DISSERTATION SUBMITTED FOR THE MASTER'S DEGREE IN MEDICAL MICROBIOLOGY

TITLE

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

SUBMITTED

BY

PUSHPENDRA KUMAR PATHAK

2022

DEPARTMENT OF MICROBIOLOGY

INTEGRAL INSTITUTE OF MEDICAL SCIENCES & RESEARCH

INTEGRAL UNIVERSITY

DASAULI, KURSI ROAD, LUCKNOW-226026, U. P.

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

A

DISSERTATION

Submitted to

INTEGRAL UNIVERSITY

In partial fulfillment of the requirements for the award of degree of

Masters of sciences

In

Medical Microbiology

By

PUSHPENDRA KUMAR PATHAK

ENROLLMENT NO: - 1900101002

Guide:

Dr. MOHD SAQUIB (MBBS, MD, PDCC)

Assistant professor

Dept. of Microbiology

Co-Guide:

Dr. AUSAF AHMAD (Ph.D.)

Associate professor

Department of Community Medicine

INTEGRAL INSTITUTE OF MEDICAL SCIENCE AND RESEARCH, KURSI ROAD, LUCKNOW,226026

INTEGRAL UNIVERSITY

Established Under U.P. Act No 09 of 2004 by State Legislation
Approved by University Grants Commission
Phone No.: +91 (0552) 2890812, 2890730, 3296117, 6451039

Fax No.: 0522-2890809

Kursi Road, Lucknow-226026, Uttar Pradesh (INDIA)

DECLARATION OF CANDIDATE

I hereby declare that this dissertation entitles **"SWINE FLU VIRUS – EPEDIOMOLOGY AND CURRENT STATUS AT NATIONAL & INTERNATIONAL LEVEL – META – ANALYSIS"** is bonafide and genuine research work carried out by me under the guidance of **Dr. MOHD SAQUIB** Assistant Professor, Department of Microbiology and Co-guide **Dr. Ausaf Ahmad** Associate Professor, Department of Community Medicine, Integral Institute of Medical Sciences and Research, Lucknow.

DATE: 15/07/2022 **PUSHPENDRA KUMAR PATHAK**

PLACE: Lucknow

INTEGRAL UNIVERSITY

Established Under U.P. Act No 09 of 2004 by State Legislation
Approved by University Grants Commission
Phone No.: +91 (0552) 2890812, 2890730, 3296117, 6451039

Fax No.: 0522-2890809

Kursi Road, Lucknow-226026, Uttar Pradesh (INDIA)

ENDORSEMENT BY THE HOD

This is to certify that the dissertation entitles **"SWINE FLU VIRUS – EPEDIOMOLOGY AND CURRENT STATUS AT NATIONAL & INTERNATIONAL LEVEL – META – ANALYSIS"** is a bonafide and genuine research work carried out by **Pushpendra Pathak** under the guidance of **Dr. MOHD SAQUIB** Assistant Professor, Department of Microbiology and co-guide **Dr. AUSAF AHMAD** Associate Professor, Department of Microbiology, IIMS&R, Lucknow in partial fulfilment of requirement for the degree of Master of Science in Medical Microbiology. The research methods and procedure described have been done by the candidate and the results have been observed by the guides periodically.

DATE:15/07/2022

PLACE: LUCKNOW

Dr. NOOR JAHAN

PROFESSOR AND HEAD,

DEPT.OFMICROBIOLOGY, IIMS&R

INTEGRAL UNIVERSITY

Established Under U.P. Act No 09 of 2004 by State Legislation
Approved by University Grants Commission
Phone No.: +91 (0552) 2890812, 2890730, 3296117, 6451039

Fax No.: 0522-2890809 Kursi Road, Lucknow-226026, Uttar Pradesh (INDIA)

CERTIFICATE BY THE GUIDE & CO-GUIDE

This is to certify that the dissertation entitles **"SWINE FLU VIRUS – EPEDIOMOLOGY AND CURRENT STATUS AT NATIONAL & INTERNATIONAL LEVEL – META – ANALYSIS"** is a bonafide and genuine research work done by **PUSHPENDRA PATHAK** in partial fulfilment of the necessity for the degree of Masters of Science in Medical Microbiology.

The research methods and procedures described are done by the candidate and results are observed by the guide periodically.

DATE:15/07/2022
PLACE: Lucknow

Dr. MOHD. SAQUIB
Assistant professor
Dept. of Microbiology
IIMS&R, LUCKNOW

Dr. AUSAF AHMAD
Associate professor
Department of Community Medicine
IIMS&R, LUCKNOW

INTEGRAL UNIVERSITY

Established Under U.P. Act No 09 of 2004 by State Legislation
Approved by University Grants Commission
Phone No.: +91 (0552) 2890812, 2890730, 3296117, 6451039

Fax No.: 0522-2890809

Kursi Road, Lucknow-226026, Uttar Pradesh (INDIA)

COPY RIGHT

DECLARATION BY THE CANDIDATE

I hereby declare that Integral Institute of Medical Sciences and Research, Integral University, Lucknow shall have the rights to preserve, use and disseminate this dissertation in print or electronic format for academic or research purpose.

I will publish the research paper related to my dissertation only with the consent of my guide.

DATE:15/07/2022 **PUSHPENDRA PATHAK**

PLACE: Lucknow

ETHICAL CLEARANCE CERTIFICATE

INSTITUTIONAL ETHICS COMMITTEE (IEC)

IIMS&R INTEGRAL UNIVERSITY, LUCKNOW

IEC/IIMS&R/2022/38

CERTIFICATE

This is to certify that research work entitled **"Swine Flu Virus-Epediomology And Current Status At National & International Level - Meta Analysis"** submitted by **Pushpendra Pathak, Dr.Mohd Saquib, Dr.Ausaf Ahmad** for ethical approval before the Institutional Ethics Committee IIMS&R.

The above mentioned research work has been approved by Institutional Ethics Committee, IIMS&R with consensus in the meeting held on **19 May 2022**.

Dr.Deepak Chopra
(Jt.Member Secretary)
IRC/IEC
IIMS &R

Dr.Q.S.Ahmed
(Member Secretary)
IRC/IEC
IIMS &R

ACKNOWLEDGEMENT

I take this opportunity to extend my sincere gratitude and appreciation to all the helping hands who made my dissertation work a huge success.

Thanks to the **Almighty God** for giving me strength and energy to finish this study.

I am thankful to the **Integral University, Lucknow** for providing the opportunity, laboratory equipment, materials, and its valuable support, to complete this study.

First and foremost, I am extremely thankful to **Dr. Noor Jahan**, Professor and Head, Department of Microbiology, IIMS&R, whose benevolent guidance and constant encouragement helped me a lot doing my dissertation.

I express my heartful gratitude and regards to our esteemed teacher and my guide **Dr. Mohd. Saquib, Assistant** Professor, Department of Microbiology and co-guide **Dr. Ausaf Ahmad**, Associate professor, IIMS&R, for providing excellent guidance, motivation and keep interest in my dissertation. It was a great opportunity and wonderful experience to work under their supervision.

I express my heartiest thanks to, **Dr. Tasneem Siddiqui** (Assistant Professor) **Mrs. Sandeepika Dubey**, **Dr. Karuna Katiyar**, Faculty members, Department of Microbiology, IIMS&R for their help, support and guidance.

I am also thankful to **Mr. Salman**, **Mr. Dheeraj**, **Mr. Dhirendra**, **Mr. Mohsin, Mr. Vishnu** for providing laboratory facilities and guidance during the period of work.

I would also pay my special thanks to my batchmates **Smriti Tiwari, Mohd Areeb,** and **Pooja Chauhan** for their continuous help and co-operation during the period of work.

Finally, Special thanks to my family, Father- Sri. **Keshav Prasad Pathak,** Mother- **Smt**. **Vimala Pathak** and Brother- Mr. **Mukesh Pathak, Dinkar Pathak** and my entire family members who encouraged me to work hard and not to worry about the results.

DATE:15/07/2022 **PUSHPENDRA PATHAK**

CONTENTS

DEDICATED TO

"TEACHERS"

"FAMILY"

&

"FRIENDS

INTRODUCTION

INTRODUCTION

The Orthomyxoviridae family of viruses includes the influenza viruses that are primarily along with possession of respiratory tract infections. Influenza viruses are categorized into three species of the genus influenza A, which infects birds naturally, that is also influenza B only able to infect people, as well as influenza C, that also afflicts dogs and pigs. The above viruses seem to be single-stranded negative sense viruses' genome that has been divided into eight sections that code for 11 different functional proteins. These proteins include surface glycoproteins like hemagglutinin (HA) and neuraminidase (NA), matrix proteins M1 and M2, and non-structural proteins NS1 and NS2, as well as polymerase complex proteins like PA, PB1, PB1-F2, PB2, and NP. Although birds are the primary hosts among those influenza viruses, humans, swine, birds and the influenza A able to infect other animals. [`1]

Influenza Premised on antigenic differences in the two surface glycoprotein haemagglutinin (HA) and neuraminidase, a virus could be divided into diffrent subtypes (NA) [2]. Antigenic drift is the term for the immunologic escape caused through genetic mutations that codes a variety of amino acid substitutions in the surface glycoproteins. [3-5] Additionally, genetic reassortment—the exchange of gene segments between two or more viruses—can be a key factor in the development of novel influenza viruses. [5-7]

Influenza A virus's surface consists of 11 different types of NA and 18 different types of HA. Based on the kinds of HA and NA that are present on the viral surface, they are divided into subtypes. Aquatic birds, which are typically believed to be the natural reservoir of Influenza a viruses, have been found to carry the virus subtypes H1-H16 and N1-N9. [8-10] H17-H18 and N10-N11 serotype sequence data were found in bats. [11-12]. Only a few subtypes of viruses, like the virus serotypes H1 and H3, which are now spreading in both humans and swine, have been founded in mammals. [13]

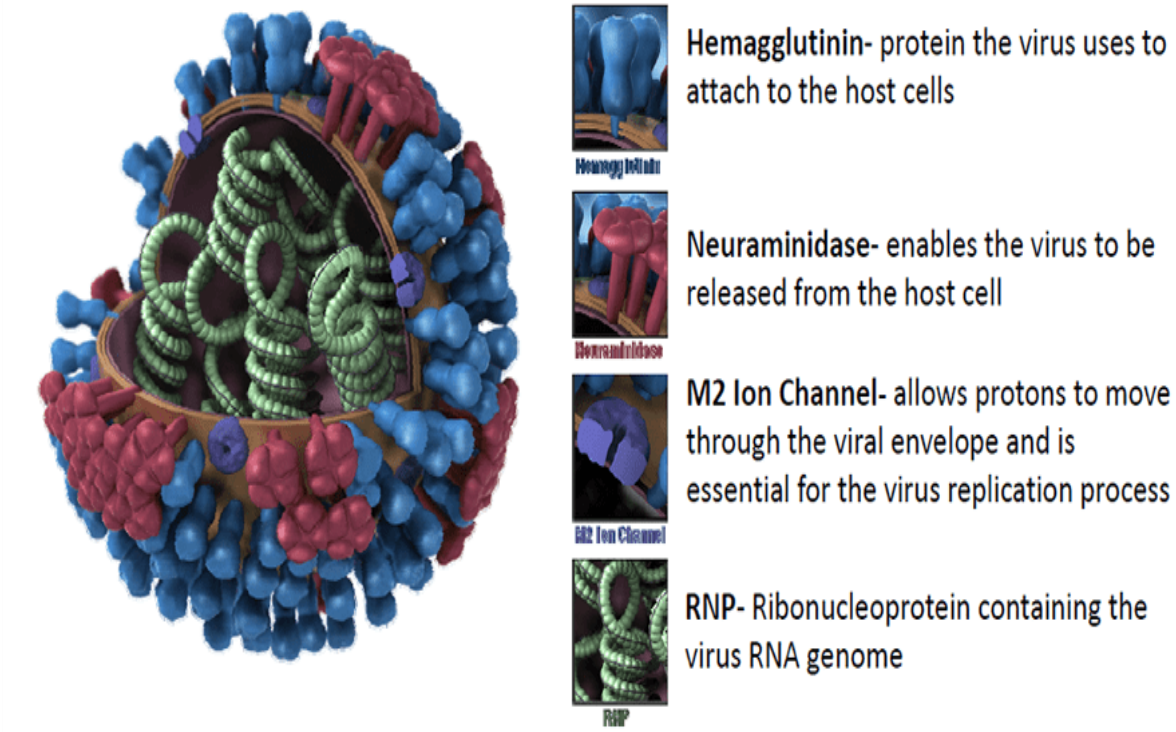


Fig.1. The H1N1 Influenza Virus from CDC - Atlanta [109].

