2014 Influenza Update

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Faculty Disclosure

The Association of Public Health Laboratories adheres to established standards regarding industry support of continuing education for healthcare professionals. The following disclosures of personal financial relationships with commercial interests within the last 12 months as relative to this presentation have been made by the speaker(s):

Dr. Pete Shult and Dr. Julie Villanueva have nothing to disclose
2014 Influenza Update

Objectives

• Describe seasonal influenza activity in the U.S. and globally this past season
• Describe the mechanisms and impact of several instances of novel influenza A emergence in humans that have recently occurred
• Describe current and future influenza testing technologies and the impact they might may have on influenza diagnosis and surveillance in the U.S.
• Describe recent outcomes of the Influenza Virologic Surveillance Right Size Project and their potential impacts
• Describe how PHL-clinical lab partnerships can benefit influenza virologic surveillance
What We’re Dealing with Now

- Ebola virus
- EV-D68
- MERS CoV
- Dengue fever
- Chikungunya
- Pertussis
- Measles/mumps

... So what’s the big deal with influenza?
Estimated Annual Burden of Seasonal Influenza in the United States

- Deaths: 3,000 – 49,000
- Hospitalizations: 54,000 – 430,000
- Cases: 15 – 60 M

Direct medical costs: $10.4 billion
2013-14 Season Virus Surveillance
2009 H1N1 Predominance

2009 H1N1 predominated – susceptible to oseltamivir
U.S. World Health Organization and National Respiratory and Enteric Virus Surveillance System Collaborating Laboratories, National Summary, 2011-14

- H3N2v
- A(2009 H1N1)
- A(H3)
- A(Subtyping not performed)
- B

Percent Positive:
- 2011
- 2012
- 2013
- 2014

Number of Positive Specimens

Percent Positive

90
80
70
60
50
40
30
20
10
0

8,000
7,000
6,000
5,000
4,000
3,000
2,000
1,000
0

40 50 10 20 30 40 50 10 20 30 40 50 10
2013-14 Pneumonia and Influenza Mortality

![Graph showing excess mortality due to H3N2 and pH1N1 strains over years 2010-11 to 2013-14. The graph indicates peaks in excess mortality during certain weeks.]

- **H3N2**
  - Peaks in excess mortality during 2011-12 and 2013-14

- **pH1N1**
  - Peaks in excess mortality during 2013-14

Excess Mortality

Weeks

% of All Deaths Due to P&I

2010-11 2011-12 2012-13 2013-14

Excess Mortality
Laboratory-Confirmed Influenza Hospitalizations by Age Group

Preliminary data as of May 10, 2014

- 0-4 yr
- 5-17 yr
- 18-49 yr
- 50-64 yr
- 65+ yr

Influenza Season:
- 2009-10
- 2010-11
- 2011-12
- 2012-13
- 2013-14

Percent
Characterization of Influenza Viruses – February 2014

- 919/920 pH1N1 viruses were antigenically similar to A/California/7/2009
- 86/86 influenza A (H3N2) viruses were antigenically similar to A/Texas/50/2012
- 21/21 (100%) influenza B/Yamagata lineage viruses were antigenically similar to B/Massachusetts/2/2012
- 19/19 (100%) viruses influenza B/Victoria lineage viruses were antigenically similar to B/Brisbane/60/2008

- 3109/3314 influenza viruses tested were sensitive to oseltamivir
- 25 pH1N1 viruses were resistant to oseltamivir
2014 Northern Hemisphere Influenza Vaccine Recommendation - WHO

• The recommended components for the 2014–15 Northern Hemisphere influenza trivalent vaccines are an A/California/7/2009 (H1N1)-like virus, an A/Texas/50/2012 (H3N2)-like virus, and a B/Massachusetts/2/2012-like (B/Yamagata lineage) virus.

• For quadrivalent vaccines, an additional component, B/Brisbane/60/2008-like (B/Victoria lineage) virus, is recommended.
Southern Hemisphere

Number of specimens positive for influenza by subtype

Data source: FluNet (www.who.int/flunet), GISRS
WHO Region of the Americas
2013 – 2014: number of influenza-positive cases by epidemiologic week and subtype

Data Source: PAHO
Global Influenza Surveillance

Data source: FluNet (www.who.int/flunet), GISRS
Characterization of Influenza Viruses – September 2014

