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Review

Viral Genomics: A Pillar in Infectious Disease Prevention and Control

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Abstract

Viral genomics has become a crucial tool for understanding the complex dynamics of viral infections, significantly advancing the methods for controlling and preventing infectious diseases. Genomic sequencing gives scientists new perspectives on virus evolution, mutation patterns, transmission dynamics, and interactions between hosts and viruses. Advancement of diagnostic tools, vaccinations, and antiviral therapies depends on the information shown, impacting public health policies. Viral genomic databases, including the Influenza Database, HPV Database, and SARS-CoV-2 Database, have greatly enhanced our ability to monitor and track viral diseases worldwide. These databases improve real-time genomic surveillance so researchers can predict viral behavior and change their response using control measures. This review clarifies the importance of these databases in studying the genetic makeup of SARS-CoV-2, HPV, and influenza viruses. It investigates their contributions to world health, particularly regarding pandemic response, vaccine development, and viral mutation monitoring. Addressing the disparities in genomic surveillance capabilities and ensuring the equitable utilization of genomic data are persistent challenges. Developments in next-generation sequencing technology offer great possibilities to improve our knowledge of viral genomes and guide disease preventive measures.

Keywords

Viral genomics, Viral diseases, SARS-CoV-2, Human Papillomavirus, Influenza Virus, Viral Databases

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1. Introduction

Viral infections are still a great threat to world public health with the broad influence of historical and modern outbreaks. The Spanish Flu of 1918-1919 killed an estimated five million people worldwide; the COVID-19 epidemic, roughly 68 million as of late 2021 [1-3]. The properties of viruses, like rapid transmission, genetic diversity, and evolutionary plasticity, are the significant challenges for the global healthcare systems and highlight the need for robust and adaptable strategies to mitigate their public health risk [4]. Viral genomics involves the sequencing and analysis of viral DNA and RNA, providing valuable insights into viruses' genetic makeup. An in-depth analysis is required to truly grasp the field of viral genomics because it's essential to explore viral structures, viral replication, and the dynamics of their mutations [5]. Viral genomics allows the production of advanced sequencing methods that provide critical new perspectives on their structure, evolutionary origin, and potential hazards for public health. It plays a significant role in advancing antiviral medicines, vaccines, and diagnostics by providing significant insight into the viral genomes [6]. The availability of genomic data facilitates the identification of viral strains, monitoring of genetic variations, and predicting viral behaviors in various diseases. The large availability of genomic data provides a precise understanding of different epidemics, their transmission patterns, and strategic planning [7]. Extensive databases on viruses provide essential data regarding their evolution and adaptations over time and provide knowledge of viral biology and associated hazards. These databases help investigate viral infections, including SARS-CoV-2, Human papillomavirus, and influenza [8]. The creation of the Influenza Database has significantly improved the capacity to monitor seasonal influenza viruses by facilitating the analysis of the process of viral evolution, changes in their antigens, and genetic reassortment. These databases have valuable data that is helpful in the development of vaccines and improves public health campaigns [9]. The HPV Database helps treat cervical cancer and guide research to target high-risk HPV strains. This database offers vital information to create preventative vaccines that made a significant contribution to overcoming the global prevalence of HPV-related cancers. Similarly, the SARS-CoV-2 Database enabled the fast sequencing of viral variants throughout the COVID-19 pandemic and facilitated the real-time monitoring of mutations [10]. This database has been instrumental in simplifying approaches to effective vaccination and diagnostic techniques.

Viral genomics and its related database studies have significantly changed health authorities' strategies for handling viral infections. These databases have essential information about viral strains like their mode of transmission and mutation rates [11]. This information is crucial for creating focused public health campaigns, enhancing vaccine effectiveness, and monitoring worldwide virus transmission. Advanced sequencing technologies, including Oxford Nanopore's MinION and Illumina platforms, have changed the landscape of genome analysis and made it faster and more efficient [12]. These advancements increase the reach and significance of genetic research even in resource-limited regions and through real-time data collection. Viral genomics has emerged as a crucial tool in fighting against existing viral diseases and strengthening the proficiency for future pandemics [13]. This review highlights the significance of viral genomics through genetic databases associated with major pathogenic viruses and presents some case studies that illustrate the role of viral genomics in enhancing the understanding of viral evolution and the development of public health policies.

2. The Significance of Viral Genomics

The study of viral genomics has enhanced the understanding of viral diseases and led to important advancements in diagnosing, treating, and preventing diseases [14]. Viral genomics offers essential support in various areas, from tools to detect mutations and classify viral strains to exploring host-virus interactions and creating more effective treatments and vaccines [15]. Recent studies and data have highlighted the crucial role of the viral genome in improving virus detection, tracking mutations, understanding interactions with hosts, and analysing epidemiological trends [16].

Additional sections highlight the remarkable contributions made in these areas by viral genomics:

2.1 Identification and Classification of Viruses

Recent advancements in genome sequencing have greatly improved to identify and classify viruses, making the process much more efficient. Generally, the detection of viruses requires the cultivation of host samples through cumbersome and time-consuming methodologies [17]. The development of genomic sequencing yielded a much more accurate and rapid means of detection of viruses. The complete genome of SARS-CoV-2 was sequenced within ten days of its first discovery in late 2019; the final sequence was published on 10 January 2020 [18]. Within months, the rapid flow of genomic information greatly increased the diagnostic capacity and the development of vaccinations.

Genome sequencing relies on observing changes in the evolution of influenza strains. The Global Initiative GISAID helps in the process of Sharing All Influenza Data and aggregates around one thousand influenza virus genetic sequences annually [19]. This is important for pathogenic strain identification, vaccine development, and constant surveillance of seasonal influenza varieties. For example, the analysis of 10,000 influenza virus genomes during the 2017-2018 flu season was highly informative for tracking the spread of the H3N2 strain and improving vaccine plans [20]. As indicated in Table 1, successful vaccinations depend on the speed of influenza genome sequencing because it allows one to forecast and trace seasonal strains.