Two significant mechanisms that contribute to the rapid evolution of influenza A virus are antigenic drift and antigenic shift. the slow concentration of mutations that affect influenza's antigenic surface HA and NA proteins Antigenic drift is caused by a virus. The seasonal influenza viruses that affect humans are caused by antigenic drift. The the influenza virus genome is segmented, which allows for the production of various reassorted viruses when two or more distinct Influenza A viruses infect a cell or host. This phenomenon is known as antigenic shift. Antigenic shift is responsible for outbreaks, among which three of the four global epidemic flu strains in recorded human history were founded (1957 Asian Flu H2N2, 1968 Hong Kong Flu H3N2, and 2009 pandemic H1N1). Swine have indeed been suggested as a mixing vessel for human, avian, as well as swine Influenza A viruses with the potential to generate a pandemic virus because they are the natural host of Influenza A viruses. **[14-16]**

Influenza A viruses seem to be respiratory organisms that are extremely contagious and can be spread from one mammalian species to another, along with living beings. two particular receptor sites have been identified: sialic acid 2,4 found of the epithelial cells of the gastrointestinal tract of wild aquatic birds and sialic acid 2,8 discovered in human respiratory tract epithelial cells. Even though their respiratory tracts possess receptors that can bind both avian and human influenza viruses, pigs are identified as a "mixing vessel." As a result, either humans or pigs may contract a disease from one another. Workers who had been exposed to swine influenza viruses had antibodies against the prevalent swine influenza viruses, according to a study of pig-to-human influenza virus transmission on Thai swine farms. **[17]**

When a hemagglutinin-containing influenza virus with which humans have little to no immunity first exists among the community as well as successfully spreading from one person to another, 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. All three global epidemic viruses, such as the Spanish flu in 1918, the Asian flu through 1957, and the Hong Kong flu in 1968, ultimately derived their HA genes from avian influenza viruses. [18-19]

Influenza A virus has been seen in a two-way transmission between humans and pigs. The inspector for the United States Bureau of Animal Industry named Koen noted there are influenza outbreaks started with any of these 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 directly in contact with pigs around the world, several of these infections have been fatal. [21] Notably, despite the fact that they caused illness in infected humans, The above swine influenza viruses have just about no or little chance to transmit from humans to humans. [21]

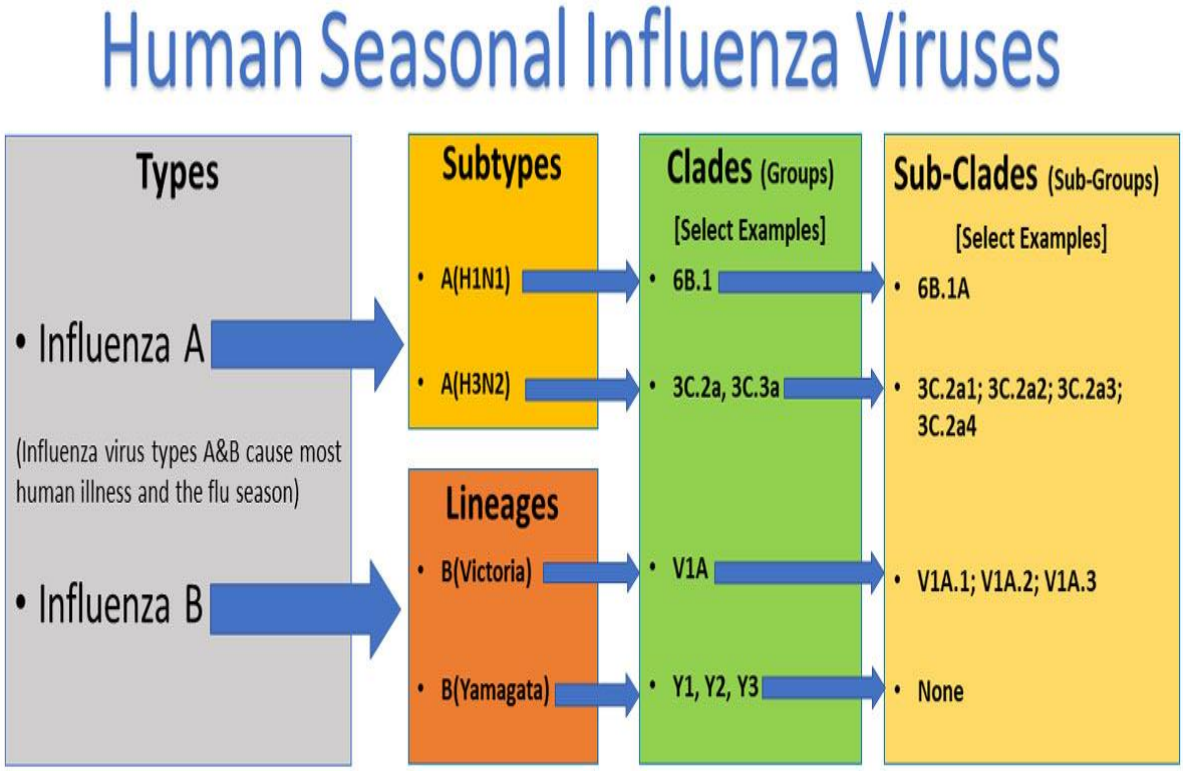


Fig.1. Influenza Virus from CDC- Atlanta

The term "swine flu" is frequently used to describe the infection of the respiratory tract induced by the H1N1 influenza A virus strain. [22] The sneezing and coughing of those who are ill allows the illness to spread from one person to another. The symptoms resemble those of the monsoonal human colds and include body aches, fatigue, body aches, fever, coughing, sore throat, runny nose, and body aches. The severe illness caused by the swine flu is notable for including pneumonia and breathlessness. [23]

Swine influenza typically results in elevated mortality rates near about 100 precent and reduced mortality in infected pigs, but it could also result in 10-15% mortality in pigs who have not previously been exposed to the illness. Because infected pigs display clinical symptoms that

are similar to those in humans, swine have been considered a better animal design for influenza research. [24]

The H1N1 pandemic is new, extremely virulent, and the product of 2 different reassortment of seasonal flu A virus can be found in human, avian, and porcine sources. [25]

EPIDEMIOLOGY

Influenza A most annually, outbreaks of variable severity take place. In the past century, the influenza virus has been responsible for the following pandemics: the Spanish flu of 1918, the Asian flu of 1957, and the Hong Kong flu of 1968. There have been variants in the disease's severity, its rate of spread, and the viral infection that has caused the outbreaks. [26]

Almost one-third of the world's people was impacted by the 1918 pandemic, which is frequently cited as the most severe and widespread of these. It was brought on by the H1N1 strain. It caused nearly 40 million deaths in its wake and may have even helped bring about 1st World War's conclusion. [27]

Following the containment of the epidemic, the virus returned to its typical pattern of causing smaller outbreaks until 1957, when such an antigenically distinct form of the virus reemerged globally in populations with immature autoimmune. H2N2 was the strain in inquiry. But only 11 years after it was discovered, this virus strain was supplanted by the H3N2 strain. It was the most prevalent strain of influenza in people up until very recently. [26]

A novel H1N1 strain that's also currently causing swine flu epidemic was revealed for the first moment in April 2009 at the Border with Mexico, and it spread quickly to be the first pandemic of the twenty-first century. [27] Previous to this, sporadic human infections with the same triple-reassorted virus were first found in swine in 1998. [28]

Within defined geographical areas of India, the disease is spreading. There had been 25 people killed as of August 17th, 1927 confirmed cases, and an approximately equivalent number of male and female cases. 8 Children under the age of 14 made up by nearly 40% of those affected. [29]

The H1N1 influenza virus that is currently prevalent is of swine origin, triple reassorted, and composed of genes from avian, swine, and human viruses [30]. The influenza pandemic of 1918–1919 is thought to have left a lasting legacy on the virus, which has developed over the past 91 years and has now acquired the capacity to not only infect but also spread within the human host. [31]

PATHOGENESIS: -

Host

Waterfowl serve as the virus's natural reservoir. The most cases of avian flu viruses are unable to instantly infect humans. Pigs are unique in that they can support acting as "fusing hosts" are both human and bird species. for the development of new strains that are adapted to humans. [32]

Transmission

In contrast to other type A influenza viruses that spread through This virus spreads via large particle respiratory droplets with small droplet nuclei, less than 6 feet must separate the source and the sensitive people for the attack to be effective. Rarely, transmission through exposure to diseased termites and small droplet particles is possible. Every bodily secretion is regarded as potentially contagious. [33]

After an incubation period of 1 to 7 days, the attack of the epithelia is the main event that follows virus transmission. [34]

The lung lesions in H1N1-infected animals were found whenever the effects of the virus on the respiratory mucosa of weanling pigs were studied and contrasted with that of the H3N2 virus were more extensive. [35]

damage to endothelial cells, airway obstruction, and peribranchial and Infiltration of periventricular mononuclear cells was among the histopathological changes observed [36]. Although bacteria commonly superinfect these endothelial damage sites, viruses can still seriously harm the lungs. Following the initial infection, the T cell activation and an increase in antibody titers are typically part of the immune response the host mounts. A decrease in virus discharge is associated with increased interferon producing in the respiratory mucosa. [37]

On average, the virus sheds for about a week (starting from 1 day before to 7 days after the onset of illness). Children regularly face longer virus going to shed periods that can last up to two weeks. [38]

CLINICAL FEATURE

Characteristics in Prevalent this same typical signs and symptoms start to a 1 to 7-day incubation period. Young adults are the most commonly affected [39].

Like any other viral respiratory illness, myalgia, fever, coughing, and sore throat are common symptoms. A trait more frequently seen in influenza of swine origin is GI upset. Nearly a 4th of patients may have vomiting and diarrhoea when they first arrive. Adolescents are more prone to the illness, and the very young are more severely affected.

RISK FACTOR OF SWINE INFLUENZA VIRUS: -

Swine influenza was caused by a variety of factors, such as temperature, environment, and breeding strategy. Everyone is aware that main characteristics such as swine influenza is its seasonality.

Minor epidemics have always happened in the winter. A swine flu infection can be brought on by abrupt temperature changes, especially in the late autumn, early spring, and winter. Rain and cold temperatures are very significant factors in the spread of the influenza virus [40–41]. With the development of breeding techniques, the pig industry grew and became more intensive, which increased the risk of swine flu in open-air rearies. [42] This modification reduced the risk of swine flu while also meeting the rising demand for pork. Variations in humidity and temperature trigger the disease to manifest almost immediately. All of this quickly spreads and is difficult to contain. The infection comes in two different forms: (1) Symptoms occur: the affected pig exhibits the typical high fever, dyspnea, depression, coughing, sneezing, and weight loss. (2) Asymptomatic: the pigs with the infection demonstrate no overt clinical signs.

Current swine influenza virus situation: -

Three main Influenza A virus subtype, H1N1, H3N2, and H1N2, have currently established themselves and are spreading throughout the world's pig herds. The 1918-like cH1N1 virus was discovered after the human pandemic of 1918 and went on to become endemic in pigs all over the world. [43].

Viruses that cause swine flu in America include: -

It is more challenging for the industry to create timely and efficient swine influenza vaccines given the highly genetically and antigenically diverse set of swine influenza viruses currently circulating in North American swine influenza vaccines.

European swine influenza viruses: -

Through Europe, medically ill European pigs have been found to have H1N1 as well as H3N2 sub - types of Influenza A virus, such as swine cH1N1, avian-like H1N1, and human-like H3N2 viruses. [32] Reducing the genotypes of circulating swine influenza viruses has become difficult due to the recombination of the 2009 pH1N1 virus with contemporary swine viruses in European pig populations. [44-46]

Asian swine influenza pathogens: -

Although it was first discovered in Asia in 1974, the cH1N1 swine virus was believed to have been present in pigs in China during in the 1918–1919 human pandemic. [47] Influenza

surveillance in the early 1980s showed that the cH1N1 virus was widely dispersed in pigs across many Asian regions and nations. [48-50] Those certain viruses were successful in establishing themselves in pigs and had no negative effects on infected animals. With some more avian influenza viruses of been introduced into swine, it is possible to develop a novel virus that is totally adapted to pigs, similar to the H1N1 virus that is found in Eurasian birds, or avian viruses can reassort with endemic viruses to produce new reassortant viruses that are highly transmittable and have the ability to endanger public health. [51]

Swine flu control is challenging.

In swine communities around the globe, there are a large number of highly diverse swine influenza viruses that are present and in circulation. [52-53] Pigs may at any time develop novel virus genotypes and subtypes as a result of infections with avian and/or human influenza viruses.

