Original Research

SWINE FLU VIRUS – EPIDEMIOLOGY AND CURRENT STATUS AT NATIONAL & INTERNATIONAL LEVEL – META – ANALYSIS

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ABSTRACT

Background: The term "swine flu" is frequently used to describe the respiratory viral infections brought on by the H1N1 influenza a virus strain. Influenza a outbreaks occur almost every year, with varying degrees of severity. The aim of this study is to review the spread of current strains of swine flu viruses.

Methods: This meta-analysis followed the PRISMA guidelines. Articles were searched on PubMed, Google scholar, Web of Science, Science Direct, and Scopus using terms related to swine flu, influenza, pandemic 2009 influenza were used. Boolean AND, OR and NOT were used.

Results: A total of 28 published studies (2009–2025) from Asia, Europe, and North America were included in this meta-analysis to assess the epidemiology and current global status of Swine Influenza Virus (SIV). Among the included studies, Asia contributed the highest number of reports (n = 15), followed by Europe (n = 7) and North America (n = 6). Full-genome sequencing and phylogenetic analyses reported in multiple studies demonstrated that genetic reassortment is a dominant evolutionary mechanism of SIVs.

Conclusions: Swine influenza prevention consists of three components: prevention in swine, prevention of transmission to humans, and prevention of spread among humans. To control the pandemic's impact, a variety of control measures such as vaccination, antiviral prophylaxis will be required. Isolation of infected individuals may be useful in the early stages of viral replication into a community.

Keywords: Swine Flu, Influenza Virus, H1N1, Epidemiology, Meta- Analysis.

INTRODUCTION

The Orthomyxoviridae family of viruses includes the influenza viruses, which are primarily responsible for respiratory tract infections. There are three different genera of influenza viruses: influenza A, which infects birds naturally, influenza B, which only infects people, and influenza C, which also infects dogs and pigs. Although birds are the primary hosts of these influenza viruses, humans, swine, birds and other animals can become infected with influenza A virus.[1]

Influenza Based on antigenic differences in the two surface glycoproteins haemagglutinin (HA) and neuraminidase (NA), a virus can be divided into various subtypes.[2]

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Antigenic drift is the term for the immunologic escape caused by genetic mutations that encode a variety of amino acid substitutions in the surface glycoproteins.[3-7]

IAVs have 18 different types of HA and 11 different types of NA on their surface. The virus subtypes H1-H16 and N1-N9 have been identified in aquatic birds, which are normally thought to be the natural reservoir of IAVs.[8-10] In bats, H17-H18 and N10-N11 subtype sequences were found.[11-12] Only a few subtypes of viruses, like the H1 and H3 subtypes of viruses, have been established in mammals and are currently circulating in both humans and swine.[13]

Antigenic drift and antigenic shift are two important mechanisms that contribute to the rapid evolution of IAVs. The gradual accumulation of mutations in the surface HA and NA proteins that cause antigenic changes in IAV is what causes antigenic drift. The seasonal influenza viruses that affect humans are caused by antigenic drift. This phenomenon is known as antigenic shift. Antigenic shift is responsible for outbreaks, which resulted in three of four pandemic influenza viruses in human history

(1957 Asian Flu H2N2, 1968 Hong Kong Flu H3N2, and 2009 pandemic H1N1). Swine's are the natural host of IAVs and have been proposed as a mixing vessel for human, avian, and swine IAVs with the potential to produce a pandemic virus [Figure 1 and Figure 2].[14-16]

Influenza A viruses are highly contagious respiratory pathogens that can be transmitted between a variety of avian and mammalian species, including humans. Two specific receptors have been identified: sialic acid (SA) 2,3 found in the epithelial cells of the gastrointestinal tract of wild aquatic birds and SA 2,6 found in the epithelial cells of the respiratory tract of humans. Pigs are known as a "mixing vessel" because their respiratory tracts contain receptors that can bind both avian and human influenza viruses. Interspecies transmission from pigs to humans or vice versa is thus possible. A study of pig-to-human influenza virus transmission on Thai swine farms found that workers who had been exposed to swine influenza viruses had antibodies against the circulating swine influenza viruses (SIV).[17]

