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Review Article

Influenza Virus Types, Subtypes and Genomic Lineage with Its Prevention and Control: A Narrative Review

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Abstract

Since influenza viruses continue to be a serious hazard to both humans and animals, they are still very important. Types A, B, and C influenza viruses are among the members of the Orthomyxoviridae family. A quick summary of the molecular factors is provided, which determine pathogenicity and clinical signs and symptoms of influenza. A review of host range and evolution highlights the genetic diversity of influenza A viruses and their capacity to successfully infect a variety of hosts, including avian and mammalian species. Moreover, influenza viruses may reassemble segments because of the way their segmented genome is designed. The significance of host sialic acid distribution and viral receptor-binding hemagglutinins in species-restricted virus binding is emphasized. It results in yearly outbreaks and necessitates the creation of novel vaccination formulations. This may ultimately result in the creation of a virus that can spread among humans and has unique antigenic qualities, perhaps sparking a pandemic. Current developments in our knowledge of the seasonality, transmission, and prevention of influenza viruses are outlined, along with their significance for halting the virus's spread.

Key Words: Acute respiratory infections; influenza virus; orthomyxoviridae; reassortment; antigenic shift

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Introduction:

Acute respiratory infections (ARIs) are prevalent worldwide and the leading cause of death in developing countries.[1] The most striking disparity between developing and developed countries with regard to ARI epidemiology is the case-fatality rate of lower respiratory infection (LRI), mainly pneumonia, bronchiolitis, and influenza,[2,3] influenza is an acute viral respiratory infection that affects all age groups and is associated with high mortality during pandemics, epidemics, and sporadic outbreaks. Nearly 10.0% of the world's population is affected by influenza annually, with about half a million deaths each year.[1] Influenza viruses are significant human respiratory pathogens that cause both seasonal, endemic infections and periodic, unpredictable pandemics.

In tropical countries, influenza activity may occur year-round as well as in outbreaks more typical of temperate regions. These infections cause serious diseases in populations weakened by malnutrition, with limited access to medical care.[4] Of note, the predisposition induced by influenza to superimposed bacterial infections, mainly Streptococcus pneumoniae, may greatly affect morbidity and mortality, mainly among impoverished populations.[5] In addition, influenza viruses can reassort or sometimes cross species barriers to generate emergent strains that may cause localized outbreaks or potentially pandemics with enormous impact for health on a global scale.[6] Since 2011, a swine-origin virus (H3N2) outbreak has been reported in the USA that predominantly involved young children exposed to swine. According to public

health laboratory specimens for the 2018-2019 season, the predominant influenza A subtype was (H1N1)pdm 09 (56.6% of positive specimens), followed by the A/H3N2 subtype (43.6%) and influenza B (4%).[7]

