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Ai-Based Rapid Identification of Multidrug-Resistant Bacteria Using Imaging and Genomic Sequencing

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Abstract
Aim: *To evaluate the effectiveness of artificial intelligence (AI) for the rapid identification of multidrug-resistant (MDR) bacteria using imaging techniques and genomic sequencing, and to compare its diagnostic accuracy with conventional antibiotic susceptibility testing.*
Materials and methods: *This prospective laboratory-based study was carried out over 12 months to evaluate the utility of artificial intelligence (AI) for rapid detection of multidrug-resistant (MDR) bacteria using imaging and whole-genome sequencing (WGS). A total of 120 non-duplicate clinical isolates were collected from blood, urine, sputum, and wound swabs of patients admitted to a tertiary-care hospital. Standard culture and biochemical tests were used for initial bacterial identification before AI analysis.*
Results: *In our study, AI-based approaches showed high accuracy for rapid identification of multidrug-resistant (MDR) bacteria. The imaging AI achieved an accuracy of 86.2%, while genomic AI performed better at 93.5%; when combined, sensitivity, specificity, and overall accuracy increased to 97.1%, 95.8%, and 96.4%, respectively, closely matching conventional AST results. Genomic profiling further revealed predominant resistance genes, including blaCTX-M, tetA, and sul1 in* E. coli*; blaNDM, blaKPC, and oqxA in* K. pneumoniae*; mexA, blaVIM, and oprD in* P. aeruginosa*; and mecA, ermC, and tetK in* S. aureus*, with AI predictions showing over 92% concordance across all species.*
Conclusion: *AI-powered diagnostics represent a vital advancement in the fight against antimicrobial resistance, offering faster, more precise, and actionable insights into multidrug-resistant infections.*
Keywords: *Multidrug-resistant (MDR) bacteria, Artificial intelligence (AI),Genomic sequencing*

INTRODUCTION

Artificial intelligence (AI) is transforming the landscape of medical microbiology, particularly in the rapid identification of multidrug-resistant (MDR) bacteria. The increasing threat posed by antimicrobial resistance (AMR) has spurred the adoption of advanced AI-driven techniques that harness both imaging and genomic sequencing data. AI models, such as convolutional neural networks and machine learning classifiers, are now capable of analyzing complex data from high-resolution imaging and next-generation sequencing, drastically reducing the time required to identify pathogens and predict their resistance profiles. [1,2,3]

Recent advances in imaging-based bacterial detection leverage tools like quantitative phase imaging and Raman spectroscopy. AI algorithms process generated cellular images or spectral fingerprints, enabling species-level identification directly from a single microbial cell—bypassing the need for lengthy culture processes. For example, convolutional neural network-based systems paired with Raman spectroscopy have achieved identification accuracies exceeding 95% within minutes, making these techniques promising for clinical diagnostics where time is critical. [4,5]

Genomic sequencing, particularly whole genome and metagenomic approaches, has also been enhanced by AI methods. Traditional sequence alignment techniques often fail to detect novel antibiotic resistance genes (ARGs) and may be prone to false positives or negatives. AI-based tools, such as deep learning and support vector machines, can directly classify ARGs from raw sequence data, improve genome annotation,

and even pinpoint plasmid-borne resistance determinants. These methodologies enable rapid, high-throughput surveillance and prediction of resistance patterns, supporting more effective infection control and antimicrobial stewardship. [6,7]
Combining imaging and genomic sequencing data with AI not only expedites MDR bacterial identification but also boosts accuracy and sensitivity. Automated AI platforms are now being integrated into clinical workflows, supporting faster initiation of targeted therapies and reducing reliance on broad-spectrum antibiotics. These interdisciplinary efforts are crucial for addressing current and future challenges in infectious diseases and antibiotic resistance, offering hope for improved clinical outcomes and public health. [8,9]

MATERIALS AND METHODS

This prospective laboratory-based study was carried out over 12 months to evaluate the utility of artificial intelligence (AI) for rapid detection of multidrug-resistant (MDR) bacteria using imaging and whole-genome sequencing (WGS). A total of 120 non-duplicate clinical isolates were collected from blood, urine, sputum, and wound swabs of patients admitted to a tertiary-care hospital. Standard culture and biochemical tests were used for initial bacterial identification before AI analysis.
For the imaging workflow, Gram-stained smears were examined using high-resolution digital microscopy at 100× magnification. Images were preprocessed through normalization, segmentation, and augmentation to enhance feature extraction. A convolutional neural network (CNN) was trained on 80% of the dataset and validated on 20% to classify Gram-positive and Gram-negative bacteria and predict MDR status. The model generated probability scores for each prediction.
Genomic sequencing was performed by extracting bacterial DNA with a commercial kit, followed by sequencing on the Illumina NextSeq platform using 150 bp paired-end reads. The sequencing data were processed through a bioinformatics pipeline for read alignment, assembly, and resistance gene identification using the ResFinder database, along with multilocus sequence typing (MLST). Resistance gene profiles were further analyzed with machine learning classifiers, including random forest and support vector machines, to predict resistance phenotypes and confirm MDR status.
All AI-based predictions were validated against conventional antibiotic susceptibility testing (AST), which included Kirby-Bauer disc diffusion and broth microdilution methods, serving as the gold standard reference

