi Arabia and their common resistance mechanisms, including ESBL production,

efflux pumps, mecA gene expression, and bla_OXA genes. It highlights the primary bacterial species impacted and their contribution to the AMR burden in clinical settings.

## 6. Comparative Analysis: Regional and Global Context

The landscape of AMR in Saudi Arabia has many similarities with this phenomenon among other Gulf and Middle Eastern countries; however, it also has some distinguishing features. Therefore, it would be important to understand these peculiarities for strategizing approaches in the region towards AMR. Some of the most significant areas of comparison from the available literature include the following.

*Prevalence of Resistant Pathogen:* According to studies, Saudi Arabia shares a common resistant population across the Gulf countries, these were primarily constituted by Escherichia coli, followed by Klebsiella pneumonia and that most commonly carry genes responsible for beta-lactamase resistance as reported by Aldawsari et al. In this case, high rates of antibiotic-resistant strains were found in Riyadh with a focus on the stringent stewardship programs required to manage antimicrobial-resistant infections (Aldawsari et al., 2020). Similarly, a systematic review by Bindayna et al. indicated that Klebsiella pneumoniae in the Arabian Gulf countries had an overall high rate of resistance; thus, it is a regional challenge (Bindayna et al., 2020).

Now moving towards the development of antimicrobial stewardship programs (ASPs) within Gulf countries for a common response to the worsening AMR threat. Saudi national ASPs for antimicrobial stewardship were introduced to support the proper use of antibiotics and minimize the rates of resistance. However, some sharp differences exist based on the effectiveness and program implementation in the said coastal regions. For instance, although Saudi Arabia has made several strides in guideline development, it faces many challenges with compliance and monitoring (Aldawsari et al., 2020).

*Self-Medication Practices:* The most prevailing of the issues in Saudi Arabia, for example, according to Alduhaimi et al. (2022) is self-medication with antibiotics. This practice has also been quite widespread within the Middle East region itself which has been one more portal of entry of the antibiotic resistance. A systematic review presented an alarming rate of self-medication throughout the region in general, and Saudi Arabia at its helm (Khalifeh et al., 2017). It highlights how this situation demands education on public health that may awaken people to perils of using antibiotics irresponsibly.

*Surveillance and Reporting:* Saudi Arabia is involved in national and international surveillance networks operating the WHO's Global Antimicrobial Resistance Surveillance System (GLASS). Such participation in surveillance is important to monitor the patterns of resistance and for guiding public health strategies. Other Gulf states have different levels of engagement and capacity in AMR surveillance, which affects the richness of data gathered across the Gulf states (Aly & Balkhy, 2012).

*Resistance Mechanisms:* Mechanisms that cause AMR in Saudi Arabia are of similar types found in the rest of the Gulf and Middle Eastern nations. Examples include the production of beta-lactamases, as well as efflux pump usage. It is revealed in the findings that resistance

mechanisms, which are categorized into the production of ESBLs and carbapenems, cut across the Saudi nation and the other neighboring nations (Aly & Balkhy, 2012). This establishes a regional aspect to the issues caused by AMR.

*Education and Awareness of the Public:* Between healthcare professionals and the public, the educational program varies from one region to another. At the high school level, Saudi Arabia has educational programs to improve awareness (Almutairi, 2023). Generally, the public's knowledge of AMR remains low, just like many other countries in the region of the Middle East (Alnasser et al., 2021). This is a call for concerted education to address the situation of AMR holistically.

*Research and Collaboration:* Saudi Arabia is very active in research on AMR, providing critical data to the international body of knowledge about resistance patterns. There is also research collaboration observed in other Gulf countries, although the scope and nature of research can differ. For instance, while Saudi laboratories are very active in studying trends in resistance, other countries might have a limited research capacity or may focus on other aspects of AMR (Alkheraije, 2024).

