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Introduction

- Antimicrobial resistance (AMR) is a major global public health challenge (1).
- While whole-genome sequencing (WGS) provides comprehensive insights into resistance mechanisms, its clinical utility is often limited by the complexity of data interpretation.
- Artificial intelligence (AI) offers a promising approach to assist in translating genomic data into actionable clinical insights (2).
- This study aimed to:
 - develop an AI-assisted workflow to support the clinical interpretation of bacterial WGS data to identify AMR genes, generate predicted antibiograms, visualize resistance patterns across clinical isolates
 - evaluate multiple AI-generated pipelines to determine an optimal approach for accurate, rapid, and reproducible decision support in clinical microbiology settings.

Methodology

- WGS data from 40 clinical isolates of *Escherichia coli* and *Klebsiella pneumoniae* (n=20/species) were analyzed
- The isolates were obtained from patients with various types of infection attending hospitals in the United Arab Emirates
- Publicly available large language models (LLMs), including ChatGPT, Claude AI, Gemini, and DeepSeek, were used to generate and refine R-based scripts for AMR gene detection and data visualization (3).
- The final workflow employed a fast, sequential, string-based exact-match approach for AMR gene detection, followed by an AI-assisted interpretation module that mapped detected genes to antibiotic classes
- The methods used in this study are summarized in **Figure 1**.

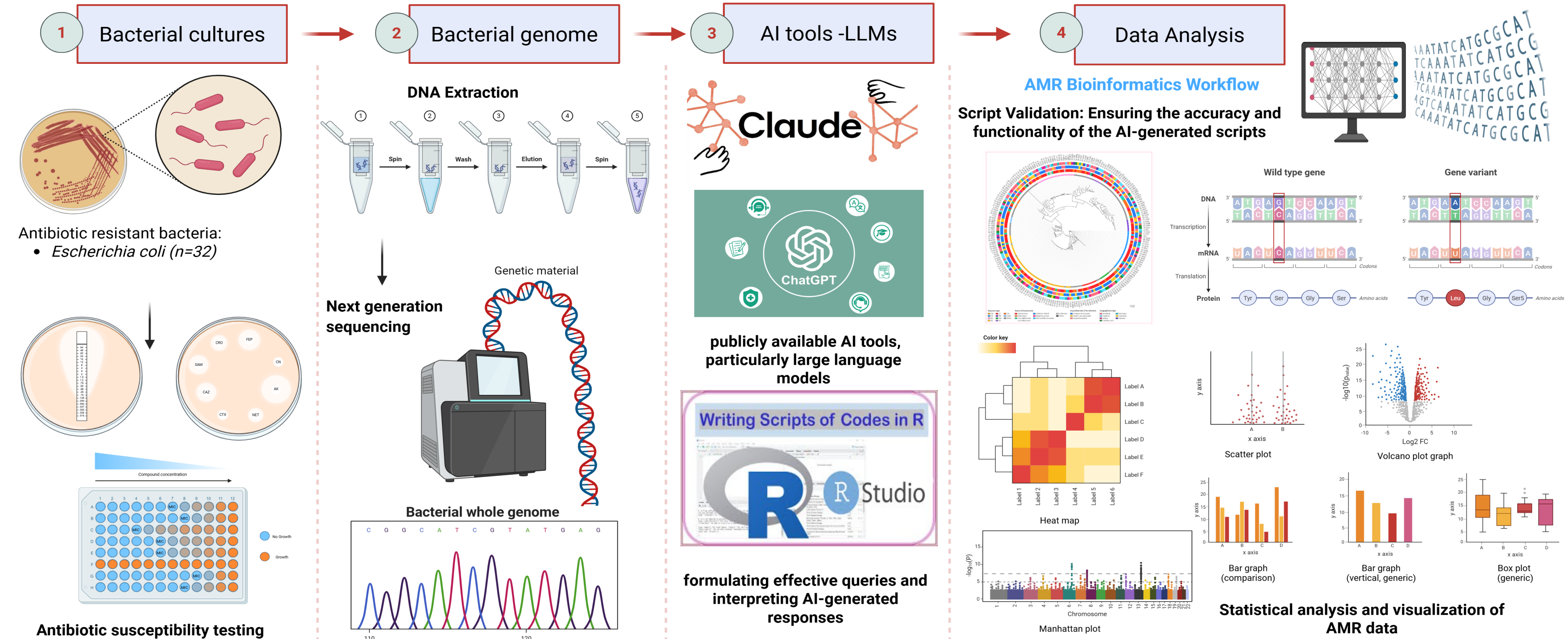


Figure 1. Methods. Steps 1-4 summarize the approach followed in this study, from collection of bacterial isolates, extracting DNA and sequencing the whole genome, then designing AI-analysis workflow to detect AMR genes, and mutations, and annotating the entire genome, followed by data analysis and visualization.

