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The Surveillance in Infectious Disease Control Role of Genomic

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Abstract

Infectious disease surveillance is central to global public health, enabling the early detection, monitoring, and control of outbreaks. Traditional surveillance methods—relying on clinical diagnoses, laboratory confirmation, and epidemiological investigations—are often constrained by delays, underreporting, and limited resolution in differentiating pathogen strains. The integration of genomic technologies has transformed infectious disease control, offering unprecedented precision and timeliness. High-throughput sequencing, whole-genome sequencing, and metagenomic approaches allow for rapid pathogen identification, antimicrobial resistance (AMR) detection, and real-time outbreak investigation. The COVID-19 pandemic highlighted the power of genomic surveillance in tracking variants, informing vaccine updates, and guiding public health responses. Beyond viral threats, genomics has proven critical in monitoring multidrug-resistant tuberculosis, methicillin-resistant *Staphylococcus aureus* (MRSA), and foodborne pathogens. Despite these advances, challenges remain, including disparities in global sequencing capacity, data-sharing limitations, privacy concerns, and high infrastructure costs. This review underscores the transformative potential of genomics in infectious disease surveillance while emphasizing the need for equitable access, international collaboration, and ethical governance. As sequencing becomes increasingly affordable and integrated with bioinformatics and artificial intelligence, genomic surveillance is poised to become a cornerstone of resilient, responsive, and precision-driven public health systems worldwide.

Keywords: Infectious Disease, Genomic, COVID-19, Antimicrobial Resistance (AMR)

1. Introduction

Infectious disease surveillance is the most important part of public health systems around the world. It means the ongoing, organized gathering, analysis, interpretation, and use of health data to find, stop, and control the spread of disease outbreaks. Classical surveillance methods, while are important, sometimes rely on clinical diagnoses, lab tests, and epidemiological investigations, which can take time and can be wrong. Genomics has been added to surveillance efforts during the past ten years, and this has changed the way public health authorities find, track, and respond to infectious diseases in ways that have never been possible before [1]. In the past, passive reporting systems were used for infectious disease surveillance. In these systems, labs and healthcare practitioners told health authorities about particular infections that needed to be reported. Health authorities utilize both active and passive systems. Active surveillance means that health authorities look for cases directly by staying in touch with providers or examining hospital records on a regular basis. Syndromic surveillance, which looks at clinical symptoms instead of proven diagnoses, is now a crucial way to find outbreaks early, especially in emergencies [2]. These methods are important, but they have their limits. For instance, underreporting is common, especially in places with few resources where it may be hard to make a diagnosis. It might be hard to respond quickly to public health issues when there are weeks or more between when a case starts and when it is reported. Traditional surveillance also doesn't provide you the level of detail you need to tell different strains of diseases apart. This capacity can help you figure out where an outbreak started or how it spreads [3].

Genomic surveillance is the use of high-throughput sequencing tools to look at the genetic material of a pathogen. Scientists can find mutations, track transmission chains, and signal new variants with a high level of accuracy by looking at the genomes of bacteria, viruses, and other infectious organisms [4]. The COVID-19 pandemic has brought attention to the use of genomes

in tracking infectious diseases all across the world. Scientists were able to keep track of novel variants like Delta and Omicron in real time because the SARS-CoV-2 genome sequencing was so fast. Genomic data were very important for changing vaccinations, diagnostics, and public health advice. The epidemic showed how useful genomics may be and how important it is for countries to work together, share knowledge, and invest in sequencing technology.

Genomic information adds to what we already know about epidemiology. For example, it might be able to tell if cases in different places are linked or if they represent distinct introductions of an infectious agent. This helps health officials decide how to use their resources and what control techniques to use. Genomics is the latest way to look into foodborne diseases. It replaces current subtyping procedures with speedier ways to find outbreaks and sources. One of the best things about genomics is that it can find and classify pathogens before they cause big outbreaks. Genomic monitoring can give early warnings of zoonotic spillovers by keeping an eye on pathogens in animal reservoirs or the environment. This is significant because new infectious diseases are becoming more common as a result of climate change, globalization, and environmental devastation [5].

Another big benefit is that it helps keep an eye on antimicrobial resistance (AMR). Whole-genome sequencing can find genes that are resistant to antibiotics. This helps keep track of where resistant strains are going and helps doctors decide how to treat them. This skill is very important because AMR is still a worldwide health problem. Genomic surveillance also helps with real-time investigations of epidemics. If the right infrastructure is in place, sequencing can be done fast and findings may be shared around the world. This makes responses from different countries more coordinated. Phylogenetic trees and monitoring mutations are two examples of applications that can help us learn about how pathogens change and spread over time [6].

Genomic monitoring has a lot of potential, but it also has certain problems. Even while the cost of sequencing tools is going down, it still costs a lot to buy the equipment, hire bioinformatics experts, and hire people. It also takes skill to analyze and evaluate data, especially when it comes to telling the difference between harmful mutations and harmless ones. Equity is another important issue. Countries with low and intermediate incomes have a harder time getting genetic tools, which means that data and epidemic detection are not as widely available around the world. For a global health security network to perform well, low- and middle-income countries need to be able to keep an eye on things better [7].

