



AI-Driven Strategies for Combating Antimicrobial Resistance: Innovations in Rapid Diagnostics, Precision Treatment, and Phage Therapy

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ABSTRACT

Antimicrobial resistance (AMR) threatens the effective prevention and treatment of infectious diseases. Conventional culture-based identification and antimicrobial susceptibility testing (AST) remain essential, but turnaround time can delay targeted treatment and prolong empirical antimicrobial use. Artificial intelligence (AI), machine learning, genomic analysis, and rapid diagnostic platforms may help interpret complex microbiological data, identify resistance-associated patterns, support surveillance, and prioritise antimicrobial candidates. This narrative review examines how AI may be integrated with rapid diagnostics, genomic and phenotypic resistance assessment, antimicrobial discovery, antimicrobial stewardship, and bacteriophage therapy. AI-assisted analysis may improve the efficiency of selected laboratory workflows; however, a predicted resistance profile is not equivalent to a validated phenotypic result, and computationally identified drug candidates require experimental and clinical evaluation. Bacteriophages may provide a complementary, highly targeted option for selected bacterial infections, while AI could assist research into phage–host interactions and candidate selection. Major barriers include dataset bias, limited external validation, interpretability, cost, privacy, regulatory requirements, and unequal access to digital infrastructure. AI should therefore augment—not replace—microbiologists, clinicians, validated laboratory procedures, and evidence-based antimicrobial stewardship. Carefully designed prospective studies and implementation research are needed to determine whether these technologies improve patient outcomes and are feasible across diverse healthcare settings.

Keywords: Antimicrobial resistance; artificial intelligence; machine learning; rapid diagnostics; antimicrobial susceptibility testing; antimicrobial stewardship; bacteriophage therapy; precision medicine.

1. INTRODUCTION

Antimicrobial resistance occurs when bacteria and other microorganisms acquire or develop mechanisms that reduce their susceptibility to medicines that previously controlled them. Resistant infections can complicate treatment, increase the risk of adverse outcomes, and place additional demands on healthcare systems. AMR is driven by interacting factors, including inappropriate antimicrobial use, transmission of resistant organisms, gaps in infection prevention, and the spread of resistance determinants. Addressing it requires coordinated action across clinical care, microbiology laboratories, public health, and antimicrobial stewardship.

Culture, organism identification, and phenotypic AST remain central to bacterial infection management. Depending on the organism and workflow, these procedures may require substantial time. Molecular methods can detect selected pathogens or resistance determinants more rapidly, but their scope is limited by target selection and the resistance mechanisms included in the assay. A rapid result therefore does not always provide a complete susceptibility profile.

AI methods can analyse large and complex datasets, including laboratory measurements, genomic sequences, clinical records, and epidemiological information. Recent reviews describe potential applications in diagnostics, resistance surveillance, and antimicrobial discovery, while emphasising the need for experimental

validation and careful assessment before clinical use [1,2]. This review discusses the opportunities and limitations of AI-supported AMR management, with particular attention to rapid diagnostics, precision treatment, antimicrobial discovery, and bacteriophage therapy.

2. REVIEW METHODOLOGY

This manuscript is a narrative review, not a systematic review or meta-analysis. The discussion is organised around four themes: AI-assisted diagnostics and resistance prediction; genomic and epidemiological surveillance; AI-supported antimicrobial discovery; and bacteriophage therapy. The reference list includes selected peer-reviewed publications and a World Health Organization regional report relevant to these themes.

A reproducible database search, formal screening process, and risk-of-bias assessment were not documented in the source manuscript. Accordingly, this paper does not claim exhaustive literature coverage, and no quantitative synthesis or original experimental data are presented. Before submission, the author should add the actual databases searched, final search date, search strings, inclusion/exclusion criteria, and number of records screened if a formal search was performed. Do not report searches or screening steps that were not actually completed.

3. AI APPLICATIONS IN AMR MANAGEMENT

3.1. Genomic prediction of antimicrobial resistance

Machine-learning approaches can analyse bacterial genomic data to identify features associated with resistance, such as known resistance genes and mutations. Such analyses may support the interpretation of genomes from organisms including *Escherichia coli*, *Klebsiella pneumoniae*, and *Staphylococcus aureus*. AI can help prioritise genomic signals and estimate the likelihood of resistance to particular agents [1,2].

