Review Article

NOVEL AVIAN INFLUENZA H7N9 VIRUS PANDEMIC THREAT IN CHINA: A REVIEW

Tunio Muhammad Tarique¹, ²*, Shuming Yang¹, Zubair Mohsina¹, Jing Qiu¹, Yan Zhao¹, Gang Chen¹, Yu Chow¹ and Ailliang Chen¹

*Corresponding Author: Tunio Muhammad Tarique, tarique_tunio@hotmail.com

Outbreaks of H7N9 avian influenza in human in 5 provinces and 2 municipalities of China have reawakened concern that avian influenza viruses may again cross species barriers to infect the human and poultry population and thereby initiate a new influenza pandemic threat. Evolutionary analysis showed that human H7N9 influenza viruses originated from H9N2, H7N3 and H11N9 virus of avian and was identified to be a novel reassortment influenza virus. Avian influenza infections have caused heavy economic losses to the poultry industry in China as well as numerous other regions worldwide. A novel Avian Influenza (H7N9) are among the most prominent viruses affecting animal and public health. Based on data this review provides information on the current situation regarding the avian influenza A (H7N9) outbreak in China. However, at present, no evidence of sustained human-to-human transmission were observed. In this review article, therefore, an attempt has been made to summarize the latest available studies and findings to serve as the scientific basis to inform technical briefing to public health authorities and others involved in pandemic influenza planning and that are also interesting to the general public. Public health authorities and clinicians need to be aware of surveillance guidance and laboratory testing needs to be made available. A comprehensive human and veterinary surveillance strategy is needed to detect extension of the infection towards China.

Keywords: Novel Avian Influenza, H7N9, Pandemic, Threat, China

INTRODUCTION

Though man has made impressive advances in the field of medicine over the last century, we remain vulnerable to a host of diseases, ranging from the common cold to those that can only be characterized as frightening. Influenza pandemics (worldwide) have occurred at various times in the 19th and 20th centuries. Several pandemics have been recorded; the first Asiatic (Russian) occurred in 1889-91 when one million people died.

¹ Institute of Quality Standards & Testing Technology for Agro products, Chinese Academy of Agricultural Sciences, State key laboratory of Agri-food safety and Quality, Ministry of Agriculture, Beijing 100081, PR China.
² Department of Agricultural Sciences, Faculty of Sciences, Allama Iqbal Open University, Islamabad, Pakistan.

This article can be downloaded from http://www.ijasvm.com/currentissue.php
In 1918-19 a second pandemic suspected to have originated in Europe, known as Spanish Influenza, took millions of lives worldwide. Pandemics keep occurring regularly, in 1932-33; 1947-48; 1957, when the Asian flu killed 1 to 1.5 million people; and the 1968-69 Hong Kong flu outbreaks, which killed 0.75 to 1 million. The possibility of a new type of pandemic influenza due to mutated strains of Influenza, particularly H7N9 is nightmarish.

The People’s Republic of China was the first country to detect H5N1 HPAI viruses in Asia in 1996 and experienced the first reported outbreaks of disease in 2004. Due to the H7N9 virus, the country’s poultry industry has suffered losses worth more than 40 billion yuan (US$6.5 bn), according to the China Animal Agriculture Association (www.news.xinhuanet.com). AI virus belongs to the Order “Mononegavirales” and Family Orthomyxoviridae, and on the basis of their Nucleocapsid and M protein antigens. In current review we are mainly focusing on Influenza virus Type A, the most virulent human pathogen and cause of all flu pandemics. Avian Influenza (AI) is a highly contagious disease caused by either of the subtypes of influenza virus. The influenza viruses mostly infect birds and mammals and are classified into three subtypes A, B and C on the basis of their Nucleoprotein (NP) and Matrix Protein (MP). The type A virus is further classified into subtypes on the basis of its surface glycoproteins: hemagglutinin (H) and neuraminidase (N). Total 16 H and 9 N serotypes are present in aquatic wild birds (Fouchier et al., 2005). Wild waterfowl (Figure 1), are a natural reservoir for these viruses and introduces the viruses into poultry (Kawaoka et al., 1988). All of the subtypes of avian influenza virus are not highly pathogenic (HPAI) but arise from low pathogenic avian influenza (LPAI), viruses introduced into poultry flocks from wild birds (Kawaoka et al., 1988). Three H subtypes (H1, H2 and H3) and two N subtypes (N1 and N2) are circulating in human beings (DeJong and Hien, 2006; Peiris et al., 2007). There were repeated cases of avian H9N2 and H5N1 influenza viruses in human beings since 1997 in Southern China, Thailand, Vietnam and Indonesia (Guan et al., 1999; Xu, 1999; Mukhtar, 2007). Avian influenza virus has raised the concerns for public health, posing a pandemic threat to the whole world. Many conventional diagnostic tests have been developed for identification of the avian influenza viruses but AI isolation, via., Chicken Embryos (CE) remains the gold standard (Alexander, 2000). The H and N based subtypes of avian influenza viruses are mostly identified by Hemagglutination Inhibition (HI) test, neuraminidase inhibition tests and reverse transcriptase polymerase chain reaction (RT-PCR) (Nicholson et al., 1998; Steininger, 2002). Most of the research work is conducted on avian influenza A viruses isolated during outbreaks. In markets, healthy birds are aggregated from different sources and kept in close proximity. Lack of Biosecurity in such markets can contribute to avian influenza subtype H7N9 persistence and dissemination.

