Experiences and Lessons Learned from Strengthening Thailand's Influenza Surveillance Network

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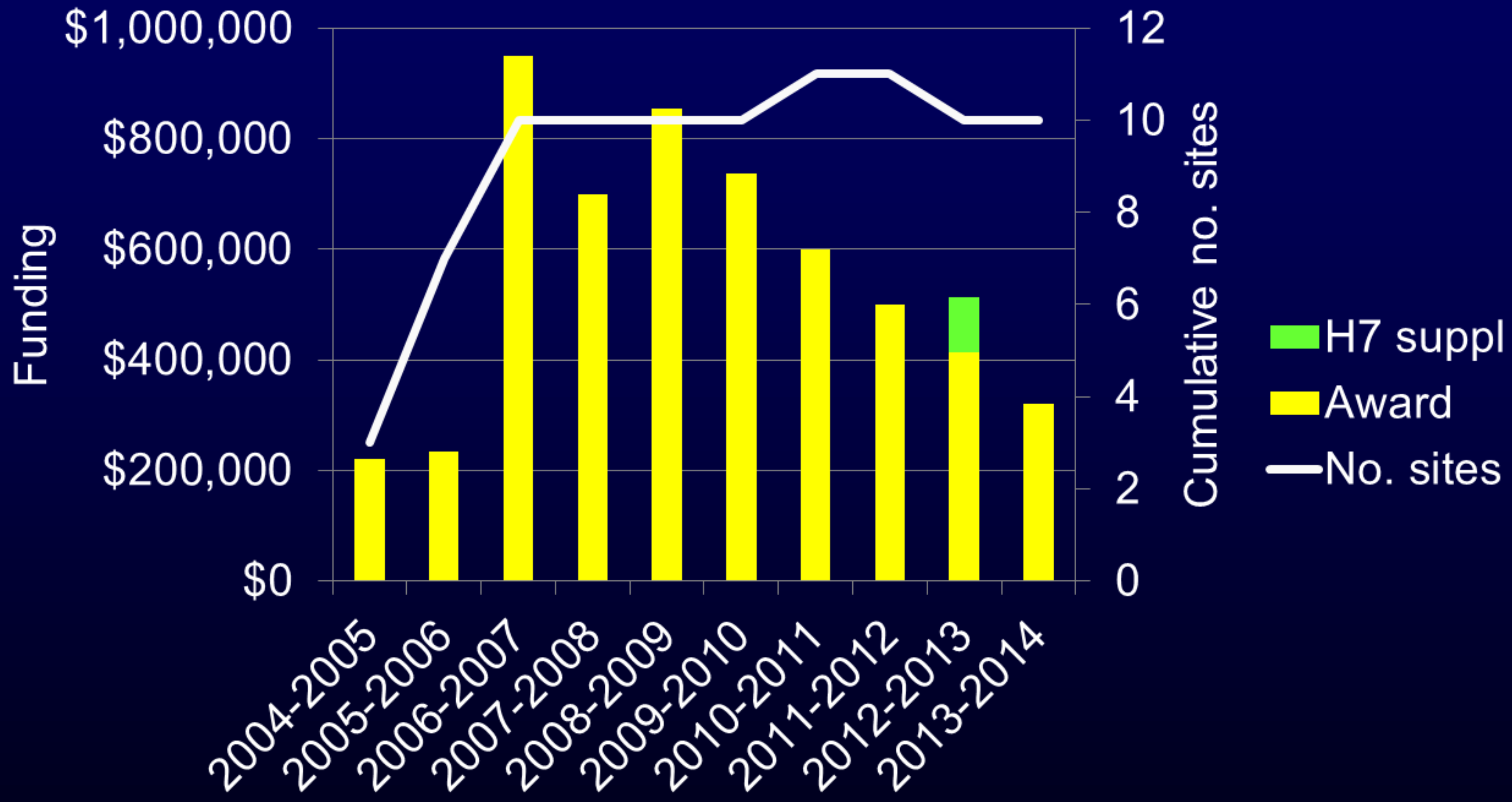
Influenza Surveillance Established in 2004

- In response to the spread of avian influenza A (H5N1) viruses
- In recognition that pandemic influenza preparedness is a core communicable disease control function

