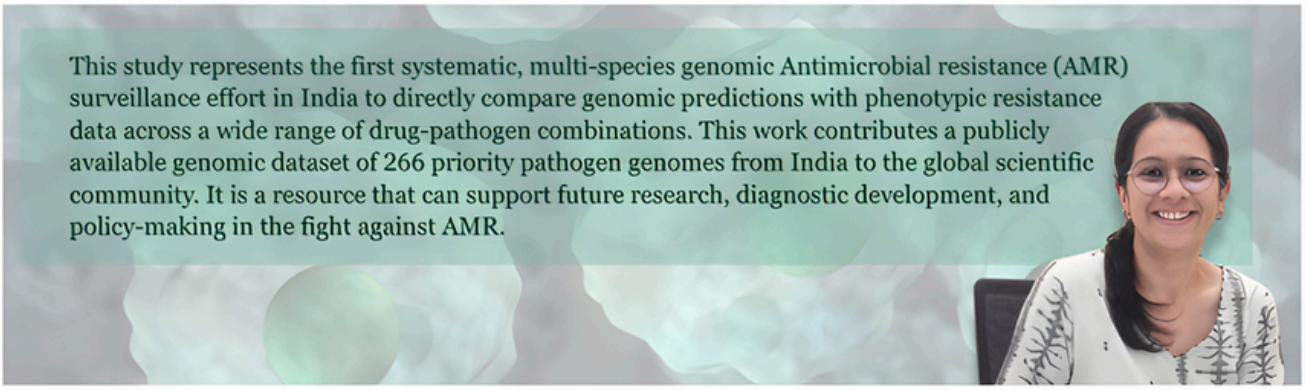
Research Blogs

What Can Genomics Tell Us About Drug Resistance in India? Insights From Recently Published Research Paper by Professor Shradha Karve

In this article, Shradha Karve, Assistant Professor of Research at Koita Centre for Digital Health, Ashoka University, discusses her recently published paper, "Genomic landscape of antimicrobial resistance in India: findings from a multi-species surveillance study". Decoding drug resistance, the study systematically examines the gap in antimicrobial resistance (AMR) genomic landscape using samples from Northern and Western India between 2022 and 2024, the first of its kind in India.



What Does this Research Paper Talk About?

Antimicrobial resistance (AMR) – the ability of bacteria and other microbes to survive and grow in the presence of antibiotics that would have otherwise killed them – is one of the most pressing public health crises of our time. When bacteria develop resistance to the drugs designed to kill them, common infections become life-threatening, routine surgeries become risky, and medical care becomes harder to deliver.

The problem is especially acute in low- and middle-income countries (LMICs) like India, where the burden of infectious disease is high, and surveillance resources are limited. Most AMR monitoring in India has traditionally relied on antibiotic susceptibility testing (AST) – a lab method that checks whether a bacterium is killed by specific antibiotics. While useful, this approach does not reveal which genes underlie resistance, how those genes spread between bacteria, or how India's resistance landscape compares to global trends. Without the understanding of this genomic layer, our ability to design better diagnostics and treatments remains constrained.

What Did the Study Aim to Find?

This study was motivated by a critical gap: the lack of large-scale datasets in India that link AST with whole-genome sequencing (WGS) data across multiple bacterial species.

Professor Karve and her lab set out to build such a dataset – one that would allow us to map the genomic underpinnings of AMR in Indian clinical settings, test how well genomic tools predict resistance compared to standard lab tests, and understand how resistance genes are spread and shared among bacteria.

The ultimate goal, along with knowledge building, is to support the development of faster, more accurate molecular diagnostic tools for AMR in India- tools that could one day replace or supplement the slow, culture-based methods currently in use, particularly in critical care settings like ICUs, where rapid diagnosis can be life-saving.

