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INFLUENZA VIRUS GENETIC DIVERSITY AND EPIDEMIOLOGICAL PROFILE IN HUMAN POPULATION

Examining the evolutionary mechanisms driving genetic variation, alongside the global epidemiological landscape, provides insights into transmission patterns, seasonal outbreaks, and pandemic potential. This review explores the complex interplay between influenza virus genetic diversity and epidemiological dynamics within human populations. Insights gained from this synthesis inform public health strategies, emphasizing the importance of surveillance, vaccination, and pandemic preparedness to mitigate the impact of influenza. Influenza viruses exhibit significant genetic variation due to mechanisms such as antigenic drift and shift, as well as their segmented genome. New strains evolve through genetic alterations, enabling them to overcome existing immunity and spread both seasonally and globally. Understanding genetic diversity is essential for predicting strain evolution and developing effective vaccines. Influenza, a highly contagious respiratory virus, spreads via respiratory droplets. It affects individuals of all ages, but those at increased risk for severe disease include the elderly, young children, pregnant women, and individuals with underlying medical conditions. Influenza follows seasonal trends, with higher transmission rates in colder months in temperate regions, while tropical regions may experience year-round circulation. Epidemiological factors influencing influenza transmission and outcomes include population density, travel behavior, and healthcare infrastructure. Monitoring influenza's epidemiological dynamics and examining genetic variants are critical tasks for surveillance systems. Effective control of influenza requires integrated strategies that address both genetic and epidemiological aspects. Controlling influenza epidemics, especially during a pandemic, involves using antiviral medications, early detection, and containment measures.

Key words: Influenza viruses, Genetic diversity, Epidemiology, Human population, Public health, Surveillance.

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Тұмау вирусының генетикалық әртүрлілігі және адам популяциясының эпидемиологиялық профилі

Жаһандық эпидемиологиялық ландшафтпен қатар, генетикалық вариацияны тудыратын эволюциялық механизмдерді зерттеу жұғу үлгілеріне, маусымдық індеттерге және пандемиялық әлеуетке жарық түсіреді. Бұл шолу тұмау вирусының генетикалық әртүрлілігі мен адам популяциясындағы эпидемиологиялық динамика арасындағы күрделі өзара әрекеттесуді зерттейді. Осы синтезден алынған түсініктер тұмау вирустарының адам денсаулығына әсерін азайту үшін қадағалаудың, вакцинациялаудың және пандемияға дайындықтың маңыздылығына баса назар аудара отырып, қоғамдық денсаулық сақтау стратегияларын хабарлайды. Антигендік дрейфа пен ығысу механизмдерінің, сондай-ақ олардың сегменттелген геномының арқасында тұмау вирустары үлкен генетикалық вариацияны көрсетеді. Жаңа штамдар генетикалық өзгерістер нәтижесінде дамиды және бұл штамдар бұрыннан бар және маусымдық немесе ғаламдық таралатын иммунитет жеңу қабілетіне ие. Генетикалық әртүрлілікті түсіну штаммдардың эволюциясына болжау және тиімді вакциналарды жасау үшін өте маңызды. Тыныс алу тамшылары тұмаудың, өте жұқпалы респираторлық вирустың таралуын мүмкіндік берді. Бұл барлық жастағы адамдарға әсер етеді, бірақ кейбіреулерінде, мысалы, қарттарда, кішкентай балаларда, жүкті елдерде және негізгі медициналық бұзылулары бар адамдарда ауыр аурулар мен зардаптардың қаупі жоғарылайды. Тұмау маусымдық тенденцияларға сәйкес келеді, қоңыржай елдерде суық айларда жұқтыру жылдамдығы жоғарылайды. Дегенмен, тропикалық жерлерде

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болады. Тұмау індетінің берілу мен салдарына әсерін ететін эпидемиологиялық элементтерге халықтың тығыздығы, саяхаттағы мінез-құлық және денсаулық сақтау инфрақұрылымы алады. Тұмаудың эпидемиологиялық динамикасы қадағалау және генетикалық нұсқаларды қадағалау жүйелерінің маңызды міндеттері бойы табылады. Тұмаудың тиімді бақылау генетикалық және эпидемиологиялық аспектілерді ескеретін біріктірілген стратегияларын қажет етеді. Тұмау эпидемиясын бақылау, әсіресе пандемия жағдайында, вируса қарсы препараттарды, ерте анықтау әдістерін және оқшаулау шараларын қолдануды талап етеді.