Epidemiology

Influenza viruses have made an impact throughout the world, causing highly contagious respiratory infections with high morbidity and mortality (in seasonal peaks), specially, in infants and the elder people. Influenza has already been associated with an average of 5% of ARIs leading to physician contact in developing countries.[8,9] This low proportion probably represents only the most intense cases, since 30% to 50% of under-five children in tropical Africa have been found to seroconvert in one outbreak.[9] Prior to that, healthy children less than [1] year of age are hospitalized for influenza at rates similar to those for adults at high risk, and influenza accounts for a great number of outpatient visits and courses of antibiotics in children of all ages.[10] Despite the seasonal dependency, influenza infections in the respective countries can also occur outside the normal influenza epidemics and can even lead to locally and temporally limited outbreaks. According to degree of severity, the influenza epidemics can also be clearly distinguished from each other. Approximately 500000 people are dying in every year worldwide.[11] Influenza pandemics are characterized by the recurrence of influenza A subtype against majority of non-immunized human population, and causing a worldwide epidemic. The past century was characterized by three major pandemics: one is, Spanish Flu of 1918 (H^1N^1) caused about 40 million deaths, second one is Asian influenza of 1957 (H2N2) and third one is Hong Kong Flu of 1968 (H2N3) were estimated at 1–2 million and 0.75–1 million deaths, respectively.[11] In 2001, Madagascar experienced high morbidity and mortality rates associated with a conventional influenza A/H3N2 subtype virus due to limited access to care and malnutrition within the population. Conversely, while influenza A outbreaks in temperate countries show sharp seasonality, the seasonal patterns of influenza in tropical countries have shown variability across different studies. In southern India[12] and Thailand,[13] influenza has been present throughout the year with occasional outbreaks. Consistent outbreaks have occurred in June–July and November–January, coinciding with the winter seasons in the southern and northern hemispheres. However, there seems to be no clear association with meteorological factors.[14] In the Philippines, influenza has been more common between November and January,[15] while in Senegal, Nigeria, and Taiwan, there has been a distinct association with increased rainfall. In southeastern Brazil,[16] Argentina,[17] and South Africa,[18] seasonal outbreaks of influenza A have occurred annually from May through August (mid-autumn through winter), in conjunction with cold temperatures but not with rainfall. Influenza B outbreaks occur periodically, yet less frequently than influenza A, in both temperate and tropical regions,[19,20] whereas influenza C is generally nonseasonal.[20] Antigenic drift, minor changes in antigenicity, is caused by accumulation of point mutations in the genes coding for influenza HA and NA, generate new strains and spread in annual epidemics. Influenza B and influenza C are less prone to antigenic drift. Major and abrupt antigenic changes in influenza A are called antigenic shift and resulting in novel HA subtype with or without new NA to which humans lack significant immunity.[21] It may be caused by acquisition of new gene segments through genetic rearrangements in hosts infected with both human and non-human viruses (usually avian), or by the re-emergence of subtypes in reservoir. Pigs are susceptible to both human and avian influenza viruses and can serve as host for recombinant or mammalian species. Novel influenza virus subtypes resulting from the shift, have caused catastrophic pandemics, including three in the last century. In February 2004, a highly pathogenic H7N3 virus emerged in domestic poultry in British Columbia with two documented human cases of conjunctivitis and mild “flulike” illness.[22] Recent clusters of human infections caused by avian influenza (particularly H5N1 subtype viruses) in Asia continent, have raised concerns about new pandemic threats.

Agents

The name "Influenza" is derived from the Latin word "influence," and the pathogens that cause this disease are single stranded RNA virus with segmented genome, pleomorphic, enveloped, and belong to Orthomyxoviridae family. These RNAs are negative-sense molecules, meaning that they must be copied into positive-sense molecules in order to direct the production of proteins. On the basis of antigenicity of the nucleoprotein (NP) and matrix protein, Influenza viruses are distributed in three (03) genera—A, B, and C. Influenza A virus is further classified in subtypes based on its two surface

glycoproteins: hemagglutinin (HA) and neuraminidase (NA).[23] Among the 15 HA and 9 NA subtypes recognized in nature, six HA (H1, H2, H3, H5, H7, and H9) and three NA (N1, N2, and N7) subtypes have been identified in human isolates of influenza A viruses.[22] Among these, only three subtypes of HA (H1, H2, and H3) and two of NA (N1 and N2) have caused pandemics in human populations in recent years.[24] The genomes of influenza viruses contain eight RNA segments in influenza A and B viruses, and seven RNA segments in influenza C.[23]

The glycoprotein HA is responsible for binding the virus to sialic acid containing cellular receptors and mediating fusion and penetration. Proteolytic cleavage of HA by cellular serine proteases exposes the hydrophobic fusion domain that mediates membrane fusion. NA cleaves terminal sialic acid from glycoconjugates present on respiratory mucins, cells, and progeny virions. This effect destroys the receptors recognized by HA, allowing the budding virus to be released from infected cells and spread in the respiratory tract. Influenza C virus contains a single surface glycoprotein that binds to receptors, promotes membrane fusion and cleaves sialic acid.[23]