Figure 1: A Wild Water Fowl One Possible Reservoir of Avian Influenza Virus
INFLUENZA A (H7N9) INFECTION IN HUMANS IN CHINA

On March 31, 2013 the Chinese Authorities (the National Health and Family Planning Commission, previously the Ministry of Health) announced the identification of a novel influenza A virus infection, A (H7N9) in three seriously ill people in two Chinese provinces (WHO, 2013). Two cases in Shanghai were men aged 87 and 27 years who became ill in mid to late February and later died (on and March 10). A third case is a 35-year-old woman from Anhui Province who became ill on 9 March. As of April 1, 2013, she was in critical condition in Nanjing (Jiangsu Province). The cases presented with acute high fever onset, cough and respiratory tract infection symptoms at the ear stage of the disease. After approximately seven days, the patients developed severe pneumonia progressing rapidly into acute respiratory distress syndrome. The viruses were confirmed as A (H7N9) infection by RT-PCR, virus isolation and then sequencing by the Chinese CDC in Beijing. The three virus strains were isolated from the three cases were found to be almost identical. China CDC posted an announcement in English on the CCDC website on March 31 (CDC, 2013), and lodged the genetic information on the GISAID website. There was no evidence of an epidemiological link between the cases. Moreover, there was no reported links with bird die offs or animals although the young male patient in Shanghai was a butcher. The third case had exposure history to poultry before the onset of symptoms. Over 80 close contacts were followed-up. The Jiangsu Provincial Health Department had set up an avian flu prevention and control work leading group organizing prevention and response activities, notably around Nanjing city in Jiangsu Province. The Health authorities in Shanghai has ordered hospitals to strengthen monitoring and supervision of respiratory illness cases (AFP, 2013). Standard advice is being given on personal hygiene, avoiding contact with dead livestock and symptomatic persons seeking medical attention. With these investigations, a number of patients were being tested for possible A (H7N9) infection and while no additional cases have been officially confirmed as of April 2, 2013 it seems likely that more will follow and be confirmed as confirmatory testing has been distributed to the provinces in China. Some other authorities in the Asia Region are adding A (H7N9) to their pre-existing guidance on detecting A (H5N1) cases from China or occurring within the country. This includes Thailand that has set-up nationwide surveillance for H7N9 bird-flu virus 7 Hong Kong (STM, 2013), and Taiwan’s Centers for Disease and Table 1 shows Global Statistics of Avian Influenza and the affected areas.