**Table 2:** Recommended Strategies to Combat AMR in Saudi Arabia.

| Strategy | Description | Expected Outcome |
|---|---|---|
| Antimicrobial Stewardship Programs (ASPs) | Implementing guidelines for rational antibiotic use in healthcare settings. | Reduction in inappropriate antibiotic prescriptions and resistance rates. |
| Surveillance Systems | Establishing laboratory-based and electronic systems for tracking AMR patterns. | Early detection of resistance trends; data for public health policy formulation. |
| Public Awareness Campaigns | Educating the population on the risks of antibiotic misuse and the importance of prescriptions. | Improved public behavior towards antibiotics; reduction in self-medication practices. |
| One Health Approach | Coordinating AMR strategies across human, animal, and environmental health sectors. | Comprehensive understanding and mitigation of resistance transmission dynamics. |
| Advanced Molecular Techniques | Using WGS, PCR, and metagenomics for resistance mechanism identification and outbreak tracking. | Enhanced precision in diagnostics; improved understanding of resistance mechanisms. |
| Regulatory Measures | Enforcing prescription-only antibiotic sales and restricting over-the-counter antibiotic availability. | Decrease in antibiotic misuse; reduction in emergence of resistant strains. |

## 7. Future Directions in Research and Policy

The priorities for molecular epidemiological research on AMR in Saudi Arabia are critical to understanding resistance dynamics, informing public health strategies, and improving clinical outcomes. Because of the unique health-care landscape and the challenges AMR faces, the following key research priorities can be discerned. There must be characterization of

mechanisms regarding the molecular aspects explaining the emergence of AMR so targeted intervention programs could be developed. That basically means that in studying such mechanisms as characterization of resistance genes, for example, like the ESBLs, carbapenemases, studies on this character must be directed particularly among the common pathogenic groups like Klebsiella pneumoniae and Escherichia coli. Further research performed by Alhazmi et al. revealed that it is possible for isolates of K. pneumoniae to harbor both the blaNDM and blaOXA-48 resistance genes Alhazmi et al. (2022). This should be extended to include all the pathogens and resistance mechanisms.

To make it perceptible for those being incorporated of monitoring the trends of AMR, monitoring trends of AMR is necessary to know the epidemiology for resistant infections. The research must be focused on developing strong integrated surveillance systems from health settings such as hospitals and community health centers. This also goes with the point given by Alkheraije, which cited the need for concerted efforts to reduce the increasing rate of AMR in the Middle East (Alkheraije, 2024). Such systems would identify emerging resistance patterns and inform public health responses.

*Monitoring Effectiveness of ASP:* It is to be monitored regarding the efficiency of ASPs in reducing the AMR rates. Studies are to be initiated at a later stage regarding the effects of these programmes on prescription practices, outcome measures in patients and trends in resistance. Studies done by Aldawsari et al. indicate that active stewardship guidelines are necessary to curb irrational antibiotic use (Aldawsari et al., 2020). Such knowledge can be used to make policy decisions in the future.

*One Health Approach:* The only way to deal with AMR is to take a One Health approach, which incorporates human, animal, and environmental health. Research on the dynamics of transmission of resistant pathogens should be done across sectors in agriculture and veterinary medicine. Integration of data from these sectors will provide insights into factors that drive resistance and will help in coordination of interventions (Alkheraije, 2024).

The public awareness and education should be furthering to improve understanding on AMR by understanding the effectiveness of interventions for creating public awareness, this should also include research studies on the knowledge, attitudes, and behavior of healthcare providers and the community about antibiotic use and resistance in public. In such public education could be possible only possible by bringing these types of intervention, as in the case of Almutairi (Almutairi, 2023) when the effects of intervention will also be demonstrated to improve future programs.

*The Inheritance Epidemiology of Healthcare-Associated Infections:* This research should survey thorough resistant pathogenic organisms in hospitals as related to their transfer pathways and genetic divergence for efficacy in catering appropriate infection control policies necessitated increasing patient safety as infected-nature itself has turned more problematical in Saudi Arabia. A paper focusing on tuberculosis was written by Al-Ghafli and Al-Hajoj; however, their investigation describes how molecular epidemiology studies would be used to have a glimpse of the understanding of infectious diseases (Al-Ghafli & Al-Hajoj, 2018).