Influenza A viruses are primarily viruses of waterfowl, particularly duck and include in all subtypes. Selected subtypes naturally infect a range of terrestrial mammals (pigs, horses, humans) and aquatic mammals (seals). Influenza B viruses infect humans and, in rare cases, seals, dogs, cats, and pigs, while influenza C viruses are primarily human viruses. Depending on the virus type and subtype, experimental infections can be induced in mice, ferrets, chickens, pigs and primates, and mainly in renal cells, continuous cell lines (MDCK, Vero, PER. C6 and LLC- MK2), also present in embryonic eggs.[24] The biological properties of influenza virus binding to red blood cells can be used for early detection of the virus in cell culture and the development of serological tests through hemagglutination inhibition.[24] Temperature above 50°C as well as lipid solvents, acids, formaldehyde, ionizing radiation and ultraviolet (UV) can inactivate influenza viruses.[24]

Mechanisms of influenza virus evolution – antigenic drift and shift

Antigenic shift and antigenic drift are the two main mechanisms that propel the evolution of influenza viruses. When two distinct influenza viruses co-infect the same cell, their genomic RNA segments reassort, resulting in the formation of novel strains and/ or subtypes that have the potential to cause serious illness and/or spread swiftly in a population lacking prior protection, is known as antigenic shift. A review of the influenza virus reassortment mechanism has been conducted.[25] A primary factor in the development of pandemic or zoonotic strains is antigenic shift or reassortment. Recombination of an H3 avian virus and a human H2N2 virus produced the 1968 pandemic influenza virus, whereas reassortment of an H2N2 avian virus and a human H1N1 virus produced the 1957 pandemic influenza virus. Multiple reassortment events in swine led to the generation of the 2009 H1N1 pandemic virus (2009 H1N1pdm). Avian H5N1 and H7N9 viruses, which are highly fatal zoonotic illnesses that infect people, are produced by reassortment with other subtypes of birds, particularly H9N2 viruses. The accumulation of mutations in the viral genome during replication due to the absence of RNA-dependent RNA polymerase proofreading activity is known as antigenic drift.[26] Mutations in the surface envelope proteins' HA and NA antibody epitopes can lessen the recognition of pre-existing antibodies produced in response to earlier viral strains. Seasonal influenza infections and the requirement for yearly influenza booster vaccinations are explained by antigenic drift.

Transmission

Seasonal flu is highly contagious and spreads quickly, especially in crowded places like schools and nursing homes. When an infected person coughs or sneezes, they release droplets containing viruses into the air, potentially infecting those nearby. The virus can also be passed on through contact with surfaces contaminated with the influenza virus. To reduce the risk of transmission, it's important for people to cover their mouth and nose when coughing and to regularly wash their hands. In regions with temperate climates, seasonal flu outbreaks are most common in the winter, whereas in tropical areas, influenza can occur at any time of year, leading to less predictable outbreaks. The incubation period for the flu is typically around 2 days, but it can range from 1 to 4 days.

Pathogenesis and Immunity

The virus infects the respiratory mucosa, where it causes lytic infection of cells and desquamation of the respiratory epithelium, mononuclear cell infiltrates in the lamina propria, and altered mucociliary clearance. Tracheobronchitis is a typical feature and often associated