2. Traditional Methods of Infectious Disease Surveillance

For years, traditional surveillance methods including closed-circuit television (CCTV), physical security patrols, and static monitoring stations have been very important for keeping people safe and protecting sensitive areas. However, as society changes and becomes more dangerous, traditional ways of watching people have a lot of problems and restrictions that make them less useful in today's world [8]. The most significant problem with traditional surveillance is that it can't be easily supervised and used in many places. Static cameras can only see certain angles and areas, which can leave blind zones that are easy to miss. Adding more cameras, cabling, and command centers to increase coverage costs a lot of money in terms of infrastructure. Adding these systems to buildings that are already there is also a disruptive and time-consuming process, especially in older structures or vast open areas [9].

Another big problem is relying too much on human operators. Security workers have to see and understand a lot of material from surveillance equipment. People's attention is restricted by nature, and it is impossible to stay on guard all the time. This makes it more likely that things will be missed, responses will be late, or judgments will be wrong. People may also view and respond to security film differently because they are tired, distracted, or even prejudiced [10]. Traditional surveillance also has to deal with the difference between reactive and proactive capabilities. Most traditional systems work by documenting occurrences instead of predicting or stopping them. Instead of stopping threats in real time, they are more often employed for forensic purposes, such as reporting evidence after an event has happened. This ability to react makes monitoring less efficient at stopping crime or quickly responding to emergencies [11].

Another big problem is privacy. There are moral and legal issues with static surveillance systems in public places because they allow for a lot of mass observation and take away people's privacy. People may not trust the system or file lawsuits if there aren't clear rules or regulations about how to store film, who may access it, and how long to keep it. Without proper oversight, surveillance technology could be used for intrusive or unauthorized monitoring [12]. Also, technology that is out of date is always a problem. Most old-fashioned surveillance systems use old technologies that aren't adaptable or able to work with other systems, which is what we need in today's digital world. They might not be able to do things like real-time analysis, remote access, or high-definition photography, which makes them less useful in fast-moving or complicated circumstances. Upgrading legacy systems is frequently too expensive and requires making big changes to the current infrastructure [13]. Finally, people are also quite worried about how to store and handle data. Surveillance systems create a lot of data that needs to be kept safely, sorted, and made easy to find. Traditional methods may not have the tools to handle this much data properly, which could lead to lost data or trouble getting vital footage at the wrong time [14].

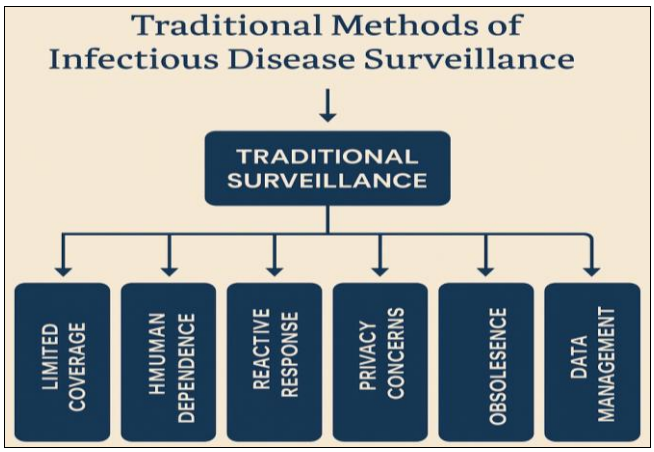

Fig 1: Traditional Methods of Infectious Disease Surveillance

Although traditional methods of surveillance have helped with security and monitoring in the past, but they are no longer able to meet today's needs. Their problems, like limited coverage, dependence on human observation, reactive response, privacy concerns, obsolescence, and data management, show how much we need better, more integrated, and smarter ways to keep an eye on things to meet current and future security needs [15].

3. Genomics in Infectious Disease Control

Genomic technologies have changed the biological sciences by giving us more knowledge than ever about the structure, function, and evolution of genomes. Genomic technologies are a lot of different tools and methods for looking at all of the genetic material in a genome. Their main goal is to figure out how genes work, how they are controlled, and how they interact with one other in living things by sequencing, interpreting, and changing DNA and RNA [16]. DNA sequencing, or next-generation sequencing (NGS), is one of the oldest genomic technologies. It lets you quickly sequence complete genomes or specific areas with a lot of accuracy and capacity. NGS can sequence millions of pieces of DNA at the same time, which makes it great for complex analysis like whole-genome sequencing, exome sequencing, and RNA-seq (transcriptome profiling) [17]. Polymerase Chain Reaction (PCR) is another important tool that can make some DNA sequences bigger. It is widely used in cloning, diagnostics, and forensic science. Real-time PCR (qPCR) and digital PCR have taken this method even farther by adding quantitative analysis and higher sensitivity [18].