The World Health Organization has been reporting on a novel situation in China where several human cases have been confirmed infected with avian influenza–like H7N9 virus (Table 2). There are reports of up to 14 cases and 6 deaths so far in the regions of Shanghai, Anhui, Jiansu and Zhejiang regions (WHO, 2013). The ages of the human patients range between 4 and 87 years old, with the majority in middle age. There was no confirmed evidence of human to human transmission and most, but not all cases had some contact with the poultry industry or handling poultry meat. The virus has been isolated from several patients and genetically characterized revealing that it is a novel reassortant virus with apparently genes from both avian H7N9 and H9N2 influenza A viruses but of
Global statistics of avian influenza and affected areas
(As of 12 May 2013)

### Table 1: Confirmed Human Cases of avian influenza A (H5N1)

<table>
<thead>
<tr>
<th>Country</th>
<th>Date of Last Report of Either Human or Animal Case</th>
<th>Human Cases</th>
<th>Poultry Cases</th>
<th>Wild Bird Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>China</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Anhui</td>
<td>23/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Beijing</td>
<td>13/04/2013</td>
<td>Y*</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Fujian</td>
<td>09/05/2013</td>
<td>Y*</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Guangdong</td>
<td>05/05/2013</td>
<td>-</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Guizhou</td>
<td>15/02/2013</td>
<td>Y*</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>Henan</td>
<td>25/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Hong Kong</td>
<td>29/01/2013</td>
<td>N</td>
<td>N</td>
<td>Y*</td>
</tr>
<tr>
<td>Hunan</td>
<td>01/05/2013</td>
<td>Y*</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Jiangsu</td>
<td>26/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Jiangxi</td>
<td>07/05/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Shandong</td>
<td>28/04/2013</td>
<td>Y*</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Shanghai</td>
<td>20/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
<tr>
<td>Taiwan</td>
<td>24/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>N</td>
</tr>
<tr>
<td>Zhejiang</td>
<td>28/04/2013</td>
<td>Y*</td>
<td>Y*</td>
<td>-</td>
</tr>
</tbody>
</table>

**Note:** Remarks: Y: Yes; N: No; Sources: World Health Organization, World Health Organization Western Pacific Region, World Organization for Animal Health (OIE), National Health and Family Planning Commission, provincial health authorities and Ministry of Agriculture of the People’s Republic of China.* Most recent occurrences in different area of China.

### Table 2: In China with Documented Highly Pathogenic Avian Influenza A(H7N9) Infection in Birds or Human in the Recent 6 Months

Source: WHO, 2013

This article can be downloaded from http://www.ijasvm.com/currentissue.php
putatively low pathogenicity for poultry. In all gene segments the virus is most closely related to avian strains. In addition the Chinese Authorities have reported a case of H7N9 Low Pathogenicity Avian Influenza (LPAI) in doves for consumption in a market in Shanghai. The sequence is reported to be closely aligned to that of viruses isolated from human cases (OIE, 2013).

**AVIAN INFLUENZA H7N9 PATHOLOGY**

Typically, the AI virus refers to Influenza A, found chiefly in birds. Infected birds show clinical symptoms like a sudden drop in egg production, brittle or soft-shelled and even shell-less eggs, swollen wattles and combs, congestion, and swollen skin under the eyes. Usually the risk of human infection from birds is through coming in close contact with bodily fluids or with contaminated surfaces. Infection can be transmitted from infected bird droppings, aliva, nasal secretions, feces, or blood. These viruses can remain infectious for about 1 week at human body temperature or a month at 32°F, and can survive at very low temperatures indefinitely. Main symptoms of AI in infected humans are mild fever, myalgia, sore throat, cough, conjunctivitis, myositis, and myoglobinuria. However, some people develop life-threatening complications like respiratory distress syndrome, pneumonia, and multiorgan failure. In 1997, the first documented infection of humans with an avian influenza virus occurred in Hong Kong. Studies determined that the infection occurred when the virus jumped directly from birds to humans due to close contact with infected poultry. A pandemic was averted by rapid mass killing/burning of over a million birds the entire poultry population of Hong Kong (Chan, 2002; Yuen et al., 1998). In December 2003, a highly pathogenic form of H5N1 caused another outbreak in poultry in The Republic of Korea (Lee et al., 2005). Another human infection was confirmed in February 2004 when two fatal cases were reported in Hong Kong due to H5N1 (Peiris et al., 2004), followed by 112 cases (57 fatal) from Thailand, Cambodia, Indonesia, and Viet Nam. Until now the cumulative number of confirmed human cases is 317 (191 fatal) (WHO, 2007). RnH5N1 viruses also have been isolated from ducks in Southern China (Chen et al., 2004) and antiviral antibodies have been found in pigs in Viet Nam (Choi et al., 2005). These cases could be the result of new strains due to reassortant viruses, antigenic shift or antigenic drift, as explained earlier. People are not immune to these different strains. Generally speaking, an individual has immunity to only those microbes or viruses to which they are earlier exposed. The possibility of dreadful new strains is thus worrying, as people either have no immunity or extremely delayed immunity depending upon the individual’s health and age. However, many new harmless strains causing symptomless infections go unnoticed. It was noticed that the Spanish flu was most lethal in young adults, who generally are most able to fight off severe infections. One theory for why the Spanish flu preferentially killed young people is because they are the one with robust and reactive immune systems and therefore were most likely to mount a self destructive response (Brown, 2007).