Түйін сөздер: Тұмау вирустары, Генетикалық әртүрлілік, Эпидемиологии, Адам популяциясы, Қоғамдық денсаулық сақтау, қадағалау.

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Генетическое разнообразие вируса гриппа и эпидемиологический профиль в человеческой популяции

Изучение эволюционных механизмов, влияющих на генетическую вариацию вируса, на фоне глобальной эпидемиологической ситуации позволяет понять закономерности передачи, сезонные вспышки и потенциал для пандемий. Этот обзор исследует сложное взаимодействие между генетическим разнообразием вируса гриппа и эпидемиологической динамикой в человеческой популяции. Полученные данные способствуют разработке стратегий здравоохранения, подчеркивая важность мониторинга, вакцинации и подготовки к пандемиям для смягчения воздействия гриппа на здоровье человека. Вирусы гриппа демонстрируют значительное генетическое разнообразие благодаря таким механизмам, как антигенный дрейф и сдвиг, а также из-за сегментированного генома. Новые штаммы эволюционируют через генетические изменения, что позволяет им обходить существующий иммунитет и распространяться как сезонно, так и глобально. Понимание генетического разнообразия имеет ключевое значение для прогнозирования эволюции штаммов и разработки эффективных вакцин. Грипп – высококонтагиозный респираторный вирус, распространяющийся через капли, образующиеся при кашле и чихании. Он поражает людей всех возрастных групп, однако наибольший риск тяжелых заболеваний существует у пожилых людей, маленьких детей, беременных женщин и людей с сопутствующими заболеваниями. Грипп подвержен сезонным колебаниям: в умеренных странах наблюдается повышение заболеваемости в холодное время года, в то время как в тропических регионах вирус может циркулировать в течение всего года. К эпидемиологическим факторам, влияющим на передачу вируса и тяжесть заболевания, относятся плотность населения, путешествия и состояние инфраструктуры здравоохранения. Мониторинг эпидемиологической динамики гриппа и исследование его генетических вариантов являются важными задачами для систем наблюдения. Эффективное управление гриппом требует комплексных стратегий, учитывающих как генетические, так и эпидемиологические аспекты. Эффективная борьба с эпидемиями гриппа требует интегрированного подхода, включающего как использование противовирусных препаратов, так и организацию своевременной диагностики и изоляции больных.

Ключевые слова: Вирусы гриппа, Генетическое разнообразие, Эпидемиология, Популяция, Общественное здравоохранение, Эпиднадзор.

Introduction

Influenza viruses are members of the family *Orthomyxoviridae* and include influenza virus types A, B, and C. Influenza has had a significant historical impact and continues to pose a considerable threat to public health. Since the transmission of H5N1 avian influenza from birds to humans in 1997, virologists and public health officials anticipated the global human spread of this virus. The pandemic spread of a novel H1N1 influenza virus arose from an unpredicted source; precursors of the pandemic influenza A (H1N1) 2009 virus have been circulating among pigs for over a decade [1]. The influenza virus is one of the most effective, enduring, and unpredictable human diseases. Worldwide, influenza is still the cause of frequent and fatal zoonotic breakouts, erratic pandemics, and regular seasonal epidemics. The influenza virus spreads by aerosols and causes "flu," an acute fever respiratory illness especially severe in young children, the elderly, and people with weakened immune systems. The influenza virus substantially negatively impacts the world's population and economy [2].

Antigenic shift, which exposes the human population to a novel strain of influenza and might result

in increased or decreased morbidity or mortality, causes flu epidemics every six to ten years. Influenza A (H1N1) pdm09 subtype virus, which originated from the reassortment of Eurasian Avian (EA) related viruses of swine and North American Triple reassortment (TRIG), caused the first human influenza outbreak of the twenty-first century. Due to a unique strain of Influenza A (H1N1) pdm09, the world experienced a pandemic in 2009 [3].