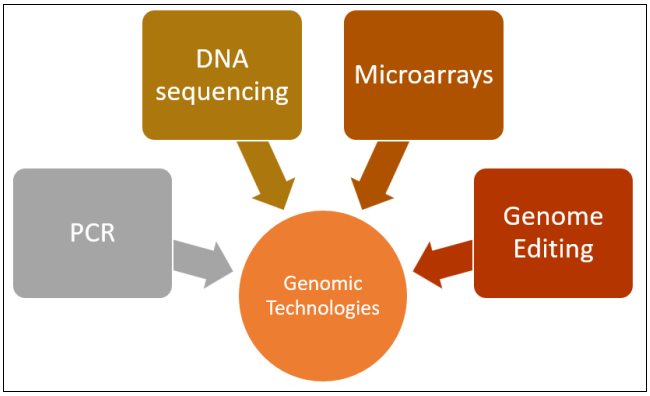

Fig 2: Genomics in Infectious Disease Control

Microarray technology isn't as common these days because of NGS, but it's still valuable for genotyping and gene expression studies. It is a way to hybridize tagged DNA or RNA with a chip that has hundreds of probes on it. This lets scientists look at expression levels or detect SNPs across the whole genome. Functional genomics has reached a new level with CRISPR-Cas9 and other genome-editing techniques. Researchers can now accurately edit the genome, which lets them remove or change specific genes to study how they work or make gene therapies. More and more people are choosing CRISPR because it's simple, effective, and flexible [19].

There are many different ways to employ these genetic tools. They have made personalized or precision medicine possible in the medical world, where therapies are made to fit a person's genetic composition. Genomic studies help find mutations that cause diseases, forecast how drugs will work, and plan tailored treatments, especially for cancer, uncommon genetic diseases, and infectious diseases. Genomic technologies are used in farming to increase crop yields, make crops more resistant to disease, and improve their nutritional value through marker-assisted selection and genetic enhancement. Genomic selection is also used in cattle breeding operations to generate animal populations that are more productive and stronger [20]. Genomics helps with biodiversity study, conservation, and ecosystem monitoring in environmental science. For example, metagenomics can look at genetic material taken directly from environmental samples. Forensic genomics is also utilized to solve crimes, identify victims of disasters, and trace family trees. It uses DNA profiling and other genetic markers to find a person or figure out how they are related to other people. Genomic technology has completely changed biological research and how it is used in various fields. As these technologies develop better faster, cheaper, and more generally available they will help us learn more about life at the molecular level and open us new ways to innovate and discover [20].

4. Pathogen Identification and Tracking Using Genomic Data

In the past, culture procedures, biochemical assays, and microscopy were used to find infectious agents. These methods are helpful to some extent, but they take a lot of time, are only somewhat sensitive, and might not find new or picky infections. Since they became available, genomics, especially next-generation sequencing (NGS) and whole genome sequencing (WGS), have changed the way we identify microbes. Genomics is now a key part of both speeding up and making the identification of infectious agents more accurate. This makes it an essential tool in modern microbiology, epidemiology, and clinical diagnostics [21].

One of the best things about genomics is that it can find pathogens without having to grow them first. This is very helpful for finding organisms that grow slowly or can't be grown in a lab, like Mycobacterium leprae or some viruses. For instance, metagenomic sequencing lets you look directly at the genetic material in a sample, such blood, cerebrospinal fluid, or tissue, and find all the microbial species that are present. This speeds up diagnosis and also makes it more likely that rare or unexpected pathogens may be found [22]. Genomics also gives us incredibly accurate genetic data that makes diagnoses more accurate. Because their phenotypic traits are similar, traditional methods sometimes don't work to correctly identify closely related species. Genomic sequencing, on the other hand, may tell different strains of organisms apart by looking at their unique genetic signatures. This level of accuracy is very important in clinical settings where the right identification is needed to make treatment regimens, especially when it comes to antibiotic resistance or emerging infectious diseases [23].

Genomics also does better when it comes to speed. It can take days to weeks for conventional cultures to grow, especially in the case of pathogens like tuberculosis. In comparison, genomic technologies can give results in a matter of hours to a few days. Rapid sequencing technology makes it possible to track the spread of pathogens almost in real time, which makes public health interventions happen faster. Genomic surveillance has been very important for keeping an eye on viral changes and transmission chains

during disease outbreaks like COVID-19 or Ebola. This has made containment efforts much more effective [24]. With multiplex sequencing, genomics also makes it possible to find numerous infections in one test. Genomics can help figure out how different microbes interact with each other in polymicrobial illnesses, which are infections caused by more than one type of microbe. It can also find each pathogen that is involved. This whole-person view leads to better treatment plans and better outcomes for patients [25].

Genomics is also used to find and figure out antimicrobial resistance (AMR), in addition to identification. Genomic data can find resistance genes in bacterial DNA, which can tell us how the microbe will respond to different drugs. This genomic information can help doctors make smart treatment decisions with fewer broad-spectrum antibiotics, which lowers the risk of microorganisms becoming resistant. Genomics has a lot of effects on public health, not only on how doctors treat individual patients. Being able to quickly and accurately identify pathogens at the genome level makes it possible to effectively find and track outbreaks. Genomic epidemiology methods, for example, can help improve infection management and policymaking by tracking the sources of infections in hospital-acquired infections or foodborne outbreaks [26].

Genomic diagnostics have their pros and cons, though. High costs, the need for specialist equipment, and the need for skilled bioinformatics support might make it hard to get to, especially in places with few resources. Still, genomic technologies are becoming more widely available thanks to continual improvements in portable sequencers, automated pipelines, and cloud computing analytic tools [27]. Finally, genomics has changed the way we find infectious pathogens, making it faster and more accurate than ever before. The use of genetics in the management of infectious disease has improved our ability to respond swiftly and effectively to both known and unknown threats, from individual diagnosis to multinational surveillance. As technology continues to improve, genomics will play an increasingly important role in finding viruses that are harmful to humans and public health [28].