*Collaboration and Data Sharing:* Their coordination of researchers against healthcare providers and public health officials shall strengthen than echo to Effective Action. Networks for data sharing and collaboration will give access to augmented research surveillance capabilities-these correspond with the opinions of Shrestha et al., as this was more documented balanced collaboration on AMR research (Shrestha et al., 2022).

## 8. Conclusion

This represents one of the more important challenges to public health, even in Saudi Arabia; antimicrobial resistance mirrors this pattern at a global scale by the increased number of multi-drug-resistant pathogens, with significant impacts upon health care. The adequate surveillance of resistance trends urgently demands support from advanced molecular epidemiology. It would include combat against inappropriate use of antibiotics, which would be addressed by putting in place antimicrobial stewardship programs and public education. This would call for collaborations that bring together human, animal, and environmental health into the one-health approach, further research, and partnerships between nations to reduce the burden of AMR. All these would improve the patient outcomes, decrease the costs associated with healthcare, and reduce the burden of AMR at a global level.

Conflict of Interest

The authors declare they don't have any conflict of interest in the form of finance and other.

Author contributions

All authors reviewed and approved the final manuscript for submission and agreed to be accountable for all aspects of the work to ensure integrity and accuracy. The first author gives the concept and writes the original draft of manuscript and corresponding author supervised the manuscript overall and provided substantial critical revisions and approved the final manuscript for submission.

Acknowledgement

Authors are thankful to national antibacterial societies and world health organization for taking global action plan on epidemiology of AMR and effectiveness of antibiotics for public health challenge universally. Authors are also sincerely grateful to open access library and publisher to compile the article.

Ethical Approval

Not Applicable

Funding

No funding is received from external and internal sources

## WORKS CITED

Baron, S., Granier, S., Larvor, E., Jouy, É., Cineux, M., Wilhelm, A., … & Chauvin, C. (2017). Aeromonas diversity and antimicrobial susceptibility in freshwater an attempt to set generic epidemiological cut-off values. Frontiers in Microbiology, 8. https://doi.org/10.3389/fmicb.2017.00503

Cassini, A., Högberg, L., Plachouras, D., Quattrocchi, A., Hoxha, A., Simonsen, G., … & Monnet, D. (2019). Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the eu and the european economic area in 2015: a population-level modelling analysis. The Lancet Infectious Diseases, 19(1), 56-66. https://doi.org/10.1016/s1473-3099(18)30605-4

Garau, J. and Bassetti, M. (2018). Role of pharmacists in antimicrobial stewardship programmes. International Journal of Clinical Pharmacy, 40(5), 948-952. https://doi.org/10.1007/s11096-018-0675-z

Perovic, O., Ismail, H., & Schalkwyk, E. (2018). Antimicrobial resistance surveillance in the south african public sector. Southern African Journal of Infectious Diseases, 33(4), 118-129. https://doi.org/10.4102/sajid.v33i4.161

Silva, L., Ramos, V., Silva, L., Paraizo, J., Silva, A., Galindo, M., … & Silva, F. (2022). Indiscriminate use of antimicrobials. Ijs - International Journal of Sciences, 4(2), 39-41. https://doi.org/10.29327/229003.4.2-12

Spellberg, B., Blaser, M., Rj, G., Hw, B., Js, B., Bi, E., … & Dn, G. (2011). Combating antimicrobial resistance: policy recommendations to save lives. Clinical Infectious Diseases, 52(suppl_5), S397-S428. https://doi.org/10.1093/cid/cir153

Ungureanu, D. (2023). An overview on the structure-activity relationship in novel antimicrobial thiazoles clubbed with various heterocycles (2017-2022).. https://doi.org/10.20944/preprints202312.0276.v1

Bandy, A. and Tantry, B. (2021). Esbl activity, mdr, and carbapenem resistance among predominant enterobacterales isolated in 2019. Antibiotics, 10(6), 744. https://doi.org/10.3390/antibiotics10060744