**SITUATION ASSESSMENT**

This is the first time this particular strain has been reported in humans. Avian origin H7 influenza viruses have been reported previously in humans, but generally only in association with
mild clinical symptoms (barring one exception in the Netherlands in 2003 when a vet died following infection with H7N7 HPAI). Given the recent finding of the H7N9 LPAI virus in doves in a market, it would not be unexpected if other similar infections were detected elsewhere in animal populations. The EU/OIE/FAO International Reference Laboratory for Avian Influenza and Newcastle Disease at AHVLA-Weybridge, UK is working closely with international partners on the situation to identify source infections. The reference laboratory has also confirmed that recommended EU protocols for detecting and characterizing H7 viruses would be applicable to this virus should it spread outside China. The European Centre for Disease Prevention and Control has produced an initial rapid risk assessment which concludes that the risk of spread to Europe is considered low, although individual cases travelling from China cannot be ruled out (ECDC, 2013). The animal source is not confirmed yet, however if there were a strong link with poultry or pigs, then the risk of introduction is mitigated by China not being approved for trade in live animals, fresh or frozen meat or pigs or poultry, captive or wild birds or other poultry products such as eggs. Further risk is mitigated by thorough cooking and safe handling of all poultry meat, as recommended by the Food Standards Agency. The risk of introduction of this virus through illicit movements, such as personal items cannot be assessed during the outbreak. The trade in captive live birds is still banned in the EU. However the UK Border Force has been already aware of the risk of disease introduction through infected pig or poultry products from this region.

**PANDEMIC RISK**

Pandemic risk cannot be determined in any meaningful way at present. Previous A (H7) infections in humans have tended to be mild (Puzelli et al, 2003; Kurtz et al, 1996). The exception is one death during a large outbreak in the Netherlands involving highly pathogenic A (H7N7) (Koopmans et al., 2004). The death in the Netherlands case was associated with an E627K substitution in PB2 of the H7 influenza virus (Koopmans et al., 2004). The same E627K substitution has been associated with high virulence, host range adaptation and airborne transmission in H5 viruses though the significance of its presence here is yet to be clarified (Subbaro et al., 1993). It may be significant that the three H7N9 viruses also have this E627K substitution. Whether this substitution has the same effect in the H7N9 virus as in the H5 and H7 viruses remains to be confirmed in the laboratory. Additionally there is reason for concern over human infections with A (H7) viruses in general (Belser et al., 2009). This is an A (H7N9) -A (H9N2) reassortant, and laboratory studies of A (H9N2) viruses with animals have suggested those viruses have pandemic potential (Wan et al., 2013). LPAI H9N2 virus infections of humans have usually resulted in uncomplicated influenza illness, but one case of lower respiratory tract disease in an immune compromised adult has been reported (Cheng et al., 2011). There is much that could be determined about these new viruses but international authorities, including WHO, the US CDC and ECDC will now be concentrating on the limited number of parameters of the greatest public health and clinical importance using tools like the Influenza Risk Assessment Tool (Trock et al., 2012).
UPDATE ON CURRENT METHODS USED FOR MOLECULAR DETECTION OF HUMAN INFECTION WITH AVIAN INFLUENZA A (H7N9) VIRUS BY RT-PCR

