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# Strategies for Integrating Whole-Genome Sequencing into Antimicrobial Resistance Surveillance

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## Background

- Antimicrobial resistance remains a growing concern in global public health, requiring improved strategies for surveillance and response.
- While conventional methodologies including culture-based susceptibility testing and gene-targeted molecular diagnostics remain central, their limitations in resolution, speed, and scalability pose challenges to effective resistance monitoring.
- In this context, whole-genome sequencing (WGS) complements conventional antimicrobial susceptibility testing, jointly enhancing the ability to reveal genetic determinants, trace transmission, and strengthen surveillance frameworks.

## Methods

- WGS was reviewed as a complementary approach, enabling high-resolution characterization of resistance determinants, virulence factors, and mobile genetic elements.
- A WGS-based surveillance framework was proposed based on five analytical domains: pathogen identification, molecular epidemiology, resistance gene detection, virulence profiling, and mobile genetic element analysis.
- For each domain, key bioinformatics tools were identified and organized into structured workflows applicable to both web-based and locally installed environments.

## Results

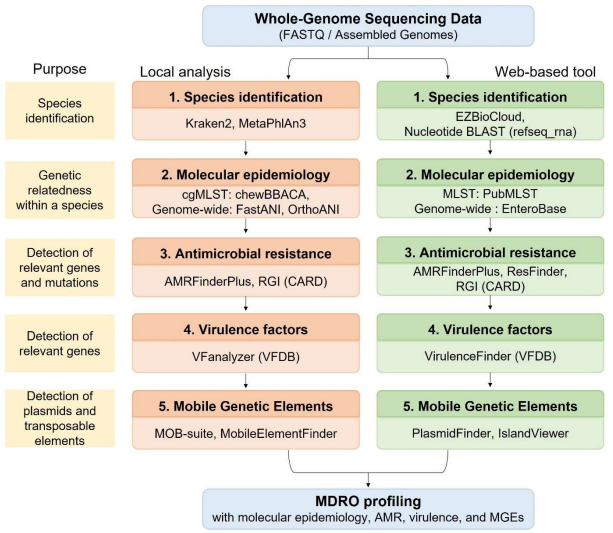


**Figure 1. Schematic presentation of the WGS-based workflow.**

- A practical workflow comprising five core analytical stages is proposed for effective WGS-based AMR surveillance: one based on locally installed computational pipelines for advanced genomic resolution and another utilising web-based tools for accessibility.

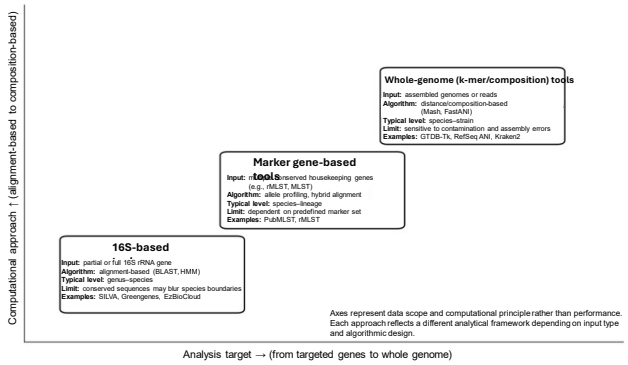


**Figure 2. Comparative spectrum of species identification methods**

- The diagram illustrates three analytical frameworks—16S rRNA-based, marker gene-based, and whole-genome k-mer/composition-based tools—positioned according to input data scope and computational principles.
- 16S rRNA-based methods rely on alignment of conserved regions for genus–species classification but are limited by low resolution among closely related taxa.
- Marker gene-based tools use allele profiling across multiple housekeeping genes to achieve species–lineage differentiation, though results depend on predefined loci and curated schemes.
- Whole-genome approaches utilize genome-wide k-mer or compositional signatures for strain-level resolution, yet are sensitive to assembly quality, contamination, and computational demand.

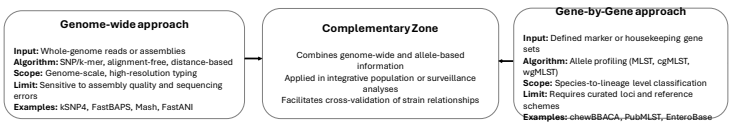


**Figure 3. Conceptual spectrum of bacterial typing approaches.**

- Genome-wide and gene-by-gene frameworks represent two complementary strategies for genomic typing.
- Genome-wide methods capture continuous variation across the entire genome, providing high-resolution strain differentiation but requiring high-quality assemblies and greater computational resources.
- Gene-by-gene methods classify isolates through allelic profiles of predefined loci, ensuring standardized and comparable results but offering lower resolution when loci are limited.
- The complementary zone bridges both frameworks, integrating the broad comparability of allele-based schemes with the fine-scale discrimination of genome-wide analyses. This conceptual spectrum highlights their combined value in achieving both resolution and standardization in genomic epidemiology.

