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Genomic Surveillance in Infectious Disease Control: Opportunities and Challenges

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ABSTRACT

This article promotes the implementation of pathogen genomic surveillance to address and alleviate health risks associated with infectious illnesses and Antimicrobial Resistance (AMR), drawing on the successes of extensive genome-wide analyses of corona variants in informing COVID-19 tracking and public health strategies while endorsing the concept of One Health (OH). The efficacy of laboratory-based monitoring and epidemic warning systems must be improved by promoting (1) universal availability of real-time Whole Genome Sequence (WGS) information on pathogens to guide clinical prevention of infections, health policy, and the study and creation of vaccines and AMR agents. Unification of diagnostic microbiology information, testing data from asymptomatic persons, pathogen sequencing data, medical information, and epidemiological information into monitoring systems. Enhanced intersectoral partnerships across medical care, public safety, the health of animals, and environmental monitoring and research utilizing OH methodologies to comprehend the natural world and transmission routes of diseases and AMR across habitats. International cooperation and connectivity of monitoring networks, harmonizing laboratory methodologies, and regulation of surveillance techniques for worldwide reporting, incorporating pathogen genetic variation or strain naming. Appropriate information sharing among surveillance systems, records, and platforms by principles of Findability, Availability, Interconnection, and Reuse (FAIR). and (vi) investigation into applying genomic monitoring techniques and their cost-effectiveness for various diseases and AMR risks in diverse contexts. Regional and global OH regulations and oversight activities must promote the coordinated advancement and practical application of pathogen genome monitoring to safeguard the health of individuals, creatures, and the environment.

Keywords: *Genomic Surveillance, Infectious Disease, Disease Control, Analysis*

INTRODUCTION

The discovery and swift proliferation of coronavirus, the pathogen responsible for COVID-19 [1], has led to a global epidemic, resulting in approximately 620 million illnesses and 6.5 million fatalities since late 2019. CoV-2, like all viruses, undergoes continuous mutations during transmission, leading to novel viral strains that exhibit phenotypic variations in reproduction and/or interactions between hosts and pathogens [11] [2]. Mutations that provide a selection advantage in specific circumstances enable a particular variant to surpass others and proliferate among the population. The World Health Organization (WHO) [3] classifies variations that proliferate swiftly or provide a public health threat due to increased transmissibility, heightened risk of severe illness, or immune escape as variations concerning [4]. Scientists and healthcare specialists primarily depend on genomic monitoring to monitor the appearance of novel variations and evaluate their potential dangers to One Health (OH) [12]. Genomic monitoring integrates epidemiological evaluation, genome sequencing, and bioinformatics to elucidate the connections between virus Whole Genome Sequence (WGS) [5] and health-related effects. Genomic tracking at the individual level facilitates the swift detection of newly emerging variations and the strategic implementation of mitigation measures by OH authorities to avert their dissemination. Connecting sequencing with medical and genetic data facilitates the correlation of individual mutations to pathogenic effects or therapeutic effectiveness, offering essential insights for establishing optimal clinical procedures [13]. Recent advancements in sequencing methods, their availability, and the worldwide immediacy of the COVID-19 global epidemic have led to unprecedented genomic monitoring of CoV-2 compared to any other virus thus far [6].