The Strategy

Between July 2022 and July 2024, the team collected 266 bacterial isolates from two groups of tertiary healthcare hospitals, one in Northern India (New Delhi) and one in Western India (Pune). The isolates represented priority pathogens, including Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii, Pseudomonas aeruginosa, Staphylococcus aureus, and Enterococcus, as well as a few other emerging threats.

The researchers selected isolates belonging to high-concern resistance categories: carbapenem-resistant (CR), carbapenem-and-colistin-resistant (CR-Col), extended-spectrum beta-lactam-resistant (ESBL), methicillin-resistant (MR), and vancomycin-resistant (VR).

For each isolate, two parallel analyses were carried out:

1. AST is the gold-standard laboratory method that tests how bacteria respond to antibiotics.
2. WGS, which allows us to read the complete DNA of each bacterial isolate and identify resistance genes (ARGs), their locations (chromosomes or plasmids), and the mobile genetic elements that can transfer them between bacteria.

Professor Shradha Karve's Lab used standard bioinformatic tools, including the Resistance Gene Identifier (RGI) linked to the Comprehensive Antibiotic Resistance Database (CARD) for genomic resistance prediction, and MOBsuite and MobileElementFinder for plasmid and mobile element analysis.

Results and Conclusion

The study produced several important findings relevant to how AMR is understood and tracked in India.

Professor Shradha Karve and her team found that genomic tools tend to over-predict resistance. Compared genomic resistance predictions against actual AST results across more than 5000 drug-pathogen combinations, the team found significant discrepancies. The most common pattern was the genomic tool predicting resistance when the bacterium was actually sensitive in the lab, and was found in more than 400 cases. This 'over-prediction' likely reflects the tool flagging genes that confer only a moderate increase in resistance, not enough to breach clinical treatment thresholds. Crucially, these false positives highlight important gaps that need to be addressed before genomic tools can be reliably used for patient diagnostics.

A rich and diverse resistance gene landscape has also been discovered. Over 80 distinct beta-lactamase genes (enzymes that break down beta-lactam antibiotics) were detected. The NDM (New Delhi Metallo-beta-lactamase) family – genes that confer resistance to carbapenem antibiotics, the last-resort drugs – were the most prevalent. Notably, blaNDM-5 was far more common than blaNDM-1 among E. coli and K. pneumoniae isolates, a finding that contrasts with some prior Indian studies and underscores the evolving resistance landscape.

A significant proportion of resistance genes were found on plasmids. Plasmids are small, circular pieces of DNA that bacteria can share with each other, enabling rapid, horizontal spread of resistance. K. pneumoniae showed the highest burden of plasmid-associated ARGs, highlighting its role as a key vehicle for resistance gene dissemination. Mobile genetic elements like insertion sequences and transposons were also found associated with ARGs, further facilitating spread.

Professor Shradha Karve's Lab discovered several well-known pathogenic lineages (such as E. coli ST131 and K. pneumoniae ST147), but also noted the diversity and regional specificity of Indian lineages, reinforcing that global AMR data cannot simply be applied to the Indian context.

Impact and Benefits of the Study (Bird-Eye-View)

This study represents the first systematic, multi-species genomic AMR surveillance effort in India to directly compare genomic predictions with phenotypic resistance data across a wide range of drug-pathogen combinations. The findings have several important implications.

- By identifying which drug-pathogen combinations are well-predicted by genomics and which are not, this work provides a roadmap for improving the accuracy of molecular diagnostic tools for AMR. Rapid genomic diagnostics could transform care in ICUs, where delays in identifying the right antibiotic can cost lives.
- The findings underscore the urgent need for continued, expanded genomic surveillance in India. Resistance gene variants detected, the plasmid diversity, and the regional specificities of the isolates all highlight that India's AMR landscape has features that are not captured by global datasets.
- Understanding how resistance genes are distributed across bacterial species, plasmids, and chromosomes is critical for designing effective infection control strategies. The finding that no pathogen relies solely on chromosomal or plasmid-based resistance means that reducing antibiotic use alone may not eliminate resistance: chromosomal ARGs can persist even after plasmid-borne ones are lost.