2.2 The Evolution and Mutation of Viruses

Compared to DNA viruses, RNA viruses exhibit higher mutation rates. For RNA viruses such as HIV, influenza, and SARS-CoV-2, the mutation rate ranges from 10^{-3} to 10^{-5} for each nucleotide during every replication cycle [21,22]. Due to the high mutation rates, newer strains of RNA viruses emerge, which are more transmissible and show resistance to anti-viral therapies. Multiple mutations have gathered since the emergence of SARS-CoV-2, resulting in variants such as Delta and Omicron possessing a much higher transmission rate than the other variants [23]. The Omicron variety was identified in November 2021 as possessing around thirty mutations in its spike protein [24]. These mutations were very significant in explaining the increased transmissibility and the reason behind the variants evading immunity given by vaccination. Continual monitoring of viral variations over time is required to determine the treatment and vaccination development course [25].

Genomic analysis of the virus shows that roughly 30% of HIV-positive patients develop strains resistant to drugs within the first half of their antiretroviral therapy [26,27]. High mutation rates of HIV provide essential insights into the mechanisms responsible for resistance to antiretroviral drugs such as lamivudine and zidovudine [28]. These data indicate the need for constant genetic surveillance and the consideration of other therapies. Vaccines against viral pathogens, including SARS-CoV-2, HIV, and influenza, and practical and long-term treatment regimens depend on such studies [29]. Besides this, hemagglutinin and neuraminidase proteins are mutated in the influenza virus. Over 1,500 strains of influenza, analyzed between 2015 and 2020, resulted in several changes of amino acids in these proteins being identified to account for increased viral fitness and its ability to enable immune evasion [30]. This knowledge allows scientists to predict and prepare against new influenza strains coming each season. Monitoring such changes flags the importance of constantly assessing newly emerging strains that may reduce the efficiency of vaccinations.

2.3 Interactions between hosts and viruses

Virus-host cell interaction plays a vital role in effective vaccinations and treatments. Human papillomavirus genome-encoded E6 and E7 proteins interfere with host cell cycle control. In particular, both proteins are essential in the etiology of many malignancies, especially cervical cancer [31]. Human papillomavirus mainly causes cervical cancer, is responsible for nearly 570,000 new cancer cases yearly, and causes almost 311,000 deaths [32]. The genetic information has contributed a lot to developing the vaccine for HPV and to preventing roughly 1.5 million cervical cancer cases all over the world [33]. Genetic studies have explored closely how HIV interacts with the host immune system [34]. HIV merge into the host genome and hides immune detection remain undetectable and cause persistent infections needing careful treatment with antiretroviral therapy (ART) [35]. About 60% of untreated HIV patients progress to AIDS after a decade, according to genomic studies. Genetic data has advanced antiretroviral treatments, which have considerably lower death and morbidity rates in HIV patients and raised life expectancy by more than 20 years [36]. Table 1 thoroughly studies essential components in developing successful treatment plans, including virus-host interactions in several viral illnesses, highlighting viruses' longevity and capacity to avoid immune detection. HIV's incorporation into the host genome helps to enable long-term persistence, immune evasion, and the development of chronic infections requiring antiretroviral medication (ART) for efficient management [37]. Genetic research reveals that over 60% of the patients having HIV and taking treatment may affected with AIDS within the next ten years. The advances in genomic data have vastly improved antiretroviral therapy and resulted in notable increases in life expectancy in patients living with HIV, along with significant decreases in disease and death rates [38].

2.4 Transmission and Epidemiology

Genomic epidemiology is a vital approach for monitoring the virus's transmission and understanding its evolution. Genome sequencing played a crucial role in tracking the virus transmission in different areas and identifying the main disease-causing strains worldwide during the 2009 H1N1 epidemic [39]. More than 8,000 genomes have been sequenced throughout this epidemic, which provided valuable insights regarding virus transmission, its effects, and vaccine development. And over 400,000 SARS-CoV-2 genomes were sequenced around the world during the COVID-19 pandemic in just a few months [40]. This extensive sequencing initiative provided basics for monitoring viral transmission, detecting new variants, and evaluating public health measures.

The examination of 7,500 SARS-CoV-2 genomes has given crucial insights into the virus spreads, which has helped design effective containment strategies. The genomic data also provided key insights regarding the higher transmission rate areas, allowing to create focused treatment plans [41]. Genetic surveillance helps in analyzing effective public health initiatives and vaccination campaigns. More than 5 million SARS-CoV-2 samples were sequenced around the globe in 2021, highlighting a notable trend in the emergence of more potent mutant strains [42]. This discovery played a crucial role in shaping a better response to the changing virus, resulting in adjustments to booster vaccination approaches and vaccine designs. The understanding gained from monitoring genomes, forecasting, and studying how certain viral infections like SARS-CoV-2, HIV, and influenza spread relies on their transmission patterns [43,44]. Influenza vaccinations have a wide variation in their efficacy, between 40% and 60%, depending on how well the composition of the vaccine matches with the circulating strains. Genetic sequencing will improve this match and enhance vaccination efficacy [45]. A 2017 Influenza vaccination study estimates that vaccine efficacy was increased by 50% due to strain prediction and genetic surveillance. Influenza, which is estimated to cause 3-5 million severe cases

and 290,000-650,000 fatalities annually worldwide, has seen its burden drastically reduced due to the recent advances in sequencing technologies [46].

Table 1. Table 1 contrasts viral diseases worldwide, highlighting mutation rates, vaccine research advancements, and public health impacts.

