



Why Genomic Surveillance Must Remain a Global Health Priority

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Abstract

Genomic surveillance has emerged as one of the most transformative developments in modern infectious disease research. Advances in next-generation sequencing (NGS), bioinformatics, and global data-sharing platforms have revolutionized the detection, monitoring, and control of viral pathogens. The COVID-19 pandemic demonstrated the critical role of genomic surveillance in identifying emerging variants, understanding transmission dynamics, and supporting evidence-based public health interventions. Beyond SARS-CoV-2, genomic surveillance has become increasingly important for monitoring influenza viruses, dengue virus, mpox virus, avian influenza viruses, respiratory syncytial virus (RSV), and other emerging pathogens with epidemic or pandemic potential. Despite remarkable progress, significant disparities remain in sequencing capacity, bioinformatics infrastructure, and access to genomic technologies, particularly in low- and middle-income countries. These limitations may delay outbreak detection and weaken global preparedness. This mini review summarizes recent advances in viral genomic surveillance, discusses its expanding applications in infectious disease control, highlights current challenges, and explores future opportunities for strengthening global surveillance systems. Sustained investment, international collaboration, and equitable access to genomic technologies will be essential for improving preparedness against future infectious disease threats.

Keywords: Genomic surveillance; viral genomics; next-generation sequencing; emerging viruses; public health; bioinformatics; pandemic preparedness; viral evolution

Abbreviations: NGS: Next-Generation Sequencing; WHO: World Health Organization; SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2; COVID-19: Coronavirus Disease 2019; RSV: Respiratory Syncytial Virus; RNA: Ribonucleic Acid; DNA: Deoxyribonucleic Acid

Introduction

The emergence and re-emergence of viral diseases continue to pose major challenges to global public health. Over the past two decades, outbreaks caused by Ebola virus, Zika virus, influenza viruses, SARS-CoV, Middle East respiratory syndrome coronavirus (MERS-CoV), SARS-CoV-2, mpox virus, and highly pathogenic avian influenza

viruses have demonstrated how rapidly infectious diseases can spread across countries and continents. These events have highlighted the need for surveillance systems capable of detecting pathogens early, monitoring viral evolution, and providing timely information to guide public health responses.

Traditionally, infectious disease surveillance relied on clinical observations, laboratory diagnostics, and epidemiological investigations. Although these approaches remain essential, they often provide limited information about viral evolution and transmission pathways. The introduction of genomic sequencing has fundamentally changed this landscape by allowing researchers to analyze

the complete genetic makeup of viruses with remarkable speed and accuracy. Genome sequencing not only confirms the identity of a pathogen but also reveals mutations, evolutionary relationships, geographic spread, and potential changes in transmissibility or pathogenicity.

The COVID-19 pandemic marked a turning point in the application of genomic surveillance. Thousands of viral genomes were generated and shared through international databases, enabling researchers to monitor the emergence of variants such as Alpha, Delta, and Omicron almost in real time. These genomic data informed vaccine updates, supported public health interventions, and enhanced understanding of viral transmission dynamics. More importantly, the pandemic demonstrated that genomic surveillance is no longer confined to research laboratories but has become an integral component of routine public health practice.

Beyond COVID-19, genomic surveillance is increasingly being used to monitor a wide range of viral pathogens. Seasonal influenza surveillance relies heavily on genomic information to identify circulating strains and guide annual vaccine formulation. Similarly, genomic analysis has supported investigations of mpox outbreaks, monitored the spread of dengue virus serotypes, and identified mutations associated with antiviral resistance in several clinically important viruses. These applications illustrate the growing importance of viral genomics across diverse areas of virology and infectious disease research.

Despite these achievements, important challenges remain. Many countries continue to experience limited access to sequencing technologies, insufficient bioinformatics expertise, fragmented surveillance systems, and inadequate long-term funding. Addressing these limitations is essential if genomic surveillance is to become a sustainable component of global health security rather than an emergency response measure activated only during major outbreaks.

This mini review discusses the evolution of genomic surveillance, its expanding role in infectious disease control, current challenges affecting implementation, and future priorities for strengthening global preparedness against emerging viral threats.