The best way to prevent and manage influenza in both humans and animals is through vaccination. It has been demonstrated that whole inactivated virus vaccines, which are frequently used in the swine industry in many countries, are effective in preventing pigs from contracting infections brought on by homologous or genetically related viruses. [54] A live-attenuated influenza virus vaccine based on NS1 deletion has been authorised for use in pigs in the United States because commercial whole inactivated virus vaccines only offer a modest level of protection against contemporary swine influenza viruses. [55] Live-virus vaccines have the advantage of providing good heterovariant and partial heterosubtypic protection while not enhancing disease [56-57]. In swine farms that used the live-attenuated influenza virus vaccine,

novel variant viruses have been discovered as a result of reassortment with endemic viruses. [58]

Some cases of influenza are treated with two types adamantanes (amantadine, rimantadine) and neuraminidase inhibitors are examples of antiviral medications (zanamivir, oseltamivir, peramivir, and laninamivir) [59-63]. Although both drug groups are capable of preventing some influenza A viruses, they both have potential side effects. Antiviral medications can be used in severe or high-risk cases that develop after this window of time, but they are most effective when taken within the first 48 hours of the onset of clinical signs. [59-61] As members of the new class of medications known as neuraminidase inhibitors, zanamivir and oseltamivir are effective against both influenza A and B. Inhaled dry powder is how zanamivir is administered. It is approved to treat patients aged 7 and older who have had uncomplicated acute influenza A or B symptoms for less than 48 hours. You can buy oseltamivir as an oral capsule. It is authorised to treat mild cases of influenza A or B in adults and children over the age of one who have had symptoms for under 48 hours Zanamivir has been given the go-ahead to prevent influenza in patients five years old and older. Oseltamivir is allowed for use in people older than one year old in order to avoid virus infection. [64]

From time to time this virus undergoes genetic shift & new strain are formed which have the potential to cause pandemics. Through our meta-analysis we will look for the recent and past epidemiological changes in the disease trend & genetic changes this virus has undergone.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

A pandemic is believed to emerge when a virus with such a novel HA subtype adapts to effective spread in humans. The latest H1N1 pandemic was caused by a swine H1N1 virus that had undergone genetic genetic recombination with modern human flu viruses. [65-66]

The pathological characteristics of this lethal H1N1 influenza infection include lymphocytic cell infiltrates that are suggestive of a primary viral pneumonia, haemorrhage intercellular pneumonitis, and diffuse alveolar damage. Recent studies suggest that there is uncontrolled release of immune mediators leading to cytokine storm and that one of the probable cause of high mortality and morbidity. Also, secondary bacterial pneumonia results in severe disease manifestation. [67-68]

Fever and upper respiratory symptoms like a cough, runny nose, and sore throat are considerable clinical features of swine influenza. Additionally reported symptoms include diarrhoea, vomiting, fatigue, and body aches.

PATHOPHYSIOLOGY: -

CYTOKINE STORM

These dangers are primarily derived from the influenza virus, which annually results in millions of severe cases and 250 000–500 000 fatalities. [69] During a pandemic year, the situation can become even worse. The 1918 H1N1 Spanish flu, the most virulent influenza, infected about 6% of the world's population and killed 3%. [70] while 2009 H1N1 pandemic influenza case fatality rate was revealed to be decreased, with an estimated rate of 0.3 percent or low. [71]

They pose an increasing risk of transmission from person to person [72-73]. In humans, these infections are associated by a forceful pro-inflammatory response and inadequate anti-inflammatory response control, a phenomenon Called **"cytokine storm."**

In the case of infections are caused by the 1918 H1N1 influenza viruses, however, the impedance became overactive, likely to result in an infection. exaggerated inflammatory response known as the cytokine storm phenomenon. [74] Multiple experimental studies and clinical trials suggested that cytokine storm was directly related to tissue damage and a poor diagnosis and management of severe influenza. [75]

Respiratory epithelial cells, that are primary targets of influenza virus, also orchestrate cytokine amplification while infection. [76] Presenting initial infection, progeny viruses that multiply within these cells can infect other cells, including alveolar macrophages. [77] Inflammatory reactions are brought on by the death of infected cells through necrosis or apoptosis. An organism's first reaction to harmful stimuli is acute inflammation, which is characterised by increased blood flow, which allows plasma and leukocytes to reach extra-vascular sites of an injury, elevation of local temperatures, and pain. [71]

The activation of pro-inflammatory cytokines or chemokines is another characteristic of the acute inflammatory response. Inflammatory cells may be attracted by those pro-inflammatory cytokines or chemokines. [77-78] Then, there is a significant infiltration of immune cells and tissue damage along with an increase in apoptotic, antiviral, and inflammatory gene

expressions. [75,79] In the same manner, regenerative processes and damage solution are initiated. This reparative process can usually completely restore function. [80]

Much severe pathological changes, such as diffuse alveolar damage, hyaline membrane formation, fibrin exudates, and fibrotic healing, are observed in severe inflammation associated with cytokine storm. Those kind of symptoms of severe capillary damage, immunopathologic damage, and chronic organ dysfunction. [78]

Furthermore, drastic inflammatory cytokines/chemokines can enter the circulation and cause systemic cytokine storms, which are responsible for multi-organ dysfunction. [75]

According to the manufacturer's instructions, IL-2, IL-4, IL-6, IL-10, TNF-a, and IFN-c levels were assessed using by ELISA.[81]

In this study, human case was found who had committed a novel reassorting virus that had obtained six internal genes (PB2, PB2, PA, NP, M, and NS) from human A(H1N1) pdm09 pathogens and HA and NA gene segments from swine influenza A(H1N2) viruses that may have been revolving in Taiwan for decades. The phylogenetic analysis showed that the HA and NA genes are each unique to Taiwanese swine and belong to different clades, suggesting that they were introduced from humans at different times. The next pandemic threat is posed by the bidirectional transmission of influenza viruses between humans and swine. [82]

This research demonstrates how the Pt/TiO2-SiO2 bionanocatalysts created in our lab reduce the spreading of influenza the virus (H1N1) upon contact. From this work, the following conclusions can be drawn: • The maximum reduction in viral replication under the conditions was 65.2 3.3 percent, but we think that by increasing the concentration of NPs, or the nanoparticle/virus ratio, we will achieve a 100 percent reduction. • Despite the nucleotide arrangement being predetermined, the nanoparticles' RNA interaction-based mechanism allows them to catalyse the cleavage of the bonds (unlike conventional vaccines, which interact with surface proteins). This speculative mechanism implies that various viricidal mechanisms may be possible for bionanocatalysts. **[83]**

Various techniques are available like EpiCC which enable us to do studies on the effectiveness of vaccines based on invariant T cell epitopes for influenza and other pathogens in comparison to whole antigen vaccines The newly emerging G4 influenza, African swine fever, and human influenza strains versus candidate vaccines are just a few viral populations that the EpiCC tool is likely applicable.**[84]**

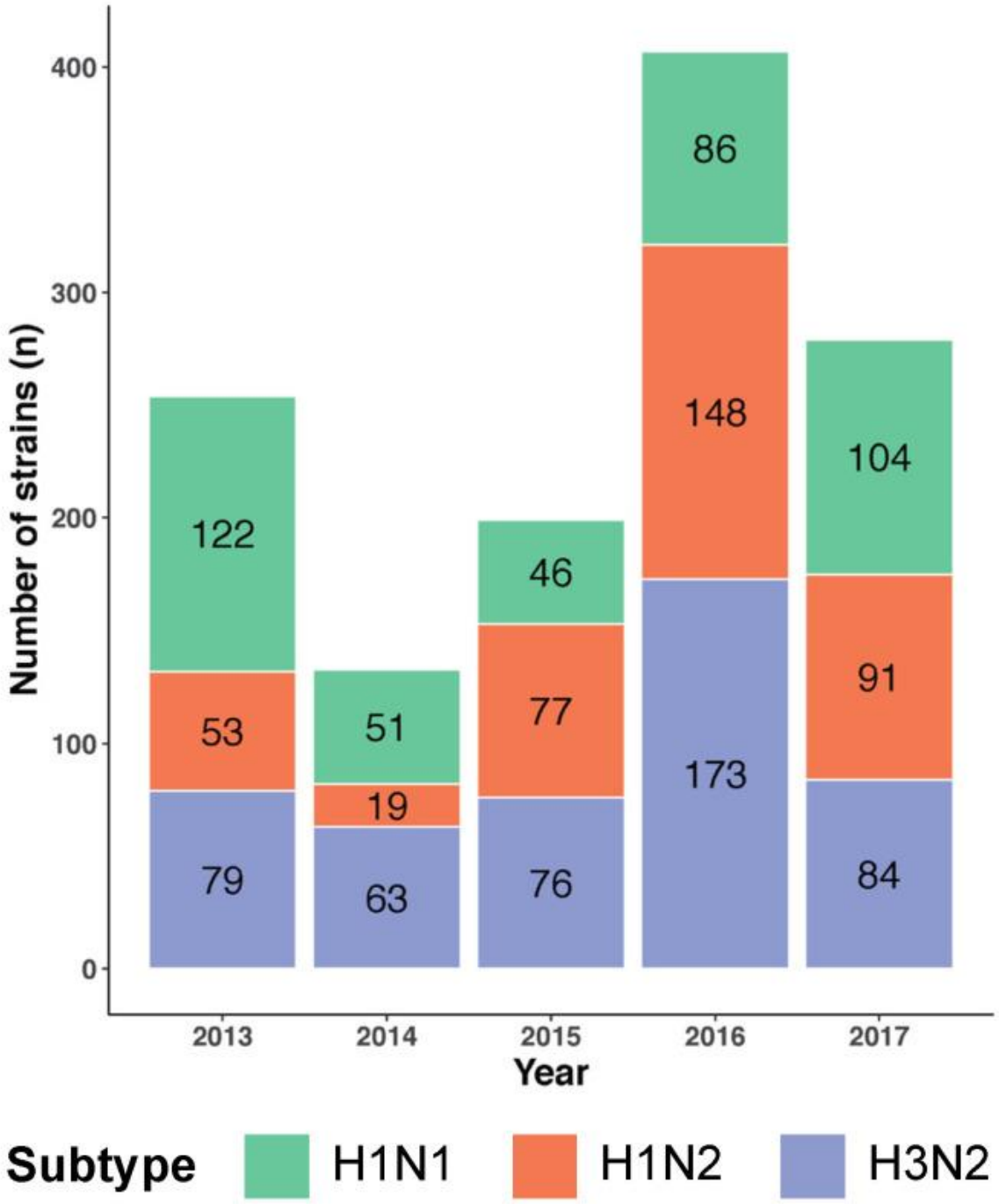


Figure 3. This study included swine Influenza A virus genome sequences from the H1N1, H1N2, and H3N2 subtypes from 2013 to 2017. The three subtypes are represented by the color-coded stacked bar chart, with So every loaded component showed how many strains were found during that year. **Courtesy-Tan S, Gutiérrez AH.et. al**.

This review describes the genetic characterization of a swine H3N2 influenza A separate (A/P17-4/2017). BLASTN analysis revealed that the 8 gene sequences shared a high degree of nucleotide similarity (97.0 to 99.0%) with porcine strains found in the Republic of Korea and the United States. The nucleotide matrix gene in particular showed a high degree of similarity to recent isolates from North Carolina in this study.[85]

In this review, it is discussed how viruses of human and non - human origin can spread to new hosts through viral transfer among both human and nonhuman hosts. We discovered the first instance of an influenza A(H1N1) pdm09 infection in a human in this study. this demonstrates that not only do these viruses circulate in swine hosts, but they are also evolving and distinguishing theirself from previously circulating influenza viruses of human origin. For the continued monitoring influenza virus activity, it is necessary to create methods for telling human- and swine-origin viruses apart. The results of this study demonstrate that distinct genetic signatures of influenza A(H1N1) pdm09 can differentiate circulating human-associated strains from distributing swine-associated strains and that these signatures can be used to enhance swine flu surveillance. [86]

This study discovered the wide variety of swine influenza virus genotypes and subtypes that are currently circulating in pigs, as well as their high diversity worldwide poses a significant challenge to developing widespread vaccination programmes and disease prevention. It's significant to note that the swine influenza virus can infect people regardless of species and even started the 2009 influenza pandemic. [87]

The findings of this study revealed that serum antibody responses of immunocompetent Belgians to major H1 swine Influenza A virus clades vary depending on the swine Influenza A virus tested, relationship to human seasonal Influenza A virus's, and the person's birth year. Total seroprevalences of classical swine (1A.3.3.2, 1A.3.3.3) but also European human-like (1B.1.2.1) swine influenza have been high (50 percent). A virus that also is low ((7,20-25) swine influenza A virus and intermediate (24%) for Asian avian-like (1C.2.3) and North American human-like (1A.1.2.1) swine influenza A viruses.[88]

Researchers found that EAS-H1N1 or a reassortant EAS-H1N1virus infection in humans could result in mild to severe clinical symptoms. Whole genome sequencing has revealed a number of gene mutations encoding amino acid substitutions in a number of virus proteins, those who have linked to increased virulence and the likelihood of transmission to other mammals and humans. It is critical to continue and expand influenza surveillance in swine because they are a host species capable of producing novel virus reasortants that could lead to another human pandemic, as seen with A(H1N1) pdm09 viruses. [89]

The work is completed in this study. Tetraplex RTqPCR identified two Influenza B virus, one Influenza D virus, but no Influenza C virus infections. Conventional RTPCR and partial sequence analysis were used to confirm the Influenza B virus and Influenza D Virus results. The tetraplex RTqPCR proved to be an efficient tool for studying influenza virus transmission at the humananimal interface because it was sensitive, specific, and high throughput. better comprehend the true incidence and prevalence of swine influenza virus types B, C, and D infections, active virological and serological surveillance must be supplemented with closemeshed active virological and serological surveillance.[90]