More broadly, this work contributes a publicly available genomic dataset of 266 priority pathogen genomes from India to the global scientific community. It is a resource that can support future research, diagnostic development, and policy-making in the fight against AMR.

This blog has been adapted from the original article, available here.

Koita Centre for Digital Health - Ashoka (KCDH-A)

WHO Global Strategy on Digital Health (2028–2033) : Southeast Asia Region Multi-Stakeholder Consultation:

The WHO **Global Strategy on Digital Health (2020-2025)**, extended to 2027, is now transitioning toward its successor framework for 2028-2033. This marks an important moment for regions to reflect on lessons learned, identify emerging priorities, and contribute constructively to the future direction of digital health globally.

To support the development of the next **Global Strategy on Digital Health (2028-2033)**, WHO-SEARO is convening a series of multi-stakeholder consultation webinars across the South-East Asia Region (SEAR). Designed as a participatory, decentralized, and inclusive process grounded in a whole-of-society and whole-of-ecosystem approach.

Events at Ashoka

As part of this initiative, four regional consultations will be held in March 2026 and two in April 2026 in collaboration with potential WHO Collaborating Centres.

Koita Centre for Digital Health at Ashoka University (KCDH-A), also hosted its inaugural regional consultation webinar on 6 March 2026 as a part of this. The session brought together diverse voices from across the Region to contribute perspectives to this global process. The session focused on reflecting on achievements and lessons from the current Global Strategy and identifying regional priorities and contextual considerations for 2028-2033.

The Indian EXPRESS

ANURAG AGRAWAL

THE SPATE of misinformation on the rollout of human papillomavirus (HPV) vaccination, as part of the national immunisation programme, reminds me of the saying, "every rationalist doubts, but not all doubts are rational". What matters is whether we use doubt as a tool to eliminate bias or to amplify it. That distinction is the difference between using evidence to guide health policy and cherry-picking fragments to promote conspiracy theories.

Let us first ask why virtually every major scientific body in the world — including ICMR and CDC — and about 160 countries, including almost every high-income nation, recommend HPV vaccination. HPV is responsible for an overwhelming majority of cervical cancers, in addition to a large proportion of anal, oropharyngeal, vulvar, vaginal and penile cancers. While men are at risk of HPV-mediated cancer, the risk is greatest for women. While some countries recommend vaccination for men, there is a near-universal consensus on vaccinating women.

India has one of the highest burdens of cervical cancer globally. The vaccines now in use, including Gardasil, part of India's rollout, have been found to be effective in large trials and, more importantly, in real-world programmes involving tens of millions of adolescents across multiple countries.

These are not small pilot studies. These are population-scale interventions followed over years. The findings are consistently striking: Dramatic reduction in HPV infection and precancerous lesions, and, where sufficient time has elapsed, a decline in cervical cancer itself.

Now, let us consider the concerns. Some point to adverse events reported in earlier studies, particularly an Indian study in 2009 in which seven young women who had received the Gardasil vaccine died. The concern deserves examination, not dismissal. Indeed, it was thoroughly investigated, and the public report showed that while there were deficiencies in the trial, there was no evidence that vaccination led to these deaths. For the record, two deaths were due to poisoning, one drowning, and one was a confirmed case of cerebral malaria.

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isolated reports is irrational.

Another line of concern is a
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Scepticism strengthens scienc
tured doubt weakens public he

The writer is dean, Trivedi School o
Ashoka University. Views

It is rational to demand an effective adverse effect monitoring system. However, to ignore a vast amount of high-quality evidence and give credence to isolated reports is irrational

In a recent publication in The Indian Express, Professor Anurag Agrawal, Head of the Koita Centre for Digital Health and Dean of BioSciences, Health Research at Ashoka University, tackles misconceptions surrounding the HPV vaccination. Advocating for evidence-led public health policy, noting that every year the vaccine is delayed, and real harm accrues to thousands of young women across India.