Evolution of Genomic Surveillance in Infectious Diseases

Advances in sequencing technology have transformed the study of infectious diseases. Early genomic investigations depended on Sanger sequencing, which provided accurate results but was labor-intensive and relatively slow. The introduction of next-generation sequencing (NGS) enabled simultaneous analysis of millions of DNA or RNA

fragments, dramatically reducing turnaround time while increasing sequencing capacity. These developments have made genomic surveillance faster, more affordable, and increasingly accessible to public health laboratories.

One of the greatest advantages of NGS is its ability to detect viral pathogens without requiring prior knowledge of the infectious agent. Metagenomic sequencing allows researchers to identify known viruses, discover previously unrecognized pathogens, and characterize mixed infections directly from clinical or environmental samples. This capability has expanded opportunities for investigating unexplained disease outbreaks and identifying viruses before they become widespread.

The increasing availability of portable sequencing platforms has further broadened the application of genomic surveillance. During recent outbreaks of Ebola virus disease and COVID-19, portable sequencing devices enabled near real-time genomic analysis in field settings, allowing researchers to generate sequence data much closer to the point of care. Such technologies have reduced delays associated with sample transportation and accelerated public health decision-making.

Equally important has been the development of bioinformatics tools capable of analyzing large genomic datasets. Phylogenetic analysis, mutation tracking, lineage assignment, and transmission network reconstruction have become routine components of genomic epidemiology. These approaches provide valuable insights into viral evolution and facilitate early identification of variants with potential epidemiological or clinical significance.

Applications of Viral Genomics in Disease Surveillance

Genomic surveillance has become an indispensable component of modern infectious disease control. By integrating genome sequencing with epidemiological investigations, researchers can better understand how viruses emerge, spread, and evolve over time.

One of its most important applications is early outbreak detection. Sequencing viral genomes from clinical samples allows investigators to identify newly emerging pathogens and determine whether infections originate from local transmission or imported cases. This information supports timely public health interventions and helps limit further spread.

Another major application is tracking viral evolution. RNA viruses, including influenza virus and SARS-CoV-2, accumulate genetic mutations as they replicate. Most

mutations have little biological significance, but some may alter viral transmissibility, pathogenicity, or immune recognition. Continuous genomic surveillance enables researchers to monitor these changes and assess their potential impact on disease control strategies.

Genomic data also contribute to vaccine development and evaluation. Monitoring viral evolution helps identify antigenic changes that may reduce vaccine effectiveness and informs the selection of vaccine strains. Seasonal influenza vaccination is a well-established example of how genomic surveillance directly supports immunization programs, while similar approaches are increasingly being explored for other viral pathogens.

In addition, genomic surveillance facilitates the detection of antiviral resistance. Sequencing viruses isolated from treated patients allows researchers to identify mutations associated with reduced susceptibility to antiviral drugs, supporting clinical management and informing treatment guidelines.

Conclusion

Genomic surveillance has become an indispensable pillar of modern infectious disease control, providing critical insights into viral evolution, transmission dynamics, and outbreak detection. The experiences gained during recent outbreaks, particularly the COVID-19 pandemic, have demonstrated that integrating genome sequencing into routine public health surveillance enables faster, evidence-based responses and strengthens preparedness against emerging viral threats. Beyond pandemic response, genomic surveillance continues to support vaccine development, monitor antiviral resistance, and improve understanding of pathogen evolution across diverse viral diseases.

Despite these advances, important challenges remain, including unequal access to sequencing technologies, limited bioinformatics capacity, fragmented surveillance systems, and inconsistent data-sharing practices. Addressing these gaps requires sustained investment, international

collaboration, and stronger laboratory networks that can generate and interpret genomic data in real time. Making genomic surveillance a routine component of global health systems, rather than an emergency measure, will enhance early detection of emerging pathogens and improve collective preparedness for future infectious disease outbreaks.

Declarations

Conflict of Interest

The author declares no conflict of interest.

Author Contributions

The author conceived the topic, reviewed the literature, drafted the manuscript, and approved the final version.

Ethical Approval

Not applicable. This mini review is based on published literature and does not involve human participants or animals.

Data Availability

No new data were generated or analyzed in this study.

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