Aldawsari, A., Tawfik, K., & Al-Zaagi, I. (2020). Antimicrobial-resistant bacteria and prescription of antibiotics at a tertiary care hospital in riyadh, saudi arabia. Cureus. https://doi.org/10.7759/cureus.12098

Alasmary, M. (2021). Antimicrobial resistance patterns and esbl of uropathogens isolated from adult females in najran region of saudi arabia. Clinics and Practice, 11(3), 650-658. https://doi.org/10.3390/clinpract11030080

Balkhi, B., Mansy, W., Alghadeer, S., Al-Nuaim, A., Alshehri, A., & Somily, A. (2018). Antimicrobial susceptibility of microorganisms causing urinary tract infections in saudi arabia. The Journal of Infection in Developing Countries, 12(04), 220-227. https://doi.org/10.3855/jidc.9517

Almutairi, K. (2023). The effects of health education on the awareness of antimicrobial resistance among high school students in riyadh, saudi arabia during 2023: a quasi-experimental study. Cureus. https://doi.org/10.7759/cureus.41639

Shorman, M. and Al-Tawfiq, J. (2013). Risk factors associated with vancomycin-resistantenterococcusin intensive care unit settings in saudi arabia. Interdisciplinary Perspectives on Infectious Diseases, 2013, 1-4. https://doi.org/10.1155/2013/369674

Al-Ghamdi, H. (2024). Prevalence of extensively and pan-drug-resistant acinetobacter spp. in nosocomial infections in western saudi arabia. Journal of Pure and Applied Microbiology, 18(2), 886-899. https://doi.org/10.22207/jpam.18.2.02

Bazaid, A., Saeed, A., Alrashidi, A., Alrashidi, A., Alshaghdali, K., Hammam, S., … & Aldarhami, A. (2021). Antimicrobial surveillance for bacterial uropathogens in ha'il, saudi arabia: a five-year multicenter retrospective study. Infection and Drug Resistance, Volume 14, 1455-1465. https://doi.org/10.2147/idr.s299846

Almutiri, A., Mohd, A., & Rahbeni, T. (2020). Antimicrobial-stewardship knowledge, attitude, and practice among professional physicians in saudi hospitals. International Journal of Research in Pharmaceutical Sciences, 11(4), 5665-5673. https://doi.org/10.26452/ijrps.v11i4.3208

Harris, S., Cole, M., Spiteri, G., Sánchez-Busó, L., Golparian, D., Jacobsson, S., … & Verbrugge, R. (2018). Public health surveillance of multidrug-resistant clones of neisseria gonorrhoeae in europe: a genomic survey. The Lancet Infectious Diseases, 18(7), 758-768. https://doi.org/10.1016/s1473-3099(18)30225-1

Warner, W., Kuang, S., Hernandez, R., Chong, M., Ewing, P., Fleischer, J., … & Xu, H. (2016). Molecular characterization and antimicrobial susceptibility of acinetobacter baumannii isolates obtained from two hospital outbreaks in los angeles county, california, usa. BMC Infectious Diseases, 16(1). https://doi.org/10.1186/s12879-016-1526-y

Wi, T., Lahra, M., Ndowa, F., Bala, M., Dillon, J., Ramón-Pardo, P., … & Unemo, M. (2017). Antimicrobial resistance in neisseria gonorrhoeae: global surveillance and a call for international collaborative action. Plos Medicine, 14(7), e1002344. https://doi.org/10.1371/journal.pmed.1002344

Hegstad, K., Mikalsen, T., Coque, T., Werner, G., & Sundsfjord, A. (2010). Mobile genetic elements and their contribution to the emergence of antimicrobial resistant enterococcus faecalis and enterococcus faecium. Clinical Microbiology and Infection, 16(6), 541-554. https://doi.org/10.1111/j.1469-0691.2010.03226.x

Jiang, T. and Chen, X. (2020). Outcome impacts due to pathogen-specific antimicrobial resistance: a narrative review of published literature. International Journal of Environmental Research and Public Health, 17(4), 1395. https://doi.org/10.3390/ijerph17041395