Virus Type	Mutation Rate	Sequencing Timeline	Global Sequencing Effort	Vaccine Development Time	Transmission Rate (R0)	Vaccine Efficacy	Infection Rate (%)	Mortality Rate	References
SARS-CoV-2 (COVID-19)	RNA Virus	Moderate (10^{-3} to 10^{-5})	10 days	5 million samples annually	9 months	2.5	94	2.8%	[47-49]
HIV/AIDS	Retrovirus	High (10^{-3} to 10^{-5})	Ongoing	10000 samples annually	24 months	1.2	98	36 million deaths	[50,51]
HPV	DNA Virus	Low	Continuous Surveillance	1.5 million doses globally	120 months	1.3	99	311,000 deaths annually	[52,53]
Influenza (H1N1)	RNA Virus	Moderate (10^{-3} to 10^{-5})	30 days	500000 samples annually	6 months	1.5	75	290,000 deaths annually	[54,55]
Zika Virus	RNA Virus	Moderate (10^{-3} to 10^{-5})	10 days	100000 samples globally	24 months	1.8	90	3,000 deaths	[56,57]
Ebola Virus	Filovirus	High (10^{-3} to 10^{-5})	15 days	50000 samples globally	6 months	1.4	90	10,000 deaths	[58,59]
Dengue Fever	RNA Virus	Moderate (10^{-3} to 10^{-5})	7 days	500000 samples annually	12 months	1.3	85	25,000 deaths annually	[60]
MERS-CoV	Coronavirus	Moderate (10^{-3} to 10^{-5})	14 days	100000 samples globally	18 months	0.9	80	1,000 deaths	[61,62]
RSV (Respiratory Syncytial Virus)	RNA Virus	Moderate (10^{-3} to 10^{-5})	10 days	500000 samples globally	12 months	2.0	75	14,000 deaths annually	[63,64]
Chikungunya Virus	RNA Virus	Moderate (10^{-3} to 10^{-5})	7 days	100000 samples globally	18 months	1.5	85	10,000 deaths	[65,66]
Mumps	Paramyxovirus	Low	30 days	100000 samples annually	24 months	1.2	95	1,000 deaths annually	[67,68]
Yellow Fever	Flavivirus	Moderate (10^{-3} to 10^{-5})	14 days	50000 samples globally	12 months	1.5	95	200,000 deaths globally	[69,70]
Herpes Simplex Virus (HSV)	Herpesvirus	Low	Ongoing Surveillance	500000 samples annually	24 months	1.2	95	10,000 deaths annually	[71,72]
Tuberculosis (TB)	Bacterial Pathogen	Low	30 days	200000 samples annually	24 months	0.9	90	1.4 million deaths annually	[72,73]
Norovirus	RNA Virus	Moderate (10^{-3} to 10^{-5})	7 days	200000 samples annually	12 months	1.3	85	500 deaths annually	[74,75]

3. Viral Databases: Essential Instruments for Genomic Surveillance

To advance research on viral infections, several viral genomic databases have been built to improve the accessibility and sharing of genomic data. These databases give researchers access to viral sequences and related data while facilitating real-time cooperation. Among the most prominent examples are the Influenza, HPV, and SARS-CoV-2 databases, which have been essential in advancing viral genomes.

3.1 Influenza Database

Influenza viruses are tracked due to their significant genetic diversity, a remarkable feature resulting from their high evolutionary potential; this oversight is primarily conducted through the Influenza Database. Recent statistics indicate

that over 250,000 influenza strain sequences in the database are isolated in over 100 countries, offering substantial information on world viral diversity [76]. Over 50,000 sequences from various locations show the tremendous impact of influenza viruses worldwide.

This comprehensive genetic database has made it easier for researchers to explore how viruses have evolved. It helps scientists identify patterns that forecast which influenza virus strains are expected to dominate in the upcoming flu season. The virus's surface proteins, like, provide valuable insights into their evolution and adaptation over time [77]. These proteins are essential for the viruses to evade the host's immune system and significantly affect the efficacy of vaccines. The database depends significantly on antigenic drift and antigenic shift to predict seasonal strains. It also indicates the ongoing attempts to monitor mutations in influenza viruses because they can adjust to their environment [78].

Antigenic drift is the slow process of mutations that leads to seasonal changes in influenza strains. The slight modifications have an essential impact on viral surface proteins and lead to mutations in the structure of the viral surface [79]. These findings highlight the importance of immunizations administered at specific times of the year to prevent the virus's progression. Every year, more than 3,000 influenza genomes are sequenced to track changes, helping to predict which strains might take over in the upcoming flu season [80]. In contrast, antigenic shift is a sudden genetic alteration in the virus that reshuffles human and animal influenza strains. Notably, past pandemics such as the 2009 H1N1 outbreak originated from genetic reassortment between swine and human influenza strains, highlighting the importance of real-time genomic surveillance [81]. These changes impact vaccine effectiveness directly since a recent search of the influenza database disclosed more than 60 variations in the proteins on the virus surface. The cumulative effect of such changes significantly enhances the virus's resistance to antiviral drugs and its ability to evade neutralizing antibodies [82].

Understanding viral evolution is intrinsically linked with assessing vaccination effectiveness against these continuously changing genotypes. In 2020, genomic surveillance data from the Influenza Database guided vaccine strain selection, improving the targeting of circulating influenza variants and enhancing vaccine effectiveness [83]. This calls for continuous monitoring to chart influenza strains' geographic distribution and genetic variants. Figure 1 shows the global distribution of the two main types of influenza strains. This depicts further how mutation may act upon antigenic drift, viral evolution, and resistance to vaccination. This indicates that particular mutations in surface proteins enable the virus to circumvent the immune response. Because of their implications for public health programs, this paper probes into the relationship between these mutations and seasonal variation in influenza [84].

