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Can AI and Genomic Surveillance Help India Detect Antimicrobial Resistance Earlier?

Whole-genome sequencing can reveal how resistance moves, while machine learning can help prioritise what public-health systems need to act on.

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ABSTRACT

Antimicrobial resistance is usually detected through laboratory susceptibility testing, which remains essential for patient care. Yet conventional surveillance often reveals only that resistance is present, not how it emerged, whether cases are connected, or how a resistance gene is moving among hospitals, farms, food systems, animals, and the environment. Whole-genome sequencing can add that missing resolution. Machine-learning methods can then help predict resistance, identify unusual clusters, and prioritise samples for investigation. For India, where antimicrobial use, healthcare access, laboratory capacity, and agricultural systems vary sharply across regions, the opportunity is substantial but technically demanding. This Article argues that AI-enabled genomic surveillance should not be built as a replacement for microbiology laboratories. It should be designed as a layered national capability that links reliable phenotypic testing, representative sampling, sequencing, epidemiological metadata, and rapid public-health response. The central challenge is not simply generating genomes. It is creating a trusted system in which genomic signals lead to action before resistant organisms become widely established.

KEYWORDS antimicrobial resistance; genomic surveillance; artificial intelligence; One Health; India; whole-genome sequencing

ARTICLE AT A GLANCE

- Phenotypic susceptibility testing remains essential; genomics adds mechanism and transmission context.
- Machine learning is most useful for prediction, triage, and anomaly detection, not autonomous public-health decisions.
- Representative One Health sampling is more important than sequencing the largest possible number of isolates.

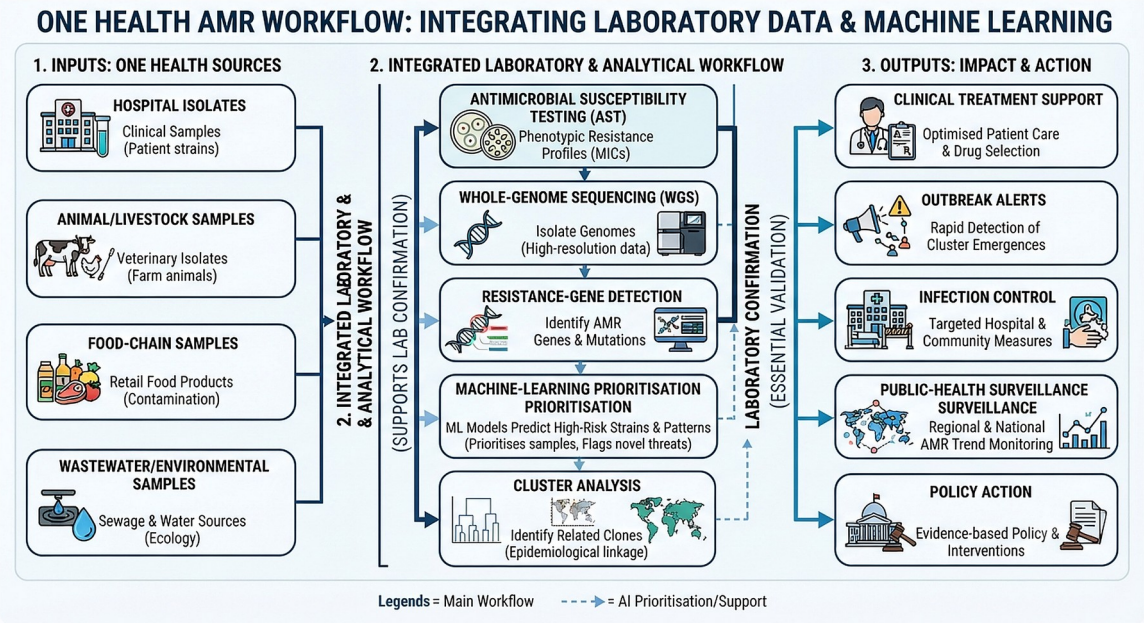

Figure 1. A One Health antimicrobial-resistance workflow integrating field, clinical, laboratory, genomic, and machine-learning data for public-health action.