Ou, H., Kuang, S., He, X., Molgora, B., Ewing, P., Deng, Z., … & Xu, H. (2015). Complete genome sequence of hypervirulent and outbreak-associated acinetobacter baumannii strain lac-4: epidemiology, resistance genetic determinants and potential virulence factors. Scientific Reports, 5(1). https://doi.org/10.1038/srep08643

Dai, Y., Liu, J., Guo, W., Meng, H., Huang, Q., He, L., … & Liu, Q. (2019). Decreasing methicillin-resistant staphylococcus aureus (mrsa) infections is attributable to the disappearance of predominant mrsa st239 clones, shanghai, 2008–2017. Emerging Microbes & Infections, 8(1), 471-478. https://doi.org/10.1080/22221751.2019.1595161

Mubita, S., Simbile, W., & Mulunda, B. (2021). Characterization and antimicrobial susceptibility profiles of bacteria isolated from various specimens among mary begg health facilities. International Journal of Health Sciences and Research, 11(5), 41-52. https://doi.org/10.52403/ijhsr.20210506

Viñas, M., Tuduri, E., Galar, A., Yih, K., Pichel, M., Stelling, J., … & Galas, M. (2013). Laboratory-based prospective surveillance for community outbreaks of shigella spp. in argentina. Plos Neglected Tropical Diseases, 7(12), e2521. https://doi.org/10.1371/journal.pntd.0002521

McDermott, P., Tyson, G., Kabera, C., Chen, Y., Liu, C., Folster, J., … & Zhao, S. (2016). Whole-genome sequencing for detecting antimicrobial resistance in nontyphoidal salmonella. Antimicrobial Agents and Chemotherapy, 60(9), 5515-5520. https://doi.org/10.1128/aac.01030-16

Cardoso, A., Silva, A., Almeida, d., & Em, M. (2019). Insights on antimicrobial stewardship in the microbiology laboratory: a review. Journal of Microbiology & Experimentation, 7(1). https://doi.org/10.15406/jmen.2019.07.00237

Fouz, N., Pangesti, K., Yasir, M., Al-Malki, A., Azhar, E., Hill-Cawthorne, G., … & Ghany, M. (2020). The contribution of wastewater to the transmission of antimicrobial resistance in the environment: implications of mass gathering settings. Tropical Medicine and Infectious Disease, 5(1), 33. https://doi.org/10.3390/tropicalmed5010033

Alahmadi, T., Alahmadey, Z., Organji, S., Elbanna, K., Ahmad, I., & Abulreesh, H. (2021). First report of multi-drug-resistant staphylococcus haemolyticus in nosocomial infections in northwestern saudi arabia. Journal of Pure and Applied Microbiology, 15(2), 725-734. https://doi.org/10.22207/jpam.15.2.24

Alyamani, E., Khiyami, A., Booq, R., Majrashi, M., Bahwerth, F., & Rechkina, E. (2017). The occurrence of esbl-producing escherichia coli carrying aminoglycoside resistance genes in urinary tract infections in saudi arabia. Annals of Clinical Microbiology and Antimicrobials, 16(1). https://doi.org/10.1186/s12941-016-0177-6

Almaghrabi, M., Joseph, M., Assiry, M., & Hamid, M. (2018). Multidrug-resistantacinetobacter baumannii: an emerging health threat in aseer region, kingdom of saudi arabia. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 1-4. https://doi.org/10.1155/2018/9182747

Abdalla, J., Albarrak, M., Alhasawi, A., Al-Musawi, T., Alraddadi, B., Wali, W., … & Kurdi, A. (2023). Narrative review of the epidemiology of hospital-acquired pneumonia and ventilator-associated pneumonia in gulf cooperation council countries. Infectious Diseases and Therapy, 12(7), 1741-1773. https://doi.org/10.1007/s40121-023-00834-w

kraiem, A., Zeng, Y., Huo, X., Yang, K., kraiem, F., Qin, J., … & Chen, T. (2019). Identification of salmonella bredeney resistant to third-generation cephalosporins in saudi arabia. Frontiers in Cellular and Infection Microbiology, 9. https://doi.org/10.3389/fcimb.2019.00390

