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ARTIFICIAL INTELLIGENCE FOR ADDRESSING ANTIBIOTIC RESISTANCE IN BACTERIAL PATHOGENS: A COMPREHENSIVE REVIEW

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ABSTRACT

Antibiotic resistance (ABR) in bacterial pathogens is a major and rapidly escalating global health challenge that threatens the effectiveness of antimicrobial therapy and contributes substantially to morbidity, mortality, and healthcare costs. The emergence and dissemination of antibiotic resistance are driven by bacterial genetic mutations, horizontal transfer of antibiotic resistance genes (ARGs), and inappropriate or excessive use of antibiotics. Although conventional microbiological, phenotypic, and sequence-alignment-based approaches have played an important role in the detection and characterization of antibiotic resistance, these methods can be time-consuming, labor-intensive, and limited in their ability to rapidly interpret the increasing volume and complexity of genomic and clinical data. Furthermore, the discovery and development of new antibiotics remain challenging because of scientific, economic, and regulatory barriers, emphasizing the need for innovative computational approaches.

Artificial Intelligence (AI) and Machine Learning (ML) have emerged as promising tools for addressing these challenges by enabling rapid analysis of large-scale genomicand epidemiological datasets. This review provides a comprehensive overview of antibiotics, their historical development and the mechanisms, causes and consequences of antibiotic resistance, followed by a critical comparison of conventional and AI-based approaches for detecting antibiotic resistance in bacterial pathogens. Particular emphasis is placed on the identification, classification and annotation of ARGs and their associated genetic determinants using AI-driven methods. Various computational approaches, including Support

Vector Machines (SVM), Convolutional Neural Networks (CNN), deep learning models, and Hidden Markov Models (HMM), are discussed in relation to their applications in resistance prediction, ARG detection, bacterial genome analysis, and antimicrobial susceptibility prediction. The review also highlights the advantages of AI, including rapid and high-throughput analysis, improved prediction accuracy, integration of heterogeneous datasets, identification of previously unrecognized resistance determinants, and potential support for precision antimicrobial therapy and novel antibiotic discovery.

KEYWORDS: Artificial Intelligence**,** Antibiotic Resistance**,** Antimicrobial Resistance Genes (ARGs)**,** Machine Learning & Bacterial Pathogens.

1 INTRODUCTION

Antimicrobial resistance (AMR) is the resistant exhibited by microorganisms to antimicrobial medications, such as antibiotics, which are used to treat infectious diseases (Tang et al., 2023). AMR has emerged as one of the greatest global health concerns due to the rapid increase in AMR infections and the limited development and introduction of new antimicrobial medications to combat this growing problem (Tang *et al*., 2023).

The initiation of the golden age of natural production of antibiotic discovery was started in 1928 with the discovery of penicillin which has reached its peaks in the mid-1950s. Subsequently, a gradual decline in antibiotic discovery and development, coupled with the evolution and spread of drug resistance among human pathogens, has contributed to the current antimicrobial resistance crisis. The introduction of antibiotics into clinical practice was arguably one of the greatest medical breakthroughs of the 20th century. In addition to treating infectious diseases, antibiotics made many modern medical procedures possible, including cancer treatment, organ transplantation and open-heart surgery (Hutchings *et al*., 2019). Antibiotics have therefore transformed the treatment of bacterial infections and saved millions of lives. However, the widespread and inappropriate use of antibiotics, combined with the natural evolution and adaptability of bacteria, has resulted in the rapid emergence and dissemination of antibiotic resistance.

The mechanisms by which bacteria develop resistance to antibiotics, including drug inactivation, modification of antibiotic targets, reduced drug uptake and active drug efflux. Many of these mechanisms are mediated by antibiotic resistance genes (ARGs), which can be transferred between bacteria, particularly through mobile genetic elements such as plasmids (Reygaert, 2018)). The increasing spread of multidrug-resistant (MDR) bacteria has created a

major global health challenge, with some bacterial pathogens exhibiting resistance even to last-resort antibiotics. Therefore, there is an urgent need to develop new approaches for understanding, detecting and controlling AMR. Accurate and rapid identification of ARGs is particularly important for understanding resistance mechanisms, monitoring their transmission and developing effective strategies to control antibiotic-resistant infections.

