

## Review Article

# Application of Genomic Studies in Epidemiological Surveillance: A Mini-Overview

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**Abstract**

The 21st century has already seen the emergence of four viral pandemics (Zika virus, 2009 H1N1 influenza virus, 2014 Ebola virus in West Africa and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)). The recent upsurge in certain diseases clearly indicates the need for continuous epidemiological surveillance and real-time monitoring of infectious diseases. Incorporating genomics into epidemiological surveillance offers a route to improve the overall health system. Recent advances in genomics and next-generation sequencing approaches provide new paradigms for monitoring transmission pipelines and reducing overall morbidity and mortality. In this mini-review, we highlight the advances in genomics, how they have been critical in epidemiological surveillance and monitoring outbreaks, and how they can help predict and monitor possible future outbreaks.

**INTRODUCTION**

“In both the business world and the realm of public health, the maxim ‘You can’t fix what you don’t measure’ holds true. Epidemiological surveillance plays a vital role in measuring the scope of an epidemic, enabling us to address the issue effectively. Recent experiences with Ebola and COVID-19 have underscored the importance of continuous epidemiological surveillance, rapid diagnosis, and real-time tracking of emerging infectious diseases [1-3]. By closely monitoring the spread of disease, epidemiological surveillance allows us to identify patterns of progression and develop timely preventive and control measures [4]. Regrettably, accurately diagnosing diseases and monitoring infectious diseases still pose challenges, particularly in low- and middle-income countries (LMIC). Despite efforts to enhance epidemiological surveillance, these LMICs, particularly in Africa, struggle to accurately identify, diagnose and report communicable diseases [2,5,6].

The emergence of COVID-19 has highlighted the role of integrating genomics into disease surveillance, presenting valuable insights. Similarly, the Ebola outbreaks in sub-Saharan Africa, characterized by alarming fatality rates of up to 90% [7], served as eye-opening experiences with significant lessons learned. While progress has been made in vaccine design and discovery, preventive strategies and supportive therapy remain

the primary options available for high-risk individuals and infected patients [8]. Consequently, there is an urgent need for early and prompt detection of diseases.

Real-time investigation and epidemiological surveillance are critical for increasing awareness and timely infection control and prevention. Integrating genomic studies into disease detection is very vital for attaining and building a robust digital and pathogen surveillance system [9]. There is also a need for prompt epidemiological surveillance to understand the circulating infection clones and lineages, their genomic features and how best to control and prevent their spread. Therefore, in this mini-review, we briefly discussed the advances in genomics and how they have been critical in epidemiological surveillance and monitoring outbreak. We also highlighted how robust epidemiological surveillance can help to predict and monitor possible future outbreaks.

**Epidemiological Surveillance in Disease Tracking and Monitoring**

Epidemiological surveillance refers to the systematic gathering, analysis, and distribution of health information to facilitate the planning, execution, and evaluation of public health initiatives [10]. It involves vigilant monitoring of health events that may arise within a population. Typically integrated into healthcare systems, epidemiological surveillance serves

as a fundamental component for monitoring significant health occurrences. Its primary objective is to enhance and fortify disease surveillance and other health-related activities within public health programs [11].

The significance of epidemiological surveillance is exemplified by its crucial role in combating infectious diseases. For instance, a study conducted in Wuhan, China, employed a susceptible-exposed-infectious-removed (SEIR) mathematical model to estimate the epidemiological parameters of Covid-19 before the implementation of preventive measures. The findings revealed that if these measures had been initiated 1, 2, or 3 weeks earlier, the number of cases could have been reduced by 66%, 86%, and 95%, respectively [12]. This study underscores the vital role of surveillance not only in controlling Covid-19 but also in managing various other diseases.

According to the WHO, epidemiological surveillance contributes to combating diseases in several ways [13]. It can help to define the health problem properly. This is because a health problem must be well-defined before it can be solved. Generating data that aid public health officials in comprehending both established and emerging infectious and non-infectious diseases holds immense significance. Without a comprehensive grasp of the health problem, including its causes, distribution, and infection establishment mechanisms, addressing the issue and implementing effective improvements becomes arduous. Vital data typically gathered includes details about the pathogen, such as its specific clone and lineage, the symptoms it induces, the affected population, as well as morbidity and mortality rates [14]. In the absence of robust surveillance, public health officials would be navigating health problems blindly, squandering valuable resources.

