



Viral Genomics: Transforming the Future of Infectious Disease Surveillance

Doty KA*

Kathryn Adams Doty, University of Pennsylvania, USA

***Corresponding author:** Kathryn Adams Doty, University of Pennsylvania, USA

Opinion

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Abstract

The rapid evolution of genomic technologies has transformed the field of virology, providing unprecedented opportunities to detect, characterize, and monitor viral pathogens. Over the past decade, viral genomics has evolved from a specialized research tool into an essential component of public health surveillance, outbreak investigation, and pandemic preparedness. The COVID-19 pandemic highlighted the value of real-time genome sequencing in tracking viral evolution, identifying emerging variants, and guiding public health interventions. At the same time, recent outbreaks of mpox, avian influenza, and dengue have reinforced the importance of integrating genomic surveillance into routine infectious disease monitoring. Despite remarkable technological advances, significant disparities remain in sequencing capacity, data sharing, and bioinformatics infrastructure, particularly in low- and middle-income countries. This opinion article argues that viral genomics should no longer be regarded as an optional research capability but as a core pillar of global health security. Sustained investment, international collaboration, and equitable access to genomic technologies will be essential for strengthening preparedness against future viral threats.

Keywords: Viral genomics; genomic surveillance; next-generation sequencing; emerging viruses; public health; infectious diseases; bioinformatics; pandemic preparedness

Introduction

The ability to read a viral genome has fundamentally changed the way infectious diseases are investigated and controlled. Only a few decades ago, identifying a virus often depended on virus isolation, serological testing, and labor-intensive laboratory techniques that required considerable time and expertise. Today, advances in next-generation sequencing (NGS) allow scientists to determine the complete genetic sequence of a virus within hours, offering insights that extend far beyond simple identification. Viral genomics has become an indispensable tool for understanding pathogen evolution, tracing transmission pathways, detecting mutations associated with immune escape, and

supporting the development of diagnostics, vaccines, and antiviral therapies.

The COVID-19 pandemic demonstrated the practical value of genomic surveillance on a global scale. Genome sequencing enabled researchers to monitor the emergence of variants such as Alpha, Delta, and Omicron in near real time, informing public health decisions and helping to evaluate the performance of vaccines and therapeutic interventions. This experience represented a turning point for virology. Genomic surveillance moved from being largely confined to research laboratories into the mainstream of public health practice, illustrating how molecular data can directly influence disease control strategies.

However, the importance of viral genomics extends well beyond SARS-CoV-2. Recent outbreaks of mpox, highly pathogenic avian influenza, dengue, chikungunya, and other emerging viral infections have highlighted the need for surveillance systems capable of detecting viral change before outbreaks escalate. In an increasingly interconnected world, where international travel, urbanization, climate change, and environmental disruption facilitate the spread of infectious diseases, early detection has become more important than ever. Viral genomics offers an opportunity to move from reactive outbreak response toward proactive surveillance that identifies potential threats before they become widespread.

Yet despite these achievements, access to genomic technologies remains uneven. While some countries have established sophisticated sequencing networks integrated into national public health programs, others continue to face significant challenges related to laboratory infrastructure, trained personnel, bioinformatics capacity, and sustainable funding. This imbalance limits the effectiveness of global surveillance because pathogens do not recognize geographical or political boundaries. Strengthening worldwide genomic capacity should therefore be viewed as a shared responsibility rather than an individual national objective.

From my perspective, the next phase of viral genomics should focus not only on technological innovation but also on practical implementation. Sequencing instruments alone do not improve public health outcomes unless they are supported by efficient surveillance systems, rapid data analysis, transparent information sharing, and coordinated public health action. Future investment should therefore prioritize building resilient genomic ecosystems that integrate laboratory science with epidemiology, clinical medicine, and public health decision-making.

The Evolution of Viral Genomics

The development of high-throughput sequencing technologies has transformed virology over the past two decades. Earlier methods often required prior knowledge of the suspected pathogen, limiting their usefulness when investigating unknown or newly emerging viruses. Modern sequencing platforms have largely overcome these limitations by enabling unbiased detection of viral genetic material directly from clinical and environmental samples.

This shift has broadened the role of virology from identifying individual pathogens to understanding the dynamics of entire viral populations. Researchers can now examine how viruses evolve within individual patients,

monitor the spread of viral lineages across regions, and detect mutations that may influence transmissibility, pathogenicity, or resistance to antiviral drugs. Such information provides valuable context that cannot be obtained through conventional diagnostic testing alone.

Equally important has been the integration of genomics with epidemiology. During outbreak investigations, combining viral genome sequences with clinical and demographic information allows investigators to reconstruct transmission networks with remarkable precision. This approach has improved our understanding of healthcare-associated infections, community transmission, and cross-border spread of emerging pathogens. As sequencing technologies continue to become faster, more affordable, and more portable, their application is likely to expand into routine disease surveillance at local, national, and international levels.

In my view, viral genomics should no longer be considered an advanced research technique reserved for specialized laboratories. It has become a practical public health tool with the potential to improve outbreak detection, guide intervention strategies, and support evidence-based policymaking. The challenge now is ensuring that its benefits are distributed equitably across all regions, regardless of economic resources or healthcare capacity.

From Sequence Data to Public Health Action

Generating viral genome sequences is only the beginning of the surveillance process. The real value of genomic information lies in its ability to inform timely public health decisions. During the COVID-19 pandemic, sequencing data helped identify variants with increased transmissibility, monitor their international spread, and assess whether existing vaccines remained protective. Similar approaches are now being applied to influenza viruses, respiratory syncytial virus, mpox, and arboviruses, demonstrating that genomic surveillance has broad relevance across multiple infectious diseases.

To maximize its impact, genomic surveillance should be integrated with traditional epidemiological investigations rather than operating as an independent activity. Clinical observations, laboratory findings, environmental monitoring, and genomic analyses each contribute unique information, but together they provide a more complete picture of disease transmission. This multidisciplinary approach enables health authorities to identify emerging threats more rapidly and implement interventions before outbreaks become difficult to control.

Conclusion

Viral genomics has become one of the most influential advances in modern virology, fundamentally changing how infectious diseases are detected, monitored, and controlled. The experience gained during recent viral outbreaks, particularly the COVID-19 pandemic, has demonstrated that genome sequencing is no longer confined to research laboratories but is an essential component of effective public health surveillance. By enabling rapid pathogen identification, monitoring viral evolution, and supporting evidence-based interventions, genomic technologies have strengthened our ability to respond to emerging infectious threats.

Despite these achievements, the full potential of viral genomics will only be realized through sustained investment in sequencing infrastructure, bioinformatics capacity, workforce development, and international collaboration. Equitable access to genomic technologies, transparent data sharing, and the integration of genomic information with epidemiological surveillance should become global priorities. Looking ahead, viral genomics must evolve from an emergency response tool into a routine element of infectious

disease surveillance, ensuring that future outbreaks are detected earlier, understood more comprehensively, and managed more effectively. Strengthening these capabilities today will enhance global preparedness and contribute to a more resilient public health system for generations to come.

Declarations

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