When a hemagglutinin-containing influenza virus with which humans have little to no immunity first appears in the population and successfully spreads from person to person, this is known as an influenza pandemic. The influenza genomes Three pandemics that affected the entire world in the last century were caused by a single virus. The HA genes of all three pandemic viruses ultimately descended from avian influenza viruses, including the Spanish flu in 1918, the Asian flu in 1957, and the Hong Kong flu in 1968 [Figure 3].[18-19]

IAVs have been observed in a two-way human-swine transmission. An inspector with the U.S. Bureau of Animal Industry named Koen noted that influenza outbreaks started with either pigs or people but quickly spread from one to the other in 1919.[20] Following this, human infections with either the H1N1 or H3N2 strains of the swine influenza virus have been documented globally as a result of direct contact with pigs, and several of these infections have been fatal. Notably, despite the fact that they caused illness in infected humans, these swine influenza viruses have almost no or very limited human-to-human transmission capability.[21]

METHODS

This meta-analysis followed the PRISMA guidelines. Articles were searched on PubMed, Google scholar, Web of Science, Science Direct, and Scopus, CDC, NCDC, WHO using terms related to swine flu, influenza, pandemic 2009 influenza were used. Boolean AND, OR and NOT were used. Article titles and abstracts were screened to include relevant articles. The H1N1 strain of the influenza A virus, Current status of swine influenza viruses, risk factor of swine influenza virus, swine flu virus Epidemiology, treatment and prevention of pandemic H1N1 Influenza virus. Article titles and abstracts were screened by researchers independently to exclude irrelevant articles. At the first stage of the search, 460 articles were found, and after reviewing the titles of articles, 195 duplicate and overlapping articles were deleted and 265 articles remained. In total, 190 articles were removed due to noncompliance with the criteria, the extract of 75 potentially related articles were reviewed, and 43 articles were excluded due to lack of access to the full text of the article and 2 articles during data extraction. Finally, 30 appropriate papers were selected to enter the meta-analysis stage [Figure 4].

RESULTS

A total of 28 published studies (2009–2025) from Asia, Europe, and North America were included in this meta-analysis to assess the epidemiology and current global status of Swine Influenza Virus (SIV). The included studies comprised molecular epidemiological analyses, surveillance reports, clinical studies, immunological investigations, and experimental models.

Geographical and Temporal Distribution- Among the included studies, Asia contributed the highest number of reports (n = 15), followed by Europe (n = 7) and North America (n = 6). India and China together accounted for a substantial proportion of human H1N1-related epidemiological and clinical studies, while the United States, Korea, and European countries predominantly reported genomic characterisation and surveillance data. The majority of studies published after 2015 highlighted ongoing circulation and evolution of SIVs, indicating persistent endemicity and periodic emergence of novel variants.[22-44]

Genetic Diversity and Reassortment Patterns- Full-genome sequencing and phylogenetic analyses reported in multiple studies demonstrated that genetic reassortment is a dominant evolutionary mechanism of SIVs. Several novel reassortment strains were identified, including viruses containing hemagglutinin (HA) and neuraminidase (NA) genes of swine origin combined with internal genes from human A(H1N1) pandemic 09 viruses. Studies from Taiwan, China, and the USA confirmed the presence of multi-lineage gene constellations, involving classical swine, Eurasian avian-like swine, and pandemic H1N1 lineages. High nucleotide sequence similarity (97–99%) between swine isolates across different regions indicated cross-regional viral dissemination [Figure 3].[32-50]

Zoonotic Transmission and Occupational Exposure- Evidence of bidirectional transmission between humans and swine was reported across several studies. Serological and molecular investigations revealed higher antibody responses and exposure rates among individuals with frequent swine contact compared to the general population.