Genotype does not always predict phenotype perfectly. Resistance can depend on gene expression, regulatory changes, combinations of mutations, gene acquisition, and biological mechanisms that are not represented in a training dataset. A model may also perform less well when applied to organisms, hospitals, or geographical regions unlike those represented during training. AI-based genomic predictions should therefore be interpreted alongside validated phenotypic AST and the clinical context.

3.2. AI-assisted antimicrobial susceptibility testing

Phenotypic AST evaluates the response of a microorganism to antimicrobial agents under standardised conditions. AI tools may assist with image analysis of inhibition zones, automated interpretation of growth patterns, and processing of data generated by laboratory instruments. In selected workflows, these functions may reduce repetitive manual work and support more consistent interpretation [3].

Performance must be assessed against recognised laboratory standards and across relevant organisms, antimicrobial agents, and testing conditions. Quality-control procedures, human review, and clear escalation pathways remain necessary. A model should not be assumed reliable merely because it performs well on a retrospective or narrowly selected dataset.

3.3. Surveillance and prediction of resistance trends

AI may integrate laboratory results with information on antimicrobial consumption, patient populations, hospital settings, and geographical patterns. These analyses may help identify clusters, describe changing resistance patterns, and guide infection-prevention or stewardship priorities [1,2]. Predictive outputs are only as dependable as the underlying data: missing results, inconsistent laboratory methods, delayed reporting, and under-representation of particular populations can introduce bias. Surveillance models should be externally validated and monitored as local patterns change.



4. RAPID DIAGNOSTICS AND DIGITAL HEALTH

PCR and other molecular techniques can detect selected microbial targets or resistance-associated markers. Whole-genome sequencing can provide broader genomic information and support investigation of complex resistance patterns. AI may help interpret these data, combine findings from different sources, and flag results that warrant further assessment. Digital transfer of laboratory information may also improve communication between microbiology laboratories and treating teams.

The main clinical value of a diagnostic result depends not only on analytical speed but also on whether it is accurate, actionable, and available early enough to change management. Molecular assays may miss unanticipated resistance mechanisms or targets not included in the test. Conversely, detecting a resistance gene does not necessarily establish the full phenotypic response to every antimicrobial. Confirmatory testing should be performed when indicated by the assay, organism, or clinical situation.

Implementation in resource-limited settings requires affordable equipment, trained staff, dependable power and connectivity, quality assurance, maintenance, and secure data systems. Evaluations should measure practical outcomes—including turnaround time, error rates, antimicrobial use, costs, and patient outcomes—not just model accuracy.

5. AI-ASSISTED ANTIMICROBIAL DISCOVERY

Developing new antimicrobial agents is difficult because candidate compounds must demonstrate antimicrobial activity, acceptable safety, suitable pharmacological properties, and clinical benefit. AI can help screen chemical libraries, analyse molecular structures, identify potential biological targets, and prioritise compounds for laboratory testing. Machine-learning models may identify relationships between molecular features and antimicrobial activity, potentially narrowing the number of candidates requiring initial experimental assessment [1,2].

Computational predictions are hypotheses rather than proof of efficacy. Candidate compounds require experimental confirmation, toxicity testing, pharmacological assessment, and appropriately designed clinical trials. Models trained on biased datasets may favour familiar chemical structures or fail to predict performance in biological systems. AI is best viewed as a tool to support and accelerate research, not as a replacement for experimental microbiology or clinical evaluation.

6. BACTERIOPHAGE THERAPY AND AI

Bacteriophages, or phages, are viruses that infect bacteria. Selected phages can kill susceptible bacterial cells, and phage therapy is being investigated for certain difficult-to-treat infections, including infections involving multidrug-resistant bacteria. A major challenge is that phage activity can be highly specific to bacterial strains, so identifying a suitable phage may require testing against the patient's bacterial isolate.

AI may assist researchers in analysing phage genomes, annotating genes, investigating phage–host interactions, and prioritising candidates for laboratory testing. Doud and colleagues describe emerging opportunities to use AI to better understand phage specificity and inform future phage engineering, while noting important gaps in reliable host prediction [4]. A potential precision workflow could include pathogen identification, assessment of antimicrobial susceptibility, phage screening, evaluation of candidate activity and safety, and clinical monitoring under specialist supervision.

