

Reading the Genetic Clues: How Bioinformatics and One Health Can Help India Prevent the Next Zoonotic Outbreak

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Abstract

Emerging infectious diseases increasingly highlight the interconnectedness of human, animal and environmental health. Climate change, habitat disturbance and changing patterns of contact between species can influence the emergence and spread of zoonotic pathogens. The One Health approach addresses these challenges through collaboration among medical, veterinary and environmental sectors. Bioinformatics strengthens this approach by enabling genomic sequencing, phylogenetic analysis, metagenomic surveillance and the investigation of antimicrobial resistance across human, animal and environmental samples. Evidence from outbreaks such as Nipah virus in Kerala demonstrates how genomic comparisons can help identify relationships between pathogens detected in different hosts, although epidemiological and field investigations remain essential to confirm transmission pathways. Wastewater surveillance and machine-learning approaches also offer opportunities to identify unexpected pathogens and prioritize surveillance activities. However, fragmented surveillance systems, unequal laboratory capacity, data-sharing barriers and ethical concerns can limit effective implementation. Strengthening genomic infrastructure, developing skilled personnel and improving coordination among relevant departments are important steps towards a more integrated surveillance system. Combining bioinformatics with One Health can support earlier threat detection, evidence-based public-health decisions and more effective prevention and control of zoonotic diseases in India.

Keywords- One Health; Bioinformatics; Zoonotic diseases; Genomic surveillance; Pathogen evolution; Next-generation sequencing; Antimicrobial resistance; Disease surveillance; Public health; Emerging infectious

diseases

Some of the most important changes affecting human health begin far beyond hospitals and laboratories. They begin in forests, wetlands, farms and the environments that people and animals share. A shift in rainfall can change vector habitats; habitat loss can alter wildlife movement; and changing patterns of contact between species can create opportunities for pathogens to cross into new hosts. These processes are often gradual, but their consequences can extend from ecosystems to communities and healthcare systems.

This is particularly relevant to zoonotic diseases, which spread between animals and people. With approximately 60% of known human infectious disease pathogens considered zoonotic, understanding the links between environmental change and disease emergence has become an important public-health priority. Climate change adds urgency to this challenge, making collaboration across human, animal and environmental health essential.

What is One Health?

One Health recognises that human, animal and environmental health are deeply interconnected. It is supported by the Food and Agriculture Organization (FAO), the United Nations Environment Programme (UNEP), the World Health Organization (WHO) and the World Organisation for Animal Health (WOAH), which encourage different sectors to work together to prevent and control health threats [3, 4].

In practice, a veterinarian noticing unusual livestock deaths, a doctor treating an unexplained fever and a forest officer monitoring wildlife should be sharing information, not working in isolation.

India's zoonotic landscape

India already lives with many diseases that cross between animals and people.

Disease	Animal link	Where it matters in India
Nipah virus	Pteropus fruit bats	Outbreaks in Kerala and West Bengal
Kyasanur	Ticks and	First recognised

Forest Disease	monkeys	in Karnataka's forests, reported in neighbouring Western Ghats states
Rabies	Dogs	Countrywide; India is estimated to carry a large share of the world's human rabies deaths
Avian influenza (H5N1)	Poultry and wild birds	Poultry outbreaks reported since 2006
Brucellosis	Cattle, buffalo, goats	Widespread in livestock; spread through raw milk and contact
Japanese encephalitis	Pigs and wading birds, via mosquitoes	Recurring outbreaks in several states

Each of these involves a different animal, habitat and community, and each needs veterinary, medical and environmental expertise working together.

Enter bioinformatics: the language that connects them

Bioinformatics uses computers and statistics to analyse biological information. Its value in One Health comes from a simple fact: every pathogen carries genetic information that offers clues about its identity, evolution and likely source.

1. Tracing the family tree of an outbreak

When scientists sequence a pathogen's genome, they can compare it with sequences from other patients, animals and places. These comparisons build phylogenetic trees, which show how closely related pathogens are.

Kerala's 2018 Nipah outbreak shows how powerful this can be. Scientists at ICMR-NIV, Pune, sequenced the virus from patients and from fruit bats captured in the affected area. The human virus was almost identical (99.7–



100% similar in the gene compared) to virus from *Pteropus* bats, pointing to bats as the source, and it clustered with the Bangladesh lineage of Nipah rather than the Malaysian one [5]. That helped doctors know what kind of illness to expect and where to look for the origin.