Although antibiotics remain essential for combating bacterial infections, their misuse, overuse, and easy accessibility through over-the-counter availability have accelerated the spread of AMR at a rate faster than the development of new antimicrobial agents. This has contributed to the emergence of multidrug-resistant bacteria and created a global health crisis in which the available options for treating MDR infections are increasingly limited (Sabtu *et al*., 2015).

An important first step in combating this crisis is the rapid and efficient identification of bacterial antibiotic resistance. Early and accurate detection can help in understanding resistance mechanisms, developing strategies to overcome resistance, and reducing inappropriate antimicrobial use through targeted and effective prescription. In this context, artificial intelligence (AI) has emerged as a promising and innovative approach for the rapid and accurate identification and prediction of AMR (Sakagianni *et al*., 2023).

The principle of "survival of the fittest" reflects the remarkable genetic plasticity of bacterial pathogens, which enables them to respond to antibiotic pressure through mutational adaptation, acquisition of genetic material and alteration of gene expression. These processes can produce resistance to virtually all antibiotics currently available in clinical practice. Therefore, understanding the biochemical and genetic basis of antibiotic resistance is of paramount importance for designing strategies to limit the emergence and spread of resistance and for developing innovative therapeutic approaches against multidrug-resistant organisms (Munita and Arias, 2016).

The World Health Organization (WHO) has identified a priority list of bacterial pathogens for which the development of novel antibiotics is urgently required. However, the discovery and introduction of new antibiotics are time-consuming, costly and challenging processes. According to the WHO report on antibacterial agents in clinical development, only a limited number of novel antibiotics have been approved since 2014. This highlights the critical need for new antimicrobial agents. In recent years, artificial intelligence has been increasingly applied to drug development following major advances in computational technologies and machine learning. AI has the potential to improve the efficiency of novel antibiotic discovery by rapidly analyzing large and complex datasets and identifying promising antimicrobial

candidates. In addition to drug discovery, AI approaches have been applied to the prediction of resistance mechanisms, identification of antibiotic resistance genes, antimicrobial susceptibility prediction, antimicrobial peptide discovery, phage therapy and antibiotic stewardship.

The promising opportunity to address the fast-growing challenge of antibiotic resistance is developed with the integration of AI with microbiology, genomics and clinical research. AI-based approaches can complement conventional methods by enabling rapid analysis and prediction of resistance-associated genetic and phenotypic features. The development and significance of antibiotics, the emergence and mechanisms of antibiotic resistance, the difficulties with traditional methods and the discovery of new antibiotics, and the use of AI and machine learning techniques for the detection and prediction of antibiotic resistance and ARGs in bacterial pathogens are all covered in this review.

2. Significant Factors Causing Antimicrobial Resistance (AMR)

Antimicrobial resistance (AMR) occurs when bacteria, fungi, viruses and parasites in humans and animals do not react to antimicrobial treatments, allowing the microorganism to persist within the host. The overuse and misuse of antibiotics, continues to be the key factor causing the current crisis and raising the problem of antimicrobial resistance worldwide. It is driven by a combination of biological, social, economic and environmental factors. Understanding these factors is essential for controlling resistant infections and preserving the effectiveness of existing antimicrobial drugs.

2. 1 Overuse and Inappropriate Use of Antibiotics

Excessive and inappropriate antibiotic use, particularly for viral infections such as the common cold and influenza, accelerates the development of resistant bacteria. Self-medication, incomplete treatment courses, over-the-counter availability, and empirical prescribing without adequate diagnostic support further contribute to AMR (Peterson *et a*l., 2023).