with prolonged abnormalities in small airway pulmonary function and airway hyper reactivity. Primary influenza viral pneumonia results in diffuse alveolar damage, alveolar hemorrhage and exudate, hyaline membranes, and later reactive fibrosis. Fatal cases show pathologic changes in non-respiratory organs, such as brain congestion and swelling, myocardial inflammation, and fibrinoid changes in arterioles.[27] Viral replication in the upper respiratory tract generally peaks within 1 or 2 days of symptom onset and, depending on age and prior immunologic experience, continues for about 3 to 8 days. The severity of illness broadly correlates with upper respiratory tract viral levels. Constitutional symptoms with influenza are due in part to the release of pro-inflammatory cytokines and chemokines. Levels of interferon (IFN-α and IFN-γ), tumor necrosis factor (TNF-α), interleukins and chemokines (IL-1β, IL-6, IL-8, IL-10, MCP-10, MIP-1α and MIP-1β) are increased in nasal secretions, and IFN, IL-6, and TNF-α are increased in blood in human influenza. The tissue tropism of a strain of influenza virus depends, among other factors, on a combination of susceptibility of its HA to be cleaved by, and tissue availability of proteases with specificity to cleave it, thus rendering the virus infectious.[28] Extra-pulmonary dissemination of virus has been uncommonly documented in humans, but systemic spread is a regular feature of highly pathogenic avian viruses in chickens and sometimes in rodents or other mammalian hosts. Serum and secretory antibodies directed to HA and NA appear about 10 days after infection. Protection against reinfection by the homologous strain is durable following natural infection and is correlated with serum and nasal neutralizing antibody levels, principally directed against HA. Vaccine-induced protection may last for up to 2 to 3 years against homotypic virus. Infection also induces cell-mediated immunity, which is detectable 3 to 6 days after infection and seems to be important for recovery.[29] Cytotoxic T-lymphocyte responses against internal proteins may provide some degree of heterosubtypic immunity.

Clinical Features

After an incubation period of one to two days, classic influenza presents with fever, chills, malaise, headache, myalgia, and prostration. It is also frequently accompanied by a nonproductive cough, sore throat, and moderate rhinorrhea. While sub-sternal pain may worsen along with a sore throat, hoarseness, and cough, systemic issues typically persist three to five days. Asthenia and cough frequently last for two weeks or more. At first, respiratory symptoms may be slight or nonexistent, particularly in the elderly or young children. The main symptoms in elderly people who are weak may be lassitude, lethargy, disorientation, low grade fever, and occasionally gastrointestinal issues. While influenza C usually results in colds or bronchitis, influenza B is usually milder than influenza A.[27] Aside from these common symptoms, influenza can also cause vomiting, diarrhea, croup (laryngotracheobronchitis), unexplained fever, and neurological symptoms in young children. Subclinical influenza virus infections can account for up to 50% of adult cases.[27] Numerous viral respiratory disorders, such as otitis media, sinusitis, tracheobronchitis, pneumonia, and, in younger children, bronchiolitis and croup, are brought on by influenza. Relapses of fever, chest pain, and cough should be suspected of secondary bacterial infections, particularly pneumonia caused by Staphylococcus aureus, Streptococcus pneumoniae, and Haemophilus influenzae. These infections are common sequelae.[27] Meningococcal infections that are invasive are also linked to influenza. The additional issues include flare-ups of asthma, congestive heart failure, and chronic bronchitis. Myocarditis, arthritis, meningoencephalitis, polyneuritis, myocarditis, disseminated intravascular coagulation, myositis, and myoglobinuric renal failure are rare diseases that occur after influenza. Reye's syndrome occurs in less than 1 in 100,000 cases of influenza in people under the age of 18 who have taken salicylates. Pregnant women, immunocompromised hosts, and HIV-positive patients are particularly susceptible to severe disease and its consequences.[27]

Diagnosis

Clinicians and epidemiologists often use clinical and epidemiologic data to diagnose influenza. Outside of season, a heightened index of suspicion and laboratory tests are required, especially in isolated, rare cases or inexplicable outbreaks of febrile respiratory disease. Viral isolation from respiratory specimens is still the accepted method and can be performed in a variety of cell types, including PRMK, MDCK, and LLC-MK2.27 By hemadsorption with guinea pig erythrocytes, the virus can be found in cell cultures either before or after the cytopathic effect (CPE) becomes apparent. In nearly all positive samples, blind hemadsorption is positive three days after inoculation.[27] Immunofluorescence using