Genomic analysis helps answer such questions, although field and epidemiological investigation are still needed to confirm how transmission happened.

Open platforms such as Nextstrain and databases such as GenBank let scientists compare sequences across borders [6]. During the 2024 spread of highly pathogenic avian influenza H5N1 among dairy cattle in the United States, genomic studies helped researchers understand how the virus emerged and moved in an unexpected host [7]. For a country that is the world's largest milk producer and has repeatedly seen avian influenza in poultry, that is a lesson worth taking seriously.

2. Finding the unknown

Traditional tests look for a specific suspected pathogen. Metagenomic sequencing examines genetic material from everything in a sample, and with bioinformatics it can help identify unexpected or unrecognised infectious agents.

Sewage surveillance is another tool. India has long used sewage sampling to watch for poliovirus, and during COVID-19 wastewater was used in many places to track SARS-CoV-2 alongside clinical testing. These methods cannot detect every infection, but they can reveal signals that conventional surveillance misses.

India also built experience with large-scale genomic surveillance through INSACOG, the national network created in late 2020 to sequence SARS-CoV-2. The same laboratories, skills and data pipelines can be turned toward animal and environmental pathogens.

3. Predicting who can infect whom

Not every pathogen in animals can infect humans. Bioinformaticians study genetic features, including viral proteins that recognise host cells, to judge the potential for cross-species infection, and machine-learning models

are being explored to flag pathogens that deserve closer monitoring.

These tools cannot reliably predict the next pandemic. But they help prioritise limited surveillance resources, for example by deciding which bat colonies, livestock markets or forest edges to sample first.

4. Tracking the drug-resistance threat

One Health is not only about viruses. Antimicrobial resistance (AMR) links hospitals, veterinary practice, dairy and poultry farming, food and the environment. By sequencing bacteria from people, animals, food and water, scientists can compare resistance genes and strains across these sources.

This can support antibiotic stewardship, safer farming practices and better infection control. However, finding similar resistance genes in different settings does not by itself prove direct transmission.

From data to decisions: the hard part

The technology is advancing quickly, but several challenges remain.

- **Disconnected surveillance:** Health, animal husbandry, forest and environment departments often keep separate records, making it hard to see a shared threat.
- **Unequal laboratory capacity:** Advanced sequencing is concentrated in a few national and state centres. Many districts lack trained bioinformaticians and reliable computing infrastructure.
- **Data sharing:** Timely access to genomic data is essential, but institutions also need fair arrangements for credit and benefit-sharing.
- **Ethics and communication:** Findings must be communicated carefully to protect privacy and avoid stigma against communities, farmers or animals. Bats, for instance, are important to ecosystems and should not become targets of panic.



What a connected future could look like

Imagine a district where a veterinary officer reports unexplained livestock deaths. Samples go to a regional laboratory, and genomic analysis shows a pathogen closely related to one detected in another state.

The result is shared with veterinary, health and forest authorities. Investigators check animal movements, possible human exposures and environmental factors. Farmers receive preventive advice, local clinicians and community health workers are alerted, and targeted surveillance begins.

This is the promise of combining bioinformatics with One Health: turning scattered observations into evidence and timely action. The sequencing tools already exist. What India needs is investment in trained people, district-level laboratories, connected data systems and cooperation between departments.

What can ordinary people do?

One Health is not only for scientists and governments.

- **Report** unusual animal illness or deaths to the nearest government veterinary hospital, and unexplained fevers to the nearest health centre.
- **Handle food safely:** boil milk, cook meat and eggs thoroughly, and avoid fruit that bats or birds may have bitten.
- **Vaccinate** pets and livestock under available programmes, and seek care promptly after any dog bite.
- **Use antibiotics responsibly,** only when prescribed, for people and animals alike.

Farmers, animal handlers, ASHA workers and consumers are often the first to notice that something is wrong, which makes them essential partners in early warning.

The bottom line

The next major zoonotic outbreak may begin with something ordinary: an unexplained

animal death, an unusual fever, a pathogen in an unexpected host. We cannot prevent every spillover, and genetic information alone cannot predict the next pandemic. But we can recognise warning signs sooner and respond before a threat spreads.

Bioinformatics reads the genetic clues. One Health connects them across people, animals and ecosystems.

The threat is connected. So must be our response.

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