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ISSN: 2329-891X
Journal of Tropical Diseases & Public Health

Commentary

Evolution of H1N1 Swine Flu Virus in Human

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DESCRIPTION

Virus-borne infectious diseases are the central concern of today's world, as new types of viruses spread infections, and pre-existing viruses are becoming more virulent. One such virus is the influenza virus, which has four types A, B, C, and D. Importantly, types A, B are responsible for significant outbreaks compared to types C and D, which are more genetically stable, less virulence, and affect animals only. Influenza A is the main causative agent of infections in humans. It is classified into different subtypes based on its surface proteins. Hemagglutinin and neuraminidase are the main surface protein and are classified into 18 and 11 types respectively. Swine flu is a fatal contagious respiratory disease caused by the A (H1N1) pdm09 influenza virus of the Orthomyxoviridae family. According to the World Health Organization, almost 2 billion people report flu-like symptoms each year. It directly affects the economy of a country and its people. In April 2009, a novel influenza virus (H1N1) emerged in Mexico, which aired worldwide within the week and WHO declared it a global pandemic of phase 6 level on 11th June 2009, which ended on 10th August 2010 with several deaths worldwide. It was first detected in 1930 in pigs as classical swine H1N1 in the United States after the 1918 pandemic of H1N1. A quadruple assortment occurred in a Eurasian virus which was triply re-assorted in which one of the viruses was descendent of 1918 strain. H1N1 is a single-stranded RNA virus having eight segments with a negative sense, which codes for surface glycoproteins; Hemagglutinin (HA), Neuroaminidase (NA), matrix protein, reverse transcriptase, and nucleocapsid proteins. This spherical virus has an 80-120 nm long filament with symmetric helical nucleocapsid. HA and NA proteins help a virus in binding with sialic acid of respiratory epithelial cells and releasing new viruses from infected cells, respectively. HA antigen of different subtypes of viruses binds with specific receptors on the host cell. The human flu virus HA protein directly detects α, 2-6 glycosidic bonds between sialic acid and galactose in the tracheal cells but the bird flu virus directly detects α, 2-3 glycosidic bonds. Pigs have both types of receptors on respiratory cells for the human H1N1 virus and also for the avian flu virus. Thus, act as a mixing vessel and provides a site for genetic re-assortment, which results in antigenic shift. Symptoms show similarity with that of the common influenza virus, and it includes fever above 104°F for more than three days, nausea, headache, sore throat, vomiting, chest pain, dyspnea, hypotension, coughing, and severe dehydration.

Influenza was reported first time with certainty in 1932, but before that, it was mentioned in Greek history (412 BC) and later reported in each century. In the 20th century only, pandemics occurred four times, the first time reported in Spain known as Spanish flu (H1N1) and causes deaths of approximately 50-100 million humans globally. Initially, it was assumed as a disease of pigs, but in 1931 virus was extracted in a laboratory 1st time from an infected pig. At the same time, humans were also infected with the same virus; it was speculated that the disease transmits from pigs to humans. After 40 years, in 1957, another subtype (H2N2) caused a pandemic and was responsible for the death of 1-2 million people. It was first detected in China in February 1957, and within five months, it was found in twenty countries. It was a mild influenza pandemic with a fatality rate of 0.67%. After a decade, a new subtype of influenza A (H3N2) caused a pandemic in Hong Kong in 1968, in which 500,000-2,000,000 deaths were reported worldwide. After that, in April 2009, a novel influenza virus emerged at a pandemic level in Mexico of phase 6 declared by the World Health Organization (WHO). Every year influenza A (H1N1) takes thousands of lives worldwide, and in 2019, according to the National Center for Disease Control of India, 17366 suspected cases of swine flu were reported, with 530 confirmed deaths till 3rd March 2019.

CONCLUSION

Vaccines are available for influenza virus presenting an effective tool but have to be redesigned every year to cover all changes due to antigenic drift in RNA. Several changes have been incorporated recently to increase the effectiveness of the immune system of the body and to speed up antibody production in case of a seasonal and pandemic emergence.

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Received: 01-Nov-2022, Manuscript No. JTD-22-19392; **Editor assigned:** 04-Nov-2022, PreQC No. JTD-22-19392 (PQ); **Reviewed:** 18-Nov-2022, QC No. JTD-22-19392 (R); **Revised:** 25-Nov-2022, Manuscript No. JTD-22-19392; **Published:** 02-Dec-2022, DOI:10.35241/2329-891X.22.10.361.

Citation: Mendez R (2022) Evolution of H1N1 Swine Flu Virus in Human. J Trop Dis. 10:361.

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Importantly, universal influenza virus vaccine development is currently in its preclinical and clinical phases. Early diagnosis of the infection is crucial as the condition becomes severe. There are many diagnosis methods like virus culture, RT-LAMP, Enzyme-Linked Immuno Sorbent Assay (ELISA), Complement Fixation test (CF), Double Immuno Diffusion (DID), Hemagglutinin Inhibition (HI), and Real Time-Polymerase Chain Reaction (RT-PCR). RT-PCR is a method of choice for confirmation of disease, but it is tedious and cost a lot. This assay shows 97% accuracy, and the Limit of Detection (L.O.D) is 0.1-102 PFU/mL. This method is specific, accurate, and highly sensitive for all strains of influenza A but it also takes time and requires a well-equipped lab. Although isolation of virus from the clinical sample is one of the gold standard methods, virus culture is infectious, time taking and requires separate laboratory setups for culturing of the virus.