- 70/70 (100%) pH1N1 viruses were antigenically similar to A/California/7/2009
- 69/141 (49%) influenza A (H3N2) viruses were antigenically similar to A/Texas/50/2012
- 140/140 (100%) influenza B/Yamagata lineage viruses were antigenically similar to B/Massachusetts/2/2012
- 40/40 (100%) viruses influenza B/Victoria lineage viruses were antigenically similar to B/Brisbane/60/2008

- 325/325 viruses tested were sensitive to oseltamivir
2015 Southern Hemisphere Influenza Vaccine Recommendation - WHO

- It is recommended that trivalent vaccines for use in the 2015 influenza season (southern hemisphere winter) contain the following:
  - an A/California/7/2009 (H1N1)pdm09-like virus;
  - an A/Switzerland/9715293/2013 (H3N2)-like virus;
  - a B/Phuket/3073/2013-like virus.

- It is recommended that quadrivalent vaccines containing two influenza B viruses contain the above three viruses and a B/Brisbane/60/2008-like virus.

Expectations for 2014-2015 US Influenza Season

• US CDC and other WHO Collaborating Centers will continue to monitor influenza circulation globally

• Flu vaccine is the best way to protect against influenza
  – Vaccine Doses Anticipated by Manufacturers: 154 – 160 million doses
    • 78 million will be quadrivalent (A/H1, A/H3, B/Yam, B/Vic)
    • 41 million doses already distributed
  – Multiple Formulations
    • 21 different products from 7 manufacturers; new ACIP preference for LAIV
    • Inactivated & Live; Tri & Quadrivalent; Standard & High Dose
Recent Studies for Vaccine Effectiveness

- **August 14, 2014**
  - Among persons 65 years of age or older, high-dose influenza vaccine
    - Showed significantly higher antibody responses, and
    - Provided better protection against laboratory-confirmed influenza illness than did standard-dose vaccine.

- **September 4, 2014**
  - New study shows vaccinating mothers protects both mother and infant
  - Similar results for HIV infected mothers and their infants
Emerging Novel Influenza A Viruses

H9N2
1998-2014

H7N7

H5N1
Human Infections with H7 subtype Influenza A Viruses

- H7 virus infection in humans is uncommon and is associated with outbreaks of highly pathogenic H7 virus among poultry
- Reported human H7 infections have been generally mild, causing conjunctivitis and influenza-like illness
- Netherlands, 2003 – H7N7
  - >30 million birds either died or were culled
  - 86 humans with conjunctivitis or ILI
- Mexico, 2012 – H7N3
  - 3.8 million birds either died or were culled
  - Two human cases with conjunctivitis
- Italy 2013
  - 6 reported outbreaks in poultry
  - Three human cases with conjunctivitis

2. CDC. MMWR 2012 Sep 14;61(36):726-7
Emerging Novel Influenza A Viruses

H9N2
1998-2014
H5N1
H7N7
2009-14
pH1N1
2009-14

CDC Virologic Surveillance – 2008-10 Influenza Seasons

>600,000 Specimens Tested
- 2.5 fold increase over prior season

www.cdc.gov/flu
Emerging Novel Influenza A Viruses

- H9N2: 1998-2014
- H3N2v: 2009-14
- pH1N1: 2011-14
Emerging Issues: Swine H3N2

As the winner of the ‘Kiss a Pig’ contest, XXX kisses the pig as it takes a jumbo-sized marshmallow from his mouth. Youth Fair attendees bought votes for the person they most wanted to see kiss the pig to raise money for the 4-H swine group. http://www.thevillagenews.com/story/56324/
Novel Influenza Cases Are Increasing

Human Cases of Reported Novel Influenza A Infection, 1959-2014
includes
Avian Influenza H4, H5, H6, H7, H9, H10
Swine Influenza H1, H3 (not pH1N1)

2. Cumulative cases of H5N1. WHO.
   http://www.who.int/influenza/human_animal_interface/EN_GIP_20140124CumulativeNumberH5N1cases.pdf?ua=1
Cases of H7N9 Infection Highlight Factors Leading to Emergence of Novel Influenza

- Increasingly Crowded
  - In the affected region, around 575 million people - 45% of China, 8% of World\(^1\)

- Increasingly Connected
  - 40 Million passengers through Shanghai Airport yearly
  - Connections globally within incubation period

- Increasingly Converging
  - In the 50 km around the 60 early cases of H7N9, there were an estimated\(^2\):
    - 131 M people
    - 241M domestic chickens
    - 47M domestic ducks

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2. Butler D. Mapping the H7N9 avian flu outbreaks. www.nature.com
Factors Leading to Emergence: Internal Gene Cassettes Enable Reassortment

- Avian H9N2 Internal Gene Cassette found in:\(^1,2\)
  - HPAI H5N1 viruses that emerged in 1997
  - H7N9 viruses in 2013
  - H10N8 viruses in 2013
- Swine H1N1 Triple-Reassortant Internal Gene (TRIG) Cassette found in:\(^3\)
  - Pandemic H1N1 in 2009
  - H3N2v in 2011-12
- Either cassette (or others ?) may serve as engines for emergence of additional novel influenza viruses.