Moreover, when data from surveillance programs are compiled and analyzed, a clear picture of the issue can be seen, leading to the development of appropriate health intervention [13]. Also, continued surveillance is very vital for monitoring and evaluating an already-established program [7]. In addition, the significance of surveillance systems that collect precise data on diseases and geographic regions cannot be overstated in assessing the importance of a particular health event [15]. Accurate information regarding the distribution and prevalence of diseases is indispensable and typically forms the foundation for decision-making by funders and governmental authorities.

### The Role of Genomics in Epidemiological Surveillance

There are different classification of genomics which has been studied and exploited for different purposes. For example, structural genomics involves determining the structure of every protein encoded by the genome [16,17]. It involves characterizing the genome structures in terms of the protein constituent [18]. There is also functional genomics which involves describing gene and protein functions by using sequencing techniques [19]. Functional genomics seeks to unravel the collaborative functioning of individual elements within a biological system to manifest a specific phenotype. It specifically investigates the

dynamic expression of gene products in a given context [20]. Additionally, comparative genomics endeavours to scrutinize genomic attributes across diverse species. By doing so, it facilitates the examination of evolutionary alterations among organisms, aiding in the identification of genes that are either conserved or shared across species, as well as genes responsible for unique characteristics exhibited by each organism [21]. Essentially, comparative genomics utilizes diverse tools to juxtapose complete genome sequences of distinct species, enabling the discovery of genetic and genomic variations and similarities [22].

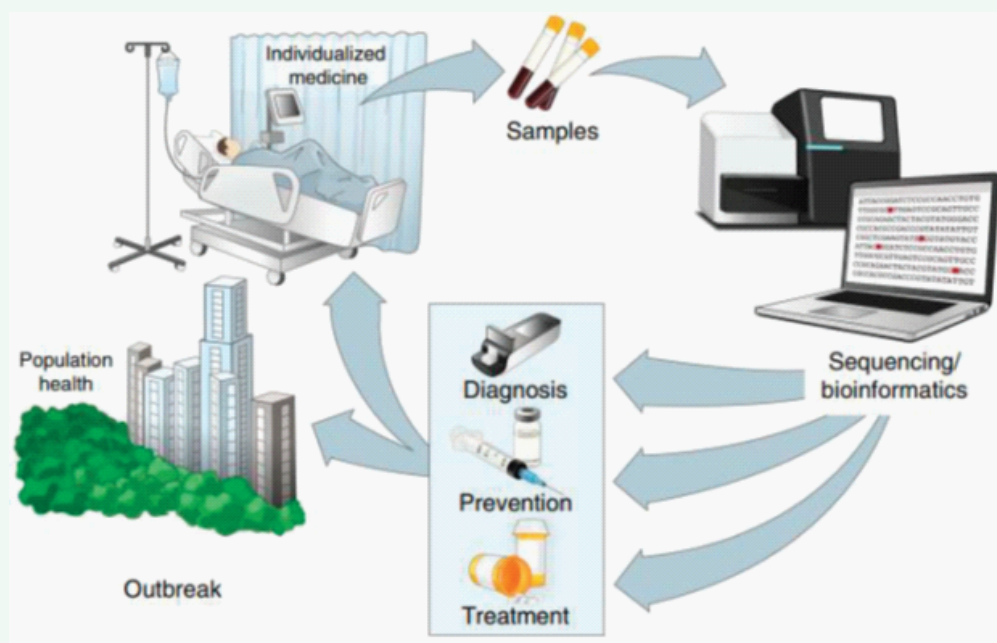
Therefore, when genomic and epidemiological data analyses are integrated, they can provide a real-time picture of an outbreak. Genomic epidemiology can inform the rapid deployment of targeted interventions (Figure 1) to protect the public as an outbreak unfolds. The application of genomic studies and epidemiological studies to combat infectious is very vital and needs to be implemented at all levels in different regions. This also requires certain comprehensively collaboration to efficiently harness the potential in mitigating and containing outbreaks and the spread of infectious variants.