5. Genomic Epidemiology and Outbreak Investigation

Genomic monitoring is now an important tool for keeping an eye on epidemics of infectious diseases as they happen. Scientists can see how illnesses change, spread, and respond to restrictions by looking at the genetic material of the pathogens. The COVID-19 pandemic brought genomic monitoring to the world's attention, but it can be used for more than just one virus. Genomic monitoring gives public health officials the important information they need to respond more swiftly and effectively to new threats, from tracking epidemics of different strains of influenza to tracking antibiotic resistance [29]. Pathogen genome sequencing from patient samples is a key part of genomic monitoring. Researchers can use this information to find mutations and compare virus or bacterial strains from different places and times. Genomic surveillance gives public health agencies a head start in halting the spread of novel variations or outbreaks when it is used in real time. For instance, genomic surveillance helped governments change their response plans when novel COVID-19 variations like Delta and Omicron were found [30]. The ability to find and follow transmission chains is one of the best things about real-time genomic surveillance. Researchers can figure out how an outbreak is going by comparing the genetic fingerprints of different diseases. They can also tell if there are several introductions or just one source. This information is very important for making plans for things like focused lockdowns, vaccination efforts, or travel bans. Genomic surveillance also helps us figure out how well vaccinations and treatments work. If a pathogen changes, some of those modifications might help it get around the immune system, making medicinal countermeasures less effective. Researchers can quickly find these changes and use them to improve vaccines or create new therapies by watching them in real time. During the COVID-19 pandemic, this was especially essential because sequencing data was used to adjust booster tactics to work with new strains [31]. To do real-time genomic monitoring, you need a lot of infrastructure, like sequencing capacity, bioinformatics tools, and skilled workers. To build and keep up this kind of capacity, governments, universities, and international organizations need to work together. GISAID and Nextstrain are two platforms that have made it easier to share data around the world. They let genetic data be shared quickly and show how pathogens adapt across national borders [32].

Genomic surveillance does have some problems, though, especially in places with few resources. Data sharing can be less effective when there aren't enough resources, infrastructure, or people who don't want to share data. Fixing these problems is necessary for the world to be able to work together to fight infectious illnesses. For genetic surveillance systems to work well in the long term, they will need money for training, capacity building, and fair access to data. Genomic surveillance is a game-changing way for public health to keep an eye on outbreaks in real time. It helps us detect, understand, and respond to infectious threats better by giving us a lot of information about how viruses' genomes change over time. As infectious diseases continue to pose a threat to global health, improving genomic surveillance will be essential for building strong, flexible health systems that can stop the spread of new outbreaks [33].

6. Antimicrobial Resistance (AMR) and Genomic Insights

Antimicrobial resistance (AMR) is an increasingly large-scale global health crisis poised to undermine years of medical advances. While pathogens adapt to resist the action of antibiotics and other antimicrobial products, infections become more difficult and even impossible to cure. Here, genomics the examination of the total genetic material of organisms—has become a formidable tool to identify, comprehend, and fight AMR threats more effectively and accurately than before [34]. Among the most important functions of genomics in the identification of AMR is fast and precise detection of genes that cause resistance. Whole genome sequencing (WGS) enables researchers to study the entire DNA composition of bacterial pathogens, which makes it possible to identify resistance genes. In the case of multi-drug resistant (MDR) bacteria, such identification is especially significant because classical phenotypic tests can take days or even weeks. Genomic information can reveal insights within a matter of hours and direct clinicians to choose the right treatments early on and prevent the abuse of ineffective antibiotics [35].

Genomics also plays an important role in surveillance and monitoring the dissemination of resistant strains. Through

the comparison of bacterial isolate genomes from various patients, locations, or time points, public health officials can trace the source and transmission patterns of resistant pathogens. This has been crucial in monitoring hospital outbreaks and following the global spread of high-risk clones such as carbapenem-resistant Enterobacteriaceae (CRE) or methicillin-resistant Staphylococcus aureus (MRSA). This information informs infection control practices and national policy reactions [35].

Another important use is the discovery of resistance mechanisms. Genomics not only detects known resistance genes but also new mutations and mechanisms of resistance. Detailed comprehension is useful for creating new antibiotics or other treatments and forecasting future patterns of resistance. For instance, detection of mutations in bacteria's gyrA gene can forecast resistance to fluoroquinolones so researchers can anticipate treatment problems before they become unmanageable [36].