Developing long-term monitoring plans for swine influenza in North Vietnam was the aim of this study. The development and field testing of monitoring procedures lasted for 14 months in 2013–2014. Six virus genotypes were discovered through genetic analysis, including the H1N1 2009 pandemic (H1N1pdm09) viruses, H1N2 with H1 of human origin, triple-reassortant H3N2 viruses, and H3N2 and H1N1pdm09 reassortants. In contrast to H1N1pdm09 establishing itself as a long-term distinct lineage in swine, repeated spillover from humans to swine was shown by phylogenetic studies of swine and human H1N1pdm09 viruses. [91]

swine's influenza A virus dynamic and complex diversity was demonstrated in this study while infection of pigs on farrow-to-wean farms. We were able to characterise the whole genomes of Influenza A virus with greater precision over time thanks to complete genome amplification and NGS technologies. This study found that Influenza A virus could be sustained for long periods of time and that different swine's influenza A virus can coexist within and between subpopulations on these farms. Pigs on farrow-to-wean farms are thus repeatedly exposed to

swine's influenza A virus that are either closely related or clearly distinct. The findings also suggested that pig population dynamics, as well as viral mechanisms of genetic diversification, should be considered when studying the variety and development of swine Influenza A virus. It is speculated that if swine's influenza A virus transmission is reduced on farrow-to-wean farms, the spread of swine's influenza A virus to other pig sites after weaning will be reduced. **[92]**

This research focuses on the key features of the recent influenza outbreak in Andhra Pradesh from 2017 to 2018. The outbreak began in the late monsoon of 2017 and had two peaks: one in the summer and one in the winter. The virus's silent spread is primarily due to a lack of awareness. The importance of raising public awareness about the modes of transmission and preventive steps that can be taken to stop the influenza virus from spreading among the general public was recognised. **[93]**

This study focused on the Early in 2015, Rajasthan, India, experienced a high morbidity rate due to the H1N1 pandemic, especially among the young and mid- population as well as pregnant women. The study emphasises the value of routinely monitoring influenza-like diseases, early diagnosis, and timely start of treatment in reported incidents. **[94]**

This study on Prevention in swine, prevention of transmission to humans, and prevention of spread among humans are the three parts of swine influenza prevention. Environmental control, including vaccination of high-risk populations and awareness programs, are crucial to swine influenza outbreak control due to the few available treatments, the high risk of severe infection, and the common need for intensive care for patients with H1N1 pneumonia.

Findings: Anti - viral medications can be used in severe or high-risk cases that emerge after this window of time, but they are most effective when started within the first 48 hours after the onset of clinical signs. Zanamivir or oseltamivir (Tamiflu, Genentech) are recommended by the Centers for Disease Control and Prevention. [95]

The work done in this study a correlation of the genome sequences of the subtype H3N2 isolates retrieved from humans and swine from each fair revealed nucleotide identities of >99.8%, verifying zoonotic transmission among swine and humans. Despite of host species or fair, every influenza A(H3N2) virus isolated in this study was >99.5% identical, displaying that a single virus strain was widely disseminated among exposition swine in Ohio in 2012.[96]

This analysis aims to develop the swine influenza virus's history, the serological epidemiology of swine influenza virus infection, the clinical characteristics of swine influenza, the formation of swine influenza vaccines, and the strategic planning of the swine influenza development of China.[97]

This study showed that experimentally inoculated nursery pigs were affected by acute respiratory illness caused by The influenza viruses pH1N1 and rH1N1 that were isolated from naturally infected pigs. Spite of the fact that animals in the rH1N1-infected cohort presented more severe clinical symptoms, had some more pigs shed the virus, were mentioned to have enhanced histopathological severity of lung lesions, and had increased viral antigen in lung

tissue, the results were not statistically significant when compared to the pH1N1-infected group. It is indeed interesting to note that viral genetic information from both viruses was still detectable in the nasal swabs after experiment was over. Comparable to other swine influenza viruses, rH1N1 and pH1N1 only led to pathological lesions and somatic manifestations in the respiratory tract. [98]

In the wake of the spread of the influenza A(H1N1) pdm09 viruses in India, the aim of this study is to record the previously unknown burden of hospitalisation for influenza in a rural town. In the community, influenza positivity was found in 20% of all hospital admissions during the monsoon season, when influenza activity flow was at its peak. These findings can aid India in creating influenza prevention efforts.[99]

Work completed for this paper Inadequate adherence to authorised vaccination suggestions is the primary cause of the low uptake of pandemic influenza vaccines during the pandemic season 2009–2010. During the German H1N1 pdm09 influenza pandemic, public relations efforts and vaccination campaigns were unsuccessful. The findings raise questions about whether contentious debates over the efficacy and Pandemic influenza vaccines are essential. may have influenced the first post-pandemic season's lower uptake of seasonal influenza vaccines.[100]

In this study, we conducted extensive phylogenetic analysis of global epidemic A/H1N1/09 (H1N1pdm09) influenza virus genome sequence data to determine the degree to which influenza viruses jump between human and swine hosts. Overall, the findings in this review show how frequently Swine are revealed to influenza viruses that are distributed by people. contribute significantly highlight the importance of enhancing preventative measures at the

human-swine interface, including influenza vaccination of swine workers. to the genetic diversity of influenza viruses in swine.[101]

Pandemic H1N1 virus 2009 (2009 H1N1) is still spreading the disease all around world, mainly in younger groups, according From this paper After each virus was administered nasally to mice, morbidity, mortality, viral replication, hemostatic parameters, cytokine production, and lung histology were all assessed. Those 2009 H1N1 viruses were extremely infectious and efficiently replicated in the lungs of mice, but they did not cause lethal illness or spread extrapulmonaryly. Losing weight, lymphopenia, and the production of proinflammatory chemokines were temporary side effects of 2009 H1N1 virus infection, but these levels were typically lower than those of a triple-reassortant swine virus and the 1918 virus. Lung lesions ranging from mild to moderate respiratory infections, with scattered bronchiolar epithelial necrosis, and mild to moderate peribronchiolar alveolitis have been managed to bring on by 2009 viruses infection. These study shows that when compared to highly pathogenic viruses, the 2009 H1N1 viruses used to have a mild to moderate level of virulence in mice.[102]

The whole paper focuses on the fact that as the global epidemic (H1N1) 2009 influenza virus continues to infect human populations around the world, reports of endemic linked animal infections are also going to rise. Since December 2009, pandemic (H1N1) 2009-like viruses have been discovered in pigs from numerous South Korean swine farms. Numerous instances of human-to-swine transmission were found through genetic and phylogenetic analyses of viral segments, with no obvious evidence of reassortment. These result suggests that in South Korea, the disease outbreak (H1N1) 2009 influenza viruses have been widespread transmitted from persons to animals. Since pigs are important to the ecosystem of influenza viruses, it is

important to closely monitor and limit these transmission events to avoid creating viruses that are more dangerous for health.[103]

This paper's work is on the high prevalence of seasonal-A cases and pandemic Cases of H1N1 in the urban agglomeration of Pune during the research period. Compared to cases who tested favourable for those who have seasonal influenza-A viruses, tested positive for the pandemic H1N1 virus had a significantly higher risk of hospitalisation (OR: 1.8). 56 and 8 of the 94 influenza-related deaths in Pune (urban) and 26 and 1 of the 94 influenza-related deaths in Mumbai (rural) were caused by pandemic H1N1 positive and seasonal-A positive cases, respectively.[104]

The work in this paper focuses on the pandemic's prevalence. An A(H1N1) virus that has been making the rounds in humans since April 2009 has a rare confluence of gene segments from both North American and Eurasian swine lineages, according to the study's main theme. It is possible that previously unknown molecular determinants are to blame for human transmission since 2009 A(H1N1) viruses do not currently contain molecular markers indicative of adjustment to humans. Although the viruses are homogenous and genetic makeup similar to North American swine A(H1N1) viruses, they differ from seasonal human A viruses (H1N1).[105]

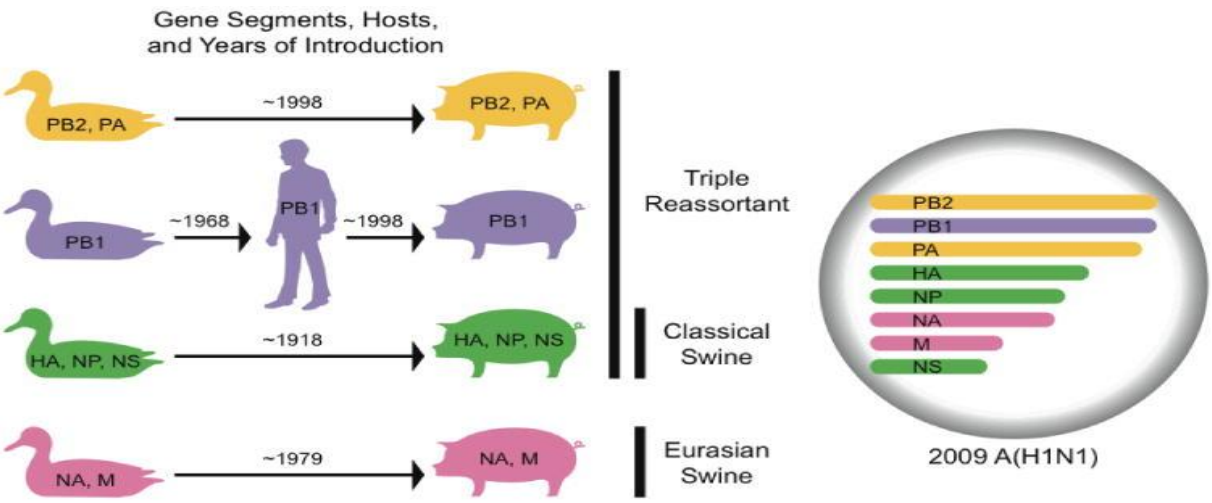


Fig. 2. The following sections of the 2009 A(H1N1) virus's genome have Origins of the host and lineage for the following proteins: HA hemagglutinin, NP nucleoprotein, NA neuraminidase, M matrix gene, and NS non-structural gene. The host is noted by the colouring of the gene segment in the circular pattern. [105] **Courtesy- Garten RJ, Davis CT.et. al**.

The work done in this paper is concentrated on A common name for viral respiratory infections is "swine flu." brought on by the H1N1 strains of the influenza A viruses. Early 2009, this disease was first identified from Mexico. It quickly spreads throughout world and claimed close to 4000 lives. It has been determined that this infection is caused by an upgraded and more virulent strain of the original H1N1.

The current H1N1 pandemic's occurrence, spread, and mortality have all been covered from this review. also talked about the present situation of H1N1 research and the state from Andhra Pradesh's efforts [106].

The purpose of this paper's work is to the first pandemic in forty years is currently being brought on by a new H1N1 virus. Although the illness is moderately severe, there are some important distinctions from seasonal influenza. In contrast to seasonal influenza, people 62 are generally unaffected, which is probably because they have H1N1 cross-neutralizing antibodies. This article examined pertinent information from previous pandemics, including To emphasise, we will use the influenza season and H5N1 avian influenza important pathogenesis and immunology-related issues [107].

The work done in this paper is focused on the first pandemic of swine influenza, which has been discovered for the first time in the Mexico-U.S. border region in April 2009. A triple reassortment process resulted in the current H1N1 influenza strain, which has genes from avian, swine, and human viruses. Transmission occurs through droplets or fumites. During incubation, 2 to 7 days pass. Patients under the age of five, Risk groups for developing serious

illness include the elderly, pregnant women, people with chronic system - wide illnesses, and youngsters taking aspirin. Pneumonia and respiratory failure are the two most common symptoms of serious swine influenza.

Less than 1% of cases of swine origin influenza have been fatal up to this point. Based on the data available (6), the case fatality rate is approximately 0.8 percent, with 1462 deaths reported worldwide as of August 6, 2009 **[108]**.

AIMS

AND

OBJECTIVES

AIMS & OBJECTIVE

AIMS: -

The aim of this study is to review the spread of current strains of swine flu viruses.

OBJECTIVE:-

To look at the disease profile of different strains of swine flu virus

To look at the current strains of swine flu viruses prevalent in different parts of the world.

MATERIALS AND METHODS

MATERIALS AND METHODS

TYPE OF STUDY:- Meta-analysis

DATA TYPE: - Data for this meta-analysis were collected from following sources.

a) Data from various publications in indexed journals.

b) Data from recent editions of textbooks.

c) Data from websites of CDC, NCDC, WHO.