Generic Influenza A virus Detection Capability

Review of data provided accurate information about which exact molecular target sequences all laboratories are using for generic influenza A detection is not available, as some laboratories may be using commercial kits for which specific assay information is not available. Data from the WHO Influenza External Quality Assurance Project (EQAP) Panel 11 (2012) which consisted of nine gamma-ray inactivated influenza A (H1N1) pdm09, A (H3N2), A (H5N1), A (H9N2) and B viruses and one negative sample, show that among the 60 participating laboratories that returned results, 40 (67%) laboratories reported correct results for all 10 samples. When considering the influenza A (H9N2) sample only, 50 out of 60 participants (83%) correctly reported this sample as influenza A unsubtypeable. Nine (15%) laboratories from eight countries successfully identified this sample as influenza A (H9). Based on the data from WHO EQAP Panel 11, the predicted ability of several assays (CDC, PHE/HPA, RIVM) in use by the network, and the on served nature of the internal genes, most countries are expected to have reasonable capability for detection of H7 Eurasian lineage as influenza A using existing reagents and protocols for detection of M gene targets. For existing influenza type A virus tests where the molecular target sequence contains differences from the avian influenza A (H7N9) virus that may affect molecular detection, the sensitivity cannot be reliably evaluated until avian influenza A (H7N9) viruses are available in Europe. Laboratories relying on an influenza type A RT-PCR test for which the molecular target sequence is not available (commercial assays), will need to seek confirmation about test adequacy from the provider. NICs are also advised to explore/ascertain the adequacy for detecting the avian influenza A (H7N9) virus of the influenza type A tests used in primary diagnostic laboratories within their country where samples may undergo primary testing.

Specific Influenza A (H7) HA Detection Capability

Due to the emerging nature of the disease caused in humans by this novel influenza virus strain of avian origin, the validation of some nucleic acid amplification and hybridization assays and reagents designed for clinical detection has been limited to in silico genomic modeling and in vitro analytical validation of strain sensitivity and specificity in the absence of clinical data. It should be emphasized that clinical validation studies of diagnostic performance (clinical sensitivity and specificity) are still either lacking or only preliminary for some of the described H7-specific assays. Therefore, the clinical diagnostic performance is uncertain for such assays and interpretation for patient management should be made with appropriate caution and bringing into use new molecular assays for human clinical diagnosis for emerging infections. To assist with making an informed decision about clinical result interpretation, application of such assays for routine clinical diagnostic purposes is subject to national regulations. Decisions about how to disseminate H7 testing capability is a matter for individual countries, but all countries should have
an idea about what kinds of generic influenza A tests are being used, to evaluate the potential for missing detection of cases of H7 virus within health systems. Understanding how testing algorithms for generic influenza A detection as opposed to H1, H3 and influenza B are undertaken may also be an important consideration.

**Receipt of Avian Influenza A (H7N9) Virus Control Material**

Handling virus stocks and propagation of live avian influenza A (H7N9) viruses in laboratories undertaking human diagnostics requires BSL3 laboratory containment (Public Health Agency of Canada, 2013) The various resources can be used to support individual laboratory biorisk management (European Committee for Standardisation., 2011). (CWA 15793) assessments for specimen collection, handling, and other specific laboratory requirements to comply with the relevant EU legislation (Directive., 2009 and 2000). Different types of control materials can be provided and will be governed by a number of factors including the provider, and facilities and assays available in recipient laboratories.

**Vaccines Against Influenza A (H7N9)**

It is unknown whether current H7 candidate vaccine viruses are cross-protective and candidate vaccine viruses based on the A (H7N9) virus will be developed (WHO, 2013). Influenza candidate vaccine strains are normally developed in WHO collaborating laboratories, WHO Essential Regulatory Laboratories or research laboratories, and then shared with all vaccine manufacturers.