1. Resistance is a biological problem and an information problem

Antimicrobial resistance (AMR) occurs when microorganisms survive medicines that previously controlled them. The consequences are clinical, economic, and ecological: infections become harder to treat, hospital stays lengthen, and resistant organisms or genes can circulate across human, animal, food, and environmental systems. A global analysis estimated that bacterial AMR was directly responsible for more than one million deaths in 2019 and associated with several million more, demonstrating that resistance is already a major cause of mortality rather than a distant threat (Murray et al., 2022).

Routine antimicrobial susceptibility testing answers a critical question: is an isolate resistant to a particular drug? Surveillance programmes aggregate these results to describe resistance patterns. However, two isolates with the same resistance profile may be unrelated, while isolates that appear different phenotypically may share a mobile resistance gene. Genomic data can identify species, sequence types, mutations, plasmids, and resistance determinants in a single analytical framework. This makes it possible to distinguish repeated local emergence from transmission of a successful resistant clone (Ellington et al., 2017).

The information problem is therefore one of resolution and timing. Public-health teams need to know whether an unusual resistance pattern is isolated or spreading, whether it is linked to a healthcare facility or food chain, and whether a gene has crossed into a new bacterial host. Genomic surveillance can answer these questions, but only when sequence data are linked to dates, locations, specimen types, clinical context, animal or environmental sources, and reliable laboratory results. A genome without metadata is scientifically interesting but operationally weak.

2. What whole-genome sequencing adds

Whole-genome sequencing reads most of an organism’s genetic material rather than testing a small set of markers. For bacterial AMR, this allows laboratories to identify known resistance genes and mutations, reconstruct relatedness among isolates, and track mobile elements. Sequencing has been integrated into national surveillance in settings such as the Philippines, where genomic data improved interpretation of resistant bacterial lineages and supported public-health capacity building (Argimón et al., 2020). The lesson is that genomics becomes useful when embedded in an existing surveillance programme, not when operated as a disconnected research project.

Prediction of resistance from sequence is possible for several organism-drug combinations, especially where mechanisms are well characterised. Yet genotype and phenotype do not always match. A gene may be present but poorly expressed; a novel mechanism may be absent from the reference database; or resistance may depend on multiple interacting mutations. Phenotypic testing therefore remains the clinical reference. Genomics adds explanation,

transmission context, and speed for recognised mechanisms, while laboratory assays reveal the actual behaviour of the organism under defined conditions (Boolchandani et al., 2019; Ellington et al., 2017).

Metagenomic sequencing extends surveillance beyond cultured isolates. It can detect resistance genes directly in mixed samples such as sewage, soil, animal waste, or hospital wastewater. A global analysis of urban sewage demonstrated that metagenomics could compare AMR gene abundance across countries and identify geographic patterns (Hendriksen et al., 2019). Such approaches are particularly relevant to One Health because they observe the shared microbial environment rather than separating human, animal, and ecological compartments.

3. Where artificial intelligence can contribute

Machine learning can classify sequences, predict resistance genes, and detect patterns across large genomic datasets. DeepARG, for example, used deep learning to improve recognition of antibiotic-resistance genes from metagenomic sequences, including sequences that were only distantly related to curated examples (Arango-Argoty et al., 2018). Similar models can combine k-mer patterns, gene content, and mutations to estimate phenotypic resistance. The practical advantage is triage: laboratories can flag isolates that require urgent confirmation or epidemiological investigation.

AI can also support anomaly detection. A surveillance system receives streams of data from many organisms, hospitals, districts, and sample types. Algorithms can identify an unexpected rise in a clone, a new gene-organism combination, or a resistance profile appearing outside its usual geography. These signals should not automatically trigger policy. They should trigger human review, repeat testing, and field investigation. In this role, AI functions as an early-warning filter rather than an autonomous decision-maker.

The strongest models will integrate multiple evidence layers. Genomic data alone may show related organisms, but epidemiology determines whether transmission is plausible. Antibiotic consumption data can explain selection pressure. Patient movement, animal trade, wastewater flows, and food distribution may reveal routes that genomes cannot. A useful Indian platform would therefore connect sequence analysis with laboratory, clinical, veterinary, agricultural, and environmental information while applying strict privacy and governance controls.