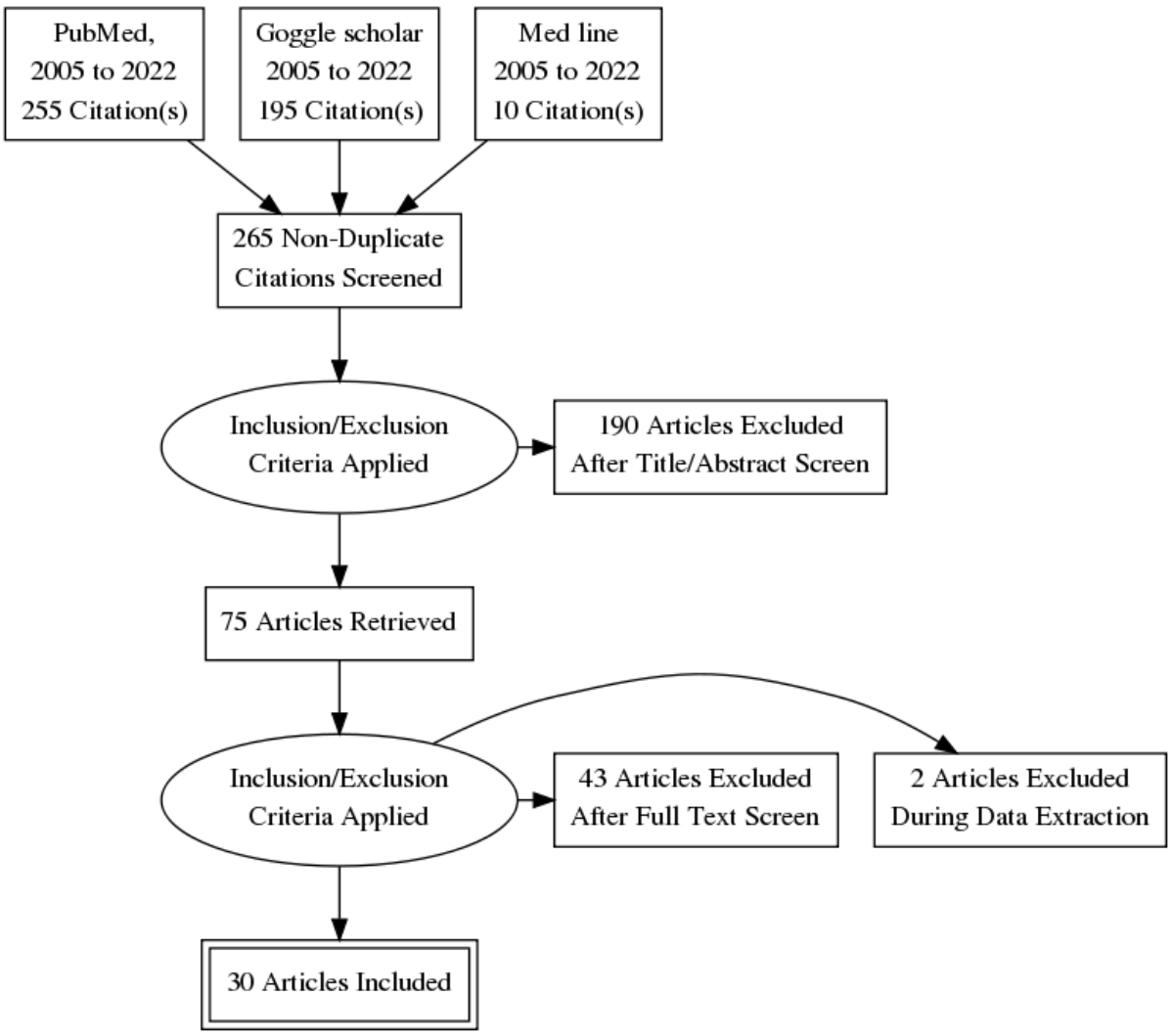
TIME FRAME: - All the studies in indexed journal from year 2005 to 2022.

SEARCH STRATEGY: - 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.

INCLUSION CRITERIA: - 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.

EXCLUSION CRITERIA: - Article titles and abstracts were screened by researchers independently to exclude irrelevant articles.

Study Selection Process: followed by PRISMA**,** 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 2 article excluded during data extraction. Finally, 30 appropriate papers were selected to enter the meta-analysis stage.



OBSERVATION AND RESULTS

OBSERVATION AND RESULTS

S. No.	AUTHOR	YEAR	COUNTRY	STUDY FINDING
1.	Yang JR, Kuo CY. et. al.	2022	Taiwan	whole-genome sequencing and phylogenetic analyses revealed that A/Taiwan/1/2021(H1N2)v is a novel reassortant virus containing hemagglutinin (HA) and neuraminidase (NA) gene segments derived from swine influenza A(H1N2), and there is another 6 internal genes (PB2, PB2, PA, NP, M and NS) are from human A(H1N1)pdm09 viruses.
2.	Tan S, Gutiérrez AH et. al.	2021	Switzerland	a previously created preservedT cell epitope-based vaccine and determine the persistence of T cell epitope conservation over time. Twenty-nine of the 58 total T cell epitopes included in the epitope-based vaccine were highly conserved and found in >1001 circulating swine IAV strains over the 4-year period.
3.	Tessy Lopez-goerne et.al.	2021	Mexico	The antiviral properties of a microparticles were demonstrated, along with a maximum reduction in viral proliferation of 65.03 3.04 percent. Pt/TiO2-SiO2 bio micro catalysts were able to reduce Influenza A (H1N1) viral infection 65.03 ± 3.04%

				The outcome of the present work suggests the possibility of implementing bionanocatalysts as treatments for Influenza A (H1N1) virus infection
4.	**Wenjun Ma. et. al.**	**2020**	**Columbia**	That review focuses on current status of swine influenza viruses in America, Europe and Asia. The lot of variety and varied distribution of different subtypes and genotypes of swine influenza viruses circulating in pigs globally is a major challenge to produce broadly effective vaccines and control disease. Importantly, swine influenza virus is able to cross species barrier to infect humans and even caused influenza pandemic in 2009.
5.	**Peter W. Cook. et. al.**	**2020**	**USA**	As a result of next generations sequencing suggest infection with an influenza A(H1N1) variant influenza A(H1N1) virus depend on similarities of various internal genes to those of swine influenza viruses circulating in America.
6.	**Song D, Kim HK. et. al.**	**2020**	**Korea**	A/swine/P17-4/2017 influenza A H3N2 separated has been genetically characterised. The nucleotide similarity between the 8 gene sequences and found so in Republic of Korea, as well as in the United States was high (97.0 to 99.0%), according to BLASTN analysis of the sequences.

7.	**Van Reeth K. et. al.**	**2019**	**Belgium**	study compared antibody responses in nonswine workers to those in people who had frequent swine contact.
8.	**Dong X, Su X, Gu Q.**	**2019**	**China**	A/Tianjin-body/1606/2018(H1N1) is a novel reassortant EAS-H1N1 virus with gene segments from EAS-H1N1 (HA and NA), classical swine H1N1(NS), and A(H1N1)pdm09(PB2, PB2, PA, NP, and M).
9.	**Peiris M. et. al.**	**2018**	**China**	H1N1 2009 pandemic (H1N1pdm09) viruses, H1N2 with H1 of human origin, H3N2 and H1N1pdm09 reassortants, and triple-reassortant H3N2 viruses were discovered through genetic analysis.
10.	**Dinah Henritzi**	**2018**	**Germany**	Tetraplex RT-qPCR identified two Influenza B viruses, one Influenza D virus, but no Influenza C virus infections. Conventional RT-PCR and partial sequence analysis confirmed the Influenza B virus, Influenza D virus results.
11	**Diaz A, Marthaler D. et. al.**	**2017**	**Kuwait**	The findings also suggested when studying the diversity and evolution of swine influenza, pig population dynamics as well as viral mechanisms of genetic diversification should be taken into account It's a virus.
12	**Malhotra B. et. al.**	**2016**	**India**	In early 2015, the H1N1 virus caused significant mortality and morbidity throughout Rajasthan, India,

				especially among young and middle-aged people, as well as pregnant women. Research highlighted the importance of routine influenza-like illness surveillance, early diagnosis, and prompt treatment initiation in suspected cases.
13	**Rewar S. et. al.**	**2015**	**India**	Antiviral medications are most effective when administered within the first 48 hours after clinical symptoms appear, but they can also be used in severe or increased cases that arise after this time.
14	**Janke BH. Et. al.**	**2014**	**USA**	The more dangerous viruses exhibit the the succeeding infection features: (1) increased or extended virus replication (2) increased cytokine initiation, as well as (3) Lower respiratory tract hybridization. Virulence is aided by nearly all viral proteins. detection of viruses and antibodies in pig oral fluids is a recent development that allows for the efficient sampling of large numbers of animals.
15	**Simonsen L. et. al.**	**2013**	**UK**	And though pandemic mortality was similar to seasonal influenza mortality, there was a significant shift toward mortality among people over 65 years old, resulting in many more life-years lost.
16	**Kong W. et. al.**	**2013**	**China**	This investigation seeks to introduce the legacy of the swine influenza virus, the serological epidemiology of swine influenza virus infection, swine influenza

				document focuses, the development of swine influenza vaccines, and the control of the swine influenza situation in China.
17	**Charoenvisal N. et.al.**	**2013**	**Thailand**	According to the findings, pigs infected with both viruses displayed typical flu-like clinical signs as well as histopathological lesions of varying severity. Both groups of influenza-infected pigs had mild to moderate pulmonary signs on 1-4 DPI. Surprisingly, both groups of pigs had viral RNA detected in nasal swabs until the end of the experiment (12 DPI).
18	**Chadha MS. et. al**	**2013**	**India**	The consequences of influenza hospitalisation in a sparsely populated Indian society following the emergence of influenza A(H1N1)pdm09 viruses. During peak influenza activity circulation periods, such as the monsoon season, influenza positivity was found in 20% of all society hospital admissions.
19	**Ye Liu. et. al.**	**2012**	**China**	Patients suffering from influenza H1N1 Infection in 2009 had biochemical changes, including variable increases in ALT, AST, CK, and LDH. Along with patients infected with influenza H1N1 2009, TLR2, TLR3, and TLR9 expression increased; no overt changes in TLR4, TLR7, or TLR8 expression were found. The main pattern-recognised receptor that can

				identify and bind to the H1N1 virus is thought to be TLR9.
20	**Nelson MI. et. al.**	**2012**	**USA**	These findings expose The presence of human influenza viruses in swine suggests that humans are at risk. contribute significantly towards the genetic diversity of influenza viruses in swine, as well as the need for improved biosecurity measures at the human-swine interface, such as influenza vaccination of swine workers
21	**Böhmer MM,**	**2012**	**Germany**	Monsoonal influenza vaccine uptake in the pre-pandemic season 2008/09 was 52.7 percent between many people over 62, 30.5 percent among health care workers, and 43.3 percent among chronically ill people. Vaccination coverage fell among all target groups in the first post-pandemic season, 2010/11. (50.6 percent, 25.8 percent, and 41.0 percent, respectively).
22	**Belser JA. et. al.**	**2010**	**U.S.**	Lung lesions caused by the 2009 viruses values range from mild to moderate bronchiolitis with occasional bronchiolar epithelial necrosis and mild to moderate peribronchiolar alveolitis. These studies show that when compared to highly pathogenic viruses, the 2009 H1N1 viruses had mild to moderate virulence in mice.

23	**Song MS, Lee JH. et. al.**	**2010**	**Korea**	In South Korea, 2009 disease outbreak (H1N1) influenza viruses were widely transmitted such as person to person. Given pigs' importance Those kind of transmission events as in ecology of influenza viruses should be closely monitored and minimised to avoid the risk of generating viruses that pose greater human health risks.
24	**Mishra AC**	**2010**	**India**	The H1N1 influenza pandemic becomes less likely. severe than 'Spanish flu 1918,' however it is more severe over other twentieth-century pandemics As a result, pandemic influenza should be regarded as a serious public health threat, warranting an unprecedented global response.
25	**Garten RJ. et. al.**	**2009**	**USA**	Molecular markers which predict human adjustment are not currently present in 2009 A(H1N1) viruses, implying that previously unknown molecular determinants are responsible for human transmission. The viruses are antigenically homogeneous and similar to swine A(H1N1) viruses in North America, but distinct from seasonal human A(H1N1) viruses (H1N1).
26	**R. Sebastian. et. al.**	**2009**	**India**	Children under the age of five, the elderly, pregnant women, patients with serious systemic illnesses, and teenagers taking aspirin are all at risk of developing

				severe disease. Pneumonia and respiratory failure are the most common severe manifestations of swine influenza.
27	**Peiris JS, Tu WW. et. al.**	**2009**	**China**	A latest H1N1 virus of swine origin (H1N1v) is causing a pandemic in humans, the first in 40 years. The illness is mild, but it differs significantly from seasonal influenza. Animal studies show that the novel H1N1v pandemic virus causes more severe illness than seasonal influenza viruses and appears to prefer the alveolar epithelium.
28	**Musturi Venkataramana et.al.**	**2009**	**India**	It has been determined that this infection is caused by an upgraded and more virulent strain of the original H1N1. The H1N1 pandemic is a brand-new, extremely virulent virus that developed through double reassortment using pieces of the genomes along with influenza A virus from pigs, birds, and humans.

DISCUSSION

DISCUSSION

This meta-purpose analysis's is to examine the epidemiological traits of SI in various nations and to identify elements that have been essential for Swine influenza virus isolation and subsequently for Swine influenza monitoring. This meta-analysis included all articles discovered in scientific open-access databases that provided information on SI, including pig-level and herd-level seroprevalence, isolation and detection rates, and risk factors from studies conducted from 2005 to 2022.

One laboratory-confirmed human case of infection with the influenza A(H1N1) virus of swine origin in the German state of North Rhine-Westphalia was reported to WHO by Germany on May 11, 2022. 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 Center. Influenza RT-PCR were used to identify virus. 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.

On April 25, 2022, One confirmed case of human infection with the avian influenza A(H3N8) virus was reported to the World Health Organization by the Republic of The union of China's National Health Commission.

