

Final Abstract Number: 53.027
 Session: *Epidemiology & Public Health*
 Date: Saturday, June 16, 2012
 Time: 12:45-14:15
 Room: Poster & Exhibition Area

Characterizing the transmission dynamics and severity of 2009 H1N1 influenza pandemic in Hong Kong

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Background: We tested 14,766 sera collected during the first wave of pandemic influenza H1N1 (pdmH1N1) in Hong Kong using viral microneutralization (MN). Each serum specimen was tested for seropositivity at MN titers of 1:20 and 1:40. Combining these serologic data with clinical surveillance data, we estimated the transmission and severity parameters using an age-structured SIR model with four age groups: 0-12, 13-19, 20-29, and 30-59.

Methods: Combining data from serological study and clinical surveillance data obtained from E-Flu database in Hong Kong, we use an age-structured SIR transmission model to estimate transmission and severity parameters of pdmH1N1, such as basic reproductive number and case hospitalization probability.

Results: We estimated that the basic reproductive number was 1.49. Older age groups were more likely to possess immunity before the pandemic and were less susceptible to pdmH1N1 infections if they did not have pre-pandemic immunity. School closure reduced within-age-group transmission by 75% among the 0-12 year olds but only 26% among the 13-19 year olds. The mean delay between symptoms onset and seropositivity at MN titers 1:20 and 1:40 were around 3 and 10 days, respectively.

Conclusion: Serial cross-sectional serologic data together with clinical surveillance data can be used to completely characterize the transmission dynamics and severity of an influenza pandemic. Serologic monitoring should be considered in pandemic surveillance.

<http://dx.doi.org/10.1016/j.ijid.2012.05.427>

Type: Poster Presentation

Final Abstract Number: 53.028
 Session: *Epidemiology & Public Health*
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The seroepidemiological profiles of dengue virus infection in southern Taiwan 2008-2010 and public health implications

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Background: During the last decade, Southern Taiwan has experienced several epidemics of dengue, caused by the virus (DENV)

having annual outbreaks with predominant single serotype of DENV, of which viral transmission has been rarely detected before and after the epidemic. In addition, most Taiwanese cases were dengue fever cases in adults in contrast to SEA, where primarily were pediatric dengue hemorrhagic fever (DHF) cases. Nevertheless, profiles of seroprevalence in the regions where dengue outbreaks mainly occurred can provide an overall picture to fully understand the transmission of different serotypes of DENV.

Methods: Two seroepidemiological studies in Tainan City and Kaohsiung City were conducted from 2008 to 2010. Tainan's study aimed to measure the seroprevalence after the DENV-1 epidemic in 2007, the largest epidemic since 1988. We chose 3 communities with the most dengue cases in 2007 to conduct cross-sectional serological surveys in August and September in 2008, and additional 4 schools in May 2009. Kaohsiung's study aimed to measure the seroincidence among subjects in community- and primary school-based cohorts, which encountered the DENV-3 epidemic in 2009. DENV-specific antibody was tested by ELISA.

Results: The overall seroprevalence of anti-DENV IgG was 7.2% of 167 Tainan's residents, significantly lower than those in two Kaohsiung's communities [27% (n=96) in November 2009 and 35% (n=71) in March 2010]. The overall infection rates of DENV in schoolchildren were quite low in both cities (3.3% versus 2.2% in 1,108 Tainan's and 1,153 Kaohsiung's schoolchildren, respectively) and 1 Kaohsiung's child living in Xiaogang district had seroconversion.

Conclusion: DENV transmission in Kaohsiung was higher than Tainan. However, the vector control program did succeed in containing the transmission among schoolchildren. Further works on serotyping is in progress to clarify the magnitude of infection by different serotypes of DENV.

<http://dx.doi.org/10.1016/j.ijid.2012.05.428>

Type: Poster Presentation

Final Abstract Number: 53.029
 Session: *Epidemiology & Public Health*
 Date: Saturday, June 16, 2012
 Time: 12:45-14:15
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A matched case-control study identifies activities of daily living associated with acquisition of melioidosis in northeast Thailand

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Background: Melioidosis is a fatal infectious disease caused by the Category B select agent and environmental saprophyte, *Burkholderia pseudomallei*. Naturally acquired infection is common in Thailand after exposure to soil and water. The relative importance of bacterial inoculation, inhalation and ingestion as routes of infection and the relevance of a range of activities of daily living are not known. This is a barrier to the development of guidelines for prevention.

Methods: We conducted a prospective hospital-based matched case-control study in northeast Thailand. Cases were patients

with culture-confirmed melioidosis, and controls were patients admitted with non-infectious conditions during the same period, matched for gender, age, and presence or absence of diabetes mellitus (a major risk for melioidosis). A questionnaire was designed to record activities of daily living, and home visits were performed to obtain all sources of drinking water and culture this for the presence of *B. pseudomallei*.