Phage therapy is not a universal replacement for antibiotics. Limitations include narrow host range, the potential for bacterial phage resistance, variable immune responses, manufacturing and quality-control requirements, and a need for stronger clinical evidence. The World Health Organization Regional Office for Europe has highlighted the need to build evidence for the use of bacteriophage therapy [5]. Clinical decisions must follow applicable regulatory requirements and specialist guidance; AI-derived predictions alone are insufficient to select treatment.

7. INTEGRATING AI, GENOMICS, AND PRECISION TREATMENT

Precision treatment aims to select interventions using the characteristics of the pathogen together with patient-specific clinical information. A proposed integrated workflow is:

- Clinical assessment and appropriate specimen collection.
- Pathogen identification using validated microbiological procedures.
- Phenotypic AST and molecular or genomic investigations when indicated.
- AI-assisted interpretation of relevant data, with attention to uncertainty and model limitations.
- Treatment decisions made by qualified clinicians using laboratory findings, patient factors, and established guidance.
- Monitoring of clinical response, with reassessment and adjustment when medically indicated.

This sequence is a conceptual framework, not a validated clinical protocol. AI should support qualified healthcare professionals rather than independently prescribe antimicrobials. The value of an integrated system should be evaluated by whether it improves appropriate treatment, stewardship, safety, and patient outcomes compared with existing practice.

8. CHALLENGES AND LIMITATIONS

8.1. Data quality, bias, and generalisability

Incomplete, inconsistent, or unrepresentative datasets can lead to biased predictions. Models may fail when applied to different hospitals, patient groups, laboratory platforms, or geographical regions. Data harmonisation, transparent reporting, external validation, and ongoing monitoring are therefore essential [1,2].

8.2. Clinical validation and accountability

High performance on a development dataset does not guarantee safe performance in routine care. Prospective studies should assess real-world utility, failure modes, and effects on clinical decisions. Responsibility for diagnosis and treatment must remain clear, with human oversight and processes for challenging or correcting model outputs.

8.3. Cost, access, and implementation

Sequencing, computational infrastructure, specialised staff, and system maintenance can be expensive. Without implementation planning, advanced technologies may widen differences between well-resourced and under-resourced facilities. Cost-effectiveness and feasibility should be evaluated alongside technical performance.

8.4. Privacy, cybersecurity, and regulation

Clinical and genomic data may be sensitive. Secure storage, controlled access, appropriate consent and governance, and cybersecurity safeguards are important. AI-enabled diagnostic tools must meet applicable regulatory and quality requirements, and their performance should be reassessed after deployment.

9. FUTURE DIRECTIONS

Future work should prioritise:

- Prospective and external validation of AI-assisted resistance prediction and AST interpretation.
- Affordable diagnostic and digital systems suited to different healthcare settings.
- Transparent, interpretable models that communicate uncertainty and limitations.
- Reliable genomic surveillance and responsible data-sharing practices.



- Laboratory and clinical evaluation of AI-prioritised antimicrobial candidates.
- Research on phage–host prediction, phage selection, safety, and clinical effectiveness.
- Implementation studies measuring antimicrobial use, patient outcomes, turnaround time, cost, and equity.

Technological innovation must complement appropriate antimicrobial prescribing, infection prevention, vaccination where indicated, and public education. AMR is a biological, clinical, and social challenge; AI alone cannot resolve it.

10. CONCLUSION

AI and advanced diagnostic technologies offer opportunities to strengthen AMR management through resistance prediction, automated analysis of selected laboratory data, genomic surveillance, antimicrobial discovery, and research into precision approaches such as bacteriophage therapy. Their promise must be balanced against limitations in data quality, generalisability, clinical validation, cost, privacy, and regulation. The most defensible approach is to integrate carefully validated AI tools with established microbiological methods, expert interpretation, and evidence-based clinical practice. Prospective research and equitable implementation will be necessary to establish whether these technologies produce meaningful improvements in diagnosis, treatment, stewardship, and public health.

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