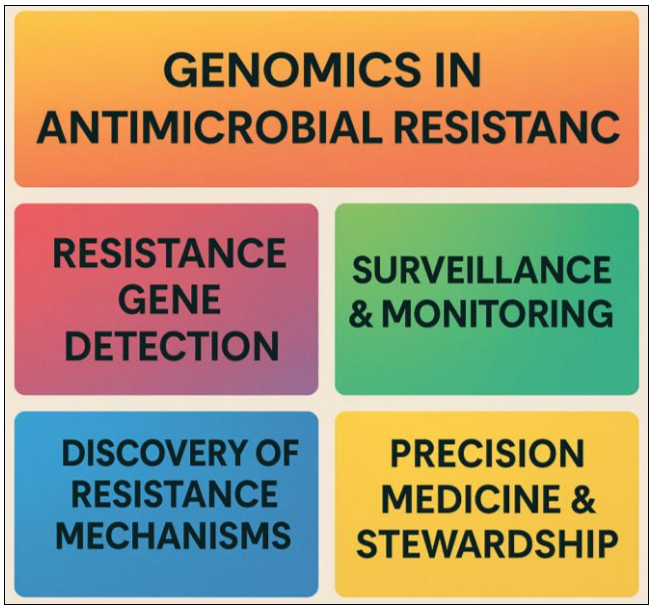

Fig 3: Antimicrobial Resistance (AMR) and Genomic Insights

In addition, genomics enables precision medicine and antibiotic stewardship. By correlating genomic information with clinical data, clinicians are able to individualize treatment regimens and reserve broad-spectrum antibiotics for only those situations where they are truly needed, reducing the selection pressure favoring resistance. Genomic databases, including the Comprehensive Antibiotic Resistance Database (CARD), and software programs such as ResFinder are becoming more widely utilized in diagnostic laboratories to aid real-time decision-making [37]. The combination of genomics with bioinformatics and artificial intelligence is again augmenting the capacity to counter AMR. Machine learning algorithms, based on training with genomic data, can accurately predict resistance, facilitating more rapid diagnosis and preparedness for outbreaks. With decreasing cost and increasing accessibility of sequencing technology, even low-resource environments can be supported with portable sequencers for local monitoring of AMR [38]. Genomics is transforming the identification and control of AMR risks. It allows for quicker, more precise diagnosis, in-depth surveillance, and evidence-based treatment choices. Although challenges persist—data sharing, infrastructure, and ethical issues—sustained investment in genomic technologies is essential for global AMR control efforts. The full realization of genomics potential might be a keystone in maintaining the effectiveness of antibiotics and securing public health for generations to come [39].

7. Integration of Genomic Data with Public Health Systems

Using genomic data in public health is a game-changing step in stopping, finding, and treating diseases. As sequencing technology have improved and become more widely available, the large amount of genetic information has given public health officials additional tools to make better and faster judgments. To turn genomic data into useful public health plans, you need to gather, analyze, interpret, and put the data into action.

7.1 Sequencing and collection of genomic data

The initial step in using genomics for public health is to get DNA or RNA samples from creatures that are important to study, like humans, diseases, or vectors. Researchers can quickly figure out the genetic makeup of these samples using technologies like next-generation sequencing (NGS). For example, genome sequencing of viruses or bacteria helps public health labs figure out the exact strain or mutation that caused an outbreak of an infectious disease [40].

7.2 Analyzing and interpretation of data

The raw genomic data is then analyzed using bioinformatics. Algorithms and computer programs help find mutations, patterns of gene expression, and other disease-related traits. Genomic data can show where a virus came from, how it is spreading through populations, and whether it is becoming resistant to therapies for infectious diseases. Genomics can help find genetic factors that make people more likely to get chronic diseases like cancer or heart disease. This lets doctors intervene early [41].

7.3 Surveillance and responding to outbreaks

Genomic data is very important for surveillance systems. For instance, genome sequencing let scientists keep an eye on new variations like Delta and Omicron during the COVID-19 pandemic. These insights helped governments change their immunization plans, put in place targeted lockdowns, and change how they test people. In the same way, genome sequencing can help doctors identify better therapies for bacterial infections by keeping an eye on antibiotic resistance genes [42]. Genomic surveillance helps public health officials find epidemics early and track how they spread. When a novel pathogen is found, comparing genomes can help figure out if the infections came from one source or numerous sources. This knowledge affects how resources are used whether to focus on confinement, mass testing, or interventions at the community level [43].

7.4 Personalized and Precision Public Health

Genomic data has the potential to help with more than just infectious diseases. Genomic research backs up "precision public health" for non-communicable diseases (NCDs). This is a concept where interventions are made to fit certain groups of people depending on their genetic risk factors. For instance, initiatives for public health can focus on testing for BRCA mutations in communities where breast and ovarian

cancer is more likely to happen. Pharmacogenomics is the study of how different genes affect how drugs are broken down in the body. This knowledge helps doctors prescribe drugs that are safer and more effective, especially when they are part of big public health programs that involve distributing medications [44].

8. Global Case Studies and Success Stories

Genomic monitoring has become a game-changing tool in public health because it gives us real-time information about how infectious diseases evolve, spread, and spread. Public health experts can find new risks, keep an eye on variants, and take action quickly by deciphering the genetic material of viruses. This has been very helpful during global health emergencies including the COVID-19 pandemic, Ebola outbreaks, and efforts to control tuberculosis (TB). Here are some important global case studies that show how genetic surveillance has had a big effect.