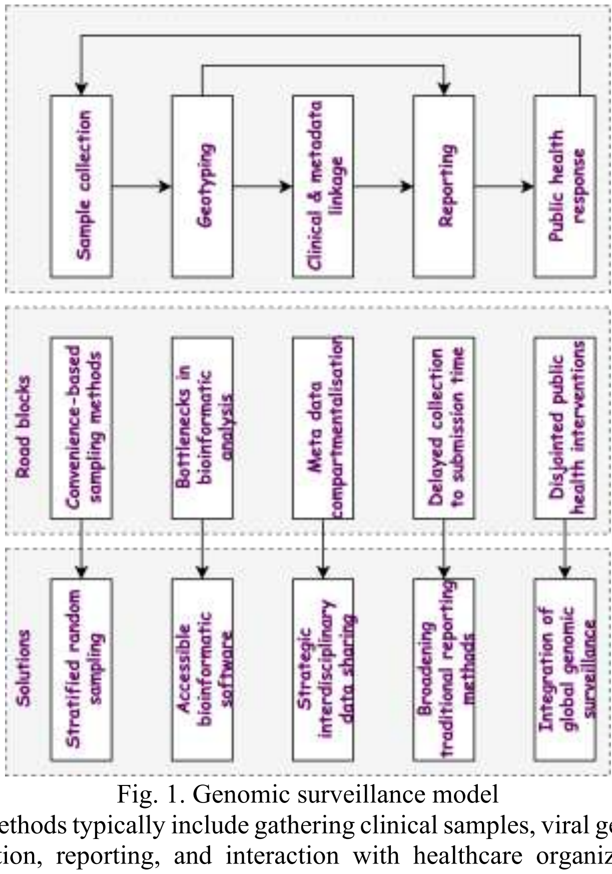

Fig. 1. Genomic surveillance model

Genomic surveillance methods typically include gathering clinical samples, viral genetic testing, integration with metadata information, reporting, and interaction with healthcare organizations for reaction and communication (Fig. 1). A resilient and sustainable framework for genomic surveillance programs to monitor CoV-2 variants worldwide can significantly alleviate the Antimicrobial Resistance (AMR) [7] burden by facilitating the prompt distribution of data to enhance research goals, therapeutic growth, prevention efforts, and clinical care. Regrettably, numerous constraints within the global genomic monitoring framework have hindered this opportunity, leading to significant delays in accessing information and inconsistent communication by Findability, Availability, Interconnection, and Reuse (FAIR) principles [8]. This study aims to evaluate the present status of CoV-2 genomic monitoring, pinpoint deficiencies in the system, and underscore possible remedies to mitigate the effects of future epidemics [10].

Obstacles and remedies for genetic disease monitoring
The research and others have previously evaluated the advantages and limitations of various genomic assays, including Sanger-based assays, point mutation tests, and Next-Generation Sequencing (NGS) approaches [14]. Many nations depend on Sanger-based assays, although NGS is increasingly utilized for diverse applications. Due to the comparative benefits regarding cost, extensive applicability, and the breadth of information accessible by NGS-based approaches, this Personal View has been confined to debates on NGS.

2.1Development of infrastructures and enhancement of human capacity
2.1.1 DNA sequencing, data processing, and storage architecture
An evaluation of sequencing ability indicates that it is limited and focused in several nations. Most capability resides outside national government health institutions [9]. This split underscores the necessity to enhance competence in national OH institutions and establish effective networks with research and educational institutions and between nations. Instructions for establishing sequencing equipment have been addressed in other sources. 2, 25, 45, 50 The preliminary investment required to build sequencing capability is projected to be between 100k and 750k, contingent upon the platform for sequencing utilized. Substantial expenditures are needed for supplementary technology for library preparation and quality assurance. The selection of a platform is contingent upon the application's type, including read depth, duration, and error rates, and necessitates trade-offs in precision, effectiveness, time, financial investment, reagent costs, and computing demands.

2.1.2 Proficient Labor Force
A diverse array of specialists is required to facilitate genomic monitoring, encompassing geneticists for testing in laboratories, bioinformaticians, and cellular researchers for interpreting and analyzing data, field researchers in epidemiology, illness experts for analyzing information, and health insurance professionals for integrating findings into regulations. Cultivating local proficiency in technology maintenance and setup is essential to avert prolonged delays and supplementary expenses associated with outsourcing to other countries.

2.2 Incorporating genomes into current laboratory monitoring frameworks
2.2.1 Establishing a multi-pathogen laboratory
The research anticipates a limited number of multipathogen core facilities will adequately support various national disease prevention programs [15]. In contrast to isolated pathogen-specific arranging research facilities, multipathogen core sequencing units offer several advantages: (1) optimizing the utilization of facilities (such as sequencing and computational) and staff members; (2) reducing servicing of equipment expenses; (3) potentially augmenting distributing and afterward arranging cost efficiencies; (4) enabling bulk purchasing; (5) improving the monitoring of ignored illnesses and pathogens; and (6) standardizing and streamlining processes across various pathogens.