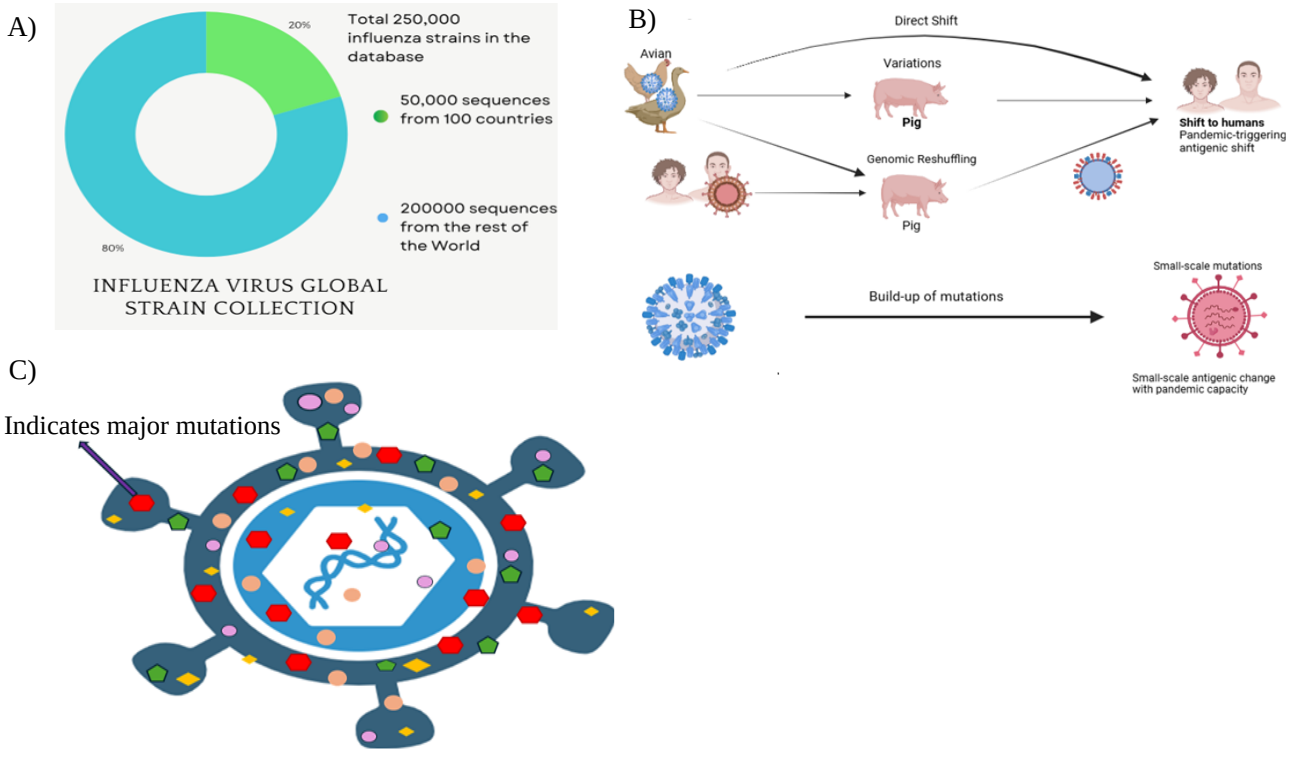

Figure 1. Figure 1 shows three sections that illustrate the genetic diversity of influenza viruses. A) a pie chart represents the global prevalence of 250,000 influenza strains, including 50,000 sequences collected from over 100 countries. This graphic highlights the critical significance of genetic surveillance in improving vaccination strategies and understanding the evolution of influenza viruses. B) A flowchart that shows the difference between antigenic drift and antigenic shift. Antigenic drift is the progressive mutations resulting in seasonal variations, whereas antigenic shift is the genetic reassortment between human and animal strains that can trigger pandemics. C) A diagrammatic illustration of the influenza virus indicating the 60 mutations in the surface proteins that affect the efficiency of vaccination and increase the viral resistance to antiviral medication.

3.2 Human Papillomavirus Database

The Human Papillomavirus (HPV) Database is an essential resource for researching the genetic diversity of the HPV, which is the leading cause of the development of cervical and other types of cancers. This database has valuable data on 200 distinct HPV genotypes and a vast collection of genomic sequences to monitor genetic mutations linked with cancer development [85]. Notably, the HPV Database has the genomic data of high-risk strains of HPV, including HPV-16 and HPV-18. These strains are responsible for approximately 70 % of cervical cancer cases caused by HPV worldwide [86]. Most research efforts on vaccination are focused on these strains because these strains significantly impact the pathophysiology of cancer, producing targeted vaccinations such as Cervarix and Gardasil. The findings of these genomic studies have provided essential new insights into the viral replication mechanism and their ability to stay within host cells [87]. The E6 and E7 oncoproteins encoded by HPV disrupt the function of tumor suppressor proteins Rb and p53, increasing the progression of cervical cancer. The HPV Database is an invaluable tool as it has more than 200 different HPV genotypes, which are valuable for understanding the role of HPV in the development of cancer [88]. Researchers monitor mutations that enhance HPV's ability to evade immune detection, influencing vaccine design and therapeutic strategies.This knowledge will advance the treatment approaches and improve the efficacy of HPV vaccinations. Ongoing surveillance of HPV evolution through the HPV Database allows scientists to predict strains that may lead to future cancer cases and refine vaccination strategies accordingly [89].

Figure 2 highlights the database's emphasis on crucial features of high-risk strains, particularly HPV-16 and HPV-18, while also providing a thorough analysis of the various HPV types associated with cervical cancer. By spotlighting the significant proportion of cancer cases linked to these two strains, the image explores the involvement of multiple HPV types in cancer development [90]. The representation effectively illustrates the clear connection between HPV strains and global cancer statistics, thus reinforcing the necessity to monitor genetic changes to improve cancer prevention strategies. On a global scale, public health policies are informed mainly by data derived from the HPV Database, which is essential for steering vaccination initiatives and cancer prevention efforts. This helps to lower the incidence of HPV-related cancers [91].