COVID-19: Tracking Variants in Real Time: The global reaction to the COVID-19 pandemic is one of the best examples of genomic surveillance in action. Scientists all over the world started sequencing the SARS-CoV-2 virus early on in the outbreak to learn more about how it spreads and changes. In January 2020, Chinese scientists published the virus's first genome sequence. This made it possible for researchers all around the world to create diagnostic tests and start working on vaccinations [44]. Genomic surveillance became even more important as variations started to show up. The COVID-19 Genomics UK Consortium (COG-UK) made the UK a pioneer in sequencing large numbers of SARS-CoV-2 genomes. This work led to the discovery of the Alpha variant (B.1.1.7) in late 2020, which led to travel warnings and tests of the effectiveness of vaccines around the world. In the same way, South Africa and India were very important in finding the Beta and Delta varieties, respectively. Sharing genetic data around the world through systems like GISAID made it possible for people to work together and make decisions in real time. Countries might quickly change their public health responses, update vaccines, and put travel restrictions in place when new variants appeared. It would not have been feasible to quickly find and keep an eye on these mutations without genomic surveillance.

Ebola: Containing Outbreaks with Precision: Genomic surveillance has also been very important in stopping Ebola outbreaks, especially in West Africa from 2014 to 2016 and the Democratic Republic of Congo from 2018 to 2020. Researchers sequenced the Ebola virus genome from patient samples during the West African outbreak. This showed how the virus propagated and changed over time. This enabled epidemiologists figure out how the disease spread and find events where it spread quickly [45]. Scientists were able to keep an eye on viral mutations and plan vaccination methods with the rVSV-ZEBOV Ebola vaccine in the DRC thanks to real-time genomic surveillance. Genomics made it possible to find transmission sources more quickly, especially in hard-to-reach and complicated areas [46].

Tuberculosis: Tackling a Silent Epidemic: Genomic surveillance has become an important technique in fighting TB, even if it doesn't get as much attention as Ebola or COVID-19. Mycobacterium tuberculosis is the bacteria that causes TB. It is noted for becoming resistant to several medicines. Old ways of diagnosing can be slow and miss drug-resistant strains too late. Genomic sequencing makes it possible to quickly find drug-resistant mutations, which leads to better treatment plans. Genomic surveillance is helping public health officials tailor treatments, stop the spread of multidrug-resistant TB (MDR-TB), and keep an eye on outbreaks in places like South Africa and India, where TB is a big problem [47].

9. Conclusion

Genomic technologies have transformed infectious disease surveillance by rectifying the substantial shortcomings of traditional methods. Conventional surveillance approaches, such as clinical diagnoses, epidemiological studies, and static monitoring systems, remain significant; nevertheless, they are often impeded by delays, underreporting, restricted spatial coverage, and the necessity for human data analysis. Genomics provides high-resolution, real-time data regarding the identity, evolution, and transmission dynamics of diseases. This enables us to adopt a proactive strategy toward public health rather than a reactive one. Genomics has emerged as a crucial instrument for evidence-based policymaking, rapid diagnosis, and tailored interventions. It can identify resistance genes in antimicrobial-resistant bacteria promptly and monitor the transmission of diseases such as COVID-19 in real time. The integration of whole-genome sequencing, metagenomics, and genome-editing technologies into surveillance systems has accelerated outbreak investigations and improved antibiotic stewardship and precision medicine. Genomics is crucial as it can identify novel variants and resistance mechanisms before to their emergence as significant public health issues. These technologies provide physicians and policymakers with the required skills to make prompt decisions, reduce unnecessary antibiotic usage, and implement targeted control strategies. Nonetheless, challenges persist, including disparities in global sequencing capabilities, a shortage of bioinformatics specialists, elevated infrastructure expenses, and ethical concerns over data protection and equitable access. In the absence of continuous international collaboration, standardized data-sharing procedures, and expenditures in capacity building, the benefits of genetic monitoring may be inequitably distributed, disproportionately impacting low- and middle-income countries. Genomics is at the forefront of a transformative era in the management of infectious illnesses. It offers a method to develop robust, responsive, and accurate public health systems by enhancing and augmenting conventional surveillance. Ongoing innovation, along with global collaboration and ethical governance, will be crucial for genomics to realize its full promise in safeguarding health security and combating emerging threats, such as the escalating issue of antibiotic resistance.

10. References

1. Armstrong GL, MacCannell DR, Taylor J, Carleton HA, Neuhaus EB, Bradbury RS, *et al*. Pathogen genomics in public health. New England Journal of Medicine. 2019; 381(26):2569-2580. Doi: https://doi.org/10.1056/NEJMsr1813907
2. Baker M, Fidler DP, Murray CJ. Infectious disease surveillance and the role of global governance. The Lancet. 2021; 397(10275):1016-1018. Doi: https://doi.org/10.1016/S0140-6736(21)00369-8
3. Barzon L. Next-generation sequencing in clinical virology: Discovery of new viruses. World Journal of