**Epidemiological Characteristics**

At this stage of the investigations in China, the data are not complete enough to fully understand the nature of the animal reservoir, how poultry becomes infected, the routes of transmission, the potential for human-to-human transmission, the incubation period and the risk factors for infection. The reservoir and routes of transmission to humans are under investigation by the Chinese authorities. The detection of A (H7N9) virus in samples from pigeons, chickens, ducks and environmental specimens at eight markets in all four provinces indicates that poultry, or other birds, might play an important role in transmission to humans. While a proportion of the cases have mentioned exposure to poultry, it should be kept in mind that it is common to buy live poultry for domestic consumption in China. Other possible animal reservoirs remain to be investigated. There is no information available about analytical studies of risk factors. The cases are widely distributed in mid-eastern China and the affected area has been expanded. One recent case was reported from a city 600 km north-west of Shanghai. This suggests that the virus is widely distributed in its animal reservoir. Poultry density is very high in this part of China and the extensive poultry trade might contribute to the distribution of the virus. There is no convincing evidence for human-to-human transmission at this stage of the outbreak. Chinese authorities have followed-up more than 700 close contacts and taken samples for RT-PCR from many of them without detecting infections. There is on going investigation into a few symptomatic cases among close contacts, but they have not so far been laboratory confirmed to have A (H7N9) infections. If the two small potential family clusters under investigation were to be confirmed A (H7N9)
infections, it would remain to be determined if they resulted from human-to-human transmission or from a common exposure to an animal or environmental source. Though the virus appears to cause no or mild disease in poultry, it seems to be highly pathogenic to humans. The casefatality rate has so far been 26% and most cases had severe disease. However, the reporting of the first three mild cases suggests that the clinical spectrum may be wider than initially presumed. Human influenza surveillance in China is currently based on Severe Acute Respiratory Infections (SARI). Broader surveillance could detect more mild cases which currently remain undiagnosed. The median age of the cases is high, at 65 years, with a large proportion being retired, and only one child has so far been found to be infected. That higher age is a risk factor could be explained by higher exposure to poultry in this age group, but this needs to be explored further. There do not seem to be notable clinical risk factors so far, but the information remains incomplete. Dates of disease onset are from 19 February to 4 April. It is unclear how well the reported cases reflect the true epidemiology or rather reflect the availability of the test (case ascertainment bias). Future serosurveys, yet to be developed, might shed a better light on the zoonotic and human-to-human transmissibility. The strong influenza surveillance system in China is not reporting an overall increase in influenza virus detection or atypical pneumonia cases in the most recent reporting period, although even this is hard to interpret at a time when rates of influenza virus transmission are expected to be falling. However, transmission would have to be advanced for those systems to show a signal.

Scientists from various USGS science centers are involved with avian influenza research that has included collaboration with China and other countries over the past 5 years. This research has focused on other influenza virus in wild birds, specifically the highly pathogenic avian influenza (HPAI). The avian influenza A (H7N9) virus is a reassortant virus; that is, a combination of at least three different wild birds and domestic poultry avian influenza viruses. The hemagglutinin (HA) gene is most similar to recent H7 viruses of ducks and waterfowl, the neuraminidase (NA) gene is most similar to a H7N9 virus isolated from wild bird feces collected in South Korea in 2011, and the six remaining gene segments are most similar to a H9N2 virus isolated from a brambling (a finch) sampled in Beijing in 2012. The brambling virus, in turn, is highly similar to other H9N2 viruses that are present in Chinese poultry.

**REASSORTMENT**

This theory (Figure 2), is based on the view that the new virus subtypes are reassortant viruses resulting from dual infection. The eight ssRNA segments of each strain reassort with each other, producing a new subtype. IA viruses can cross the "species barrier," and pigs are postulated as the most likely "mixing vessel."

![Figure 2: Reassortment of Human H2 with Avian H3 Virus: e.g., Emergence of the H3N2 Pandemic Virus in 1968](http://virology-online.com/viruses/Influenza.htm)
CONCLUSION

Although rigorous control measures have been implemented in commercial poultry in China, in this scenario, the earlier identified presence of H7N9 in poultry in China and in other countries in the region, poses a continuous threat for the emergence of more pathogenic strains of both avian and human influenza viruses. For this purpose there is a constant need to carry out a coordinated surveillance for influenza viruses both in birds and humans in the country. Continuous screening of live bird markets in major cities for AIV may help scientists to control outbreaks by preventive measures. It is expected that for China and their respective regions, it will take a few years to achieve freedom from the virus.

ACKNOWLEDGMENT

The author acknowledges Graduate School of Chinese Academy of Agricultural Sciences Beijing China, Allama Iqbal, Open University, and the Higher Education Commission Pakistan.

REFERENCES


This article can be downloaded from http://www.ijasvm.com/currentissue.php


32. WHO (2013), Influenza A (H7N9): Five additional cases detected in China", http://www.wpro.who.int/en/


35. www.news.xinhuanet.com x.html