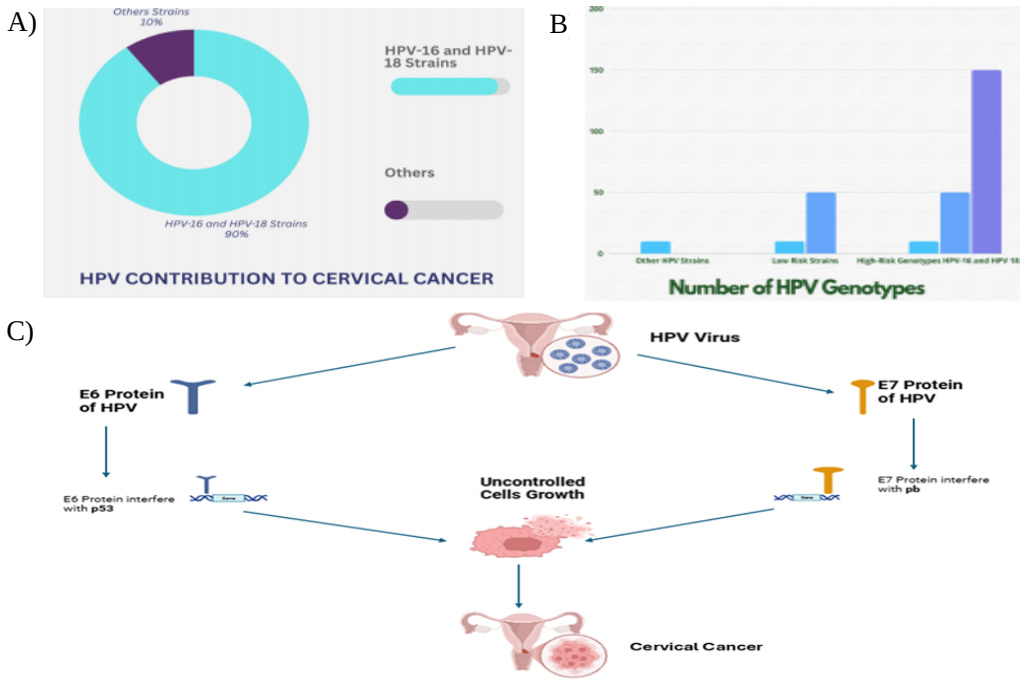

Figure 2. Figure 2 provides a comprehensive analysis of the distribution of HPV strains and their relationship with cancer progression. A) pie chart illustrating that HPV-16 and HPV-18 account for approximately 70% of cervical cancer cases and nearly 90% of all malignancies associated with HPV. The residual segment refers to different HPV variants that have a reduced impact on cervical cancer. B) A bar chart illustrating the distribution of over 200 HPV genotypes within the database, utilizing color coding to distinguish between low-risk and high-risk infections. C) A flowchart depicts how HPV E6 and E7 oncoproteins negatively affect the p53 and Rb tumor suppressor proteins, resulting in uncontrolled cell growth and cancer development.

3.3 SARS-CoV-2 Database

Monitoring the evolution of the SARS-CoV-2and supporting worldwide public health projects has made the SARS-CoV-2 Database indispensable throughout the epidemic. By the end of 2023, the database had around 2 million SARS-CoV-2 genomic sequences worldwide via GISAID [92]. Regular tracking of viral alterations in the database revealed novel variants. As shown in Figure 3A, the fast increase in sequence data highlights the notable expansion of SARS-CoV-2 from the start of the epidemic in early 2020 to the end of 2023. Research has focused on critical mutations in the SARS-CoV-2 spike protein since they significantly affect the virus's transmissibility and immune evasion ability,

increasing transmissibility by 30% to 50% [93]. The most common mutation by the middle of 2020 was the D614G mutation, which considerably helped the virus to propagate globally. The E484K mutation has been shown to reduce the antibody-neutralizing ability of Beta and Gamma variants by 70%, raising the virus's resistance to natural and vaccination-induced immunity [94]. Furthermore, ascribed to these higher mutation rates is the emergence of highly transmissible variants such as Delta and Omicron. By increasing the binding affinity of the virus to the human ACE2 receptor, the N 501Y mutation in the Alpha and Omicron variants boosts its capacity to infect host cells [95]. The global proliferation of the Delta variant is primarily attributed to the P681R mutation, which is associated with a noticeable increase in infectivity. These mutations facilitate the virus's ability to persist and elude immune responses [96]. As illustrated in Figure 3C, these alterations significantly impact vaccine efficacy. Vaccines developed for the Alpha variant exhibited a 20–30% reduction in antibody-neutralizing capacity resulting from prior vaccination or infection [97]. Highlighting its immune evasion capabilities, the Omicron variant demonstrated a substantial 70% decrease in vaccine effectiveness relative to its predecessor. This research, aimed at encompassing a wider range of mutations, has played a pivotal role in developingbivalent and multivalent vaccines, thereby enhancing our capacity to address emerging variants effectively [98]. In particular, mutations integrated in the SARS-CoV-2 Database and numerical data highlight the critical need for ongoing genomic surveillance. Real-time tracking of mutations, including D614G, E484K, and N501Y, will help one to understand viral evolution and direct the development of effective vaccinations [99]. Constant research on newly emerging variants shapes effective public health programs. This guarantees fast modification of treatments and immunizations to combat the most recent virus strains.