This review addresses several key research issues related to the epidemiological composition and genetic diversity of influenza viruses in humans. The review aims to analyze the genetic elements associated with influenza virus pathogenicity, assess the impact of antigenic drift on vaccine efficacy, and explore ways to improve vaccine formulation. It also examines the kinetics of influenza virus propagation, the impact of climate and environmental factors, the dynamics of host immune responses, and the effectiveness of current influenza surveillance systems. Additionally, it considers the effects of behavioral and societal factors, such as vaccination uptake, travel habits, and public health initiatives. The review highlights the importance of a One Health approach to understanding the interactions between human, animal, and environmental factors in the spread of influenza.

Main body

Large population sizes and densities at mass gatherings such as the Hajj (Makah, Saudi Arabia) can contribute to outbreaks of respiratory virus infection by providing local hot spots for transmission followed by spread to other localities [4]. It has previously demonstrated that antigenic variations of H3N2 co-circulated with clades of H1N1/2009 and that seasonal H3N2 and pandemic H1N1 viruses, both of which were present during the initial wave of the H1N1 pandemic in Hong Kong, have similar transmission potential in home settings. Together with the pandemic H1N1 virus, sporadic H3N2 transmission was also noted at the same period in other areas of the world. Nasopharyngeal swabs from index cases with confirmed influenza and their household contacts were used for whole genome deep sequencing to characterize patterns of viral evolution at a finer scale, precisely, the amount of genetic diversity transmitted among hosts. Crucially, spatiotemporal transmission chains were constructed, and donor/recipient pairs in suspected transmission events were identified with relatively high confidence using household epidemiological data. These pairs have also been compared with unrelated pairs [5].

Influenza seasonally, despite extensive preexposure and vaccination, influenza A viruses (IAVs) are predicted to cause tens of billions of dollars in economic expenditures and thousands of deaths annually in the United States alone. IAV continues to spread across the human population because it constantly develops resistance to herd immunity. This is not a universal characteristic of all viruses, though; certain viruses (such as measles) have mutation rates comparable to that of IAVs yet do not successfully develop immunological resistance in humans and are effectively suppressed by vaccination. Identifying the specific factors that influence influenza virus development is a critical unresolved issue in virology that must be addressed to create future vaccines and therapies that are resistant to escape. IAV populations show remarkable levels of genomic and genetic diversity. Genetic diversity, which IAV and the majority of other RNA viruses have in common, is the number of nucleotide sequence polymorphisms resulting from the relatively high rate of mutation of the viral polymerase. Genomic diversity is the difference in each virus particle's ability to code for different genes or which viruses are successfully expressed during infection. The extent to which IAV populations exist as extremely diverse swarms of genetically and phenotypically heterogeneous particles is becoming more visible because of new technologies and methods. IAV populations comprise large groups of genetically diverse minor sequence variants that are closely connected, sometimes (though not always correctly) referred to as "quasispecies." In other RNA virus systems, the impact of this variety on viral pathogenicity and fitness has been thoroughly studied. When new selection pressures arise, preexisting genetic variety is fuel for adaptation, leading to mutations that may enhance fitness. Because both processes depend on the accumulation of advantageous substitutions, this process of evolutionary innovation promotes the persistence of seasonal influenza virus strains in the human population and the emergence of zoonotic strains with pandemic potential into human circulation. The vast majority of random mutations are harmful. Thus, there are costs associated with this diversity and the tremendous potential advantages. A virus's ability to evolve probably rests partly on its ability to weigh the advantages and disadvantages of preserving a high-standing diversity. The mutation-prone replication mechanism produces the mutational landscape found in IAV populations,

which is influenced by selection and other evolutionary processes like genetic drift. In this section, I will summarize our current understanding of the virologic characteristics and evolutionary processes that control the genetic composition of IAV populations [6].

Influenza viruses cause severe global economic and public health burdens. From 1990 to 1999, annual influenza epidemics in the US caused over 30,000 fatalities annually. Frequent pandemics cause noticeably larger mortality tolls [7]. Over 20 million religious visitors visit Saudi Arabia, and it receives 3 million pilgrims annually. Every year, tourists from more than 180 countries congregate in a small space, increasing the danger of respiratory illnesses, such as influenza viruses, spreading among pilgrims. Influenza infection is among the most significant contributors to public and international health issues. During their time in Makah and the sacred sites, pilgrims endure harsh climatic conditions, with temperatures sometimes rising beyond 45 °C. [8].

