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Letter to the Editor

Influenza Virus and Its Preparedness in Nepalese Scenario

Bimalesh Kumar Jha[1]*, Raj Kumar Mahato[2], Bishnu Prasad Upadhya[2] and Krishna Das Manandhar[1]

[1]*Central Department of Biotechnology, Tribhuvan University, Nepal*
[2]*Department of Health Services, National Public Health Laboratory, Nepal*

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***Corresponding author**

Bimalesh kumar jha, Central Department of Biotechnology, Tribhuvan University, Teku, Kathmandu, Nepal,
Tel: 00977-9849672299;
Email: bimujnp@yahoo.com

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The threat of a human influenza (Swine Flu, Seasonal Flu and Bird Flu) pandemic has greatly increased over the past several years with the emergence of highly virulent avian influenza viruses, notably H5N1 viruses, which have infected humans in several Asian and European countries. Previous influenza pandemics have arrived with little or no warning, but the current widespread circulation of H5N1 viruses among avian populations and their potential for increased transmission to humans and other mammalian species may afford us an unprecedented opportunity to prepare for the next pandemic threat. The Ministry Of Health, Department of Health and Human Services is coordinating a national strategy to respond to an influenza pandemic that involves multiple agencies, including the Centers for Disease Control and Prevention, the Food and Drug Administration, and Word Health Organization National Influenza Centre (NIC). Within NIC, conducts basic and clinical research to develop new vaccine technologies and antiviral drugs against influenza viruses. We describe recent research progress in preparing for pandemic influenza.

Case Report

The influenza viruses belong to the family Orthomyxoviridae and are classified into three types (A, B and C) according to antigenic differences among their Nucleoprotein (NP) and matrix (M) proteins [1]. Influenza A viruses circulate naturally in a global avian reservoir; however, some viral strains have crossed the species barrier establishing in pigs, horses and most notably, infecting humans. Influenza B viruses almost exclusively infect humans although they present a less pathogenic profile than Influenza A viruses. Influenza C viruses are rare and have been known to infect humans, dogs and swine. Influenza A viruses are enveloped negative- stranded RNA viruses comprised of eight gene segments that encode 10 proteins: Hemagglutinin (HA), Neuraminidase (NA), Matrix Proteins (M1 and M2), Nonstructural Proteins (NS1 and NS2), the Nucleocapsid (NP), and the three Polymerases (PB1, PB2 and PA) [2]. Until recently, a total of 16 HA subtype (H1-H16) and 9 NA subtypes (N1-N9) had been identified in avian hosts. Of the 144 total possible combinations, only three combinations of the HA/NA subtypes have been established as human influenza (H1N1, H2N2, and H3N2) [3]. More recently, H7 and H9 subtypes have been known to cause infection in humans [4]. RNA polymerases lack the proof reading ability of DNA polymerases resulting in high mutation rates, specifically point mutations of the HA or NA antigens. These mutations from its predecessors, known as "Antigenic Drift", can lead to new, distinct antigenic variants and is well characterized in human and poultry influenza viruses [1]. Further research on the magnitude of antigenic difference among variants and specific amino acids directly related to antigenic difference may provide insight on how best to develop and utilize vaccinations as a control strategy. Additionally, the eight individual gene segments of the influenza virus allows for genetic re-assortment when two influenza viruses infect the same cell. The host animal consequently serves as a "Mixing Vessel" and the result is an "Antigenic Shift" with generations of novel influenza viruses acquiring characteristics of both parent viruses [2]. These two mechanisms permit a genetic diversity among influenza viruses that describe the recurring seasonal influenza epidemics of varying pattern and severity as well as the continuing risk of the emergence of a novel pandemic strain. Avian influenza viruses are divided into Highly Pathogenic Avian Influenza (HP) or Low Pathogenic Avian Influenza (LP). The distinction between LP and HP avian influenza is their local versus system replication, respectively [3-5].

Although several studies conducted in Europe have described the impact of influenza and common infective complications such as otitis media in children; few studies have been conducted on more severe influenza-associated complications including Febrile Seizures (FS) and acute encephalopathy. Febrile Seizures account for approximately 20% of all hospitalized infants and young children with influenza [5].

National Public health Laboratory (NPHL) is the government national reference laboratory under the Department of Health Services (DoHS) and Ministry of Health and Population (MoHP). It is directly linked with different levels of 277 government laboratories in the country. It was established in 1968 as Central Health Laboratory. The name was changed to National Public Health Laboratory in 1991 with the mandate for organizational and administration responsibilities for the health laboratory services (public health and clinical diagnostic) in both public and private sectors throughout the country. Networking, Licensing, monitoring, supervision, capacity, strengthening and conducting research activities and NEQAS of the laboratories are the major functions of NPHL. Currently, NPHL has facility of biosafety level (BSL-3) lab with real time PCR (RT-PCR) which is in use for testing viral load & virus culture for Human Influenza including Swine flu.

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