Genomic similarity between human variant influenza viruses and circulating swine strains supported the role of pigs as reservoirs facilitating zoonotic spill over and viral adaptation to humans.[24-55]

Clinical and Epidemiological Findings in Humans- Clinical studies from India and China reported that Influenza A(H1N1) pdm 9 infection was associated with significant morbidity and mortality, particularly among pregnant women, young children, elderly individuals, and patients with chronic illnesses. Hospital-based surveillance data showed increased influenza positivity during peak seasonal periods, with pneumonia and respiratory failure being the most common severe manifestations. Biochemical and immunological analyses demonstrated elevated inflammatory markers and altered toll-like receptor expression, suggesting host immune dysregulation during severe infection.[56-64]

Pathogenesis and Virulence Characteristics- Experimental and animal model studies revealed that virulent SIV strains exhibited prolonged viral replication, enhanced cytokine responses, and lower respiratory tract involvement. Histopathological findings included bronchiolitis, alveolitis, and epithelial necrosis of varying severity. These findings were consistent with moderate to severe pathogenic potential, particularly for pandemic-associated strains.[33-49]

Advances in Diagnostics, Surveillance, and Therapeutic Approaches- Several studies reported the use of next-generation sequencing, multiplex RT-qPCR, and oral fluid sampling as effective tools for enhanced surveillance and early detection of SIVs.[32-44] Novel antiviral strategies, including Pt/TiO_2-SiO_2 bionanocatalysts, demonstrated a reduction of up to 65.2 ± 3.3% in Influenza A(H1N1) viral replication under experimental conditions, indicating potential future therapeutic applications.[64-72]

Discussion

Pandemic believed to arise, when a virus with a novel HA subtype adapts to efficient transmission in humans. The recent H1N1 pandemic arose from a swine H1N1 virus adapting to human transmission due to genetic reassortment with current human influenza viruses.[65-72]. The pathological findings of this fatal H1N1 influenza disease have been those of diffuse alveolar damage and haemorrhagic interstitial pneumonitis with lymphocytic cell infiltrate suggestive of a primary viral pneumonia. Recent studies suggest that there is uncontrolled release of immune mediators leading to cytokine storm and this is one of the probable causes of high mortality and morbidity. Also, secondary bacterial pneumonia results in severe disease manifestation.[69-72] A new influenza A (H3N2) virus subclade J.2.4.1, also called “H3N2 subclade K,” was first identified by CDC through analysis of sequence data in August 2025. Subclade K influenza viruses have a number of changes that make their hemagglutinin gene different, and they have been characterized as “antigenically drifted” in comparison to other recently spreading A (H3N2).[73] The 2023-2024 influenza season was for shorter durations as compared to previous seasons. In all surveillance systems, influenza A (H1N1) pdm09 viruses predominated during the season, followed by A (H3N2).[74] On May 11, 2022, Germany notified WHO of one laboratory-confirmed human case of infection with a swine-origin influenza A(H1N1) virus in the German state of North Rhine-Westphalia. The case is an adult between the ages of 30 and 40 who was discovered during routine sentinel surveillance for influenza. The case first showed signs of an influenza-like illness on March 21. These symptoms included fever, coughing, sore throat, headaches, and muscle pain. A nasal swab sample was taken on March 24; on March 29, the influenza A virus was discovered.

The sample was examined at the German Robert Koch Institute's National Influenza Centre. Influenza Reverse transcriptase-polymerase chain reaction was used to identify a virus (RT-PCR). On May 5, whole genome sequencing revealed a swine A(H1N1) virus with Eurasian avian similarities. More virus characterization is currently being done. The patient has since recovered and was not hospitalised. Although there was no direct contact with swine in this case, the person did live in a region with a lot of swine farms and knew people who farmed swine. Several influenza A(H1) virus infections have been detected in Europe in recent years. Although infections with A(H1N1) variant virus do occur on occasion, they are considered rare and unusual.[75] On April 25, 2022, the People's Republic of China's National Health Commission notified WHO of one confirmed case of human infection with an avian influenza A(H3N8) virus.[76]

On April 29, 2022, WHO received notification of a human case of avian influenza A (H5N1) in Colorado State, United States of America. The incident occurred during the culling of poultry at a farm where the influenza A (H5N1) virus was confirmed in the poultry. The US Centres for Disease Control and Prevention confirmed avian influenza A (H5) in the case on April 27, and subtype N1 was confirmed later by sequence analysis. Close contacts and people involved in poultry culling have been identified, tested, and are being tracked down. Based on available data, WHO considers the risk posed by this virus to the general population to be low, and the risk to occupationally exposed individuals to be moderate.[77]