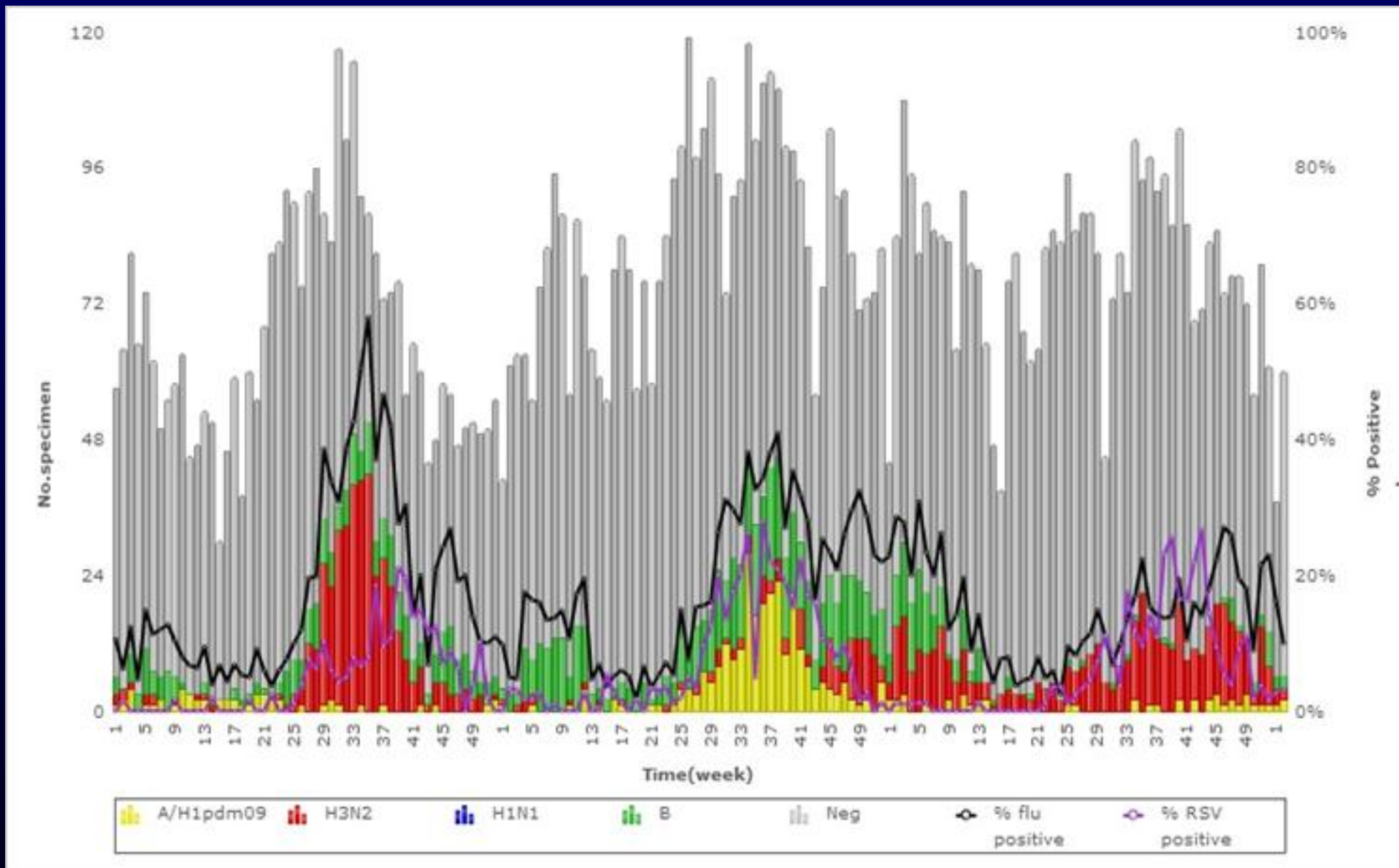
Establishment of the System



Utility of Surveillance

- Viral monitoring
  - Antiviral resistance
  - Type/subtype dominance
  - Strain changes
  - Novel viruses
- Epidemiologic monitoring
  - Seasonality
  - Geographic spread
  - Age distribution
  - ILI vs. SARI