Results: Multivariable conditional logistic regression analysis based on 288 cases and 515 controls showed that activities associated with a risk of melioidosis included working in a rice field (conditional odds ratio [cOR]=2.1; 95% confidence interval [CI] 1.4–3.3), other activities associated with exposure to soil or water (cOR=1.4; 95%CI 0.8–2.5), an open wound (cOR=2.0; 95%CI 1.3–3.3), eating food contaminated with soil or dust (cOR=1.5; 95%CI 1.0–2.2), drinking untreated water (cOR=1.8; 95%CI 1.2–2.8), being in the rain (cOR=2.1; 95%CI 1.4–3.2), water inhalation (cOR=2.4; 95%CI 1.6–3.8), current smoking (cOR=1.6; 95%CI 1.0–2.4) and steroid intake (cOR=2.1; 95%CI 1.1–4.1). *B. pseudomallei* was detected in water source(s) consumed by 8% of cases and 4% of controls (cOR=2.1; 95%CI 0.9–5.0).

Conclusion: Inoculation, inhalation and ingestion are all important routes of *B. pseudomallei* infection. Our findings provide the basis for multi-facet evidence-based guidelines for the prevention of melioidosis.

<http://dx.doi.org/10.1016/j.ijid.2012.05.429>

Type: Poster Presentation

Final Abstract Number: 53.030

Session: Epidemiology & Public Health

Date: Saturday, June 16, 2012

Time: 12:45–14:15

Room: Poster & Exhibition Area

Investigation and analysis of melioidosis outbreak after Typhoon Namadol in Southern Taiwan, 2011

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Background: Melioidosis caused by *Burkholderia pseudomallei* is a common zoonotic disease of tropical climates, especially in South-east Asia and northern Australia. It is spread through inhalation, ingestion or direct contact between a wound and the contaminated source. In Taiwan, melioidosis outbreaks are often associated with typhoon floods. Past outbreaks occurred mostly in southern Taiwan after typhoons passed through in 2005, 2008, 2009, and 2010. In this study, we investigated the melioidosis outbreak after Typhoon Namadol struck Taiwan in August, 2011 to identify high risk groups and the transmission route, and provide public prevention measures.

Methods: The data was collected by Taiwan CDC. One month after Typhoon Namadol occurred during August 27 and 31, 2011, cases were confirmed in southern Taiwan. Taiwan FETP interviewed the cases (or their family members); determined whether the residence was flooded and whether the case had any skin wound and exposure to soil during the typhoon; and reviewed the cases' medical records and demographic characteristics.

Results: During September 6 and 28, 2011, 17 melioidosis cases were confirmed in southern Taiwan. In this outbreak, the case number peaked three weeks after the typhoon hit. The mean age of the cases was 63 years. The male to female ratio was 1.43:1. All cases had chronic diseases such as diabetes, renal disease, malignant tumor or liver disease. All cases were found to have no wound

and no exposure history to soil. Four of 17 cases (23.5%) died despite of proper medical care. The most common clinical syndrome was pneumonia (n = 12, 71%).

Conclusion: Melioidosis is highly fatal. All cases had no exposure to soil and most developed pneumonia, which indicated that the infection was associated with inhalation of contaminated dust or vapor caused by typhoon. Patients with history of chronic diseases are at increased risk for melioidosis, especially elderly. During the typhoon season, health authorities should reinforce promoting melioidosis awareness by spreading important health education messages to patients at risk and advising public to remain vigilant against melioidosis.

<http://dx.doi.org/10.1016/j.ijid.2012.05.430>

Type: Poster Presentation

Final Abstract Number: 53.031

Session: Epidemiology & Public Health

Date: Saturday, June 16, 2012

Time: 12:45–14:15

Room: Poster & Exhibition Area

The role of human papillomaviruses in oesophageal squamous cell carcinoma: a review of the evidence

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Background: Oesophageal cancer (OC) is responsible for almost half a million deaths annually, worldwide and has a multifactorial aetiology, which may account for its geographical variation in incidence. The potential of human papillomaviruses (HPV) as oncogens in the tumorigenic process of oesophageal squamous cell carcinoma (OSCC) has been widely studied, with inconclusive results. As a general trend, studies carried out in high incidence OSCC regions have reported higher rates of HPV detection in OSCC tissues in comparison to reports from low-risk settings. Since the recent introduction of prophylactic HPV vaccines, it has become more important to definitively determine whether an HPV-OSCC link exists. Case-control methodology is the most suitable study design to answer this research question. We evaluate current evidence on this topic.

Methods: The MEDLINE and EMBASE databases were searched for studies which tested for the presence of HPV DNA in OSCC tissue. Key journals in related areas were hand-searched to identify any papers which were not electronically indexed. 165 studies met our inclusion criteria, of which 23 were case-control studies. The Epi Info (CDC) 3.5.3 program was used for statistical analysis of the 23 case-control studies.

Results: Our results support previous findings of higher levels of HPV detection in high-risk OSCC regions compared to areas of low-risk. The role of HPV in OSCC remains unclear, despite an accumulation of further studies on the subject. Analysis of the case-control studies revealed 10 studies with odds ratios supporting a significant association between HPV and OSCC. The largest single