On April 29, 2022, A human case of avian influenza A (H5) has been reported to WHO in Colorado State, America. The incident took place at a farm where the influenza A (H5N1) virus had been identified in the chickens, during the culling of the flock. On April 27, the US Centers for Disease Control and Prevention confirmed avian influenza A (H5) in the case; later, sequence analysis confirmed subtype N1. Close associates and those involved in the culling of poultry have been found, tested, and are being sought after. According to the information at hand, WHO rates the risk this virus poses to the general public as low and the risk it poses to people who are exposed to it at work as moderate.

On July 21, 2021, the National IHR focal point of India informed WHO of a single human case of avian influenza A(H5N1) from the northern Indian state of Haryana. This is the first known instance of the influenza A(H5N1) virus infecting a human in India.

On May 31, 2021, One reported case of human infection with the avian influenza A(H10N3) virus was reported to the World Health Organization by the Republic of The union of China's National Health Commission. It's the first case of avian influenza A(H10N3) virus infection in humans to be documented anywhere in the world.

Typically, influenza virus infection results in significant mortality and morbidity. Because they can contract both the pigs, avian and human influenza infections are essential in the creation of

novel influenza viruses with the ability to induce a pandemic. Currently, it is known that the influenza virus subtypes H1N1, H3N2, and H1N2 co-circulated into the pigs. The influenza virus usually causes significant morbidity and mortality after infection. 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 pigs are known today to co-circulate. Because they are susceptible to infection by both the human and avian influenza viruses, pigs play a significant role in the development of novel influenza viruses with pandemic potential. H1N1, H3N2, and H1N2 subtype influenza viruses are generally recognized to founder in pigs.

EAS-H1N1 viruses have taken control after extensive evolution since 2005. According to reports, EAS-H1N1 viruses in China prefer to bind to human-type receptors, and some of the tested viruses were transmitted to ferrets by respiratory droplets. The above implies that among the influenza viruses presently present in animals, the EAS-H1N1 SIVs pose a major threat of a global epidemic. Sun et al. revealed that novel triple-reassortant EASH1N1 SIVs to gene segment from A (H1N1) pdm09 (PB1, PB2, PA, and NP), EAS-H1N1 (HA, NA, and M), and Traditional Swine influenza virus (NS) have been separated from pigs in Tianjin. This finding demonstrated that various genetic lineages of swine H1N1 virus infections were co-circulating in the Tianjin.

According to the author, Tianjin / 1607/18 decided to share close antigenic and genetic strong affinity of H1N1 virus infections that have been widespread in Chinese pigs at the period.

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 interact to genetic lineage virus dissipation within mucosal secretions and decrease viral contagiousness by ability to inhibit influenza neuraminidase activity and preventing sialic acid residue cleavage. By focusing on the rapid identification of novel strains in humans as well as initiatives to lessen the likelihood of pass infection, current surveillance efforts aim to detect and prevent a new pandemic.

CONCLUSION

CONCLUSION

Three steps make up swine flu prevention: trying to prevent swine infection, trying to prevent human infection, and trying to prevent human infection of human. Environmental control, such as vaccination of large populations, as well as awareness campaigns are crucial to swine influenza outbreak control due to the few available treatments, the high risk of secondary infection, and the frequent need for intensive care for patients with H1N1 pneumonia.

The most economical precautions are social seclusion, proper ventilation, hand washing, and respiratory manners. The use of masks in healthcare settings has been proven effective in halting the spread of the virus, but similar extrapolations to the general public are not possible.

They must also be used properly before being disposed of properly. People who are healthy should avoid being around sick people, and children with minor symptoms must be cared for at home by an assigned adult. Triage, patient separation, antiviral medication use, and personal protective equipment (PPE) should all be prioritised in healthcare settings according to the risk from exposure.

In humans, clinical symptoms from EAS-H1N1 or a reassortant EAS-H1N1virus infection can result in mild. In some virus proteins, gene mutations encoding amino acid substitutions have been known to increase pathogenicity and the likelihood of transmission to humans and other mammals. Those same mutations have been discovered across whole genome sequencing. Swine are a host species capable of producing novel virus reasortants that could cause another human pandemic, as was the case with A(H1N1) pdm09 viruses, so it is crucial to maintain and increase influenza surveillance in swine.

The newly established tetraplex RTqPCR is a suitable tool for this task and it may provide additional information regarding potential Influenza B virus and Influenza C virus reverse zoonotic transmission events and the existence of Influenza D virus in swine populations. Additionally, samples from other host species, such as humans, should be screened using the influenza ABCD tetraplex RTqPCR. Therefore, this tool may be useful for investigations into influenza virus transmission at the swinehuman interface.

Investigation upon that efficacy of whole antigen- and retained T cell epitope-based vaccines against influenza and other pathogens is made easier with the help of the EpiCC instrument. As demonstrated here, the EpiCC instrument can be used to compare vaccines to circulating field strains, but it is also useful for figuring out whether currently available vaccines might be efficient (at the T cell epitope level) vs an emerging infection. The newly developing G4 influenza, African swine fever, and human influenza strains versus candidate vaccines are just a few viral populations that the EpiCC instrument is likely applicable.

To mitigate the pandemic's impact, there will be a variety of control measures required. Vaccination, antiviral prophylaxis, and antiviral treatment are examples of these. Furthermore, simple measures such as Protective measures are crucial, especially respiratory care and proper coughing technique. In the early stages of a virus's introduction into a community, separation of infected people in assigned hospitals may be helpful. Once the infection has spread and Since so many people are diagnosed, home separation of patients with minor infections would be more practical than hospital isolation.

BIBLIOGRAPHY

REFERENCES

1. Koen J.S. A practical method for field diagnosis of swine disease. Am J Vet Med. 1919; 14:468–470.
2. Webster RG, Bean WJ, et al.. Evolution and ecology of influenza A viruses. *Microbiol Rev*. 1992;56:152–179.
3. Webster RG, Laver WG, Air GM, et al.. Molecular mechanisms of variation in influenza viruses. *Nature*. 1982;296:115–121. doi: 10.1038/296115a0
4. Drake J. Rates of spontaneous mutation among RNA viruses. *Proc Natl Acad Sci USA*. 1993;90:4171–4175. doi: 10.1073/pnas.90.9.4171
5. Hensley SE, Das SR, Gibbs JS, et al.. Influenza A virus hemagglutinin antibody escape promotes neuraminidase antigenic variation and drug resistance. *PLoS One*. 2011;6:e15190. doi: 10.1371/journal.pone.0015190
6. Bedford T, Suchard MA, Lemey P, et al.. Integrating influenza antigenic dynamics with molecular evolution. *Elife*. 2014;3:e01914. doi: 10.7554/eLife.01914
7. Rambaut A, Pybus OG, Nelson MI, et al.. The genomic and epidemiological dynamics of human influenza A virus. *Nature*. 2008;453:615–619. doi: 10.1038/nature06945
8. Fouchier RA, Munster V, Wallensten A, Bestebroer TM, Herfst S, Smith D, Rimmelzwaan GF, Olsen B. and Osterhaus AD (2005) Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. *J Virol* 79(5), 2814–22.
9. Rohm C, Zhou N, Suss J, Mackenzie J. and Webster RG (1996) Characterization of a novel influenza hemagglutinin, H15: criteria for determination of influenza A subtypes. *Virology* 217(2), 508–16.

10. Webster RG, Bean WJ, Gorman OT, Chambers TM and Kawaoka Y. (1992) Evolution and ecology of influenza A viruses. *Microbiol Rev* 56(1), 152–79.
11. Tong S, Li Y, Rivailler P, Conrardy C, Castillo DA, Chen LM, Recuenco S, Ellison JA, Davis CT, York IA, Turmelle AS, Moran D, Rogers S, Shi M, Tao Y, Weil MR, Tang K, Rowe LA, Sammons S, Xu X, Frace M, Lindblade KA, Cox NJ, Anderson LJ, Rupprecht CE and Donis RO (2012) A distinct lineage of influenza A virus from bats. *Proc Natl Acad Sci U S A* 109(11), 4269–74.
12. Tong S, Zhu X, Li Y, Shi M, Zhang J, Bourgeois M, Yang H, Chen X, Recuenco S, Gomez J, Chen LM, Johnson A, Tao Y, Dreyfus C, Yu W, McBride R, Carney PJ, Gilbert AT, Chang J, Guo Z, Davis CT, Paulson JC, Stevens J, Rupprecht CE, Holmes EC, Wilson IA and Donis RO (2013) New world bats harbor diverse influenza A viruses. *PLoS Pathog* 9(10), e1003657.
13. Ma W, Kahn RE and Richt JA (2009) The pig as a mixing vessel for influenza viruses: Human and veterinary implications. *J Mol Genet Med* 3(1), 158–66.
14. Kida H, Ito T, Yasuda J, Shimizu Y, Itakura C, Shortridge KF, Kawaoka Y. and Webster RG (1994) Potential for transmission of avian influenza viruses to pigs. *J Gen Virol* 75 (Pt 9), 2183–8
15. Ma W, Kahn RE and Richt JA (2009) The pig as a mixing vessel for influenza viruses: Human and veterinary implications. *J Mol Genet Med* 3(1), 158–66.
16. Scholtissek C. (1990) Pigs as 'Mixing Vessels' for the Creation of New Pandemic Influenza A Viruses. *Med Principles Pract* 2, 65–71.
17. Kitikoon P, Sreta D, Tuanudom R, Amonsin A, Suradhat S, Oraveerakul K, Poovorawan Y, Thanawongnuwech R. Serological evidence of pig-to-human influenza virus

transmission on Thai swine farms. *Vet Microbiol.* 2011;**148**:413–418. doi: 10.1016/j.vetmic.2010.09.019.

18. Ghosh A, Nandy A, Nandy P. Computational analysis and determination of a highly conserved surface exposed segment in H5N1 avian flu and H1N1 swine flu neuraminidase. BMC Struct Biol 2010;10:6.
19. Lim BH, Mahmood TA. Influenza A H1N1 2009 (Swine Flu) and pregnancy. J Obstet Gynaecol India 2011;61:386e93.
20. Koen JS (1919) A practical method for field diagnosis of swine disease. *Amer J Vet Sci* 14, 468.
21. Myers KP, Olsen CW and Gray GC (2007) Cases of swine influenza in humans: a review of the literature. *Clin Infect Dis* 44(8), 1084–8.
22. Moss R.B. Prospects for control of emerging infectious diseases with plasmid DNA vaccines. J Immune based Therapies Vaccines. 2009; 7:3. doi: 10.1186/1476-8518-7-3.
23. IBN live May 16 (2009) First case of swine flu confirmed in India. http://ibnlive.in.com/news/first-case-o-swne-fluconfirmed-inIndia/92733-3.h
24. Alexander DJ and Brown IH (2000) Recent zoonoses caused by influenza A viruses. Rev Sci Tech 19(1), 197–225.
25. McQueen JL, Steele JH and Robinson RQ (1968) Influenza in animals. Adv Vet Sci 12, 285–336.
26. Kilbourne ED. Influenza pandemics of the 20th century. Emerging Infect Dis 2006; 12: 9-14.
27. Taubenberger JK. The origin and virulence of the 1918 “Spanish” influenza virus. Proc Am Philos Soc 2006; 150: 86– 112.

28. Chang LY, Shih SR, Shao PL, Huang DT, Huang LM. Novel swine-origin influenza virus A (H1N1): the first pandemic of the 21st century. J Formos Med Assoc 2009; 108: 526-532.

29. Olsen CW. The emergence of novel swine influenza viruses in North America. Virus Res 2002; 85:199–210.

30. Ministry of Health and Family Welfare. Government of India. Influenza A [H1N1] - Status as on 17th August, 2009. http:// mohfw.nic.in/Status%20as%20on%2017th%20August% 202009.doc

31. Newman AP, Reisdorf E, Beinemann J, Uyeki TM, Balish A, Shu B, Lindstrom S, Achenbach J, Smith C, Davis JP. Swine influenza A (H1N1) triple reassortant virus infection, Wisconsin. Emerging Infectious Diseases 2008; 14: 1470-1472

32. Morens DM, Taubenberger JK, Fauci AS. The persistent legacy of the 1918 influenza virus. NEJM 2009; 361: 225 -229.

33. Myers PK, Olsen CW, Gray CG. Cases of swine influenza in humans: a review of the literature. Clin Infect Dis 2007; 44: 1084–1088

34. Interim guidance on antiviral recommendations for patients with novel Influenza A (H1N1) virus infection and their close contacts. Centre for disease control and prevention:H1N1 guidance 6 May 2009. http://www.cdc.gov/h1n1flu/ recommendations.htm.

35. Ministry of Health and Family Welfare, Government of India. Swine Flu- Clinical Management Protocol and Infection Control Guidelines. http://mohfw.nic.in/Clinical%20 Management-Swine%20Flu.doc

36. Sreta D, Kedkovid R, Tuamsang S, Kitikoon P, Thanawongnuwech R. Pathogenesis of swine influenza virus (Thai isolates) in weanling pigs: an experimental trial. Virology J 2009; 6: 34.