The National IHR focal point of India notified WHO on July 21, 2021, of one human case of avian influenza A(H5N1) from Haryana state in northern

India. This is India's first reported case of human infection with the influenza A(H5N1) virus.[78]

On May 31, 2021, the People's Republic of China's National Health Commission notified WHO of one confirmed case of human infection with the avian influenza A(H10N3) virus. This is the first case of human infection with the avian influenza A(H10N3) virus reported anywhere in the world.[79]

Influenza virus infection usually causes substantial mortality and morbidity. Because they can contract both the human and avian influenza viruses, pigs are crucial in the development of novel influenza viruses with pandemic potential. [24-48] H1N1, H3N2, and H1N2 subtypes of influenza viruses are currently known to co-circulate in pigs. Infection with the influenza virus typically results in significant mortality and morbidity. Because they can contract both the human and avian influenza viruses, pigs are crucial in the development of novel influenza viruses with pandemic potential. H1N1, H3N2, and H1N2 subtypes of influenza viruses are currently known to co-circulate in pigs. Pigs play an important role in the generation of novel influenza viruses with pandemic potential because they may be infected with both humans and avian influenza virus. Currently, influenza viruses of subtypes H1N1, H3N2 and H1N2 are known to co-circulate in pigs.[63-79]

After long-term evolution, EAS-H1N1 viruses have become dominant since 2009. EAS-H1N1 viruses in China have been reported to preferentially bind to human-type receptors, and some of the viruses tested were transmitted in ferrets by respiratory droplets. This suggests that the EAS-H1N1 SIVs pose the greatest pandemic threat among the influenza viruses currently circulating in animals.[49] Sun et al. reported that novel triple-reassortment EASH1N1 SIVs were isolated from pigs in Tianjin, with gene segments from A (H1N1) pdm09 (PB1, PB2, PA, and NP), EAS-H1N1 (HA, NA, and M), and Classical SIVs (NS), which showed that multiple genetic lineages of swine H1N1 viruses were co-circulating in the Tianjin swine population. TJ/ 1606/18 had close antigenic and genetic relationships with EAS-H1N1 viruses that were circulating in pigs in China.[80]

Implementing vaccines against the inactivated influenza virus will be the primary preventive measure for minimising the morbidity and mortality linked to the influenza pandemic virus Zanamivir and oseltamivir inhibit influenza neuraminidase activity and prevent sialic acid residue cleavage, interfering with progeny virus dispersal within mucosal secretions and reducing viral infectivity. Current surveillance efforts are aimed at detecting and preventing a new pandemic by focusing on the rapid identification of novel strains in humans as well as efforts to reduce the possibility of cross-infection between species. The newly developed tetraplex RTqPCR is an appropriate tool for this purpose, and it could shed more light on potential reverse zoonotic transmission events of IBV and ICV, as well as the presence of IDV in swine populations. The EpiCC tool to facilitate research on the effectiveness of whole antigen- and conserved T cell epitope-based vaccines against influenza and other pathogens. Furthermore, simple measures such as standard precautions, particularly respiratory hygiene and cough etiquette, are critical. Isolation of infected individuals in designated hospitals may be useful in the early stages of virus introduction into a community. Once the infection has spread and a large number of people are infected, home isolation of people with mild infections would be more feasible than isolation in health care settings.

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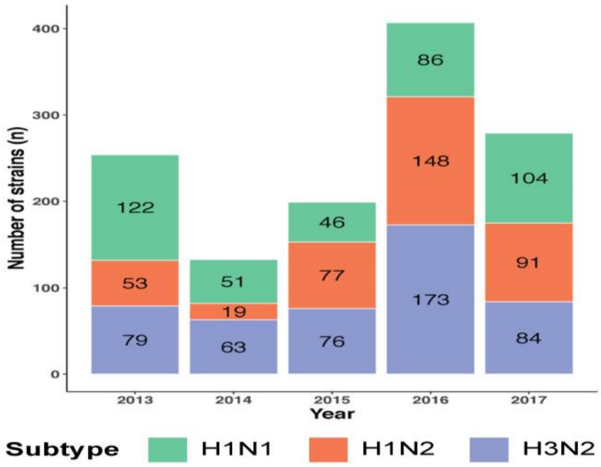