Weekly Situational Awareness



http://www.thainihnic.org/influenza/main.php

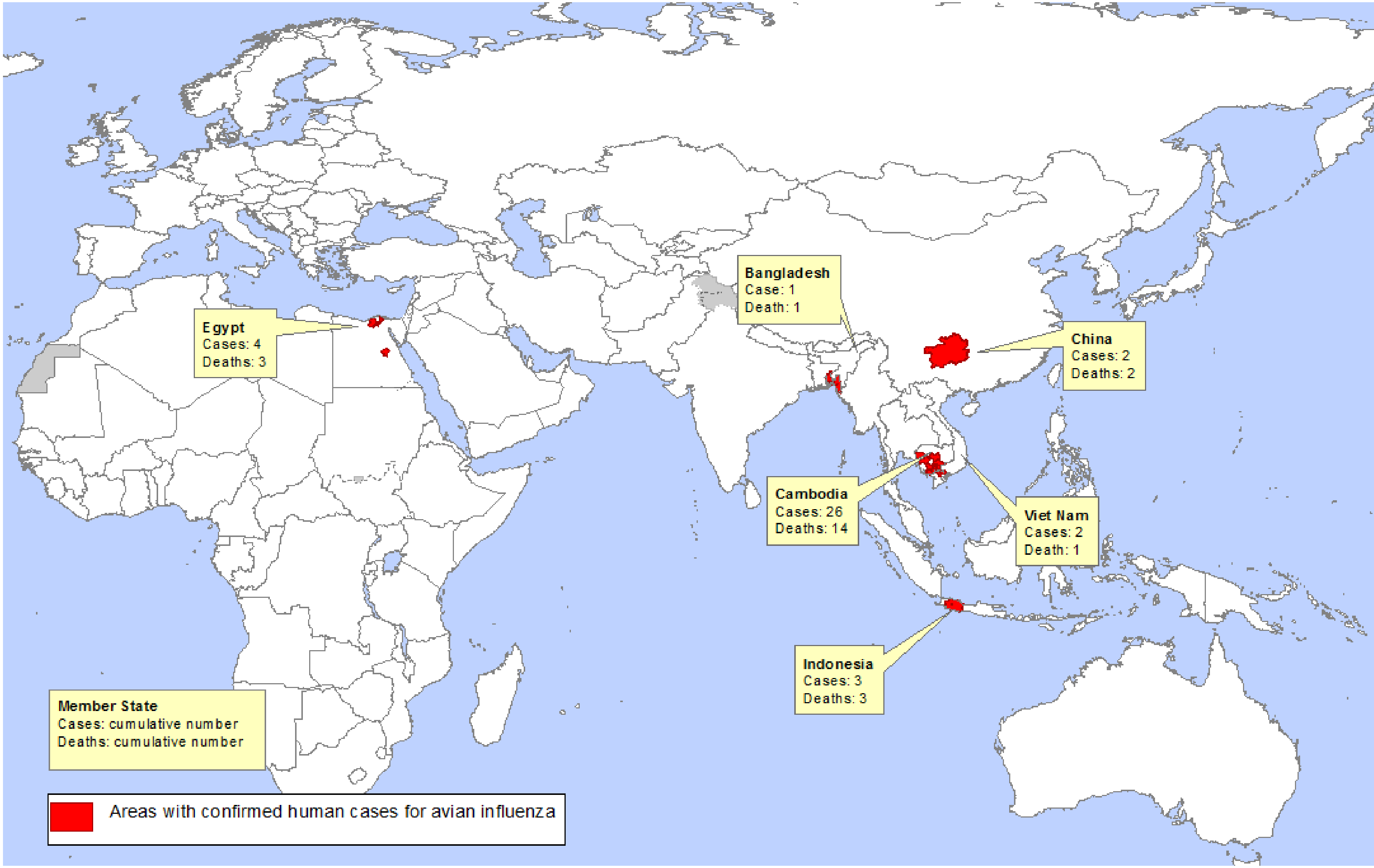
Flexibility to Expand Laboratory Testing Quickly

- Influenza A (H5N1)
- Other respiratory viruses
  - RSV
  - HPIVs
  - HMPV
  - adenovirus
- Influenza A (H7N9)
- MersCoV