Results

- Four AI-assisted AMR detection pipelines were evaluated, differing in computational strategy, sensitivity, and runtime.
- Alignment-based approaches demonstrated increased sensitivity for detecting mutated resistance genes but were computationally intensive.
- In contrast, the exact-match pipeline demonstrated high specificity, robust performance, and substantially reduced runtime.
- The final workflow, generated using ChatGPT, achieved 100% identity and coverage for detected AMR genes, with an average processing time of approximately 70 seconds per sample.
- Global heatmaps revealed resistance trends, while per-strain reports enabled intuitive interpretation of genomic findings and prediction of appropriate antibiotic classes (Figures 2).
- Clinically relevant resistance genes, including *blaNDM*, *blaCTX-M*, and aminoglycoside resistance genes, were identified across isolates (Figure 3), and aided in the prediction of the antibiotic susceptibility profiles (Figure 4).

Interactive AMR Resistance Profile Explorer

AMR Resistance Profile

Strain-Specific Antimicrobial Resistance Analysis

Strain: EC477.fq

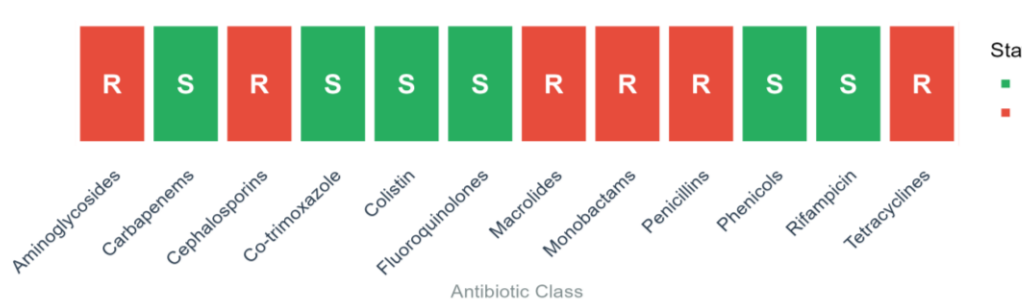
Resistant to 6

Susceptible to 6

Genes and Associated Resistance

TET (Resists: Tetracyclines); MPH (Resists: Macrolides); CTX-M (Resists: Cephalosporins, Penicillins, Monobactams); AAC (Resists: Aminoglycosides); OXA-1 (Resists: Penicillins)

Resistance Profile for This Strain



Treatment Guidance

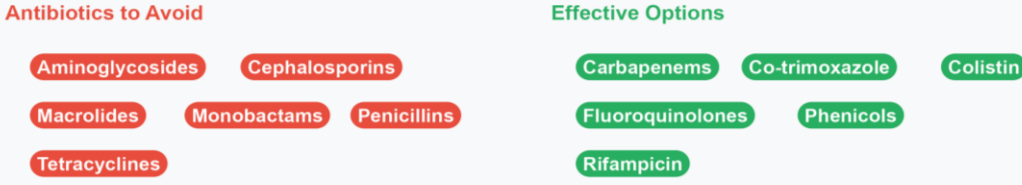


Figure 2. Report of AMR genes, predicted susceptibility profile with suggestion for antibiotic prescription based on genotype selected bacterial strain