2.2 Poor Infection Prevention and Control

Inadequate sanitation, overcrowding, poor hand hygiene, and improper sterilization in healthcare settings facilitate the spread of resistant pathogens. Healthcare-associated infections (HAIs), including those caused by MRSA and *Clostridium difficile*, are common where infection control measures are insufficient. Limited access to effective antibiotics in low- and middle-income countries also promotes resistance (Mulani *et al*., 2019).

2.3 Spread of Resistant Pathogens and Globalization

International travel, migration, and global food trade enable rapid dissemination of resistant microorganisms across countries. Resistant pathogens such as NDM-1-producing bacteria, CRE, *Salmonella*, and *Campylobacter* spread through infected individuals, contaminated food, and antibiotic-treated livestock, highlighting the need for global AMR surveillance [Walia *et al*., 2023].

2.4 Pharmaceutical Waste and Environmental Pollution

Discharge of antibiotic-contaminated waste from hospitals, pharmaceutical industries, and agriculture introduces antimicrobial residues and resistant bacteria into soil and water. These environments act as reservoi1rs of resistance genes, which spread rapidly through horizontal gene transfer (HGT), contributing to the emergence and persistence of AMR (Larsson & Flach, 2022).

3. Methods by which Bacteria show antibiotic resistance

Antibiotic resistance mainly occurs through drug inactivation, reduced drug uptake, changes in drug targets, and increased drug efflux. These mechanisms are often controlled by genetic mutations and antibiotic resistance genes (ARGs), which can be carried on plasmids and transferred between different bacteria (Muteeb *et al.,* 2023). Identifying ARGs is therefore important for understanding resistance and developing new antibiotics. Conventional NGS-based methods mainly depend on sequence alignment and may miss novel ARGs or produce false positives. Artificial intelligence (AI), particularly machine learning (ML) and deep learning (DL), offers a promising alternative by learning patterns from known ARG sequences and helping detect and annotate new resistance genes. Thus, AI can improve the analysis of large genomic datasets and support better understanding of antibiotic resistance (Roy et al., 2023).

The role of genetic elements such as plasmids, transposons, integrons, and chromosomal mutations in the acquisition and spread of resistance traits. The chapter also explores the horizontal gene transfer (HGT) mechanisms, which allow resistance genes to be transmitted between and among species in a variety of situations, including clinical, agricultural, and ecological settings. Furthermore, the impact of these genetic dynamics on existing and future therapeutic techniques is critically examined, including the development of novel antimicrobials, phage therapy, CRISPR-based gene editing, and antibiotic stewardship programs. This chapter intends to improve understanding of AMR's genetic architecture and

suggest novel approaches to combating the rise of drug-resistant infections by combining molecular biology and clinical relevance.

Machine learning (ML), as a subfield of AI that endows a computer the ability to predict certain outcomes through a learned model using a large amount of experimental data, also known as training data (Dey 2016). The CARD (Comprehensive Antibiotic Resistance Database) (Alcock *et al*. 2020) and MegaRES (Doster et al. 2020) are among the many databases that collect peer-reviewed AMR determinants data, including the species of bacteria, a brief annotation on the mechanism of action of the determinant on the class of antibiotics and the corresponding DNA and protein sequences. These data could be used to train algorithms to generate a learnt model to reliably identify known or novel AMR (Arango-Argoty *et al.* 2018) and even predict the minimum inhibitory concentration (MIC) of MDR bacteria.

Because of their extraordinary genetic adaptability, bacteria can react to a variety of environmental dangers, such as the presence of antibiotic compounds that could endanger their survival. Because they share an ecological niche with species that produce antibiotics, bacteria have developed ancient defense mechanisms to withstand the detrimental effects of antibiotics. As a result, their innate resistance allows them to flourish in the presence of antibiotics. From an evolutionary standpoint, bacteria employ two main genetic strategies to respond to the antibiotic action. First is to acquire mutations in a gene or genes frequently linked to the compound's mechanism of action, and second one is through horizontal gene transfer to obtain foreign DNA coding for resistance determinants (Vaidya, 2011).