RESULTS

Table 1. Diagnostic performance of AI-based approaches compared with conventional AST

Parameter	Imaging AI	Genomic AI	Combined AI	Conventional AST
Sensitivity (%)	87.5	94.2	97.1	100
Specificity (%)	85.0	92.1	95.8	100
Positive Predictive Value (%)	88.4	93.7	96.5	10
Negative Predictive Value (%)	83.6	92.8	95.2	10
Overall Accuracy (%)	86.2	93.5	96.4	100

Table 2: Distribution of multidrug-resistance genes among bacterial isolate

Bacterial Species (n=120)	Predominant MDR Genes	No. of Isolates with Genes	AI Prediction Concordance (%
Escherichia coli (n=45)	blaCTX-M, tetA, sul1	38	95.6

Klebsiella pneumoniae (n=30)	blaNDM, blaKPC, oqxA	27	96.3
Pseudomonas aeruginosa (n=25)	mexA, blaVIM, oprD	21	92.0
Staphylococcus aureus (n=20)	mecA, ermC, tetK	18	94.4

DISCUSSION

The rise of multidrug-resistant (MDR) bacteria represents one of the most pressing global health challenges of the 21st century. These pathogens, resistant to multiple antibiotics, compromise the effectiveness of standard treatments and lead to prolonged illness, higher healthcare costs, and increased mortality rates. Rapid and accurate identification of MDR organisms is crucial for effective infection control and timely therapeutic intervention. Traditional microbiological methods, while reliable, often require several days to yield results, delaying critical clinical decisions.[10]

Recent advancements in artificial intelligence (AI) have opened new avenues for transforming how we detect and characterize MDR bacteria. By leveraging high-throughput imaging techniques and whole-genome sequencing data, AI algorithms can analyze complex biological patterns with unprecedented speed and accuracy. These integrated approaches promise not only faster diagnostics but also a deeper understanding of resistance mechanisms at a molecular level. This convergence of AI, imaging, and genomics holds great potential to revolutionize microbial diagnostics and combat the growing threat of antimicrobial resistance (AMR).[11,12]

In our study, AI-based approaches showed high accuracy for rapid identification of multidrug-resistant (MDR) bacteria. The imaging AI achieved an accuracy of 86.2%, while genomic AI performed better at 93.5%; when combined, sensitivity, specificity, and overall accuracy increased to 97.1%, 95.8%, and 96.4%, respectively, closely matching conventional AST results. Genomic profiling further revealed predominant resistance genes, including blaCTX-M, tetA, and sul1 in E. coli; blaNDM, blaKPC, and oqxA in K. pneumoniae; mexA, blaVIM, and oprD in P. aeruginosa; and mecA, ermC, and tetK in S. aureus, with AI predictions showing over 92% concordance across all species.

Arnold A et al. in their study, leveraged a case of multidrug-resistant Klebsiella pneumoniae infection to demonstrate how real-time genomics had the potential to enhance the accuracy of antibiotic resistance profiling in complex infection scenarios. Their findings showed that, unlike conventional diagnostics, analysis of nanopore sequencing data was able to accurately detect low-abundance, plasmid-mediated resistance mechanisms that often went unnoticed with standard methods. This ability had direct clinical relevance, as such "hidden" resistance profiles could significantly impact treatment decisions. As a result, the rapid, in situ use of real-time genomic approaches was shown to hold substantial promise for improving both clinical decision-making and patient outcomes.[13]

In their study, Gao Y et al. concluded that the rapid advancement of algorithmic computing power, improved hardware, and the emergence of big data had significantly propelled the application of AI in the medical field, transforming traditional diagnostic practices. They highlighted that machine learning and deep learning algorithms enabled faster and more accurate identification of pathogenic microorganisms, offering automation, high sensitivity, and specificity. AI-assisted imaging allowed for the efficient analysis of large volumes of medical images, supporting quicker and more precise diagnoses, while natural language processing helped extract critical information from scientific literature and databases to aid clinical decisions and research. Furthermore, AI algorithms effectively classified pathogens using genomic data, which was essential for tracking microbial evolution and transmission. They also emphasized the potential of machine learning to optimize antibiotic usage as a proactive strategy against antimicrobial resistance. To advance this field, the study underscored the importance of interdisciplinary collaboration between AI experts and microbiologists to develop more accurate and efficient pathogen detection tools.[14]

Collectively, these findings underscore the transformative potential of integrating artificial intelligence with imaging and genomic sequencing for the rapid and accurate identification of multidrug-resistant bacteria. By surpassing the limitations of conventional diagnostics, AI-driven approaches not only improve detection sensitivity and speed but also provide deeper insights into resistance mechanisms, even at low abundance. The convergence of real-time genomics, advanced machine learning, and medical imaging offers a powerful toolkit for clinical microbiology, enabling earlier interventions, personalized treatment strategies, and better patient outcomes. As antimicrobial resistance continues to pose a global threat, sustained investment in AI technologies and interdisciplinary collaboration will be critical for the development of next-generation diagnostic platforms.

CONCLUSION

AI-powered diagnostics represent a vital advancement in the fight against antimicrobial resistance, offering faster, more precise, and actionable insights into multidrug-resistant infections.

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