The utilization of genomic data holds significant practical implications for the field of public health, specifically in infectious disease control. By employing whole genome sequencing (WGS) techniques, it is now possible to analyze pathogens directly from clinical samples, thereby providing valuable information during disease outbreaks, especially when prior knowledge of mutation-related characteristics such as virulence, drug susceptibility, and antigenicity is available [23]. This data can further facilitate point-of-care molecular diagnostics and aid in tailoring personalized treatment approaches, similar to the application of human genetic data in precision medicine [24].

At a broader population level, the integration of genomics with epidemiological data enables the identification of pathogen mutations as indicators of transmission events. This approach offers a detailed understanding of epidemic transmission patterns at a fine-scale resolution, empowering the development of more precise and targeted large-scale public health interventions compared to traditional methods [11]. In essence, the genomic sequencing of pathogens aligns with the One Health approach, which encompasses the interconnectedness of human, animal, and environmental health. By employing genomic epidemiology, the surveillance, prevention, and control of diseases can be facilitated within the framework of the One Health approach [9].

### Improving Preparedness and Response to Epidemics through the Application of Genomic Studies in Epidemiological Surveillance

The emergence of infectious diseases, such as COVID-19 and the Ebola virus disease, represents a significant peril to public health [2]. Despite the Ebola virus being present in central and west Africa for many years, numerous African nations have not fully embraced the use of genomic studies and epidemiological surveillance in public health. The inclusion of genomic data is



**Figure 1:** Precise Interventions Informed by Pathogen Sequencing during Infectious Disease Outbreaks [25]. 2019).

crucial for achieving a sufficient level of detail in monitoring local transmission and understanding the routes and timing of pathogen importation between countries. Additionally, the genomic surveillance of evolving pathogens in LMIC has the potential to guide the development of tailored and effective molecular assays for treatment and prevention. It can also aid in monitoring factors that contribute to the adaptation and virulence capabilities of these pathogens.

Furthermore, data from genomic surveillance is very crucial for vaccine design. For most viral diseases, there are commercially available vaccines [3]. However, there are no available vaccines for other pathogens like bacteria and even fungi. Genomic data is crucial to developing and designing an efficient vaccine to help curtail the infectious disease crisis. This data type is essential in understanding the exact clones and lineages circulating in most regions. Identifying antigenic components (usually surface-exposed materials) that could be leveraged to design vaccines is also important, and this type of data can only be generated with the help of genomics.

Therefore, genomic data is not only utilized in investigating known outbreaks or epidemics; they have other crucial importance. Another important aspect of omics techniques is metagenomics and transcriptomics [25]. The utilization of these two advancements holds great potential for diagnosing unknown infections and enhancing our understanding of circulating microbial pathogens. Such knowledge is vital for informed preparedness and control measures against future epidemics. Particularly in regions with limited resources and infrastructure, like LMIC, significant investments in infrastructure for research

and capacity development are still required to fully harness the benefits of genomic studies. By offering adequate support to local institutions engaged in genomics research, these institutions can serve as key hubs for investigating future epidemics or pandemics. It is also imperative to advocate for the widespread adoption and integration of genomics in public health across various regions and at all levels. However, strengthening genomic-based epidemiological surveillance systems requires collaborative efforts at different levels as previously mentioned.

Given the continuous shifts in climate, biodiversity, and human behaviour, it is imperative to recognize the immense significance of genomics. In view of the fact that LMICs, particularly Africa bear the greatest burden of endemic infectious diseases, the integration of genomics into public health holds the potential to save countless lives, both within the affected regions and beyond.

### Limitations and Challenges in Integrating Genomics Studies in Epidemiological Surveillance

While new initiatives are being established, the effectiveness of these efforts is hampered by various limitations, including inadequate funding, poor coordination, limited capacity for data integration, non-representative data, and a lack of properly trained personnel with the necessary expertise. Furthermore, instability in governance and poor policy-making at local and national levels has led to fragmented approaches and inconsistent capabilities.

Surveillance does not need to be flawless to be valuable; however, it can have limitations, particularly in terms of underreporting, lack of representativeness, and timeliness, which

undermine its usefulness. It is important effort is integrated into devising and implementing measures to overcome these challenges. For most notifiable diseases, surveillance data relies on passive reporting by physicians and other healthcare providers. Underreporting significantly delays effective action and allows preventable cases to occur due to delayed reporting and the delayed implementation of control measures.