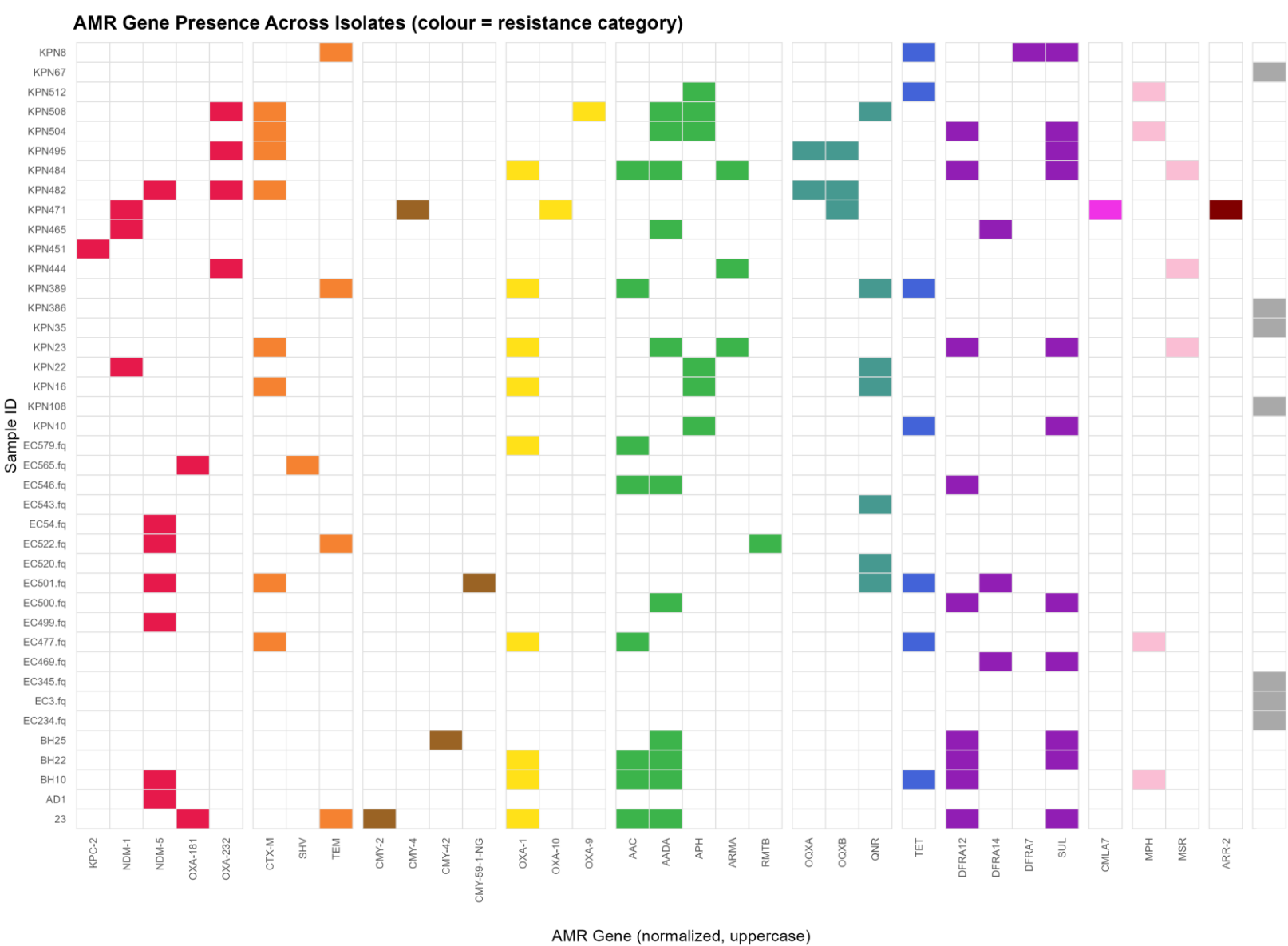


Figure 3. AMR genes detected in the whole genomes of clinical isolates tested



Figure 4. Predicated antibiotic susceptibility profiles from the clinical isolates

Conclusions

- This study demonstrates that AI-assisted workflows can effectively bridge the gap between genomic AMR data and clinical decision-making.
- The proposed workflow can facilitate prediction of the most appropriate antibiotic therapy, particularly in critically ill patients.
- The approach provides a practical, efficient, and educational framework for integrating AI-driven genomics into routine clinical microbiology practice and AMR surveillance.

REFERENCES:

- Prestinaci, F., Pezzotti, P. & Pantosti, A. Antimicrobial resistance: a global multifaceted phenomenon. *Pathog Glob Health* 109, 309–318 (2015).
- Ding, Y. et al. Artificial intelligence-assisted point-of-care testing system for ultrafast and quantitative detection of drug-resistant bacteria. *SmartMat* 5, e1214 (2024).
- Savita & Verma, N. A review study on big data analysis using R studio. *International Journal of Engineering Technologies and Management Research* 6, 129–136 (2019).

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