Between February 12, 2014 – August 27, 2014 two cases of A(H3N2)v were identified (both in August):

- two children in Ohio (2 year old female and 10 year old female)
- one child was hospitalized; both have fully recovered

Although both cases had exposure to swine at county agricultural fairs and/or farms prior to clinical onset

Both A(H3N2)v viruses from Ohio were closely related, and their genomes are comprised of swine triple reassortant A(H3N2) genes with NP and M from A(H1N1)pdm09
Full Genome H3N2v

North American H3N2 Triple Reassortant Swine

2011-2013 North American H3N2v

2013 North American H3N2v

2013 Iowa H3N2v

2014 Ohio H3N2v

H1N1pdm09

Classical Swine H1N1 – North American Lineage

Avian – North American Lineage

Seasonal H3N2

Eurasian Swine Lineage

H1N1pdm09
Table 1. Genome constellations identified in contemporary H3N2 viruses isolated from swine in the USA

Origin of each gene segment is colour-coded according to the gene lineage: blue, H3 and N2 of the TRIG human seasonal lineage; green, TRIG avian lineage; pink, TRIG swine lineage; lime green, 2009 pandemic H1N1 lineage. Genotypes 1–10 of reassorted rH3N2p and H3N2-TRIG viruses are colour-coded in the first column by the pattern of gene constellation. Similar colour-coding of genotypes is used in Fig. 1. The H3 subcluster A–F and N2 gene lineage is indicated in the HA and NA (neuraminidase) columns as denoted in Figs 1 and S6, respectively.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>PB2</th>
<th>PB1</th>
<th>PA</th>
<th>HA</th>
<th>NP</th>
<th>NA</th>
<th>M</th>
<th>NS</th>
<th>No. of isolates</th>
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<tr>
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<td></td>
<td></td>
<td></td>
<td>A, E</td>
<td></td>
<td>2002</td>
<td></td>
<td></td>
<td>23</td>
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<td>2</td>
<td></td>
<td></td>
<td></td>
<td>A, E, F</td>
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<td>1998</td>
<td></td>
<td></td>
<td>5*</td>
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<tr>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td>B, D</td>
<td></td>
<td>2002</td>
<td></td>
<td></td>
<td>2</td>
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<tr>
<td>4</td>
<td></td>
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<td>F</td>
<td></td>
<td>1998</td>
<td></td>
<td></td>
<td>14*</td>
</tr>
<tr>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td>E</td>
<td></td>
<td>2002</td>
<td></td>
<td></td>
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<td>6</td>
<td></td>
<td></td>
<td></td>
<td>D, F</td>
<td></td>
<td>1998</td>
<td></td>
<td></td>
<td>5*</td>
</tr>
<tr>
<td>7</td>
<td></td>
<td></td>
<td></td>
<td>C, E</td>
<td></td>
<td>2002</td>
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<td></td>
<td>3</td>
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<td>8</td>
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<td>A</td>
<td></td>
<td>2002</td>
<td></td>
<td></td>
<td>55</td>
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</tbody>
</table>

*2 of 5 isolates, 1 of 14 isolates, and 1 of 5 isolates from G2, G4 and G6, respectively, have N2-2002 gene lineage.

http://vir.sgmjournals.org
Influenza A(H5N1) Case Update

Cumulative human case count: 2003 – 2014 (n=667)

Vietnam = 127
Iraq = 3
Djibouti = 1
Nigeria = 1
Myanmar = 1
Canada = 1

Turkey = 12
Indonesia = 197
China = 47
Azerbaijan = 8
Laos = 2

Thailand = 25
Egypt = 176
Cambodia = 56
Pakistan = 3
Bangladesh = 7
# Influenza A(H7N9) Update