Building Laboratory Network

- 14 regional laboratories
  - Training
  - Proficiency testing twice a year
  - Distribute new reagents (H5N1, H1N1pdm09, H7N9, MERS Cov)
- University laboratories
- Close communication with NIC

Areas with confirmed human cases for avian influenza A(H5N1) reported to WHO, 2013- to-date*,



*All dates refer to onset of illness
Data as of 10 December 2013
Source: WHO/GIP

Monitoring for H7N9

- Acquired diagnostic reagents in April 2013
- Began tested for H7N9
- 418 samples tested through Jan 9, 2014
  - 382 influenza A positive from surveillance system
  - 4 SARI or death due to influenza A
  - 32 from general service
- All negative for H7N9

Site Monitoring was Useful

- Opportunity to review and revise SOPs
- Retain good relationships
- Over time, optimize sites

Epidemiology and Laboratory Integration

- Surveillance system with linked epi and lab data
- Experts from both NIH and BoE

Lessons from the Pandemic

- Number of samples can easily overwhelm the laboratory
- At-risk age may differ from seasonal influenza
- SARI is very important to assess disease severity

Expanded Laboratory Capacity

- Dramatic increase in specimens during epidemic/pandemic
- Need network of laboratories to facilitate testing
- 14 DMSC Regional Laboratories
  - Trained
  - Supply regents
  - Proficiency testing

Importance of Capturing all Ages

- Immunity to novel virus can by vary by age
- A system that captures patients of all ages can help determine age groups most at risk

Importance of SARI

- Many novel viruses (e.g., H5 and H7) cause a severe clinical presentation
- ILI surveillance would not pick up infections due to these viruses
- In a pandemic, rapid knowledge of the extent of severe disease is critical for making decisions

Recommendations for H7 Surveillance

- Focus on SARI
- Focus on points of entry (if pathogen were imported from China)
- Focus on border sites (if pathogen were brought across border)

Communicating Results

Influenza Virus Strain Data from Thailand, 2005-2012: How well does the vaccine match?

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Background:

Thailand's annual public influenza vaccination campaign begins in June and uses the Southern Hemisphere formulation. Both Northern (NH) and Southern (SH) hemisphere formulations are sold in the private sector. A national sentinel surveillance network for influenza-like illness and severe acute respiratory illness is used to monitor weekly influenza virus activity and herald an increase in influenza activity. Here we use these data to evaluate the match and timing between strains circulating in people and those in the trivalent vaccine.

A study of oseltamivir-resistant influenza viruses in Thailand, 2008-2010

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Abstract

On 25 January 2008, WHO was notified by Norway of a high prevalence of oseltamivir (Tamiflu©) resistance in seasonal influenza A(H1N1) viruses detected through routine surveillance and testing. Information about drug resistance is now an important piece of information guiding patient treatment recommendations. The Regional Influenza Reference Laboratory of SEA Region (RIRL), Thailand established the capacity to run the fluorescence-based NA enzyme inhibition assay. Throat swabs from patients with influenza-like illness or pneumonia were collected at 11 sentinel sites across the country. All swab specimens were transported to the RIRL. Specimens were identified using the standard protocol for real time reverse transcription polymerase chain reaction (rRT-PCR) from the WHO and US-CDC to detect influenza A/B virus and then A viruses were subtyped with specific primers from US-CDC. All specimens from sentinel sites which demonstrated influenza positive by rRT-PCR during 2008-2010 were selected for virus isolation in MDCK cells. A total of 1,211 representative influenza isolates were tested for susceptibility to oseltamivir by fluorometric neuraminidase inhibition Assay (phenotypic assay). All positive results or resistant isolates and some negative results obtained from phenotypic assay were subsequently performed partial NA gene sequencing which carried the oseltamivir resistance mutation at H274Y (N2 numbering) . The study results demonstrated that in 2008-2009, a steady increase in proportion of seasonal A(H1N1) oseltamivir resistance was observed, reaching 95.6% in 2009. In 2009-2010, the H274Y mutation was found in pandemic A(H1N1) viruses and the prevalence of resistance was 1.31%. Oseltamivir resistance was not found with influenza type B or H3 viruses during 2008-2010. Continued monitoring of antiviral resistance in influenza viruses is essential for guiding patient treatment recommendations .