A central facility can consolidate resources for establishing and maintaining genomics centers within national disease control programs, leading to enhanced cohesiveness and integration of various initiatives. Integrated models exhibit excessive latency when the labor is limited, the workload is substantial, or machinery malfunctions occur. A hybrid-integrated methodology is advantageous, wherein subsequent operations occur in disease-specific research facilities. At the same time, only upstream procedures, including quality assessments, DNA sequencing, and evaluation, are conducted at the central sequence and bioinformatics centers.

2.2.2 Laboratory networking and quality control frameworks

A nationwide network strategy would optimize the limited resources, particularly for national health institutions and illness control programs lacking domestic capability. A possible solution is to use a three-tiered pyramid framework analogous to that employed in other effective WHO disease systems. National-level pathogen genetic facilities are the foundation, primarily facilitating prompt and precise genomic monitoring. These facilities are connected to local laboratories that, besides functioning as national research facilities, act as regional referral centers to assist national government health institutions and illness control programs in nations lacking sequencing capabilities. These local facilities could facilitate the training and support of national referral facilities for pathogenic genomes. The specialized facilities and informatics centers might offer training, technical help, and reliability help to national and neighborhood manufacturing facilities, innovate and develop more cost-effective ways, and function as recommendation testing locations.

Facilitating mechanisms

3.1 Regulatory guidelines and structures

Incorporating genetic surveillance into health care necessitates the establishment of supportive policies and regulatory structures. These mechanisms can enhance effective practices in collecting, storing, and utilizing specimens, international specimen movement, genetic archiving, biorepository preservation, and sharing, as well as the analysis and application of pathogenic genomic information, amongst other functions. Despite the acknowledged advantages of swift data dissemination for efficient cross-border disease management and pandemic mitigation, deficiencies persist in this area. Established through consultation, a cohesive legal framework for the entire continent is necessary to identify and mitigate local obstacles. The structure should ideally utilize established international structures, such as those formulated by the WHO Science and Technology Blueprint regarding infectious agent genetic sequence information and the Nagoya Protocols on the equal distribution of benefits derived from gene collaboration. Continental organizations with involvement from various entities can support it.

3.2 Cost-reduction strategies

The per-sample expense of NGS is typically elevated and a barrier for regular application by national visible health institutions or disease control programs; however, this cost can be significantly diminished through multiplication, wherein numerous samples, each uniquely barcoded with a primer, are combined and sequenced concurrently, a method particularly advantageous in high-throughput resources. The expense of library preparation continues to be elevated despite multiplexing, necessitating negotiations with producers to render sequence more economical.

Negotiated price is essential to rectify the inequity in equipment, upkeep, and reagents expenses, which are significantly elevated compared to other regions, mainly due to earnings margins established by local enterprises and distributors and shipping and customs fees. Alternative strategies involve large-scale purchasing via regional or continental frameworks.

3.3 Community practices

A consortium of pathogen genetics specialists, including OH officials, animal welfare professionals, epidemiologists, genomics specialists, philosophers, statisticians, and computational biologists, must be formed. The community will promote the dissemination of best practices, cost-effective wet laboratory genetic norms, statistics and bioinformatics instruments, training resources, and innovations. Communities of practice will facilitate collaborative initiatives to control or eliminate common illnesses by cultivating trust between members for sharing information, enhancing technical abilities, formulating joint tactics, standardizing data reporting structures, and conducting informal periodic notifications of possible disease dangers.

3.4 Leadership and Orchestration

Creating a viable pathogen genomics system that utilizes shared assets and collaborative efforts for transnational illness control and eradication throughout the continent needs an efficient coordination system. It was founded as a continental organization to assist and collaborate with all nations in enhancing surveillance, epidemic leadership, and the avoidance of infectious illnesses. It has collaborated with regional counterparts to pioneer the integration of pathogen genetics into healthcare structures, fulfilling its goal to enhance surveillance of diseases across the continent. The partnership involves mobilizing funds for building capacities and enabling CoV-2 sequencing, which is anticipated to aid in the targeted and timely management of epidemic revival in the event of another outbreak and in monitoring the efficacy of diagnostics, treatments, and vaccinations. The institute is anticipated to formulate regulations and norms, enable bulk procurement and negotiated costs with producers, assist in training employees, create and oversee an operational testing system with sample delivery and quality-assured experiments, and manage the effective operation of neighborhoods of execution, among other tasks.