3.1 Mutational Resistance

In this scenario, a subset of bacterial cells derived from a susceptible population develops mutations in genes that affect the activity of the drug, resulting in preserved cell survival in the presence of the antimicrobial molecule. Once a resistant mutant emerges, the antibiotic eliminates the susceptible population, and the resistant bacteria predominate. In many instances, mutational changes leading to resistance are costly to cell homeostasis (i.e., decreased fitness) and are only maintained if needed in the presence of the antibiotic. In general, mutations resulting in antimicrobial resistance alter the antibiotic action via one of the following mechanisms: (i) modifications of the antimicrobial target (decreasing the affinity for the drug; see below), (ii) a decrease in the drug uptake, (iii) activation of efflux mechanisms to extrude the harmful molecule, or (iv) global changes in important metabolic

pathways via modulation of regulatory networks. Thus, resistance arising due to acquired mutational changes is diverse and varies in complexity. In this chapter, we will give several examples of antimicrobial resistance arising through mutational changes (Munita JM.Arias CA. 2016).

3.2 Horizontal gene transfer (HGT).

Classically, bacteria acquire external genetic material through three main strategies: (i) transformation (incorporation of naked DNA), (ii) transduction (phage mediated), and (iii) conjugation. Transformation is perhaps the simplest type of HGT, but only a handful of clinically relevant bacterial species are able to naturally incorporate naked DNA to develop resistance. Emergence of resistance in the hospital environment often involves conjugation, a very efficient method of gene transfer that involves cell-to-cell contact and is likely to occur at high rates in the gastrointestinal tract of humans under antibiotic treatment. As a general rule, conjugation uses mobile genetic elements (MGEs) as vehicles to share valuable genetic information, although direct transfer from chromosome to chromosome has also been well characterized (Manson JM, Hancock LE, Gilmore MS. 2010). The most important MGEs are plasmids and transposons, both of which play a crucial role in the development and dissemination of antimicrobial resistance among clinically relevant organisms (Munita JM.Arias CA. 2016).

4. Artificial Intelligence-Based Diagnostic Tools for Early Detection of Antibiotic Resistance

Antibiotic resistance represents one of the greatest challenges to global public health, as it reduces the effectiveness of antibiotic treatments and increases the risk of difficult-to-treat infections. In this context, artificial intelligence (AI)-based diagnostic tools can analyze large volumes of data, often with greater accuracy than humans, enabling faster and more targeted diagnoses. One of the main applications of AI in the diagnosis of antibiotic resistance is the analysis of microscopic images. Machine learning algorithms can be trained to recognize specific features in images (Anahtar *et al*., 2021) of bacterial cultures that are indicative of antibiotic resistance. For example, a study conducted by Hayashi et al. (Hayashi-Nishino *et al*., 2022) focused on using Convolutional Neural Networks (CNNs) to identify drug-resistant bacterial cells in transmission electron microscope (TEM) images without the need for antibiotic exposure. Their study revealed that drug-resistant strains maintain morphological changes even in the absence of drugs, suggesting a link between genetic changes during the acquisition of drug resistance and morphological changes. CNNs and Support Vector

Machines (SVMs) have been widely explored for their ability to identify complex patterns in microbiological and genetic data (Lu *et al.,* 2022).

5. ARG -AI in identification of ARG genes

Conventional ARG detection methods mainly depend on sequence alignment and reference databases. Although useful, these methods may have difficulty detecting novel resistance genes and can produce false-positive or false-negative results. The rapid growth of next-generation sequencing (NGS) has generated large amounts of genomic data, creating a need for faster and more effective analytical approaches. Artificial intelligence (AI), including machine learning (ML) and deep learning (DL), offers promising tools for analysing these complex datasets and identifying, classifying, and annotating ARGs. Thus, AI-based approaches have the potential to improve ARG detection and contribute to better surveillance and management of antibiotic resistance (Olatunji, *et al*., 2024).