Using phylogenetic analysis, whole genome consensus sequences were grouped by household for every patient group with either H3N2 or H1N1/2009. Comparisons of phylogenetic trees from each gene revealed no proof that this population underwent reassortment during the time frame of the research (no data displayed). This group was exposed to three antigenic sublineages of H3N2 (A/Brisbane/10/2007-like, A/Victoria/208/2009-like, and A/Perth/16/2009-like) and three clades of H1N1/2009. Despite the population's tiny size, one instance of mixed subtype infection was found. (Patient 781_V1 (0), suggesting that co-infection of seasonal and pandemic strains could not be uncommon. [5]. This review article has used a series of scientific and reliable articles to find the reasons for the diversity and epidemiological profile of influenza viruses in the human population. This article's goals include a thorough analysis of genetic diversity, a detailed investigation of epidemiological profiles, a synthesis of genetic and epidemiological viewpoints, implications for public health, and future directions. Epidemiological studies aim to identify factors that place some populations at greater risk of contracting an infectious disease than others. Such factors can be associated with the three legs of the "epidemiologic triad" for infectious diseases: the combination of an external causative agent, a susceptible host, and an environment that links these two together. Genetic differences contribute to variations in the immune response of different individuals to a pathogen [9].

Between the two sites, it was observed substantial diversity in A (H3N2) and A (H1N1) pdm09 viruses, with A (H1N1) pdm09 viruses having substantially less nucleotide variation at antigenic places than A (H3N2) viruses. Antigenic sites for A (H1N1) pdm09 varied from the vaccine strain by three to four amino acids, with two differences shared by all studied isolates. Antigenic sites for A (H3N2) viruses varied from the vaccination strain by six to nine amino acids, with four differences shared by all studied isolates [10]. Among the various seasonal influenza viruses, influenza A/H3N2, which has been affecting people since the 1968 "Hong Kong" pandemic, has survived even after the 2009 A/H1N1pdm virus appeared and effectively supplanted the seasonal influenza A/H1N1 that was previously circulation. Ongoing antigenic alterations in circulating seasonal A/H3N2 viruses constantly prompt new guidelines for developing seasonal influenza vaccines. The aim is to maximise vaccine-induced protection in the general public and among healthcare workers [11]. In human hosts, influenza virus populations expand exponentially at the beginning of an acute infection. Viral titers peak two to four days after the infection's start, and afterwards, titers decline for three or four days until the virus reaches undetectable levels [12].

Continuously evolving Influenza viruses accumulate changes in the viral genome, leading to the diversity of subpopulations and the introduction of novel strains. Pandemics and yearly epidemics result from this. Zoonotic vectors, host immunity, and other ecological and environmental factors can cause viral genetic variation and antigenic alteration. Point mutations causing antigenic drift, gene reassortment causing genetic shift, defective-interfering particles, and RNA recombination changing the Influenza virus genome are some processes that can cause genetic variation [13]. Influenza A predominated in all WHO regions between 2011 and 2019, frequently alternating between A (H1N1) pdm09 and A (H3N2). Between 2011 and 2019, the percentage of B/Yamagata and B/Victoria viruses stayed low. During the COVID-19 pandemic, influenza A was likewise prevalent in all WHO regions except for WPR; nonetheless, most samples tested positive for A (H3N2). About 98% and 90% of the samples found in AMR in 2021 and 2022 tested positive for A (H3N2). 90% of all positive samples in WPR in 2021 were caused by B/Victoria viruses. Nevertheless, influenza A was once more prevalent in WPR in 2022 and 2023. Furthermore, throughout the COVID-19 pandemic, hardly many B/Yamagata viruses were found [14].