## Cumulative counts by Report Date

<table>
<thead>
<tr>
<th></th>
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</thead>
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<tr>
<td><strong>Countries affected</strong></td>
<td>China</td>
<td>China, Malaysia</td>
<td>China, Malaysia</td>
</tr>
<tr>
<td>Number of provinces/municipalities/areas/SARs* with confirmed cases – China</td>
<td>11 / 2 / 1 / 0</td>
<td>12 / 2 / 1 / 1</td>
<td>14 / 2 / 1 / 1</td>
</tr>
<tr>
<td>Number of confirmed cases*</td>
<td>135</td>
<td>318</td>
<td>453</td>
</tr>
<tr>
<td>Number of confirmed cases hospitalized</td>
<td>131</td>
<td>317</td>
<td>448</td>
</tr>
<tr>
<td>Number of fatal confirmed cases</td>
<td>45</td>
<td>126</td>
<td>171</td>
</tr>
<tr>
<td>Cases of confirmed human to human transmission**</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Number of probable clusters‡</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Number of confirmed clusters††</td>
<td>5</td>
<td>4</td>
<td>9</td>
</tr>
<tr>
<td>Number of asymptomatic infections</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

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\* Special administrative region of the People’s Republic of China

\* Confirmed cases include persons with laboratory confirmation of H7N9 infection through report from China CDC or Provincial CDC

\*\* Represents transmission from between confirmed cases

‡ Probable clusters include 1 or more close contacts of a confirmed case with respiratory illness. H7N9 infection cannot ruled out because appropriate test not available.

†† Confirmed clusters are two or more confirmed cases of H7N9 that are close contacts of one another.

‡‡ Includes the asymptomatic infection who was discharged from quarantine.
Epi-Curve of Avian Influenza A (H7N9) Virus Cases by Onset of Illness Date and Province, Municipality, or Area of China, 18 Feb 2013 — 18 Sep 2014 (N=452)*

* Onset date unknown for 5 cases.

* One case was reported in Malaysia on 1/30/2014 (week 5, 2014)
H7N9 Cases in Two Waves – China, 2013-14

[Map showing distribution of H7N9 cases across China, with bars indicating cases by province and week of onset.

Legend:
- First Wave Only
- Second Wave Only
- Both First and Second Waves]
Age Distribution of H5N1 Cases Compared to H7N9 Cases in China

Median (IQR):
- H5N1: 26 years (19-25)
- H7N9: 61 years (48-73)
What might occur this fall for H7N9?

- H7N9 avian and human cases likely will return this fall, c/w H5 cases
- Lack of symptoms in poultry will allow H7N9 to spread undetected
  - Cost of first H7N9 wave estimated to be at a minimum $600 million¹,²
- Humans will continue to serve as sentinels of infection in poultry
- H7N9 likely to spill over into other countries
- H7N9 vaccine developed
  - CDC synthesized vaccine candidate
  - NIH conducting trials
In addition…

• On May 5, 2014, the Sichuan Provincial Health and Family Planning Commission of China reported a fatal human infection with avian influenza A (H5N6)
  – The patient was a poultry farmer and was reported to have had exposure to sick and dead poultry prior to his illness.
  – To date, this is the only reported human infection with a HPAI H5 virus bearing an N6 NA gene (H6N6 Eurasian lineage)
  – H5N1 clade 2.3.4.6 HA with six internal genes from 2.3.2.1 clade

• Human infections with H10N8 avian influenza virus in Jiangxi province of China
  – Three H10N8 human infection cases with two deaths were reported.
  – H10N8 virus was detected in a live poultry market
  – Internal genes are of influenza A(H9N2)
Novel Influenza Virus Summary

- Factors Leading to Recognition: Increasing Awareness, Surveillance, and Diagnostic Testing
- WHO Collaborating Centers and global public health partners continue to monitor for novel influenza A viruses
- Human infection with influenza viruses circulating in other species have occurred but without sustained human-to-human transmission
- Diagnostic assays may or may not detect novel influenza viruses in human specimens
- Contact federal, state, and/or local public health laboratories for additional guidance
Influenza
Diagnostic Technology Update

RIDTs
Multiplex
PCR
REGULATIONS
Automation
RAPID
Molecular

NGS
Influenza Molecular Tests - PCR

Available in the PHL

- CDC Flu rRT-PCR Dx Panel – FDA cleared
- Flu B lineage testing – FDA cleared
- H7N9 available under EUA
- H3v evaluation for FDA approval
  - Multi-site PHL clinical study
Influenza Molecular Tests - PCR

Commercially Available - FDA Cleared

- CDC periodically updates list
- More and more clinical labs using these
- Literature in general indicates high level of performance
- Concerns:
  - Detection of novel influenza A’s
  - Variable subtyping capabilities