type-specific antisera or hemagglutination inhibition can be used to confirm isolates. Additionally, it can make a diagnosis in one to two days. Immunofluorescence of pathogens on monolayers of MDCK cells injected using centrifugation (shell-vial).[30] A variety of methods (such as immunofluorescence [IF] and enzyme immunoassay [EIA]) can be used to directly detect conserved influenza antigens (M or NP) in clinical samples, and a number of point-of-care kits are commercially available with turnaround times of 15 to 30 minutes. A commercial assay relies on the identification of NA activity specific to influenza. These tests' sensitivity ranges from 90% in infants to 50% to 70% in adults, depending on the kind of sample and length of sickness.[27] With the added benefit of identifying non-infectious viral genomes, a variety of reverse transcription–polymerase chain reaction (RT-PCR) assay formats have been employed to identify influenza A and B RNAs in clinical samples.[27] Even though RT-PCR takes longer to complete than commercial quick antigen detection kits, it may be less expensive—especially in impoverished nations. Assays that offer quick, very sensitive quantitative detection of influenza A and B have been developed thanks to real-time RT-PCR.[31,32] Because these tests are simultaneously quick, extremely sensitive, quantitative, and amenable to being employed in multiplex format—which may include probes for numerous distinct respiratory pathogens—they have a great deal of potential to replace other approaches.[32] Nevertheless, most laboratories in developing countries still cannot afford the prices. Numerous procedures can be used to retrospectively perform a serologic diagnosis of influenza utilizing paired acute and convalescent serum, mostly for serologic survey purposes.[27]

Treatment

M2 ion channel blockers such as amantadine and rimantadine prevent influenza A virus replication during the uncoating stage.[27] Treatment with either medication might shorten the length of influenza sickness in adults with uncomplicated influenza A by about one to two days if initiated early, within 48 hours of the onset of symptoms. This applies to persons without underlying medical conditions. Whereas rimantadine undergoes substantial metabolism following absorption and fewer than 10% of the dosage is eliminated unchanged in the urine, amantadine is eliminated in its undisturbed form from the urine. Only half the dose is required for elderly people to reach comparable plasma levels. Amantadine or rimantadine adverse effects can include upset stomach and have impact on the central nervous system. Amantadine is more likely to cause central nervous system (CNS) intolerance, which can cause agitation, psychosis, seizures, and coma in severe cases. When stopped, mild side effects such as nausea, anorexia, dry mouth, anxiety, and insomnia might be resolved. Amantadine and rimantadine are available as 10-mg/mL syrup and 100-mg tablets. For people over 65, a dose of 100 mg twice daily is advised (patients under 65 should take 100 mg daily). A dose of 5 mg/kg/day (maximum 150 mg/day) of rimantadine has been recommended for children under the age of ten.[27] Dose reductions proportional to the creatinine clearance (ClCr) are suggested for patients with renal insufficiency (amantadine for ClCr <60 to 80 mL/min/1.73 m2; rimantadine for ClCr <10 to 20 mL/min/1.73 m2). About one-third of patients receiving treatment develop influenza viruses resistant to amantadine-rimantadine; these viruses can spread to close contacts and produce the common flu sickness. These medications become useless when resistance develops spontaneously, as it has in several recent human isolates of the H5N1 virus.[27] By obstructing the active site of the enzyme responsible for cleaving sialic acid, the neuraminidase inhibitors zanamivir and oseltamivir suppress influenza A and B viruses. This prevents the viruses from escaping from infected cells and from spreading throughout the respiratory system.[33] Inhaled zanamivir (10 mg twice day for 5 days) lowers illness by 1 to 2.5 days in adults and children over 5 years of age. It also reduces the need for antibiotics by 40% for lower respiratory problems. Although zanamivir is usually well tolerated, it can sporadically cause bronchospasm, especially in people who already have an underlying respiratory condition or the flu.[27] Oseltamivir (75 mg taken twice daily for five days) decreases the intensity of the sickness, the amount of time it takes to resume normal activities, and the proportion of adult problems that require hospitalization and antibiotic prescriptions by almost 50%. Oseltamivir decreases the prevalence of otitis media and, as a result, the need for antibiotic prescriptions in children aged 1 to 12. Mild to moderate nausea or vomiting are examples of side effects. There is no need to modify the dosage of neuraminidase inhibitors for older patients.[27] Resistance emergence is rare with both medications, but a recent study of kids on oseltamivir treatment found drug-resistant viruses in 18% of the patients, frequently in