Influenza is an infectious disease caused by influenza viruses which are in the Orthomyxoviridae family[1]. Influenza viruses are single-strand segmented RNA viruses. There are two genuses that commonly cause influenza in humans, Classification of influenza viruses into subtypes is labeled according to the H number (H1 to H16) and the N number (N1 to N9) which represent the type of hemagglutinin and neuraminidase respectively.[2] Although influenza spreads around the world every year as seasonal epidemics, resulting in the death of approximately 250 000 to 500 000 people every year,[3] an influenza pandemic can occur after the appearance of the new strain of a virus in humans. Often, new strains appear when an existing influenza virus transfers from animals to humans. An example of a new

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Original Article

Influenza viruses in Thailand: 7 years of sentinel surveillance data, 2004–2010

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Background The re-emergence of avian influenza A (H5N1) in 2004 and the pandemic of influenza A (H1N1) in 2009 highlight the need for routine surveillance systems to monitor influenza viruses, particularly in Southeast Asia where H5N1 is endemic in poultry. In 2004, the Thai National Institute of Health, in collaboration with the US Centers for Disease Control and Prevention, established influenza sentinel surveillance throughout Thailand.

Objectives To review routine epidemiologic and virologic surveillance for influenza viruses for public health action.

Methods Throat swabs from persons with influenza-like illness and severe acute respiratory illness were collected at 11 sentinel sites during 2004–2010. Influenza viruses were identified using the standard protocol for polymerase chain reaction. Viruses were cultured and identified by immunofluorescence assay; strains were identified by hemagglutination inhibition assay. Data were analyzed to describe frequency, seasonality, and distribution of circulating strains.

Results Of the 19 457 throat swabs, 3967 (20%) were positive for influenza viruses: 2663 (67%) were influenza A and able to be subtyped [21% H1N1, 25% H3N2, 21% pandemic (pdm) H1N1] and 1304 (33%) were influenza B. During 2009–2010, the surveillance system detected three waves of pdm H1N1. Influenza annually presents two peaks, a major peak during the rainy season (June–August) and a minor peak in winter (October–February).

Conclusions These data suggest that March–April may be the most appropriate months for seasonal influenza vaccination in Thailand. This system provides a robust profile of the epidemiology of influenza viruses in Thailand and has proven useful for public health planning.

Keywords Influenza, inpatients, outpatients, surveillance, Thailand.

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Introduction

Since 2004, a widespread epidemic of highly pathogenic avian influenza caused by influenza A (H5N1) viruses in animal populations, particularly chickens, has swept through Southeast Asia. The disease poses a considerable public health risk. Not only can viruses infect humans directly, causing severe disease with high mortality,[1] but there is also potential for these viruses to acquire the ability to transmit from human to human either by reassortment with other influenza viruses or by mutation and give rise to new pandemic strains.[2] Avian influenza viruses were first detected in Thailand in January 2004, and through 2006, there were 25 persons infected with laboratory-confirmed influenza A (H5N1) viruses, including 17 deaths, reported to the World Health Organization (WHO).[3] No cases have been identified since 2006.

In response to the spread of avian influenza A (H5N1) viruses, and in recognition that pandemic influenza preparedness is a core communicable disease control function, the Thai National Institute of Health (Thai NIH) at the Ministry of Public Health (MOPH), in collaboration with the US Centers for Disease Control and Prevention (CDC), established a series of influenza surveillance networks. In 2004, Thai NIH set up surveillance sites across the country. The surveillance system was established to monitor the frequency of influenza, identify new strains and describe seasonality.

Data to Inform Policy Decisions

- Clinical guidance
  - Herald the start of influenza season
  - Monitor changes in antiviral resistance
- Situational awareness
  - Novel viruses
  - Outbreak awareness
- Vaccine policy
  - Data contributed to vaccine decisions

Opportunities for Expanded Role

- Network could be used to evaluate vaccine program
- Monitor vaccine coverage and vaccine efficacy

Summary

- Surveillance is a core public health function
- Sustainability is critical
- System should be flexible and adapt to needs that arise during outbreak/pandemic
- For novel viruses, focus on SARI is critical
- Possible opportunities for expanded role in vaccine program