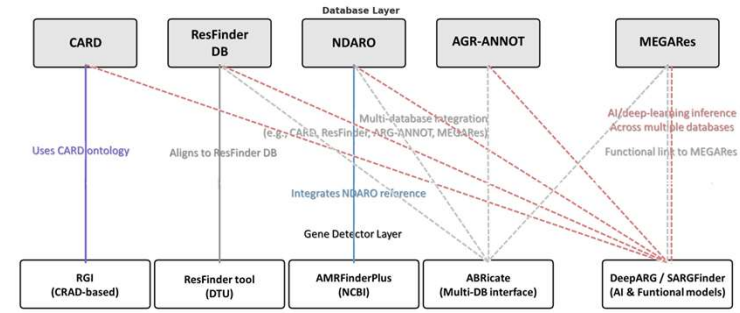


**Figure 4. Interconnected framework of AMR databases and detection tools**

- Curated AMR databases (CARD, NDARO, ResFinder, ARG-ANNOT, MEGARes) serve as foundational references for gene identification.
- Detection tools (RGI, AMRFinderPlus, ResFinder, ABRicate, DeepARG, SARGFinder) utilize these repositories via ontology, alignment, or AI inference.

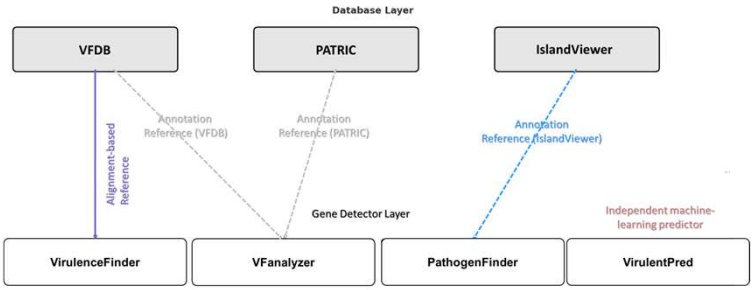


**Figure 5. Interconnected framework of virulence databases and detection tools**

- Curated virulence databases, including VFDB, PATRIC, and IslandViewer DB, provide essential reference sources for gene identification.
- Detection tools such as VirulenceFinder, Vfanalyzer, PathogenFinder, and Virulentpred utilize these repositories through sequence alignment, curated annotation, and machine-learning integration.
- VirulentPred operates as an independent machine-learning predictor that does not rely on specific virulence gene databases, focusing instead on intrinsic sequence features.

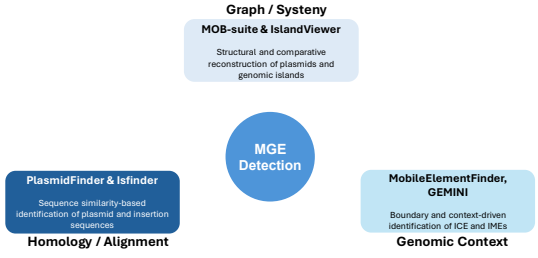


**Figure 6. Tri-domain Framework of Mobile Genetic Element (MGE) Detection Tools**

- This tri-domain framework conceptualizes the methodological landscape of MGE detection.
- Homology, context, and graph based approaches collectively provide complementary perspectives for characterizing mobile genetic elements.
- The central hub represents the integrative us of these domains within modern genomic surveillance pipelines.

## Conclusions

- The proposed framework supports practical integration of WGS into antimicrobial resistance surveillance by offering flexible, tool-based workflows tailored to diverse infrastructure levels.
- Broader application of these tools supported by advances in user interfaces and automation will enhance global capacity for genomic surveillance and antimicrobial resistance control.

## Reference

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- Sherry NL, Lee JYH, Giulieri SG, Connor CH, Horan K, Lacey JA, Lane CR, Carter GP, Seemann T, Egli A, Stinear TP, Howden BP. Genomics for antimicrobial resistance—progress and future directions. Antimicrob Agents Chemother 2025;69(5).

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