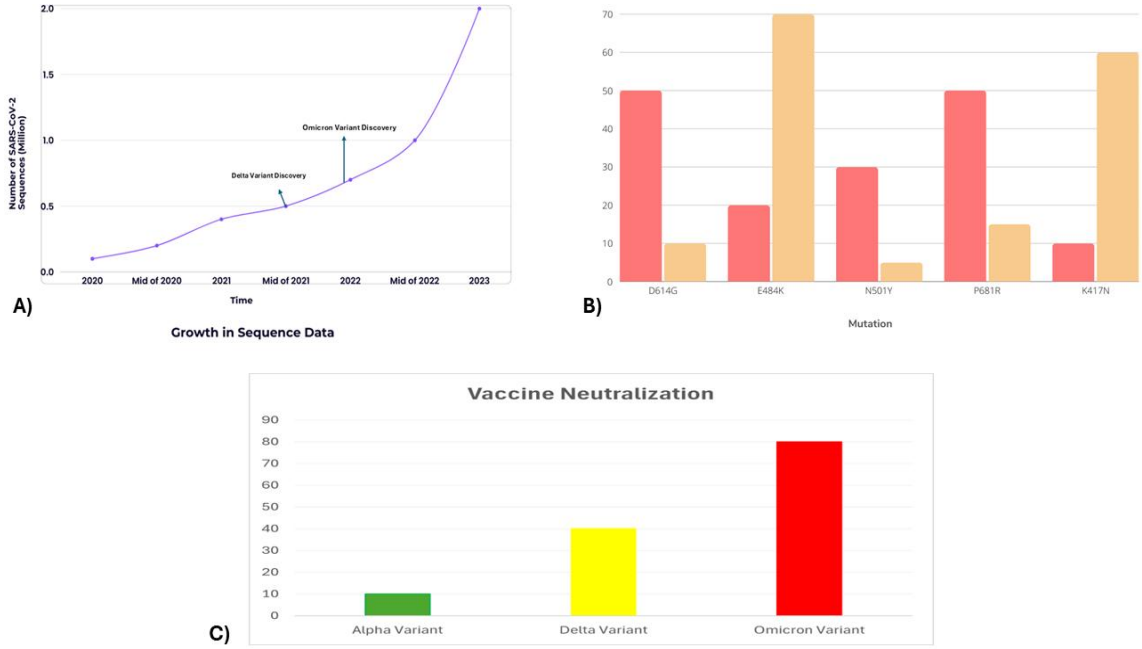

Figure 3. Figure 3 shows the critical phases of SARS-CoV-2 evolution, including the appearance of the Delta and Omicron variants via later components. A) The graph showing the spread of SARS-CoV-2 sequences from 2020 to 2023 emphasizes the immediate need for global genomic surveillance to control the pandemic sufficiently. B) A graphic representation of the opposition different mutations in the variants to vaccinations cause. C) a graph showing the drop in vaccination efficacy against variants Alpha, Delta, and Omicron. A color-coded bar system displays the data: red indicates intense immunological escape, yellow indicates moderate immune escape, and green indicates modest immune escape.

4. Case Studies in Diseases Control and Viral Genomics

Due to developments in viral genomics, the discipline of public health has seen significant change. Effective disease control plans, infection diagnosis, and mutation tracking depend on these instruments. The following case studies highlight viral genomics' importance in controlling viral diseases and its ongoing impact on preventative strategies to stop the next medical crisis.

4.1 COVID-19 Pandemic

Human health, societal interactions, and the global economy have all been drastically disrupted by the COVID-19 epidemic. Since its discovery, a thorough study has focused on the virus's structure, genome, transmission dynamics, and general public health issues [100]. The COVID-19 case study highlights how vital viral genomes are to addressing a major global health crisis. Fast identification of SARS-CoV-2 is made possible by advanced sequencing methods [101]. Table 2 shows that GISAID 2022 will have shared almost 40 million genetic sequences worldwide. The large volume of genetic data makes designing effective management strategies and necessary diagnostic techniques for early

identification simpler. The rapid identification of viral mutations through genomic monitoring technologies significantly influenced public health policies and response strategies[102]. Identifying the D614G mutation in the spike protein greatly expanded our knowledge of COVID-19's increasing transmissibility. Genomic research indicates that Omicron and other factors have about thirty mutations in the spike protein [103]. These genetic modifications highlight the need for changing immunization strategies, including booster doses, since they raise the transmissibility of the virus and assist it in escaping immunity from earlier vaccinations. Although unequal access to immunization remains a significant challenge, more than 12 billion doses of vaccines will be administered globally in 2022 [104]. While lower-income nations battled to surpass 20%, high-income nations reached immunization rates of 80% [105]. Table 2 underscores that continuous genetic surveillance is essential for supporting worldwide public health campaigns and changing vaccination policies to help lower these inequalities.

4.2 Avian Influenza (H7N9)

The entrance of H7N9 avian influenza in China in 2013 highlighted the critical relevance of viral genomes in controlling a fatal virus. The epidemic, which has recorded 1,400 cases and a 39% fatality rate, underscores the dire consequences stemming from inadequate genetic sequencing [106]. To identify changes in the hemagglutinin (HA) and neuraminidase (NA) proteins, the genomes of over 50,000 H7N9 virus samples were sequenced, as shown in Table 2. Essential insights into the evolution of the virus and the mechanics of its transmission among the human population have been uncovered as a result of this analysis [107]. Public health authorities have taken strict action to respond to the problem and slaughtered more than 10 million avians. The research on genomic data helps to advance vaccines and antiviral medicines designed to counter the genetic mutations of the H7N9 virus [108]. This case highlights gene surveillance's importance in monitoring viral mutations, improving predictive skills, and reducing possible future threats. The influence of the human papillomavirus (HPV) on the progression of cancer is a notably important area of research [109]. With HPV being one of the most prevalent among various malignancies, cervical cancer remains a leading etiological factor. Creating effective preventive strategies calls for a grasp of HPV's carcinogenic capacity and dynamics of transmission [110]. Emphasizing the importance of public health initiatives aiming at increasing vaccination coverage, HPV immunizations have evolved into a necessary tool in reducing the prevalence of HPV-related cancers. The section on viral genomics emphasizes how crucial genomics are to cancer prevention, including avoiding cervical cancer and other HPV-related diseases [111]. Thorough genomic sequencing of over 200 HPV genotypes reveals that high-risk strains, especially HPV-16 and HPV-18, are shown to be responsible for more than 90% of cervical cancer cases globally. Table 2 demonstrates that after the discovery of Gardasil, the incidence of cervical cancer in those vaccinated has dropped by 70%. Even with adequate immunization, unequal global access still poses a significant challenge [112]. While low-income countries struggle to obtain 50% coverage, high-income countries have achieved immunization rates surpassing 80%. This disparity emphasizes the urgent need for projects to improve global vaccine accessibility [113]. Through more than 20,000 HPV genomes, sequencing has yielded important new insights on the viral E6 and E7 genes, which are vital in thus compromising the tumor suppressor genes p53 and Rb, promoting cancer progression. This work has established a basis for new therapeutic approaches, greatly enhanced vaccine efficacy, and progressed more individualized cancer treatments [114].