4. India’s opportunity and its practical constraints

India already has a foundation through the Indian Council of Medical Research Antimicrobial Resistance Surveillance and Research Network, which compiles resistance data from participating centres and reports clinically important trends (Indian Council of Medical Research, 2023). Genomics could deepen this network by resolving outbreaks, characterising emerging mechanisms, and connecting regional observations. However, a national strategy must account for uneven laboratory infrastructure, differences in specimen submission, variable access to sequencing, and the high cost of maintaining trained bioinformatics teams.

Representativeness is the first challenge. If sequencing is concentrated in tertiary hospitals, the resulting map may overrepresent severe urban infections and underrepresent community, rural, veterinary, food, and environmental reservoirs. A technically advanced but biased system can generate false confidence. Sentinel sampling should therefore be designed around public-health questions, with transparent inclusion criteria and periodic assessment of geographic and population coverage. The World Health Organization’s genomic-surveillance strategy emphasises coordinated systems, standards, workforce development, and rapid sharing rather than sequencing volume alone (World Health Organization, 2022).

The second challenge is interoperability. Laboratories may use different identifiers, susceptibility methods, software pipelines, and metadata fields. Without common standards, data cannot be compared reliably. The third is turnaround time. A sequence analysed months after collection contributes to research but may miss an outbreak-control window. The fourth is governance. Patient information, hospital reputations, agricultural livelihoods, and international data-sharing obligations require clear rules on access, de-identification, attribution, and communication.

5. Building a surveillance system that leads to action

A practical model would use layers. At the base, microbiology laboratories perform quality-assured culture, identification, and susceptibility testing. A representative subset of isolates then enters sequencing based on defined triggers: unusual resistance, suspected outbreaks, priority pathogens, treatment failures, geographic gaps, or One Health sampling. Standard pipelines identify organisms, genes, mutations, plasmids, and relatedness. Machine learning flags

anomalies and estimates which findings deserve urgent review. A multidisciplinary team then interprets the result and recommends action.

Action may include infection-control audits, contact tracing within healthcare facilities, targeted environmental sampling, changes in empirical treatment guidance, veterinary investigation, or restrictions on a specific antimicrobial use. The time from sample collection to response should be measured as a core performance indicator. Other indicators should include representativeness, concordance between predicted and observed resistance, outbreak-detection yield, and the proportion of alerts that produce documented interventions.

India's scale makes the problem difficult, but it also creates an opportunity to build a globally important One Health surveillance system. The decisive investment is not only in sequencers or algorithms. It is in the connections among laboratories, epidemiologists, clinicians, veterinarians, environmental scientists, data engineers, and public-health authorities. Genomic AI can reveal patterns that were previously invisible. Its value will be determined by whether those patterns arrive early enough, are trusted enough, and are connected closely enough to institutions that can act.

6. The skills and infrastructure that matter

Building this system requires more than a central sequencing laboratory. District and hospital laboratories need quality-assured organism identification and susceptibility testing because poor input data cannot be repaired computationally. Regional hubs need sequencers, biosafety systems, contamination controls, reference materials, and stable procurement for reagents. Bioinformatics teams need version-controlled pipelines, validated databases, and the ability to reanalyse older genomes when new resistance mechanisms are discovered. Epidemiologists need access to interpretable outputs rather than raw phylogenetic trees.

Workforce design should avoid dependence on a few specialists. Training programmes can teach microbiologists enough genomics to recognise data-quality problems and teach data scientists enough microbiology to understand phenotype, plasmids, and sampling bias. Shared analysis platforms can reduce duplication, but centralisation should not prevent local teams from asking questions relevant to their region. Competency should be assessed through proficiency panels in which laboratories receive blinded isolates or sequence files and compare results.

Financing should include maintenance and response, not only capital equipment. Sequencers that cannot be serviced, databases that are not updated, and alerts that no institution owns will not improve public health. A sustainable budget should cover sample transport, phenotypic confirmation, sequencing, data storage, workforce, outbreak investigation, and communication. The most valuable pilot projects will show the complete chain from an unusual isolate to a documented intervention and measured outcome.

Key takeaways

- Phenotypic susceptibility testing remains essential; genomics adds mechanism and transmission context.
- Machine learning is most useful for prediction, triage, and anomaly detection, not autonomous public-health decisions.
- Representative One Health sampling is more important than sequencing the largest possible number of isolates.
- Common metadata standards, rapid turnaround, and governance are prerequisites for national usefulness.
- The success metric is not genomes produced but earlier, better-targeted interventions.

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