El-Tayeb, M., Ibrahim, A., Al-Salamah, A., Almaary, K., & Elbadawi, Y. (2017). Prevalence, serotyping and antimicrobials resistance mechanism of salmonella enterica isolated from clinical and environmental samples in saudi arabia. Brazilian Journal of Microbiology, 48(3), 499-508. https://doi.org/10.1016/j.bjm.2016.09.021

Mboowa, G., Sserwadda, I., & Aruhomukama, D. (2020). Re-thinking antimicrobial resistance transmission dynamics: a meta-analysis of cross-sectional studies at referral hospitals in uganda. F1000research, 9, 878. https://doi.org/10.12688/f1000research.24638.1

Faria, T. (2023). Bacterial resistance: a narrative review on staphylococcus aureus, klebsiella pneumoniae and pseudomonas aeruginosa. Research Society and Development, 12(11), e25121143640. https://doi.org/10.33448/rsd-v12i11.43640

Si, Z., Lim, H., Tay, M., Du, Y., Ruan, L., Qiu, H., … & Pethe, K. (2020). A glycosylated cationic block poly(β-peptide) reverses intrinsic antibiotic resistance in all eskape gram-negative bacteria. Angewandte Chemie, 59(17), 6819-6826. https://doi.org/10.1002/anie.201914304

Bao, Y., Sakinc, T., Laverde, D., Wobser, D., Benachour, A., Theilacker, C., … & Hüebner, J. (2012). Role of mprf1 and mprf2 in the pathogenicity of enterococcus faecalis. Plos One, 7(6), e38458. https://doi.org/10.1371/journal.pone.0038458

Chon, J., Lee, U., Bensen, R., West, S., Paredes, A., Lim, J., … & Sung, K. (2020). Virulence characteristics of meca-positive multidrug-resistant clinical coagulase-negative staphylococci. Microorganisms, 8(5), 659. https://doi.org/10.3390/microorganisms8050659

Aperce, C., Amachawadi, R., Bibber-Krueger, C., Nagaraja, T., Scott, H., Vinasco-Torre, J., … & Drouillard, J. (2016). Effects of menthol supplementation in feedlot cattle diets on the fecal prevalence of antimicrobial-resistant escherichia coli. Plos One, 11(12), e0168983. https://doi.org/10.1371/journal.pone.0168983

Fernández-Alarcón, C., Singer, R., & Johnson, T. (2011). Comparative genomics of multidrug resistance-encoding inca/c plasmids from commensal and pathogenic escherichia coli from multiple animal sources. Plos One, 6(8), e23415. https://doi.org/10.1371/journal.pone.0023415

Thabit, A. (2023). An overview of antimicrobial resistance in saudi arabia (2013–2023) and the need for national surveillance. Microorganisms, 11(8), 2086. https://doi.org/10.3390/microorganisms11082086

Sherry, N., Horan, K., Ballard, S., Silva, A., Gorrie, C., Schultz, M., … & Seemann, T. (2023). An iso-certified genomics workflow for identification and surveillance of antimicrobial resistance. Nature Communications, 14(1). https://doi.org/10.1038/s41467-022-35713-4

Kusuma, I. (2023). Revolutionizing the fight against antimicrobial resistance with artificial intelligence. Pharmacy Reports, 3(1), 53. https://doi.org/10.51511/pr.53

Ma, T., Zaheer, R., McAllister, T., Guo, W., Li, F., Yan, T., … & Guan, L. (2022). Expressions of resistome is linked to the key functions and stability of active rumen microbiome. Animal Microbiome, 4(1). https://doi.org/10.1186/s42523-022-00189-6

Sherry, N., Horan, K., Ballard, S., Silva, A., Gorrie, C., Schultz, M., … & Seemann, T. (2022). Bridging the gap between bioinformatics and the clinical and public health microbiology laboratory: an iso-accredited genomics workflow for antimicrobial resistance.. https://doi.org/10.1101/2022.05.26.493552