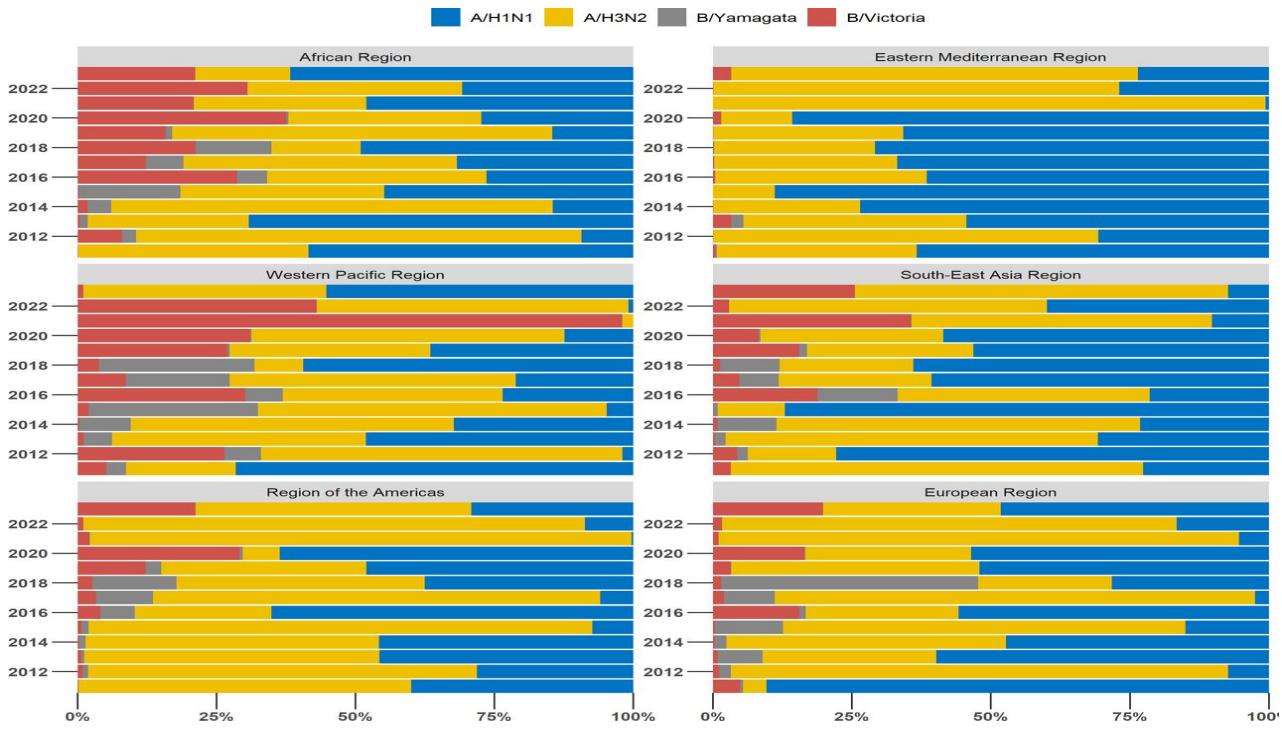

Figure 1 – Distribution of influenza B lineages and influenza A subtypes by six WHO regions from 2011 to 2023 [14]

Origins of genetic diversity

Influenza viruses (family Orthomyxoviridae) possess a negative-strand segmented RNA genome and enveloped virions. Genetic diversity in the influenza virus results from a high rate of mutation associated with replication using low-fidelity RNA polymerase and the reshuffling (or reassortment) of segments among confecting strains. The emergence of viral infections with potentially devastating consequences for human health depends on their underlying evolutionary dynamics [15]. The emergence of new influenza A virus strains can be caused by ‘‘antigenic shift,’’ resulting from reassortment of gene segments, including H and N types, ‘‘antigenic drift’’ resulting from the continuing accumulation of mutations in the H and N genes or a pathogenic virus jumping species, and acquiring the ability to infect and be transmitted among humans, as in the 1918 pandemic [16]. The influenza A virus is divided into 18 HA and 11 NA subtypes based on the antigenic differences between HA and NA. All influenza virus subtypes have been found in wild birds, the natural influenza virus reservoirs, except H17N10 and H18N11, isolated from bats. Avian influenza viruses multiply effectively in wild birds, but in other animals, they do not. However, mounting evidence shows that various animals, including dogs, cats, rhesus macaques, and even plateau pikas, can contract avian influenza viruses. Human sporadic H5N1, H7N9, and H10N8 infections have been documented in China, suggesting that other viruses of bird flu subtypes may be dangerous to people due to their natural development [7].