connection with prolonged viral excretion. This study also demonstrated that kids can still spread viruses even after five days of treatment.[34] Antipyretic-analgesic medications can be used to treat fever and pains brought on by influenza. Given its link to Reye's syndrome, aspirin should be avoided.

Prevention and Control

The two ways to prevent influenza are by immunizing against live-attenuated or formalin-inactivated multivalent influenza viruses and by administering influenza virus A chemoprophylaxis. The World Health Organization (WHO) surveillance network selects the influenza viruses most likely to circulate in the upcoming influenza season, and the influenza vaccine, which is administered prior to the influenza season, currently contains one strain of influenza B and two strains of the influenza A subtypes, H3N2 and H1N1.[27,35] In healthy children and adults, the inactivated vaccination has a about 70% to 90% efficiency in preventing disease.[35] Additionally, it lowers mortality and hospitalizations linked to influenza in elderly and high-risk individuals. The Centers for Disease Control and Prevention (CDC) advise vaccinating people who are 50 years of age or older, live in assisted living facilities, have children or adults with long-term respiratory or cardiovascular disease, including asthma, are chronically ill with diabetes mellitus, renal dysfunction, or hemoglobinopathies, are immunosuppressed patients, including those with HIV infection, have children and adolescents on long-term aspirin therapy who may develop post influenza Reye's syndrome, are pregnant women during the flu season, have children between the ages of 6 and 23 months, and are among those who can infect people at high risk, including healthcare providers and people who live with those at-risk individuals, cruise ship workers, service providers, unvaccinated visitors to regions where influenza may be prevalent (such as the tropics, the southern hemisphere between April and September), and tourists traveling in sizable organized travel groups are among the groups that fall into this category. Furthermore, the vaccination is made available to everyone who wants to lower their risk of contracting influenza.[27,35] The inactivated vaccine is safe to use during pregnancy but should be avoided in people who have a history of egg allergies. It should be given as a single intramuscular (IM) injection immediately before the influenza season (two doses in previously unimmunized children <9 years of age).[35] A thorough evaluation of the safety and effectiveness of vaccines in children has revealed a good safety profile and an efficacy rate of 77% to 91% in children aged 1 to 15. Although immunization of household contacts and caregivers should lower the risk of influenza infection in these high-risk children, inactivated vaccine is not currently advised for children under 6 months of age. vaccinations can be administered intranasally using live-attenuated vaccinations or inactivated for healthy individuals between the ages of 5 and 49 who are not in close contact with immunocompromised patients.[35] Recently, the influenza inactivated vaccine—whose composition is based on influenza viruses circulating in the southern hemisphere—was released in several tropical regions of the world. The vaccination is administered before the onset of the influenza season, which typically occurs in southern hemisphere nations between May and July. Annual immunization campaigns against respiratory infections have decreased hospitalizations and mortality rates among the elderly in South America.[36] The results of ongoing surveillance already demonstrate that while developing influenza vaccines with compositions more suitable for South America, consideration should be given to regional differences in circulating influenza virus strains.[37] In addition to being highly tolerated, genetically stable, and seldom transmissible, live-attenuated, cold-adapted vaccinations given intranasally also have the benefit of eliciting local secretory immunoglobulin A (IgA) responses. It could be necessary to give young children two doses due to possible component interference.[27] After receiving a license in 2003, this vaccine is now available to healthy individuals between the ages of 5 and 49 in the United States. This includes those who wish to avoid influenza as well as those who are in close contact with high-risk groups.[35] This vaccination is not advised for people who have hemoglobinopathies, diabetes, or other underlying medical conditions; people who are receiving immunosuppressive therapies; people with known or suspected immunodeficiency diseases; children or adolescents taking aspirin or other salicylates; people with a history of Guillain-Barré syndrome; pregnant women; and people who have previously experienced egg hypersensitivity.[35] The cold-adapted trivalent influenza vaccination has been shown in several studies to offer protection against drift variant strains and is extremely effective (92% in phase 3) in preventing culture-confirmed