Seale, A., Hutchison, C., Fernandes, S., Stoesser, N., Kelly, H., Lowe, B., … & Scott, J. (2017). Supporting surveillance capacity for antimicrobial resistance: laboratory capacity strengthening for drug resistant infections in low- and middle-income countries. Wellcome Open Research, 2, 91. https://doi.org/10.12688/wellcomeopenres.12523.1

Amin, A., Pasha, M., Hoque, M., Siddiki, A., Saha, S., & Kamal, M. (2022). Methodology for laboratory-based antimicrobial resistance surveillance in animals. Veterinary World, 1066-1079. https://doi.org/10.14202/vetworld.2022.1066-1079

Saeed, D., Hasan, R., Naim, M., Zafar, A., Khan, E., Jabeen, K., … & Rao, J. (2017). Readiness for antimicrobial resistance (amr) surveillance in pakistan; a model for laboratory strengthening. Antimicrobial Resistance and Infection Control, 6(1). https://doi.org/10.1186/s13756-017-0260-6

Alnasser, A., Al-Tawfiq, J., Ahmed, H., Alqithami, S., Alhaddad, Z., Rabiah, A., … & Alnasser, A. (2021). Public knowledge, attitude and practice towards antibiotics use and antimicrobial resistance in saudi arabia: a web-based cross-sectional survey. Journal of Public Health Research, 10(4). https://doi.org/10.4081/jphr.2021.2276

Zongo, E. (2024). On-site evaluation as external quality assessment of microbiology laboratories involved in sentinel laboratory-based antimicrobial resistance surveillance network in burkina faso. Antimicrobial Resistance and Infection Control, 13(1). https://doi.org/10.1186/s13756-023-01362-5

Bindayna, K., Joji, R., Ezzat, H., & Jahrami, H. (2020). Antimicrobial-resistant genes among klebsiella pneumoniae in the arabian gulf countries: a systemic review and meta-analysis.. https://doi.org/10.21203/rs.3.rs-38813/v1

Alduhaimi, G., Alabdulkareem, M., Alhussin, G., Alhumaid, L., Basudan, S., Masud, N., … & Bosaeed, M. (2022). Awareness of antimicrobial resistance: surveillance among visitors of a tertiary care center, riyadh, saudi arabia. Saudi Journal of Health Systems Research, 2(3), 128-135. https://doi.org/10.1159/000525891

Khalifeh, M., Moore, N., & Salameh, P. (2017). Self-medication misuse in the middle east: a systematic literature review. Pharmacology Research & Perspectives, 5(4). https://doi.org/10.1002/prp2.323

Aly, M. and Balkhy, H. (2012). The prevalence of antimicrobial resistance in clinical isolates from gulf corporation council countries. Antimicrobial Resistance and Infection Control, 1(1), 26. https://doi.org/10.1186/2047-2994-1-26

Alkheraije, K. (2024). Antimicrobial resistance from one health perspective in the middle east: a systematic review. Open Veterinary Journal, 14((1) (Zagazig Veterinary Confer), 577. https://doi.org/10.5455/ovj.2024.v14.i1.53

Alhazmi, W., Aljabri, A., & Alzahrani, I. (2022). The molecular characterization of nosocomial carbapenem-resistant klebsiella pneumoniae co-harboring blandm and blaoxa-48 in jeddah. Microbiology Research, 13(4), 753-764. https://doi.org/10.3390/microbiolres13040054

Al-Ghafli, H. and Al-Hajoj, S. (2018). Quantiferon-tb gold in-tube in saudi arabia benchmarked with other sites of the middle east: a meta-analysis review. The Journal of Infection in Developing Countries, 12(09), 687-699. https://doi.org/10.3855/jidc.10311

Shrestha, P., He, S., & Legido-Quigley, H. (2022). Antimicrobial resistance research collaborations in asia: challenges and opportunities to equitable partnerships. Antibiotics, 11(6), 755. https://doi.org/10.3390/antibiotics11060755