Annotation is the process of assigning biological information to the identified gene. Once an Antibiotic resistance genes (ARGs) are specific genes present in bacteria that enable them to survive the action of antibiotics. These genes produce proteins that destroy antibiotics, alter antibiotic targets, reduce drug uptake, or actively pump antibiotics out of bacterial cells. The rapid spread of ARGs among pathogenic bacteria has become one of the greatest threats to global public health. Therefore, early identification and accurate annotation of ARGs are essential for disease diagnosis, surveillance, and the development of new antimicrobial therapies.

Traditionally, ARGs are identified by comparing bacterial DNA sequences with known resistance genes stored in databases such as Comprehensive Antibiotic Resistance Database (CARD), ResFinder, and ARG-ANNOT. Although these conventional methods are reliable, they are time-consuming and often fail to detect newly evolved or highly divergent ARGs. Artificial Intelligence (AI), particularly Machine Learning (ML) and Deep Learning (DL), has revolutionized ARG identification by enabling rapid, accurate, and large-scale analysis of genomic data.

6. Workflow of AI-Based ARG Identification

The AI-based identification process generally follows these steps:

1. **Sample collection:** Bacterial isolates or environmental samples are collected.
2. **DNA sequencing:** Whole-genome sequencing or metagenomic sequencing generates DNA sequence data.

3. **Data preprocessing:** Low-quality sequences are removed and cleaned.
4. **Feature extraction:** AI converts DNA or protein sequences into numerical features such as k-mers, amino acid composition, conserved motifs, or sequence embeddings.
5. **AI prediction:** Machine learning or deep learning models classify genes as resistant or non-resistant.
6. **Gene annotation:** The identified genes are matched with ARG databases and annotated with gene names, resistance mechanisms, and antibiotic classes.
7. **Validation:** Predictions are confirmed through laboratory experiments or comparison with curated databases.

Traditional ARG identification methods use either direct read mapping or assembly of NGS reads into contigs, followed by comparison with reference databases. These approaches may miss novel ARGs, produce false-positive or false-negative results, and may not clearly distinguish chromosomal genes from plasmid-borne genes. AI-based methods can analyze raw NGS reads or assembled genes to identify and validate potential ARGs. Machine learning and deep learning approaches, including SVM, neural networks, HMM, random forest, and XGBoost, can recognize sequence patterns associated with antibiotic resistance and improve ARG detection and annotation (Roy *et al*., 2023).

7. AI tools used in ARG identification

AI Models Used for ARG Prediction

Several AI approaches are commonly employed:

- **Deep Learning (DL)**
- **Hidden Markov Models (HMM)**
- **Support Vector Machine (SVM):** Separates resistant and non-resistant genes based on sequence patterns.

7.1 Deep Learning (DL)

Deep learning (DL) methods use neural networks to learn complex patterns from large biological datasets and are increasingly used for ARG identification and annotation. One important tool is DeepARG, which can detect ARGs from both assembled sequences and short NGS reads and classify them into different antibiotic resistance groups with high accuracy (Arango-Argoty et al., 2018). Newer approaches such as PLM-ARG combine protein language models with machine learning to improve ARG detection and classification (Wu et al., 2023). CNN-based systems such as HMD-ARG can further classify ARGs

according to antibiotic class, resistance mechanism, and gene type, showing accuracies above 90% (Wu et al., 2023). DL is also being applied to natural language processing (NLP) to identify gene–antibiotic relationships from scientific literature, which can help improve and update ARG databases. Overall, DL provides a powerful approach for detecting, classifying, and annotating both known and potentially novel ARGs.