Another critical issue is the lack of representativeness in reported cases. Underreporting is neither consistent nor random. Two significant biases distort the completeness of reporting. Firstly, healthcare providers are more likely to report cases that involve severe illness and hospitalization, neglecting milder cases, despite individuals with mild illness being more likely to transmit the infection to others due to their unrestricted movement. Consequently, this bias leads to an inflated estimate of disease severity, such as the death-to-case ratio. Secondly, healthcare providers are more inclined to report cases when the disease garners media attention. This bias results in an underestimation of the baseline disease incidence once media coverage diminishes.

Timeliness is yet another issue. Delays in collecting, analyzing, and disseminating data on notifiable diseases can occur at various stages. The causes of these delays vary, including disease-specific factors. For instance, certain diseases require confirmatory laboratory tests before physicians can make a diagnosis. Complicated or inefficient reporting procedures can also contribute to delays. Furthermore, delays in analysis commonly occur when surveillance is not regarded as a program that provides actionable information. Ultimately, delays at any stage can lead to delays in disseminating information, leaving the medical and public health communities without the timely data they need to take swift action.

There are problems of inadequate financial resources in Africa to fund genomic studies of the entire region. Funding is an important aspect of genomic studies, which could be obtained through the government or private sources of funds. Also, most surveillance programs are complex. Traditional and outdated methods of genomic surveillance are still in place, and this should be displaced as soon as possible. Modern surveillance methods should be adopted to yield more authentic results, which will lead to more effective real-time preparedness and response to emerging epidemics.

## RECOMMENDATIONS AND CONCLUSION

There is a need for improved awareness of practitioners. It is crucial for all individuals engaged in epidemiological surveillance to acknowledge their responsibility. The health department must take an active role in disseminating information about the list of reportable diseases and the mechanisms employed for genomic surveillance. Practitioners should always develop their skills by constantly studying in order to combat the future emergence of diseases. There is also a need for simplified reporting. Genomic surveillance data should be as simple as possible.

Moreover, feedback plays a crucial role that cannot be emphasized enough. It can take various forms, such as written communication like a monthly newsletter, or oral updates provided during regular medical staff meetings. To be effective, the feedback should be timely, informative, engaging, and tailored to each healthcare practitioner. Additionally, it should encompass valuable insights into disease patterns and control activities, thus promoting awareness and reinforcing the importance of active involvement in meaningful public health initiatives.

In the past, surveillance of notifiable diseases heavily relied on reports from physicians. However, nowadays, almost all state mandate that commercial and hospital laboratories report positive cultures or diagnostic tests for notifiable illnesses. In some instances, the number of laboratory reports surpasses those from physicians, hospitals, clinics, and other sources. Expanding the scope of surveillance involves utilizing additional healthcare personnel, such as infection control personnel and school nurses, as sources of surveillance data. Another effective approach is to develop alternative methods for conducting surveillance, such as leveraging secondary sources of data. This approach has proven successful in monitoring influenza outbreaks.

Moreover, adequate financial resources, especially in LMIC, cannot be overemphasized. Therefore, there should be an adequate source of finance through the government or other financial establishments. Also, the Implementation of mathematical modelling is very vital. Therefore, mathematical fields such as modelling should be leveraged as it could help to understand past and current diseases, which gives insights and makes it easier to forecast the nature of emerging diseases.

In general, the close interactions among humans, animals, and the environment pose a risk for the emergence of infectious diseases, and this risk is increasing. Consequently, it is crucial to focus on understanding the intricate dynamics between humans, animals, and the environment, as well as the various farming systems and their bio-security levels. Preventing the introduction of diseases through vaccination, and swiftly controlling outbreaks through containment measures are essential aspects of preparing for future epidemics and pandemics. The COVID-19 pandemic has highlighted the critical significance of collaboration that goes beyond conventional infrastructures, networks, and disciplines. This collaboration also extends to leveraging genomics and open data infrastructures. The ongoing investments in global genomic surveillance hold tremendous potential, as long as we avoid repeating the mistake of developing them exclusively for the immediate situation but rather for future possible health events.

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