RESPIRATORY DISEASE SURVEILLANCE NETWORK IN ROYAL THAI ARMY HOSPITALS

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Background: Respiratory infections become the diseases of military important due to the high infection rate and rapid spreading, especially if occur in closed community as military camp. The latest influenza pandemic caused by a novel strain of A/H1N1 has caused illness, death and economic crises worldwide. On-going, comprehensive influenza surveillance is critical to detect and monitor influenza outbreaks, and to evaluate preventive and containment measures. The Armed Forces Research Institute of Medical Sciences (AFRIMS) has established a respiratory disease surveillance network in 8 Royal Thai Army hospitals located in rural areas with high border traffic near Myanmar, Malaysia, Laos, and Cambodia to determine the seasonal and regional etiology of respiratory disease, enhance outbreak response capability and to enable the safe collection of clinical samples.

Methodology: Adults presenting with influenza like illnesses (history of fever and cough or sore throat or rhinorrhea) are consented and enrolled. Respiratory samples are tested with a rapid test for influenza A and B on-site. Aliquots are sent to AFRIMS in Bangkok for influenza genotyping using realtime RT-PCR and detection of other respiratory pathogens by MassTag PCR. MassTag PCR amplifies genetic material utilizing domain-specific primers tagged with a unique molecular mass tag to allow mass spectrometric analysis and simultaneous detection of up to 30 different pathogens.

Results: During February 2007 to February 2013, total of 4,750 patients were enrolled and consented from 8 Royal Thai Army Hospitals along borders. Using rapid test performed onsite, 918 (19.3%) were positive for influenza virus (Figure 1A).

Influenza genotyping by realtime PCR demonstrated 1,211 (25.49%) were infected by influenza virus; 496 (10.4%) were influenza A/H1, 324 (6.8%) were influenza A/H3, 26 (0.6%) were unsubtyped influenza A and 365 (7.7%) were influenza B (Figure 1B). Detection of other respiratory pathogens in 1026 samples utilizing MassTag PCR revealed 343 were infected by viruses; Influenza-A,-B, Parainfluenza (PIV), Adenovirus, Coronavirus-OC43, Enterovirus, Rhinovirus, Respiratory Syncytial Virus (RSV-A,-B), human Metapneumovirus (hMPV) and bacteria; *Mycoplasma pneumoniae*, *Haemaphilus influenza Streptococcus pneumonia* (Figure 1C). In addition, co-infection of pathogens were identified such as RSV-B with *S. pneumoniae*, adenovirus with coronavirus-OC43 and *H. influenzae* with *S.pneumoniae*. Isolation of local Influenza viruses and full-length genetic characterization is ongoing. Our ongoing experiments are isolation of local influenza viruses and subsequently genetic characterization.

Discussion: The networking of respiratory disease surveillance has been established and actively operates along Thai border areas since 2007. Testing for many respiratory pathogens provides a comprehensive picture of disease burden in this population and greatly improves our ability to detect and respond to emerging diseases including avian influenza. An extensive influenza surveillance program in Asia can assist with documenting virus spread and genetic changes, and is well positioned to provide assistance during pandemics.