Deep learning, a branch of Artificial Intelligence (AI), is increasingly used to determine whether a bacterial isolate is susceptible or resistant to antibiotics. Traditionally, bacteria isolated from a patient are tested using Antimicrobial Susceptibility Testing (AST) or by measuring the Minimum Inhibitory Concentration (MIC), which indicates the lowest concentration of an antibiotic needed to stop bacterial growth. However, these methods usually analyze the bacterial population as a whole and may not detect resistant cells present in small numbers. Deep learning overcomes this limitation by analyzing microscopic images of individual bacterial cells. In this method, bacteria are first exposed to a high concentration of an antibiotic, causing visible changes in their chromosomes and cell structure. Thousands of images of both antibiotic-susceptible and antibiotic-resistant bacteria are used to train a deep learning model. The AI learns to recognize the unique patterns associated with each type of response. When a new bacterial sample is tested, the trained model compares its images with the known patterns and rapidly predicts whether the bacteria are susceptible or resistant. This approach can even detect resistance at the single-cell level, where not all bacterial cells respond equally to antibiotics. As a result, deep learning provides faster, more accurate identification of antibiotic resistance, helping doctors choose the most effective treatment for patients.

7.1.2 Identification of Plasmid Sequences

Plasmids are important agents of transfer of antibiotic resistance genes (ARGs) between bacteria. Therefore, identifying plasmid sequences become necessary to identify the possible spread of ARGs. However, distinguishing plasmid DNA from chromosomal DNA is difficult, especially when genome assemblies are incomplete. AI-based methods such as PlasFlow, DeepPlasmid, and PPR-Meta use deep learning to identify plasmid sequences (Olatunji et al., 2024).

7.2 Hidden Markov Models (HMM)

Hidden Markov Models (HMMs) are computational methods used to identify ARGs by recognizing characteristic patterns in protein or DNA sequences. HMM models trained from known ARG families can identify resistance genes and predict their possible origin with high sensitivity and specificity, often reaching 97–99% accuracy (Lakin *et al*., 2019). HMMs have

also been combined with specific sequence markers to detect antimicrobial resistance genes, toxins, and virulence factors directly from NGS reads. Thus, HMMs are useful for accurate ARG detection, particularly when sequence patterns are conserved within resistance-gene families.

7.3 Support Vector Machines (SVM)

Support Vector Machine (SVM) is a machine-learning method useful for classifying biological sequences, especially when the datasets are large and complex. SVM models have been used to identify and classify β-lactamases, which are major enzymes responsible for β-lactam antibiotic resistance. One study classified β-lactamases into different groups with 82–97% accuracy using protein sequence features (Srivastava et al., 2018). SVM has also been used to detect and classify antibiotic resistance efflux pump proteins into major families such as ABC, MFS, SMR and MATE, with high accuracy (Pandey et al., 2020). These studies demonstrate that SVM can be a useful AI tool for identifying important antibiotic resistance mechanisms from protein sequences.

8. Advantages of Artificial Intelligence

Artificial Intelligence (AI) enables rapid analysis of large and complex genomic, clinical, and microbiological datasets, making it a valuable tool for detecting and predicting antibiotic resistance. AI and machine learning models can identify and classify antibiotic resistance genes (ARGs), predict antimicrobial susceptibility, recognize resistance patterns, and support rapid clinical decision-making. AI can also assist in the discovery of novel antibiotics by screening large compound libraries and predicting potential antibacterial activity. In addition, AI-based surveillance can support the early detection and monitoring of emerging AMR trends.

9. Applications

AI-based ARG identification has a wide range of applications across healthcare, environmental, and research settings. It is used in clinical microbiology laboratories for rapid detection of resistance genes and supports hospital infection surveillance by monitoring the spread of resistant pathogens.

10. Challenges

Despite its potential, AI-based approaches face several limitations. Their accuracy depends strongly on the quality, size and diversity of available datasets, while incomplete or biased data can lead to unreliable predictions. Lack of standardized datasets and resistance