Virology. 2020; 9(1):1-20. Doi: https://doi.org/10.5501/wjv.v9.i1.1
4. Black A, MacCannell D, Sibley T, Taylor J. Genomic surveillance of antimicrobial resistance. Nature Reviews Microbiology. 2020; 18(9):478-492. Doi: https://doi.org/10.1038/s41579-020-0366-2
5. Boucher HW, Talbot GH, Bradley JS, Edwards JE, Gilbert D, Rice LB, *et al*. Bad bugs, no drugs: No ESKAPE! An update from the Infectious Diseases Society of America. Clinical Infectious Diseases. 2009; 48(1):1-12. Doi: https://doi.org/10.1086/595011
6. Brown AC, Bryant JM, Einer-Jensen K, Holdstock J, Houniet DT, Chan JZ, *et al*. Rapid whole-genome sequencing of Mycobacterium tuberculosis isolates directly from clinical samples. Journal of Clinical Microbiology. 2015; 53(7):2230-2237. Doi: https://doi.org/10.1128/JCM.00486-15
7. Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, *et al*. BLAST+: Architecture and applications. BMC Bioinformatics. 2009; 10(421):1-9. Doi: https://doi.org/10.1186/1471-2105-10-421
8. Chiu CY, Miller SA. Clinical metagenomics. Nature Reviews Genetics. 2019; 20(6):341-355. Doi: https://doi.org/10.1038/s41576-019-0113-7
9. Christaki E, Giamarellos-Bourboulis EJ. The role of genomics in bacterial pathogenesis and drug resistance. Future Microbiology. 2014; 9(8):969-980. Doi: https://doi.org/10.2217/fmb.14.59
10. Davies J, Davies D. Origins and evolution of antibiotic resistance. Microbiology and Molecular Biology Reviews. 2010; 74(3):417-433. Doi: https://doi.org/10.1128/MMBR.00016-10
11. Didelot X, Bowden R, Wilson DJ, Peto TE, Crook DW. Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics. 2012; 13(9):601-612. Doi: https://doi.org/10.1038/nrg3226
12. Duffy S, Shackelton LA, Holmes EC. Rates of evolutionary change in viruses: Patterns and determinants. Nature Reviews Genetics. 2008; 9(4):267-276. Doi: https://doi.org/10.1038/nrg2323
13. Gardy JL, Loman NJ. Towards a genomics-informed, real-time, global pathogen surveillance system. Nature Reviews Genetics. 2018; 19(1):9-20. Doi: https://doi.org/10.1038/nrg.2017.88
14. Gilchrist CA, Turner SD, Riley MF, Petri WA, Hewlett EL. Whole-genome sequencing in outbreak analysis. Clinical Microbiology Reviews. 2015; 28(3):541-563. Doi: https://doi.org/10.1128/CMR.00075-13
15. Gire SK, Goba A, Andersen KG, Sealfon RS, Park DJ, Kanneh L, *et al*. Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science. 2014; 345(6202):1369-1372. Doi: https://doi.org/10.1126/science.1259657
16. Greninger AL. Clinical metagenomics for pathogen detection. Annual Review of Pathology. 2018; 13:287-312. Doi: https://doi.org/10.1146/annurev-pathol-020117-043459
17. Gwinn M, MacCannell D, Khabbaz RF. Integrating genomics into public health surveillance: Future directions. Emerging Infectious Diseases. 2019; 25(7):1415-1420. Doi: https://doi.org/10.3201/eid2507.181646
18. Harris SR, Feil EJ, Holden MT, Quail MA, Nickerson EK, Chantratita N, *et al*. Evolution of MRSA during a hospital outbreak. Science. 2010; 327(5964):469-474. Doi: https://doi.org/10.1126/science.1182395
19. Hendriksen RS, Munk P, Njage P, Van Bunnik B, McNally L, Lukjancenko O, *et al*. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications. 2019; 10(1124):1-12. Doi: https://doi.org/10.1038/s41467-019-08853-3
20. Holmes EC, Dudas G, Rambaut A, Andersen KG. The evolution of Ebola virus: Insights from the 2013-2016 epidemic. Nature. 2016; 538(7624):193-200. Doi: https://doi.org/10.1038/nature19790
21. Hu Y, Cheng L. CRISPR-Cas systems and antimicrobial resistance. Microorganisms. 2021; 9(4):814. Doi: https://doi.org/10.3390/microorganisms9040814
22. Inouye M, Dashnow H, Raven LA, Schultz MB, Pope BJ, Tomita T, *et al*. SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. Genome Medicine. 2014; 6(11):90. Doi: https://doi.org/10.1186/s13073-014-0090-6
23. Jackson BR, Tarr C, Strain E, Jackson KA, Conrad A, Carleton H, *et al*. Implementation of nationwide real-time whole-genome sequencing to enhance listeriosis outbreak detection and investigation. Clinical Infectious Diseases. 2016; 63(3):380-386. Doi: https://doi.org/10.1093/cid/ciw242
24. Köser CU, Ellington MJ, Cartwright EJ, Gillespie SH, Brown NM, Farrington M, *et al*. Routine use of microbial whole-genome sequencing in diagnostic and public health microbiology. PLoS Pathogens. 2012; 8(8):e1002824. Doi: https://doi.org/10.1371/journal.ppat.1002824
25. Kwong JC, McCallum N, Sintchenko V, Howden BP. Whole genome sequencing in clinical and public health microbiology. Pathology. 2015; 47(3):199-210. Doi: https://doi.org/10.1097/PAT.0000000000000235
26. Ladner JT, Grubaugh ND, Pybus OG, Andersen KG. Precision epidemiology for infectious disease control. Nature Medicine. 2019; 25(2):206-211. Doi: https://doi.org/10.1038/s41591-019-0345-2
27. Leopold SR, Goering RV, Witten A, Harmsen D, Mellmann A. Bacterial whole-genome sequencing revisited: Portable, scalable, and standardized analysis for typing and detection of virulence and resistance genes. Journal of Clinical Microbiology. 2014; 52(7):2365-2370. Doi: https://doi.org/10.1128/JCM.00262-14
28. Luheshi LM, Raza S, Rueckert C. Infectious disease surveillance using big data. Nature Reviews Genetics. 2020; 21(12):751-766. Doi: https://doi.org/10.1038/s41576-020-0275-9
29. Maguire F, McConkey BJ. CARD 2020: Antibiotic resistome surveillance with the Comprehensive Antibiotic Resistance Database. Nucleic Acids Research. 2019; 48(D1):D517-D525. Doi: https://doi.org/10.1093/nar/gkz935
30. Maljkovic Berry I, Melendrez MC, Bishop-Lilly KA, Rutvisuttinunt W, Pollett S, Talundzic E, *et al*. Next-generation sequencing and bioinformatics methodologies for infectious disease research and