Since 1918, three pandemics have been brought on by influenza A viruses that infect people after spreading from wild birds. Numerous additional mammalian hosts, such as pigs, dogs, horses, bats, seals, and whales, have also contracted influenza A viruses. Influenza A viruses, like other viruses, must co-opt host factors to replicate within a host cell successfully. Influenza A virus requires host factors at many stages of its life cycle, from entry, transport of gene segments to the nucleus, replication, and packaging to exit. As a result, the virus must adapt to novel host factors to successfully emerge in a new host species. Pandemic preparedness requires us to identify mutations that allow or prevent animal viruses from using human host factors and to understand the mechanisms that enable host switching [17]. Influenza in humans is one of the first large-scale pathogen genome sequencing initiatives focused on a virus, and influenza virus genomes are frequently used to test evolutionary analysis techniques. These techniques are increasingly utilised to

comprehend antigenic drift and select vaccine variants. The initial proof of influenza's phylogenetic diversity is the identification of highly divergent and diversified viruses in fruit bats (Artibeus spp.) from Central and South America, which revealed a virus burden more significant than that of the bird-mammal 16HA-9NA model [18].

Epidemiological profile of influenza viruses in the human population

Influenza A viruses are microorganisms that cause respiratory tract infections in humans, birds, and other mammals such as swine, horses, etc. In the 20th century, three pandemics resulted in widespread morbidity and mortality. A novel H1N1 (H1N1pdm) virus surfaced in 2009 and sparked a pandemic that killed 18,449 people, according to reports, and likely infected millions more globally [19]. Regular annual epidemics have characterised seasonal influenza in temperate zones of the world for most of the last fifty years. The observed skip dynamics can be explained in relatively simple terms by basic epidemiological principles. The general population had never been exposed to the novel strain of H1N1pdm until it surfaced in March 2009. This made it possible for the pandemic to spread worldwide, even though it was outside many nations' typical influenza season. Each subsequent epidemic outbreak increased the general public's exposure to the novel H1N1pdm strain over time, strengthening population immunity and lowering the number of vulnerable people [20]. Seasonal influenza is responsible for a significant annual burden of lower respiratory tract infections (LRTIs) and other respiratory conditions (such as chronic obstructive pulmonary disease), even though the burden of influenza is frequently discussed concerning past pandemics and the threat of future pandemics. A systematic scientific attempt to measure the health loss linked to a wide range of illnesses and impairments is the Global Burden of Disease Study (GBD) 2017. An influenza pandemic in 1918 is thought to have claimed between 20 and 50 million lives, surpassing the death toll from World War 1. Seasonal influenza continues to have a significant role in the rising global incidence of lower respiratory tract infections (LRTIs) today [21]. Influenza virus infections are common in people of all ages. Epidemics occur in the winter months in temperate locations and at varying times of the year in subtropical and tropical locations. Most influenza virus infections cause mild and self-limiting disease, and around one-half of all infections occur with a fever. Only a tiny minority of infections lead to severe diseases requiring hospitalisation. During epidemics, the rates of influenza virus infections are typically highest in school-age children. The clinical severity of infections tends to increase at the extremes of age and with the presence of underlying medical conditions, and the impact of epidemics is most remarkable in these groups. Every year, Significant morbidity and mortality are caused by influenza epidemics, and influenza pandemics could have an even more significant effect than the 2019 coronavirus outbreak. To create more effective control strategies, we must know how influenza is spread [22].

A novel strain of influenza virus A H1N1, also known as "swine flu," started to spread in several nations worldwide in April 2009. Although the genomic makeup of the most recent H1N1 virus strain differs significantly from that of the previously identified isolates, it has been discovered to share close ties with the swine flu virus. The genetic features of this new virus were not previously found in Influenza A in humans, pigs, or poultry [23]. According to phylogenetic analysis of recently made public whole genome sequences of the human influenza A virus, several viral lineages commonly co-circulate within a single geographic location. This contrasts with earlier research that showed a single dominant and selectively preferred lineage in the HA1 (hemagglutinin) domain alone [24]. While influenza epidemiology varies considerably throughout the year in equatorial locations, the influenza seasons typically occur between November and April in temperate regions of the Northern Hemisphere (NH) and between May and October in the Southern Hemisphere (SH). GISN tracks the epidemiology and characteristics of influenza viruses all year round to identify the emergence and dissemination of novel antigenic variations. Based on data from GISN and assessed by a group of officials from the CC, ERL, NIC, and others, the WHO has issued official annual recommendations for the formulation of seasonal influenza vaccinations every February since 1971 [25]. On June 11, 2009, the World Health Organization (WHO) declared a pandemic alert level 6. This warning level was increased from 5 to 6 in less than 20 days, and as of right now, the infection has spread to 208 countries worldwide with 2,46,571 confirmed cases and 9596 deaths [26]. The year 2009 marked the beginning of a pandemic brought on by a fresh strain of the H1N1 influenza virus. The outbreak started in March when officials in Mexico noticed a greater-than-anticipated rise in flu-like episodes and the simultaneous development of unusual instances of pneumonia1. The pandemic influenza virus (H1N1) 2009 is the current name for the etiological agent that was identified in early