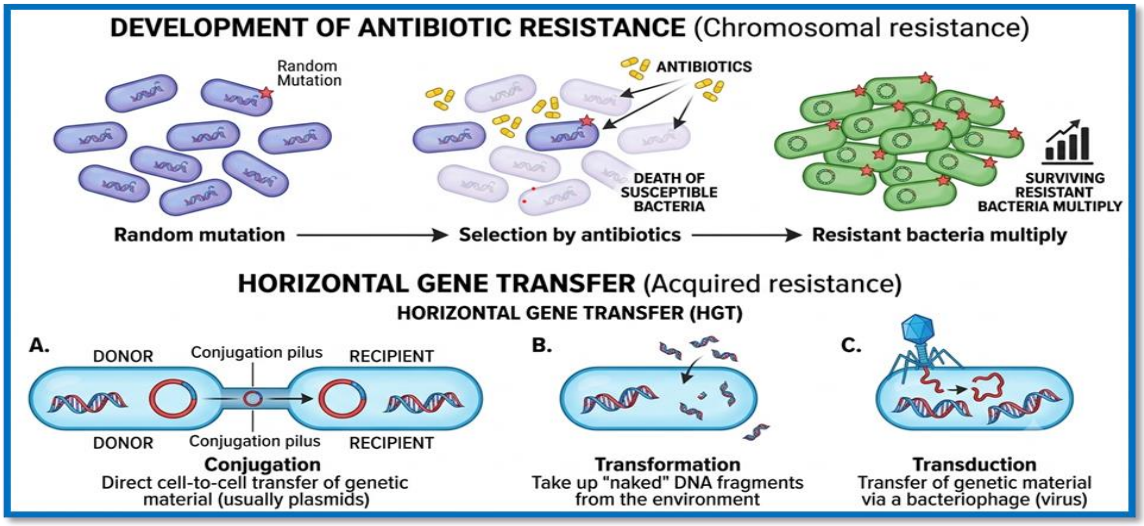
classifications also makes comparison between models difficult. Complex models, particularly deep learning approaches, may have limited interpretability, making their predictions difficult to explain. High computational requirements, limited clinical validation, and difficulties in detecting novel ARGs further restrict widespread application. Therefore, AI predictions require experimental and clinical validation before routine implementation (Olatunji et al., 2024).

11. Future Perspectives

The future of AI in antimicrobial resistance (AMR) research is promising. AI can help identify new antibiotic resistance genes (ARGs), predict resistance mechanisms, and improve AMR surveillance. When combined with whole-genome sequencing and metagenomics, AI can support faster detection of resistant bacteria and outbreaks. It may also help discover new antibiotics and predict the most effective treatment for individual patients.

AI-based tools can also improve antimicrobial susceptibility testing (AST). Disk diffusion tests are commonly used, but manual measurement can lead to errors and differences between users. An offline smartphone application developed by Pascucci et al. (2021) uses a phone camera to capture and analyze antibiogram images. It measures inhibition zones and classifies bacterial susceptibility automatically.

The application showed 90% agreement with hospital automated AST systems and 98% agreement with manual measurements. Such low-cost and portable AI tools could be especially useful in resource-limited settings. Overall, better datasets, standardized methods, experimental validation, and collaboration between AI and clinical researchers can make AI an important tool in the fight against AMR (Pascucci, *et al 2021)*.



PLM-ARG is an artificial intelligence (AI)-based tool that uses a large protein language model to identify antibiotic resistance genes (ARGs) and classify the type of antibiotic resistance they confer. Unlike traditional sequence similarity methods, which often fail to detect unknown or highly different ARGs, PLM-ARG learns patterns from protein sequences and can identify both known and novel resistance genes. Trained on a dataset containing over 28,000 ARGs across 29 resistance categories, the model achieved very high prediction accuracy and outperformed existing ARG identification tools. This approach improves the detection of antibiotic resistance in clinical and environmental samples, supporting better antimicrobial resistance surveillance and research (Wu et al., 2023).

Artificial intelligence (AI) is playing an important role in the fight against antibiotic resistance by improving the detection and analysis of antibiotic resistance genes (ARGs). Traditional sequence alignment methods often fail to identify new or highly different ARGs, whereas AI can recognize complex patterns in genetic data with greater accuracy. AI techniques can identify and classify ARGs from bacterial genomes and plasmids, predict potential resistance genes, and help discover new antibiotic targets. These advancements support faster and more reliable antimicrobial resistance surveillance and contribute to the development of effective antibiotics (Olatunji *et al*., 2024).

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