3.5 Evaluation of impact and long-term sustainability

3.5.1 Oversight and Assessment

Regular evaluations of the success and efficacy of integrating genetic data into standard OH surveillance methods will be essential. This review must encompass the assessment of data collecting accuracy and rapidity, reporting and utilization of data for policy development, the identification of deficiencies and opportunities for enhancement, and evaluating the costs and benefits of genetic data relative to alternative surveillance methods.

3.5.2 Financial support and viability

Countries ought to establish a sustainable structure for genetic surveillance. Genomic monitoring must be integrated into more significant OH initiatives, national prevention and treatment programs, response to emergencies, antibiotic resistance monitoring, and other surveillance efforts, necessitating adequate resource allocation. Mainstream financing entities, including global funds and other collaborators, must persist in endorsing the execution of proposed genomics applications, which are essential for the efficacy of disease management initiatives. Countries utilize alternative organizations that advocate for diverse genomics applications. National health service departments and national disease management initiatives should collaboratively establish definitive financial commitments and long-term maintenance plans with other countries.

Reaction to Public Health

The purpose of genetic surveillance is to provide an effective OH reaction. Advancements in technology and mathematics within pathogenic genomics offer a distinctive potential to leverage epidemiology to improve OH response. During the COVID-19 pandemic, efficient genomic surveillance systems have demonstrated their critical role in facilitating evidence-based OH communication and actions. An optimal, comprehensive intervention approach informed by monitoring would demonstrate advantages throughout the fundamental OH care system. The structure consists of concrete actions designed to implement practical solutions that universally enhance OH among all populations, highlighting four key areas: (1) evaluation, (2) policy creation, (3) confidence, and (4) equity. Prior researchers have recorded that disparities in genomic monitoring during the COVID-19 epidemic can be ascribed to insufficient infrastructure or assistance in one or more of these critical service domains.

These studies highlight the detrimental impact of neglected facilities, fragmented organizations with inconsistent OH messaging, and inadequate intervention measures to control pathogen transmission on genetic surveillance initiatives. The absence of monitoring in resource-constrained nations and the insufficient infrastructure to facilitate this work in under-sampled communities underscore opportunities for global cooperation and capacity-building initiatives. To clarify the subject, the research will examine current constraints within the general healthcare structure and evaluate efforts integrating molecular monitoring with visible OH evaluation and policy formulation to enhance equity within public well-being treatments for epidemics of illnesses.

Conclusion

Enhancing WGS technologies for the genomic study of microbes with epidemic propensity has shown effective in facilitating infectious disease exploration, early outbreak identification, and the containment of epidemics caused by various pathogens and AMR. The research must persist in tackling difficulties like those encountered during the COVID-19 global epidemic and allocate resources towards the infrastructure necessary for global incorporated OH genetic monitoring, facilitating a prompt and cohesive response to future worldwide epidemic and global health threats posed by infectious illnesses and AMR. Infectious illness preparedness encompasses various facets that genomic methodologies can significantly impact, from identifying outbreaks and establishing and disseminating novel variations to guiding intervention choices, including vaccinations and antibiotics. National, local, and international organizations are enhancing pandemic preparedness mechanisms after the COVID-19 epidemic. These initiatives will significantly benefit from expanding pathogen sequencing capabilities and laboratory expertise alongside the modernization of medical records systems. Advancement is required in standardizing pathogenic genomic terminology, monitoring, and the compatibility of medical systems. Emphasizing the seamless combination of genetic, microbiological, clinical, and epidemiological information from many domains is essential. Global agreements and cross-sector partnerships should promote consensus-driven national legislation that is FAIR-compliant and ensures accountable oversight of sharing information within and among surveillance systems and health agencies. Translational studies must identify obstacles and facilitators to adoption across many contexts. Evaluating the cost-effectiveness of genetic surveillance in mitigating illness burden will facilitate data gathering and sharing to illustrate the comprehensive wellness and economic advantages. Equally implementing those above cooperative and capacity-building measures globally while establishing comprehensive genomic monitoring of significant human and zoonotic diseases will augment the worldwide epidemic knowledge and assist in mitigating potential pandemics.

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