4.3 HIV and Antiretroviral Therapy Resistance

Research on infectious diseases mainly revolves around the interplay between antiretroviral treatment and HIV. Management of HIV infections and patient quality of life improvement depends on antiretroviral medications [115]. The tracking of mutations that confer resistance to antiretroviral therapy (ART) positions HIV as a crucial topic in the field of viral genomics. Comprehensive genomic sequencing of HIV across diverse patient populations worldwide has identified mutations in key regions, particularly within the protease and reverse transcriptase genes [116]. These findings underscore the necessity for evolving therapeutic strategies to preserve treatment effectiveness by providing a thorough analysis of the mechanisms underlying medication resistance.

Because of continuous research on viral evolution, healthcare professionals can identify mutations that confer resistance to specific antiretroviral drugs (ART). This information facilitates the development of more focused and successful therapy plans [117]. Table 2 shows the results of ongoing studies on developing second and third-line antiretroviral medications (ART) as backups should first-line treatments prove insufficient. Genomic surveillance has to be implemented if patient immunity is to be raised and drug-resistant HIV strains are to cease arising [118].

4.4 Zika Virus and Birth Defects

While the fight against HIV continues through genomic surveillance of drug resistance, viral genomics has also played a crucial role in understanding emerging infectious threats, such as the Zika virus. More recently, studies have examined the relationship between the Zika virus and congenital abnormalities. Spread mainly by mosquito bites, the Zika virus is strongly connected to several congenital anomalies, including microcephaly and other neurological problems [119]. Understanding the impact of the Zika virus on fetal development is crucial for creating effective public health campaigns and preventive policies. Clarifying the infection processes and their effects on a mother's health has lately attracted most of the attention in the study [120].

Table 2. Insights from Case Studies on the Role of Viral Genomes in the Treatment of Various Viral Diseases

Case Study	Virus	Year	Outbreak Size	Key Genomic Data/Mutations	Role of Genomic Sequencing	Vaccine/Intervention	Global Health Impact	References
COVID-19 Pandemic	SARS-CoV-2	2020-2023	40+ million sequences	D614G, E484K, N501Y, Omicron mutations	Rapid mutation tracking, diagnostic test development	12+ billion doses of vaccine globally, boosters	High mortality in unvaccinated populations has a major economic impact	[24,123,124]
Avian Influenza	H7N9	2013	1,400+ confirmed cases	Hemagglutinin, neuraminidase mutations	Genomic sequencing monitored mutations facilitating transmission models	Ten million+ poultry culled, antiviral therapy development	39% mortality rate, potential for zoonotic transmission	[125,126]
HPV Outbreak	HPV	Ongoing	200+ genotypes of HPV	HPV-16, HPV-18	Genomic data shows high-risk strains involved in cancer.	The Gardasil vaccine reduces cervical cancer by 70%	Vaccination rates globally: 80% in high-income countries and 50% in low-income countries.	[127,128]
Ebola Outbreak	Ebola Virus	2014-2016	28,000+ cases	Virus-specific mutations in glycoproteins	Genomic sequencing identified transmission chains and mutations	Ring vaccination strategy, ZMapp treatment	11,325 deaths, containment measures successful but costly	[129,130]
Zika Virus Outbreak	Zika Virus	2015-2016	1,500+ cases	NS1 protein mutations, connection to congenital disabilities	Genomic sequencing revealed a mutation link to microcephaly	Mosquito control and public health advisories	5,000+ cases of microcephaly reported in Brazil	[131,132]
HIV/AIDS Surveillance	HIV-1	1980s-present	37 million+ infected	RT mutations, drug resistance markers	Monitoring of drug resistance, vaccine development	Global ART treatment, PrEP prevention programs	Global ART coverage improved transmission rates but was prevalent in low-income regions.	[133,134]
Hepatitis C Outbreak	Hepatitis C Virus	Ongoing	71 million+ infected	NS3/4A, NS5A mutations	Genomic sequencing tracks viral mutations linked to drug resistance	Direct-acting antivirals (DAAs) leading to 95% cure rate	Reduced global incidence with antiviral access	[135,136]
Measles Outbreak	Measles Virus	Ongoing	10-30 million cases/year	F protein mutations	Sequencing is used to track strain variations, monitor outbreaks	Measles vaccination, global eradication campaigns	Resurgence due to vaccine gaps, 100,000+ deaths annually	[137,138]
Polio Eradication	Poliovirus	1988-present	350,000+ cases (1988 peak)	VP1 mutations	Genomic sequencing monitors the spread of viruses and the movement of different strains.	Worldwide initiative for polio immunization, local elimination efforts	Successful elimination in most regions, with continued initiatives in specific areas.	[139,140]
Smallpox Eradication	Variola Virus	1960s-1980s	100 million+ cases	Variola major and minor genomic differences	Viral genome sequencing guided the creation of vaccine strains.	Global Elimination Campaign 1977-1980	Smallpox has been eradicated globally, with no reported cases since 1980.	[141,142]
Rabies Control	Rabies Virus	Ongoing	59,000+ deaths annually	G-protein mutations	Genomic sequencing identifies regional viral variants	Animal vaccination, post-exposure prophylaxis	High mortality, despite control, is endemic in many regions	[143,144]
Influenza Seasonal	Influenza A/B	Seasonal	3-5 million cases/year	H3N2, H1N1, H5N1, H7N9 mutations	Genomic surveillance is used to select yearly vaccine strains	Annual flu vaccine, antiviral treatments	Reduced morbidity in vaccinated populations, mutations reduce efficacy	[145,146]
Hepatitis B Control	Hepatitis B Virus	Ongoing	257 million+ infected	S gene mutations	Genomic analysis tracks antiviral resistance in hepatitis B strains	Hepatitis B vaccination, antiviral therapy	Global incidence decreased with vaccination programs ongoing in high-risk areas.	[147,148]
Dengue Fever	Dengue Virus	Ongoing	100 million+ cases/year	DEN-2 and DEN-3 strain mutations	Genomic sequencing to track strain variation and mosquito vectors	Vector control, dengue vaccine development	Increasing burden in tropical regions, rising case numbers	[149,150]
Yellow Fever	Yellow Fever Virus	Ongoing	200,000+ cases/year	YF-17D vaccine strain analysis	Sequencing of viral strains to monitor mutation and spread	Yellow fever vaccination, mosquito control	Vaccination reducing incidence in affected regions	[151,152]