influenza in healthy youngsters. Generally speaking, the effectiveness of inactivated vaccines is similar to that of young to middle-aged persons.[35] Additional experimental methods have been investigated in the creation of influenza vaccines, such as recombinant HA generated in insect cells, virosomes containing glycoproteins on their surface, M2 protein conjugated with the core of the hepatitis B virus, and bare DNA encoding the nucleoprotein or HA of influenza viruses.[27] European approvals for cell culture-based vaccines (MDCK, Vero) may provide a substitute for the drawbacks of the existing egg-grown vaccinations. Reverse genetics has been utilized to quickly generate candidate vaccines against viruses that could pose a pandemic hazard. Amantadine and rimantadine are 70% to 90% effective in preventing influenza A during outbreaks and are licensed for use. Amantadine or rimantadine may be used as prophylaxis for individuals who are immunocompromised, elderly individuals who have not received vaccinations, patients in long-term care facilities where outbreaks are occurring, individuals who are unable to obtain vaccinations, and those who received a vaccine strain that differs from the outbreak strain. Prophylaxis should begin as soon as feasible at dosages comparable to those used for therapy and be sustained for a minimum of two weeks, or one week after the epidemic ends.[35] Influenza mutations resistant to amantadine and rimantadine Up to 30% of treated individuals had a virus, which may be linked to medication prophylactic failure.[34] Although only oseltamivir (75 mg twice daily) has been licensed for this indication in the US, both oseltamivir and inhaled zanamivir (10 mg/dose twice day) are more than 80% effective in preventing influenza during epidemics.[27,35] Antiviral medications, particularly neuraminidase inhibitors, may be able to prevent hospitalizations and lower respiratory problems associated with influenza pandemics in the future by lowering the risk of person-to-person transmission. Still, supply constraints44 provide a significant challenge. Thus, it is crucial to take into account regulations to guarantee a sufficient supply of these medications as well as guidelines to make the most use of those that are available.[22]

Conclusion

Infection with influenza A virus is the most frequent and severe type, and typically found in humans. It spreads quickly and affects people in a wide geographic area in a short period of time, causing pathology ranging from moderate to severe. The influenza A virus is mostly spread by wild aquatic birds and other animal species, including pigs, ferrets, horses, seals, whales, mink, giant anteaters, cats, and dogs. The influenza B and C viruses mostly affect humans and have a fairly narrow host range. The influenza virus acquires the potential to spread globally through a process known as "genetic shift," which involves the complete regrowth of surface antigen and a slow-moving genetic alteration caused by mutations that enable the virus to effectively adapt to the human population. Increased seasonal influenza vaccination rates are anticipated to significantly lower the disease burden in our country and improve population readiness in the event of a pandemic. By following the most recent ACIP recommendations and seizing every chance to discuss the value of yearly vaccination with students, caregivers, and staff, school nurses can contribute to an increase in the rates of influenza vaccination. In addition to providing support, school nurses and their medical colleagues may ensure that they receive their annual vaccinations on time. While research on the epidemiology of influenza infection has been conducted for a number of years, several aspects of the disease's spread remain poorly understood. To improve understanding of the pathophysiology and transmission of influenza viruses, this article summarizes key virological, epidemiological, and clinical characteristics.

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