April 2009 by the Centers for Disease Control and Prevention (CDC/Atlanta, USA) and reported to the World Health Organization (WHO) in compliance with the 2005 International Health Regulations [27]. Following the 1968 H3N2 virus pandemic, influenza A(H3N2) viruses became common in humans and have been a primary contributor to influenza outbreaks. These viruses evolve continuously by reassortment and genomic evolution. Antigenic drift is the cause for the need to update influenza vaccines frequently. Using two data sets that span the entire period of circulation of A (H3N2) influenza viruses in humans, it was shown that H3N2 influenza virus evolution can be mapped to 13 antigenic clusters [28]. The linkage between the virologic profile and clinical characteristics of individuals affected by the influenza virus offers crucial data for clinical care and epidemiological control of upcoming illness epidemics. Control of the forthcoming epidemics is based primarily on the analysis of patients and comparison of viral load in conjunction with epidemiological information. The median viral load was more significant during the pandemic than seasonal influenza. In pH1N1 (2009)-infected patients, the viral load was positively correlated with chills, myalgia, and rhinorrhea and negatively correlated with dyspnea; no correlation was seen with other symptoms or with clinical circumstances, including immunodepression, pregnancy, smoking, or comorbidities [29].

Conclusion

The comprehension and control of seasonal influenza outbreaks and pandemics heavily rely on the genetic variety and epidemiological makeup of influenza viruses within the human population. Some essential features of influenza viruses' epidemiological profile and genetic diversity in the human population followed: In the first, point mutations in the genes that encode the surface proteins hemagglutinin (HA) and neuraminidase (NA) accumulate through a process called "antigenic drift." These mutations result in minor changes to the viral surface proteins and generate seasonal flu outbreaks. This enables the virus to evade any immunity that might have previously formed. When two different influenza viruses infect the same host cell and share genetic material, a more severe genetic alteration known as an "antigenic shift" occurs. As demonstrated by the H1N1 virus that caused the 2009 flu pandemic, this mechanism may lead to novel influenza strains that can potentially produce pandemics.

The second one is the epidemiological profile, in which researching the incidence, influence on human health, and transmission patterns are all part of the epidemiological profile of influenza viruses. Essential elements consist of seasonal variation in which influenza follows seasonal trends, peaking in temperate locations in the colder months of the year. A few examples of the variables that affect this seasonality are humidity, temperature, and human behavior. The transmission dynamics, in which respiratory droplets and close contact with infected persons are the main ways influenza spreads. Comprehending transmission dynamics, encompassing variables like vaccination coverage, travel patterns, and population density, is imperative to execute efficacious control strategies. Also, influenza's effects on health can range from moderate to severe respiratory illnesses, and it can result in complications like pneumonia, particularly in susceptible groups, including the elderly, small children, and people with underlying medical disorders. The virulence and transmissibility of circulating strains of influenza can cause variations in the annual burden of the disease on public health systems.

The third one is surveillance and monitoring systems, which are respiratory droplets and close contact with infected persons, the main ways influenza spreads. Comprehending transmission dynamics, encompassing variables like vaccination coverage, travel patterns, and population density, is imperative to execute efficacious control strategies. As we know, researchers and public health officials can gain a better understanding of the behavior of influenza viruses and develop measures to prevent and control flu outbreaks and pandemics by combining data from genetic studies, epidemiological surveillance, and clinical observations so it would be better to cooperate with them from time to time and get accurate and precise information.

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