The outbreak of the Zika virus was observed between 2015 and 2016 and it revealed the major risk of congenital abnormalities, most notably microcephaly, which is linked with viral infections. Genomic sequencing provided real-time data that allowed public health organizations to track the spread of Zika and adjust control measures, such as targeted mosquito eradication, to effectively curb transmission [121]. The coordinated efforts of global health organizations (WHO) during the Zika outbreak to share genetic data were very helpful in overcoming the transmission of the virus and the development of successful public health campaigns. In addition, advances in viral genomes have helped to get a more in-depth understanding of the virus pathophysiology, and it helped to prevent and control evolving viral hazards [122].

5. Challenges and Future Directions

Viral genomics has greatly improved the monitoring, prevention, and management of viral diseases. Still, a major challenge is the difference in the capacity of genetic surveillance between high-income and low-income countries [153]. According to the World Health Organisation (WHO) investigation report, 25% of low- and middle-income countries (LMICs) can effectively sequence their genomes against viral threats [154]. This difference requires the immediate need for global measures to detect viral mutations to strengthen the preparation for potential outbreaks at the worldwide level. High-income countries conducted 90 percent of the genetic sequencing during the COVID-19 pandemic. On the other hand, low-income countries have a shortage of genomic data, restricting their ability to adjust healthcare practices effectively [155]. This gap highlights the demand for global collaboration to ensure health security and facilitate fair access to genetic data and technologies. The confidentiality of data and the ethical distribution of genetic information are two other significant challenges that must be addressed. The growing availability of genetic data poses substantial problems regarding preserving individuals' privacy, consent in advance, and the ethical use of this resource [156]. The sharing of genetic data has occasionally generated concerns about potential misuse for purposes beyond scientific research, including discrimination or exploitation. The Global Alliance for Genomics and Health (GA4GH) advocates for establishing consistent data-sharing networks that uphold ethical standards and ensure the responsible utilization of genetic data. Although these policies have been gradual, more than 100 countries have committed to enhancing data-sharing networks by 2023 [156].

The development of sequencing technologies should help fix many of these problems. Next-generation sequencing (NGS) has dramatically raised the capacity to identify viral changes [157]. 2020 alone saw about 12 million SARS-CoV-2 genomes sequenced globally, allowing real-time mutation detection. Future developments in long-read sequencing and NGS technologies might greatly help to monitor and forecast viral evolution [158]. By 2030, sequencing a human genome will cost $100, enabling comprehensive genomic monitoring even in settings with limited resources. According to a 2024 study published in Nature Biotechnology, this research is expected to hasten the identification of new viral strains and enhance vaccination development, possibly reducing vaccine production timelines by as much as 50% [159].

Constant improvements in sequencing technologies and data-sharing platforms give great possibility for more effective control of viral outbreaks. Targeted, exact, strong antiviral medicines can be developed by combining genetic data with present epidemiological monitoring techniques [160]. The increasing availability of genetic surveillance, especially in low-and middle-income countries, is projected to increase the capacity of the worldwide health system to prevent and address approaching viral risks. Recent changes in viral genomes should speed up and improve accuracy in sequencing while underscoring the need to use this powerful tool properly and sensibly to preserve global health.

6. Conclusion

Modern public health is fundamentally based on viral genomes since it helps one to understand viral evolution, illness spread, and the creation of highly targeted therapy techniques and vaccinations against certain viruses. Comprising thorough databases, the Influenza Database, HPV Database, and SARS-CoV-2 Database let researchers track viral mutations, track transmission patterns, and hasten the creation of tailored therapies. Access to genetic resources determines whether one studies the dynamic character of viruses, improves pandemic readiness, or generates more successful immunizations against recently developing variants. The field of virology has undergone a significant transformation due to advancements in bioinformatics and genome sequencing, resulting in enhanced precision and efficiency in viral genome analysis. Notwithstanding these advances, issues persist, including challenges around data confidentiality, unequal access to genetic data, and the inherent uncertainty of viral mutations. Still, the ongoing development of viral genomes has immense potential. It foresees a period when public health efforts are progressively adaptable, accurate, and successful worldwide in reducing viral illnesses and pushing for a better and more resilient planet.

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Conflict of Interest

Authors declare no conflict of interest.

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