Figure 1: The Three Subtypes H1N1, H1N2, And H3N2 from Swine IAV Genome Sequences Represented by the Color-Coded Stacked Bar Chart, with Each Stacked Component Displaying the Number of Strains for that Year.[67]

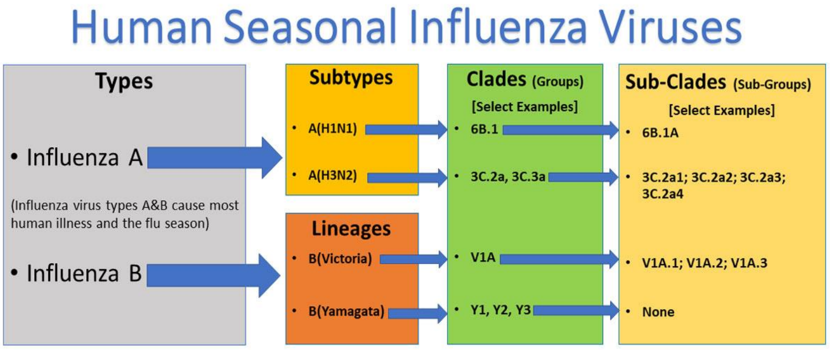

Figure 2: Human Seasonal Influenza Viruses.

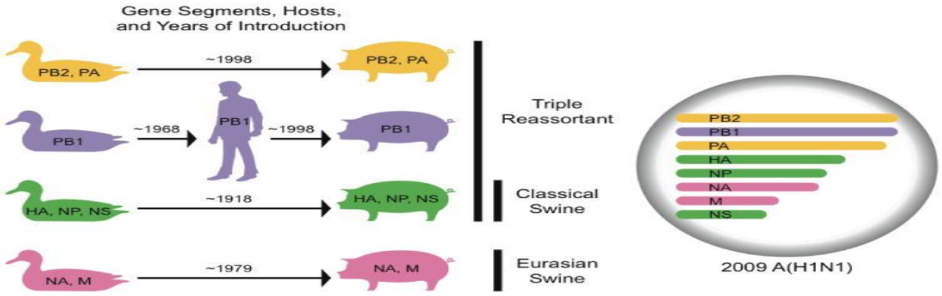

Figure 3: The Following Gene Segments of the 2009 a (H1N1) Virus Have Host and Lineage Origins

*Polymerase basic 2 (PB2), polymerase basic 1 (PB1), polymerase acidic (PA), hemagglutinin (HA), nucleoprotein (NP), neuraminidase (NA), matrix gene (M), and non-structural gene (NS). The colour of the gene segment in the circle indicates the host.[105]

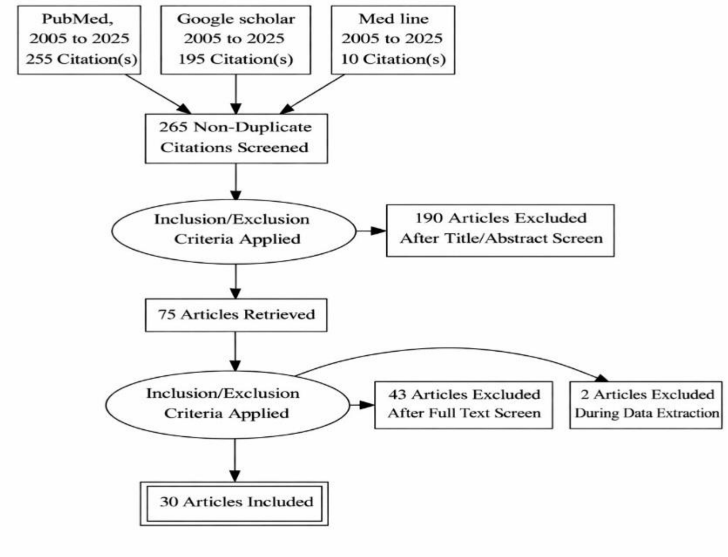

Figure 4- The Preferred Reporting Items for Systematic Reviews and Meta- Analyses (PRISMA)