Table 1. Comparison of Diagnostic Methods for Antimicrobial Resistance Detection

Diagnostic Method	Average Detection Time	Accuracy (%)	Advantages	Limitations
Culture + Disk Diffusion	24–48 hours	85	Inexpensive Widely available	Time-consuming, Less precise
Automated Analyzers (VITEK, BD Phoenix)	6–12 hours	95	Rapid, Standardized	High equipment cost
PCR and Real-Time PCR	2–4 hours	98	High sensitivity, detects resistance genes	Requires trained personnel
MALDI-TOF MS	1–3 hours	97	Identifies species quickly	Cannot detect gene-level resistance

Conclusion Modern diagnostic technologies – particularly PCR and automated analyzers – significantly improve the detection of antimicrobial resistance in clinical settings. Their broader implementation could enhance infection control and rational antibiotic use, ultimately helping to reduce hospital-acquired resistant infections.

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THE EFFECTIVENESS OF NEW COMBINATION THERAPIES AGAINST MULTI-RESISTANT BACTERIA

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Relevance. The growing resistance of microorganisms to multiple antibiotics is a serious clinical concern. Infections caused by multi-drug-resistant (MDR) bacteria often fail to respond to standard therapy, forcing clinicians to explore alternative treatment strategies. One such approach is the use of combination therapy, where two or more antimicrobial agents act synergistically. Evaluating the effectiveness of such combinations is essential for developing rational treatment protocols.

Aim. This article aims to assess the efficacy of antibiotic combination therapies against MDR bacterial strains based on current literature data. The review focuses on identifying synergistic combinations that enhance bactericidal activity, reduce the development of resistance, and improve clinical outcomes. It also seeks to evaluate the potential risks and benefits of these therapies, including adverse effects and the emergence of new resistance mechanisms, to guide optimal treatment strategies.

Materials and Methods. A systematic literature review was performed using PubMed, Google Scholar, and WHO databases. Search terms included "combination therapy," "beta-lactam inhibitors," "multidrug-resistant bacteria," and "clinical outcomes." Inclusion criteria: studies from 2018-2024, clinical or in vitro evaluations of combination treatments, and clear statistical analysis of resistance rates. Data from selected articles were analyzed qualitatively and summarized in comparative form.

Results. The review revealed that combinations of beta-lactam antibiotics with beta-lactamase inhibitors (e.g., piperacillin-tazobactam, amoxicillin-clavulanate) remain effective against many resistant bacteria. Newer combinations, such as ceftazidime–avibactam, demonstrate excellent activity against Pseudomonas aeruginosa and Klebsiella pneumoniae producing carbapenemases.

Discussion. Combination therapy demonstrates improved bactericidal activity compared to monotherapy. The synergistic effect is particularly important against organisms producing beta-lactamases or efflux pumps. Nevertheless, misuse of these combinations may accelerate resistance development, highlighting the need for rational use and continued surveillance.

Table 1. Effectiveness of Combination Therapies in Literature Reports

Antibiotic Combination	Target Bacteria	Average Sensitivity (%)	Key Findings
Piperacillin-Tazobactam	E. Coli, P. Aeruginosa	70–80	Effective in moderate resistance cases
Amoxicillin-Clavulanate	Staphylococcus aureus, Enterobacter spp.	65–75	Common in outpatient therapy
Ceftazidime-Avibactam	K.Pneumoniae, P.Aeruginosa	85–90	Active against carbapenem-resistant strains
Meropenem-Vaborbactam	Enterobacteriaceae	80–88	Broad-spectrum, costly

Conclusion. Combination therapies remain a powerful strategy for combating MDR infections. Future clinical studies should focus on optimizing dosing regimens and assessing long-term outcomes.

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PHARMACOGENETICS VARIABILITY IN DRUG METABOLISM AMONG DIFFERENT POPULATIONS

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Relevance. Pharmacogenetics examines how genetic variations influence individual responses to drugs. Differences in metabolic enzyme activity can lead to treatment failure or toxicity, emphasizing the importance of personalized medicine. With the rise of genetic testing, understanding population variability in pharmacogenes is crucial for safe prescribing.

Aim. This article aims to review and summarize the impact of genetic polymorphisms on drug metabolism and therapeutic response among different ethnic populations. The review seeks to identify clinically relevant genetic variants that affect drug pharmacokinetics and pharmacodynamics, and to understand how these variants differ in frequency and impact across various ethnic groups. The ultimate goal is to provide insights that can inform personalized prescribing practices, improve drug safety, and enhance therapeutic efficacy in diverse populations.

Materials and Methods. A literature-based analytical review was conducted using PubMed, ScienceDirect, and FDA pharmacogenomic databases. Keywords included “pharmacogenetics,” “CYP450 polymorphism,” “drug metabolism,” and “ethnic variability.” Studies from 2018–2024 were reviewed, focusing on genes CYP2D6, CYP2C9, and CYP3A4. Data were organized according to enzyme type, population frequency, and clinical relevance.

Results. Substantial interethnic variability was identified in drug-metabolizing enzyme expression. Poor metabolizers of CYP2D6 substrates were more common among European populations, while ultra-rapid metabolizers were prevalent in African groups.

Table 1. CYP450 Polymorphism Frequency and Clinical Implications

Enzyme	Population Group	Common Phenotype	Drugs Affected	Clinical Implication
CYP2D6	European	Poor metabolizer (~7-10%)	Antidepressants, beta-blockers	Reduced efficacy, toxicity risk
CYP2C9	Asian	Intermediate metabolizer (~15%)	Warfarin, NSAIDs	Dose adjustment required