public health. Pathogens. 2020; 9(11):880. Doi: https://doi.org/10.3390/pathogens9110880
31. Manoharan A, Chatterjee S. Genomics of antimicrobial resistance: A global perspective. Indian Journal of Medical Research. 2019; 149(1):14-22. Doi: https://doi.org/10.4103/ijmr.IJMR_1923_17
32. Marm Kilpatrick A, Randolph SE. Drivers, dynamics, and control of emerging vector-borne zoonotic diseases. The Lancet. 2012; 380(9857):1946-1955. Doi: https://doi.org/10.1016/S0140-6736(12)61151-9
33. Metcalf CJ, Lessler J. Opportunities and challenges in modeling emerging infectious disease dynamics. Science. 2017; 357(6347):149-152. Doi: https://doi.org/10.1126/science.aam8335
34. Moran E, O'Neill J. Tackling antimicrobial resistance: The role of genomics. Journal of Antimicrobial Chemotherapy. 2020; 75(1):1-4. Doi: https://doi.org/10.1093/jac/dkz400
35. Naccache SN, Greninger AL, Lee D, Coffey LL, Phan T, Rein-Weston A, *et al*. The role of next-generation sequencing in infectious disease diagnosis. Expert Review of Molecular Diagnostics. 2014; 14(4):421-433. Doi: https://doi.org/10.1586/14737159.2014.910036
36. O'Neill J. Tackling drug-resistant infections globally: Final report and recommendations. The Review on Antimicrobial Resistance. HM Government & Wellcome Trust, 2016.
37. Quick J, Grubaugh ND, Pullan ST, Claro IM, Smith AD, Gangavarapu K, *et al*. Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols. 2017; 12(6):1261-1276. Doi: https://doi.org/10.1038/nprot.2017.066
38. Rawson TM, Moore LS, Hernandez B, Charani E, Castro-Sanchez E, Holmes AH. A systematic review of clinical decision support systems for antimicrobial management: Are we failing to investigate these interventions appropriately? Clinical Microbiology and Infection. 2020; 26(5):520-532. Doi: https://doi.org/10.1016/j.cmi.2019.12.010
39. Robinson ER, Walker TM, Peto TE. Genomic insights into antimicrobial resistance and tuberculosis. Nature Reviews Microbiology. 2019; 17(9):471-485. Doi: https://doi.org/10.1038/s41579-019-0210-8
40. Schurch AC, Van Schaik W. Challenges and opportunities for whole-genome sequencing–based surveillance of antibiotic resistance. Annals of the New York Academy of Sciences. 2017; 1388(1):108-120. Doi: https://doi.org/10.1111/nyas.13310
41. Tang P, Croxen MA. Genomic epidemiology: Whole-genome sequencing in outbreak investigation, clinical diagnosis and public health surveillance. Clinical Microbiology Newsletter. 2017; 39(6):45-52. Doi: https://doi.org/10.1016/j.clinmicnews.2017.02.004
42. Thomson NR, Aanensen DM. Pathogen genomics and tracking infectious disease. BMC Biology. 2017; 15(1):1-4. Doi: https://doi.org/10.1186/s12915-017-0413-4
43. Van Dorp L, Acman M, Richard D, Shaw LP, Ford CE, Ormond L, *et al*. Emergence of genomic diversity and recurrent mutations in SARS-CoV-2. Infection, Genetics and Evolution. 2020; 83:104351. Doi: https://doi.org/10.1016/j.meegid.2020.104351
44. Walker TM, Merker M, Kohl TA, Crook DW, Niemann S, Peto TE. Whole genome sequencing for M. Tuberculosis. The Lancet Infectious Diseases. 2017; 17(3):262-274. Doi: https://doi.org/10.1016/S1473-3099(16)30159-7
45. World Health Organization. Global antimicrobial resistance and use surveillance system (GLASS) report 2021. WHO, 2021. https://www.who.int/publications/i/item/9789240027336
46. Yang Y, Yu Y. Machine learning for antimicrobial resistance prediction: Challenges and opportunities. Frontiers in Microbiology. 2021; 12:772742. Doi: https://doi.org/10.3389/fmicb.2021.772742
47. Zhou Y, Wang J. Application of genomic big data in public health. Frontiers in Genetics. 2019; 10:1200. Doi: https://doi.org/10.3389/fgene.2019.01200