37. Novel Swine-Origin Influenza A (H1N1) Virus Investigation Team. Emergence of a novel swine-origin influenza A (H1N1) virus in humans. NEJM 2009; 360: 2605-2615.
38. Schultz-Cherry S, Olsen CW and Easterday BC (2012) History of Swine influenza. *Curr Top Microbiol Immunol* 370, 21–8.
39. Brown IH, Harris PA, McCauley JW and Alexander DJ (1998) Multiple genetic reassortment of avian and human influenza A viruses in European pigs, resulting in the emergence of an H1N2 virus of novel genotype. *J Gen Virol* 79 (Pt 12), 2947–55.
40. Azziz Baumgartner E, Dao CN, Nasreen S, Bhuiyan MU, Mah-E-Muneer S, Al Mamun A, Sharker MA, Uz Zaman R, Cheng PY, Klimov AI, Widdowson MA, Uyeki TM, Luby SP, Mounts A, Bresee J. Seasonality, timing, and climate drivers of influenza activity worldwide. *J Infect Dis.* 2012;206:838–846. doi: 10.1093/infdis/jis467.
41. Soebiyanto RP, Adimi F, Kiang RK. Modeling and predicting seasonal influenza transmission in warm regions using climatological parameters. *PLoS One.* 2010;5:e9450. doi: 10.1371/journal.pone.0009450.
42. Maes D, Deluyker H, Verdonck M, Castryck F, Miry C, Vrijens B, de Kruif A. Risk indicators for the seroprevalence of *Mycoplasma hyopneumoniae*, porcine influenza viruses and Aujeszky's disease virus in slaughter pigs from fattening pig herds. *Zentralbl Veterinarmed B.* 1999;46:341–352.
43. Beato MS, Tassoni L, Milani A, Salviato A, Di Martino G, Mion M, Bonfanti L, Monne I, Watson SJ and Fusaro A. (2016) Circulation of multiple genotypes of H1N2 viruses in a swine farm in Italy over a two-month period. *Vet Microbiol* 195, 25–29.
44. Simon G, Larsen LE, Durrwald R, Foni E, Harder T, Van Reeth K, Markowska-Daniel I, Reid SM, Dan A, Maldonado J, Huovilainen A, Billinis C, Davidson I, Aguero M, Vila T, Herve S, Breum SO, Chiapponi C, Urbaniak K, Kyriakis CS, Brown IH and Loeffen W.

(2014) European surveillance network for influenza in pigs: surveillance programs, diagnostic tools and Swine influenza virus subtypes identified in 14 European countries from 2010 to 2013. *PLoS One* 9(12), e115815.

45. Watson SJ, Langat P, Reid SM, Lam TT, Cotten M, Kelly M, Van Reeth K, Qiu Y, Simon G, Bonin E, Foni E, Chiapponi C, Larsen L, Hjulsager C, Markowska-Daniel I, Urbaniak K, Durrwald R, Schlegel M, Huovilainen A, Davidson I, Dan A, Loeffen W, Edwards S, Bublot M, Vila T, Maldonado J, Valls L, Brown IH, Pybus OG and Kellam P. (2015) Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. *J Virol* 89(19), 9920–31.
46. Zhu H, Webby R, Lam TT, Smith DK, Peiris JS and Guan Y. (2011a) History of Swine influenza viruses in Asia. *Curr Top Microbiol Immunol* 370, 57–68.
47. Arikawa J, Yamane N, Odagiri T. and Ishida N. (1979) Serological evidence of H1 influenza virus infection among Japanese hogs. *Acta Virol* 23(6), 508–11.
48. Nerome K, Ishida M, Oya A. and Oda K. (1982) The possible origin H1N1 (Hsw1N1) virus in the swine population of Japan and antigenic analysis of the isolates. *J Gen Virol* 62 (Pt 1), 171–5.
49. Shortridge KF and Webster RG (1979) Geographical distribution of swine (Hsw1N1) and Hong Kong (H3N2) influenza virus variants in pigs in Southeast Asia. *Intervirology* 11(1), 9–15.
50. Ma W. Swine influenza virus: Current status and challenge. *Virus Res*. 2020;288:198118. doi: 10.1016/j.virusres.2020.198118.

51. Sebastian MR, Lodha R, Kabra SK. Swine origin influenza (swine flu). Indian J Pediatr. 2009 Aug;76(8):833-41. doi: 10.1007/s12098-009-0170-6. PMID: 19802552.

52. Anderson TK, Chang J, Arendsee ZW, Venkatesh D, Souza CK, Kimble JB, Lewis NS, Davis CT and Vincent AL (2020) Swine Influenza A Viruses and the Tangled Relationship with Humans. *Cold Spring Harb Perspect Med*.

53. Lewis NS, Russell CA, Langat P, Anderson TK, Berger K, Bielejec F, Burke DF, Dudas G, Fonville JM, Fouchier RA, Kellam P, Koel BF, Lemey P, Nguyen T, Nuansrichy B, Peiris JM, Saito T, Simon G, Skepner E, Takemae N, Webby RJ, Van Reeth K, Brookes SM, Larsen L, Watson SJ, Brown IH and Vincent AL (2016) The global antigenic diversity of swine influenza A viruses. *Elife* 5, e12217.

54. Van Reeth K. and Ma W. (2013) Swine influenza virus vaccines: to change or not to change-that's the question. *Curr Top Microbiol Immunol* 370, 173–200.

55. Genzow M, Goodell C, Kaiser TJ, Johnson W. and Eichmeyer M. (2017) Live attenuated influenza virus vaccine reduces virus shedding of newborn piglets in the presence of maternal antibody. *Influenza Other Respir Viruses* 12(3), 353–359.

56. Richt JA, Lekcharoensuk P, Lager KM, Vincent AL, Loiacono CM, Janke BH, Wu WH, Yoon KJ, Webby RJ, Solorzano A. and Garcia-Sastre A. (2006) Vaccination of pigs against swine influenza viruses by using an NS1-truncated modified live-virus vaccine. *J Virol* 80(22), 11009–18.

57. Vincent AL, Ma W, Lager KM, Janke BH, Webby RJ, Garcia-Sastre A. and Richt JA (2007) Efficacy of intranasal administration of a truncated NS1 modified live influenza virus vaccine in swine. *Vaccine* 25(47), 7999–8009.

58. Sharma A, Zeller MA, Li G, Harmon KM, Zhang J, Hoang H, Anderson TK, Vincent AL and Gauger PC (2020) Detection of live attenuated influenza vaccine virus and evidence of reassortment in the U.S. swine population. *J Vet Diagn Invest*, 1040638720907918.

59. Reynolds JJ, Torremorell M, Craft ME. Mathematical modeling of influenza A virus dynamics within swine farms and the effects of vaccination. PLoS One 2014;9:e106177.

60. Allerson M, Deen J, Detmer SE, et al. The impact of maternally derived immunity on influenza A virus transmission in neonatal pig populations. Vaccine 2013;31:500e5.

61. Uscher-Pines L, Maurer J, Harris KM. Racial and ethnic disparities in uptake and location of vaccination for 2009 H1N1 and seasonal influenza. Am J Public Health 2011;101:1252e5.

62. Cho KJ, Hong KW, Kim SH, et al. Insight into highly conserved H1 subtype-specific epitopes in influenza virus hemagglutinin. PLoS One 2014;9:e89803.

63. Thorlund K, Awad T, Boivin G, Thabane L. Systematic review of influenza resistance to the neuraminidase inhibitors. BMC Infect Dis 2011;11:134.

64. . Orozovic G, Orozovic K, Lennerstrand J, Olsen B. Detection of resistance mutations to antivirals oseltamivir and zanamivir in avian influenza A viruses isolated from wild birds. PLoS One 2011;6:e16028.

65. Garten, R. J., Davis, C. T., Russell, C. A., Shu, B., Lindstrom, S., Balish, A., Sessions, W. M. et al., Antigenic and genetic characteristics of swine-origin 2009 A (H1N1) influenza viruses circulating in humans. Science 2009. 325: 197–201.

66. Smith, G. J., Vijaykrishna, D., Bahl, J., Lycett, S. J., Worobey, M., Pybus, O. G., Ma, S. K., Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. Nature 2009. 459: 1122–1125.

67. World-Health-Organization, Human infection with pandemic A (H1N1) 2009 influenza virus: clinical observations in hospitalized patients, Americas, July 2009 - update. Wkly. Epidemiol. Rec. 2009. 84: 305–308.

68. Centers-for-Disease-Control, Intensive-care patients with severe novel influenza A (H1N1) virus infection – Michigan, June 2009. MMWR Morb. Mortal. Wkly. Rep. 2009. 58: 749–752

69. Influenza (Seasonal) [World Health Organization, October 2014].

70. Taubenberger JK, Morens DM. 1918 Influenza: the mother of all pandemics. *Emerg Infect Dis* 2006; 12: 15–22.

71. Knipe DM, Howley PM. *Fields Virology*. 6th ed. Philadelphia, PA: Wolters Kluwer/Lippincott Williams & Wilkins Health; 2013.

72. Liu Q, Liu DY, Yang ZQ. Characteristics of human infection with avian influenza viruses and development of new antiviral agents. *Acta Pharmacol Sin* 2013; 34: 1257–1269.

73. Zhang W, Wan J, Qian K, Liu X, Xiao Z, Sun J et al. Clinical characteristics of human infection with a novel avian-origin influenza A(H10N8) virus. *Chin Med J* 2014; 127: 3238–3242.

74. Peiris JS, Hui KP, Yen HL. Host response to influenza virus: protection versus immunopathology. *Curr Opin Immunol* 2010; 22: 475–481.

75. Tisoncik JR, Korth MJ, Simmons CP, Farrar J, Martin TR, Katze MG. Into the eye of the cytokine storm. *Microbiol Mol Biol Rev* 2012; 76: 16–32.

76. Teijaro JR, Walsh KB, Cahalan S, Fremgen DM, Roberts E, Scott F et al. Endothelial cells are central orchestrators of cytokine amplification during influenza virus infection. *Cell* 2011; 146: 980–991.

77. La Gruta NL, Kedzierska K, Stambas J, Doherty PC. A question of self-preservation: immunopathology in influenza virus infection. *Immunol Cell Biol* 2007; 85: 85–92.

78. Shinya K, Gao Y, Cilloniz C, Suzuki Y, Fujie M, Deng G et al. Integrated clinical, pathologic, virologic, and transcriptomic analysis of H5N1 influenza virus-induced viral pneumonia in the rhesus macaque. *J Virol* 2012; 86: 6055–6066.

79. Hussell T, Goulding J. Structured regulation of inflammation during respiratory viral infection. *Lancet Infect Dis* 2010; 10: 360–366.

80. Peiris JS, Cheung CY, Leung CY, Nicholls JM. Innate immune responses to influenza A H5N1: friend or foe? *Trends Immunol* 2009; 30: 574–584.

81. Liu, Ye, et al. "Antiviral role of Toll-like receptors and cytokines against the new 2009 H1N1 virus infection." *Molecular biology reports* 39.2 (2012): 1163-1172.

82. Yang, Ji-Rong et al. “Human infection with a reassortant swine-origin influenza A(H1N2)v virus in Taiwan, 2021.” *Virology journal* vol. 19,1 63. 7 Apr. 2022, doi:10.1186/s12985-022-01794-2

83. Lopez-Goerne, Tessy, et al. "Inhibition of Influenza A (H1N1) Virus Infection by Pt/TiO2-SiO2 Bionanocatalysts."

84. Tan S, Gutiérrez AH, Gauger PC, Opriessnig T, Bahl J, Moise L, De Groot AS. Quantifying the Persistence of Vaccine-Related T Cell Epitopes in Circulating Swine Influenza A

Strains from 2013-2017. Vaccines (Basel). 2021 May 6;9(5):468. doi: 10.3390/vaccines9050468. PMID: 34066605; PMCID: PMC8148565.

