

Final Abstract Number: 24.001

Session: Update on Influenza

Date: Friday, June 15, 2012

Time: 15:45-17:45

Room: Ballroom B

### Human and animal epidemiology of influenza in Southeast Asia

T. Chotpitayasunondh

*Queen Sirikit National Institute of Child Health, Bangkok, Thailand*

Influenza A viruses infect a wide range of animals especially aquatic birds which are their natural hosts and primordial reservoir. The interspecies transmission of viruses among animals result in a transient infection characterized by limited spread. Nevertheless, in certain occasion, a stable lineage can be established into other avian and mammalian hosts including swine and humans. The viral subtypes that have successfully transmitted between species in Southeast Asia are highly pathogenic avian influenza (HPAI) H5N1, H9N2, H3N2 and recently the H1N1-2009 pandemic influenza in humans was the result of reassortment of genetic material from avian, swine and human influenza viruses. The epidemiology of animal influenza is complex due to a number of factors such as environment, number of hosts, genetic and antigenic change of viruses.

Human influenza is one of the most common illness among people in all regions, however, much less attention has been paid to epidemiology of infection in Southeast Asian countries. Recent studies in this region suggested a substantial burden of disease similar to that of Europe and North America i.e., up to 11-26% of outpatient cases presenting with acute febrile illness and 6-14% of hospitalized pneumonia cases had laboratory confirmed influenza infection.

Recently, influenza viruses in animals and humans are increasingly circulating among wide range of hosts. As a result, there is the potential for the reassortment of the genetic material from the different subtypes of influenza viruses and, thus, emergence of a novel influenza with a potential to cause an influenza pandemic. As of 5 March 2012, there were a large number of outbreak in poultry and backyard chickens caused by HPAI[WV1] -H5N1 mainly in Asia with 592 human infection and 59% of fatality rate. This human-animal influenza interface reinforces the need for close monitoring, surveillance, and collaboration between public health and veterinary sectors. Avian influenza H5N1 in poultry and human in Southeast Asia creates the potential risk of the emergence of serious pandemic influenza in the near future.

<http://dx.doi.org/10.1016/j.ijid.2012.05.103>

Final Abstract Number: 24.002

Session: Update on Influenza

Date: Friday, June 15, 2012

Time: 15:45-17:45

Room: Ballroom B

### Clinical features and pathogenesis of H5N1 influenza in humans

T.T. Hien

*Oxford University Clinical Research Unit (OUCRU) Vietnam, Hoi Chi Minh, Viet Nam*

Avian influenza A (H5N1) occurred in poultry throughout Asia has had major economic and health repercussions. Infections with this virus have been identified since January 2004 and despite intensive clinical management the case fatality is still unacceptably high. We report the clinical findings among patients with confirmed cases of avian influenza A (H5N1) who presented to hospitals in Vietnam. In all 67 cases, the diagnosis of influenza A (H5N1) was confirmed by means of viral culture or reverse transcriptase-polymerase chain reaction (RT-PCR). Patients presented to hospitals after a median duration of illness of 6 days with fever (75%) cough (89%) and dyspnea (98%). Diarrhea and mucosal bleeding at hospital admission were more common in fatal than in non fatal cases. Common findings were bilateral pulmonary infiltrates on chest X-Ray (72%), lymphopenia (73%), and increased serum transaminase levels (ALT69%, ALT 61%). The most reliable predictor of a fatal outcome was the presence of both neutropenia and raised ALT level on admission (correctly predicted 91% of death and 82% of survival). Treatment of oseltamivir showed benefit but use of corticosteroid is associated with increased risk of death. Influenza H5N1 infection in humans is characterized by high pharyngeal virus loads and frequent detection of viral RNA in rectum and blood. Viral RNA in blood was present only in fatal H5N1 cases and was associated with higher pharyngeal viral loads. We observed low peripheral blood T-lymphocyte counts and high chemokine and cytokine levels in H5N1-infected individuals, particularly in those who died, and these correlated with pharyngeal viral loads. Our observations indicate that high viral load, and the resulting intense inflammatory responses, is central to influenza H5N1 pathogenesis. The focus of clinical management should be on preventing this intense cytokine response, by early diagnosis and effective antiviral treatment. Despite recent progress, knowledge of the epidemiology, natural history, and management of influenza A (H5N1) disease in humans is still incomplete. There is an urgent need for more coordination in clinical and epidemiologic research among institutions in countries with cases of influenza A (H5N1) and internationally.

<http://dx.doi.org/10.1016/j.ijid.2012.05.104>