85. Noh, Ji Yeong et al. “Complete Coding Sequence of a Swine Influenza A Variant (H3N2) Virus Isolated in the Republic of Korea in 2017.” *Microbiology resource announcements* vol. 9,7 e01355-19. 13 Feb. 2020, doi:10.1128/MRA.01355-19
86. Cook, Peter W et al. “Detection and Characterization of Swine Origin Influenza A(H1N1) Pandemic 2009 Viruses in Humans following Zoonotic Transmission.” *Journal of virology* vol. 95,2 e01066-20. 22 Dec. 2020, doi:10.1128/JVI.01066-20.
87. Ma W. Swine influenza virus: Current status and challenge. Virus Res. 2020 Oct 15;288:198118. doi: 10.1016/j.virusres.2020.198118. Epub 2020 Aug 13. PMID: 32798539; PMCID: PMC7587018.
88. Vandoorn E, Leroux-Roels I, Leroux-Roels G, Parys A, Vincent A, Van Reeth K. Detection of H1 Swine Influenza A Virus Antibodies in Human Serum Samples by Age Group[1]. Emerg Infect Dis. 2020 Sep;26(9):2118-2128. doi: 10.3201/eid2609.191796. PMID: 32818398; PMCID: PMC7454048.
89. Li X, Guo L, Liu C, Cheng Y, Kong M, Yang L, Zhuang Z, Liu J, Zou M, Dong X, Su X, Gu Q. Human infection with a novel reassortant Eurasian-avian lineage swine H1N1 virus in northern China. Emerg Microbes Infect. 2019;8(1):1535-1545. doi: 10.1080/22221751.2019.1679611. PMID: 31661383; PMCID: PMC6830285.
90. Henritzi, Dinah et al. “A newly developed tetraplex real-time RT-PCR for simultaneous screening of influenza virus types A, B, C and D.” *Influenza and other respiratory viruses* vol. 13,1 (2019): 71-82. doi:10.1111/irv.12613

91. Baudon, Eugénie et al. “Swine influenza viruses in Northern Vietnam in 2013-2014.” *Emerging microbes & infections* vol. 7,1 123. 2 Jul. 2018, doi:10.1038/s41426-018-0109-y

92. Diaz, Andres et al. “Complete Genome Sequencing of Influenza A Viruses within Swine Farrow-to-Wean Farms Reveals the Emergence, Persistence, and Subsidence of Diverse Viral Genotypes.” *Journal of virology* vol. 91,18 e00745-17. 24 Aug. 2017, doi:10.1128/JVI.00745-17

93. Mudhigeti N, Racherla RG, Mahalakshmi PA, Pamireddy ML, Nallapireddy U, Kante M, Kalawat U. A study of influenza 2017-2018 outbreak in Andhra Pradesh, India. Indian J Med Microbiol. 2018 Oct-Dec;36(4):526-531. doi: 10.4103/ijmm.IJMM_18_272. PMID: 30880701.

94. Malhotra B, Singh R, Sharma P, Meena D, Gupta J, Atreya A, Meena BR. Epidemiological & clinical profile of influenza A (H1N1) 2009 virus infections during 2015 epidemic in Rajasthan. Indian J Med Res. 2016 Dec;144(6):918-923. doi: 10.4103/ijmr.IJMR_1183_15. PMID: 28474629; PMCID: PMC5433285.

95. Rewar S, Mirdha D, Rewar P. Treatment and Prevention of Pandemic H1N1 Influenza. Ann Glob Health. 2015 Sep-Oct;81(5):645-53. doi: 10.1016/j.aogh.2015.08.014. PMID: 27036721.

96. Bowman, Andrew S et al. “Swine-to-human transmission of influenza A(H3N2) virus at agricultural fairs, Ohio, USA, 2012.” *Emerging infectious diseases* vol. 20,9 (2014): 1472-80. doi:10.3201/eid2009.131082

97. Kong W, Ye J, Guan S, Liu J, Pu J. Epidemic status of Swine influenza virus in china. Indian J Microbiol. 2014 Mar;54(1):3-11. doi: 10.1007/s12088-013-0419-7. Epub 2013 Jul 16. PMID: 24426160; PMCID: PMC3889855.

98. Charoenvisal N, Keawcharoen J, Sreta D, Tantawet S, Jittimanee S, Arunorat J, Amonsin A, Thanawongnuwech R. Experimental infection with a Thai reassortant swine influenza virus of pandemic H1N1 origin induced disease. Virol J. 2013 Mar 16;10:88. doi: 10.1186/1743-422X-10-88. PMID: 23497073; PMCID: PMC3606200.

99. Chadha MS, Hirve S, Dawood FS, Lele P, Deoshatwar A, Sambhudas S, Juvekar S, LaFond KE, Mott JA, Lal RB, Mishra AC. Burden of seasonal and pandemic influenza-associated hospitalization during and after 2009 A(H1N1)pdm09 pandemic in a rural community in India. PLoS One. 2013 May 15;8(5):e55918. doi: 10.1371/journal.pone.0055918. PMID: 23690913; PMCID: PMC3654970.

100. Böhmer, Merle M et al. "Barriers to pandemic influenza vaccination and uptake of seasonal influenza vaccine in the post-pandemic season in Germany." *BMC public health* vol. 12 938. 31 Oct. 2012, doi:10.1186/1471-2458-12-938.

101. Nelson, Martha I et al. "Global transmission of influenza viruses from humans to swine." *The Journal of general virology* vol. 93,Pt 10 (2012): 2195-2203. doi:10.1099/vir.0.044974-0

102. Belser, J. A., Wadford, D. A., Pappas, C., Gustin, K. M., Maines, T. R., Pearce, M. B., Zeng, H., Swayne, D. E., Pantin-Jackwood, M., Katz, J. M., & Tumpey, T. M. (2010). Pathogenesis of pandemic influenza A (H1N1) and triple-reassortant swine influenza A (H1) viruses in mice. *Journal of virology*, *84*(9), 4194–4203.

103. Song MS, Lee JH, Pascua PN, Baek YH, Kwon HI, Park KJ, Choi HW, Shin YK, Song JY, Kim CJ, Choi YK. Evidence of human-to-swine transmission of the pandemic (H1N1) 2009 influenza virus in South Korea. J Clin Microbiol. 2010 Sep;48(9):3204-11. doi: 10.1128/JCM.00053-10. Epub 2010 Jul 7. PMID: 20610681; PMCID: PMC2937722.

104. Mishra AC, Chadha MS, Choudhary ML, Potdar VA. Pandemic influenza (H1N1) 2009 is associated with severe disease in India. PLoS One. 2010 May 7;5(5):e10540. doi: 10.1371/journal.pone.0010540. PMID: 20479875; PMCID: PMC2866330.

105. Garten RJ, Davis CT, Russell CA, Shu B, Lindstrom S, Balish A, Sessions WM, Xu X, Skepner E, Deyde V, Okomo-Adhiambo M, Gubareva L, Barnes J, Smith CB, Emery SL, Hillman MJ, Rivailler P, Smagala J, de Graaf M, Burke DF, Fouchier RA, Pappas C, Alpuche-Aranda CM, López-Gatell H, Olivera H, López I, Myers CA, Faix D, Blair PJ, Yu C, Keene KM, Dotson PD Jr, Boxrud D, Sambol AR, Abid SH, St George K, Bannerman T, Moore AL, Stringer DJ, Blevins P, Demmler-Harrison GJ, Ginsberg M, Kriner P, Waterman S, Smole S, Guevara HF, Belongia EA, Clark PA, Beatrice ST, Donis R, Katz J, Finelli L, Bridges CB, Shaw M, Jernigan DB, Uyeki TM, Smith DJ, Klimov AI, Cox NJ. Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. Science. 2009 Jul 10;325(5937):197-201. doi: 10.1126/science.1176225. Epub 2009 May 22. PMID: 19465683; PMCID: PMC3250984.

106. Venkataramana M, Vindal V, Kondapi AK. Emergence of swine flu in Andhra Pradesh: Facts and future. Indian J Microbiol. 2009 Dec;49(4):320-3. doi: 10.1007/s12088-009-0057-2. Epub 2010 Jan 7. PMID: 23100792; PMCID: PMC3450187

107. Peiris JS, Tu WW, Yen HL. A novel H1N1 virus causes the first pandemic of the 21st century. Eur J Immunol. 2009 Nov;39(11):2946-54. doi: 10.1002/eji.200939911. PMID: 19790188.

108. Sebastian MR, Lodha R, Kabra SK. Swine origin influenza (swine flu). Indian J Pediatr. 2009 Aug;76(8):833-41. doi: 10.1007/s12098-009-0170-6. PMID: 19802552.

109. https://www.cdc.gov/h1n1flu/images.htm

turnitin

Similarity Report ID: oid:27992:20020201

PAPER NAME

pushpendra thesis.docx

WORD COUNT

12476 Words

CHARACTER COUNT

68423 Characters

PAGE COUNT

71 Pages

FILE SIZE

436.1KB

SUBMISSION DATE

Jul 22, 2022 10:47 AM GMT+5:30

REPORT DATE

Jul 22, 2022 10:51 AM GMT+5:30

18% Overall Similarity

The combined total of all matches, including overlapping sources, for each database.

- 16% Internet database
- 14% Publications database
- Crossref database
- Crossref Posted Content database
- 8% Submitted Works database

Excluded from Similarity Report

- Bibliographic material
- Quoted material
- Cited material
- Small Matches (Less then 8 words)

Summary

turnitin **Similarity Report ID:** oid:27992:20020201

18% Overall Similarity

Top sources found in the following databases:

- 16% Internet database
- Crossref database
- 8% Submitted Works database
- 14% Publications database
- Crossref Posted Content database

TOP SOURCES

The sources with the highest number of matches within the submission. Overlapping sources will not be displayed.

1	science.gov Internet	3%
2	ncbi.nlm.nih.gov Internet	2%
3	Visayas State University on 2022-07-11 Submitted works	<1%
4	raw.githubusercontent.com Internet	<1%
5	tandfonline.com Internet	<1%
6	core.ac.uk Internet	<1%
7	journals.plos.org Internet	<1%
8	brain.unboundmedicine.com Internet	<1%

Sources overview

turnitin **Similarity Report ID:** oid:27992:20020201

9	mafiadoc.com Internet	<1%
10	R. J. Garten, C. T. Davis, C. A. Russell, B. Shu et al. "Antigenic and Gene... Crossref	<1%
11	cgspace.cgiar.org Internet	<1%
12	link.springer.com Internet	<1%
13	Tessy López-Goerne, Gabriela de la Rosa-Gutiérrez, Francisco J. Padill... Crossref	<1%
14	198.246.124.29 Internet	<1%
15	hkupasteur.hku.hk Internet	<1%
16	cyberleninka.org Internet	<1%
17	Musturi Venkataramana, Vaibhav Vindal, Anand K. Kondapi. "Emergenc... Crossref	<1%
18	pubfacts.com Internet	<1%
19	Peter W. Cook, Thomas Stark, Joyce Jones, Rebecca Kondor et al. "Det... Crossref	<1%
20	research.ed.ac.uk Internet	<1%

Sources overview

21	Ma Wenjun. "Swine Influenza Virus: Current Status and Challenge", Viru... Crossref	<1%
22	pubmed.ncbi.nlm.nih.gov Internet	<1%
23	University of Wales, Lampeter on 2022-03-11 Submitted works	<1%
24	Nagaraja Mudhigeti, Rishi Gowtham Racherla, Padmalatha Anjaneyulu ... Crossref	<1%
25	wwwnc.cdc.gov Internet	<1%
26	Praveen Belagal, Hemanth Naick Banavath, Buddolla Viswanath. "Swin... Crossref	<1%
27	Christman, M.C.. "Pandemic (H1N1) 2009 virus revisited: An evolution... Crossref	<1%
28	University of Sheffield on 2009-10-26 Submitted works	<1%
29	documents.worldbank.org Internet	<1%
30	Li, Q., J. Qi, Y. Wu, H. Kiyota, K. Tanaka, Y. Suhara, H. Ohrui, Y. Suzuki, ... Crossref	<1%
31	cnic.org.cn Internet	<1%
32	Janke, B. H.. "Influenza A Virus Infections in Swine: Pathogenesis and ... Crossref	<1%

Sources overview

33	W. Ma. "Viral reassortment and transmission after co-infection of pigs ... Crossref	<1%
34	jornaldepneumologia.com.br Internet	<1%
35	nature.com Internet	<1%
36	edoc.unibas.ch Internet	<1%
37	Liverpool John Moores University on 2009-11-30 Submitted works	<1%
38	icmr.nic.in Internet	<1%
39	cdc.gov Internet	<1%
40	hampstead.qc.ca Internet	<1%
41	Frank Y. K. Wong, Celeste Donato, Yi-Mo Deng, Don Teng et al. "Diverg... Crossref	<1%
42	Imperial College of Science, Technology and Medicine on 2012-11-22 Submitted works	<1%
43	K. Pabbaraju, S. Wong, A. A. Wong, G. D. Appleyard et al. "Design and V... Crossref	<1%
44	Liverpool John Moores University on 2011-03-07 Submitted works	<1%

Sources overview

45	The University of Manchester on 2014-04-07 Submitted works	<1%
46	docplayer.net Internet	<1%
47	elib.tiho-hannover.de Internet	<1%
48	gavinpublishers.com Internet	<1%
49	hdl.handle.net Internet	<1%
50	doria.fi Internet	<1%
51	pagepress.org Internet	<1%
52	2642 on 2015-04-06 Submitted works	<1%
53	J. Brian Kimble, Meghan Wymore Brand, Bryan S. Kaplan, Phillip Gauge... Crossref	<1%
54	Molecular Virology, 2013. Crossref	<1%
55	Napier University on 2021-04-29 Submitted works	<1%
56	Patrick Saunders-Hastings, Bryson Quinn Hayes, Robert Smith?, Daniel... Crossref	<1%

Sources overview

turnitin **Similarity Report ID:** oid:27992:20020201

57	University of KwaZulu-Natal on 2019-03-11 Submitted works	<1%
58	University of Strathclyde on 2012-12-13 Submitted works	<1%
59	onlinelibrary.wiley.com Internet	<1%
60	outbreaknewstoday.com Internet	<1%
61	pt.scribd.com Internet	<1%
62	studylib.net Internet	<1%
63	pubmedcentral.nih.gov Internet	<1%
64	uptodate.com Internet	<1%

Sources overview