Multiplex PCR Respiratory Pathogen Tests

<table>
<thead>
<tr>
<th>Name</th>
<th>Manufacturer</th>
<th># Targets</th>
<th>Targets 510(k) Cleared</th>
<th>Sample &gt;Result</th>
<th>YR</th>
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<tbody>
<tr>
<td>FilmArray Respiratory Panel</td>
<td>BioFire</td>
<td>20</td>
<td>Viral &amp; Bacterial</td>
<td>Yes</td>
<td>2012</td>
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<tr>
<td>eSensor Respiratory Virus Panel</td>
<td>GenMark Diagnostics</td>
<td>14</td>
<td>Viral only</td>
<td>No</td>
<td>2012</td>
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<tr>
<td>xTAG Respiratory Virus Panel</td>
<td>Luminex</td>
<td>12</td>
<td>Viral Only</td>
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<td>xTAG Respiratory Virus Panel FAST</td>
<td>Luminex</td>
<td>8</td>
<td>Viral Only</td>
<td>No</td>
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<tr>
<td>Verigne Respiratory Virus Plus</td>
<td>Nanosphere</td>
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<td>Viral Only</td>
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<td>2011</td>
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<tr>
<td>Prodesse ProFlu+</td>
<td>Hologic Genprobe</td>
<td>3</td>
<td>Viral Only</td>
<td>No</td>
<td>2008</td>
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<tr>
<td>Simplexa FluA/B + RSV</td>
<td>Focus Diagnostics</td>
<td>3</td>
<td>Viral only</td>
<td>No</td>
<td>2012</td>
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<tr>
<td>Quidel Molecular RSV + hMPV</td>
<td>Quidel</td>
<td>2</td>
<td>Viral Only</td>
<td>No</td>
<td>2013</td>
</tr>
</tbody>
</table>
Multiplex PCR Respiratory Pathogen Tests

*Their value?*

Positivity of Respiratory Specimens by PCR at Wisconsin Laboratories (Excluding Influenza and RSV)

- Adenovirus
- Coronavirus
- Human Metapneumovirus
- Rhinovirus/Enterovirus
- Parainfluenza
Rapid Influenza Diagnostic Tests (RIDTs)

A perennial discussion

www.cdc.gov/flu/professionals/diagnosis/clinician_guidance_ridt.htm

www.jointcommission.org/siras.aspx
Rapid Influenza Diagnostic Tests
*The Next Generation*

- Incorporates reader instrument
- Reduces subjectivity
- Improved sensitivity
- CLIA-waved
- Data transmission capabilities
- A step in the right direction

**Quidel Sofia Influenza A & B**

**B-D Veritor Influenza A & B**
Rapid Influenza Diagnostic Tests
An Unique Application for Surveillance

Cellular-Linked (Cloud-Based) System for Near Real-Time Surveillance of Influenza Viruses A and B Using the Sofia® Fluorescence Immunoassay Platform

1 S Barlow, 2 L Brammer, 3 D Booker, 4 A Fowlkes, 5 A Giorgi, 6 L Mimms, 7 E Reisdorf, 8 P Shult, 9 J Tamerius, 10 J Temte

1 University of Wisconsin School of Medicine and Public Health, Madison, Wisconsin, United States; 2 Centers for Disease Control and Prevention, Atlanta, Georgia, United States; 3 Public Health Laboratory Services, Madison, Wisconsin, United States; 4 University of Wisconsin School of Medicine and Public Health, Madison, Wisconsin, United States; 5 Wisconsin State Laboratory of Hygiene, Madison, Wisconsin, United States; 6 Public Health Laboratory Services, Madison, Wisconsin, United States; 7 Seattle Biomedical Research Institute, Seattle, Washington, United States; 8 Centers for Disease Control and Prevention, Atlanta, Georgia, United States; 9 Public Health Laboratory Services, Madison, Wisconsin, United States; 10 Public Health Laboratory Services, Madison, Wisconsin, United States.

Options for the Control of Influenza VIII Meeting, Sept. 2013, Cape Town, South Africa
The Potential for “Real-time” Influenza Surveillance
Improving RIDT Performance

There are new regulations in our future

https://www.federalregister.gov/articles/2014/05/22#food-and-drug-administration

- New nomenclature proposed: **Influenza Virus Antigen Detection test**
If you are an RIDT(I VAD) user...

- **What would the new regulations entail?**
  - Reclassifying RIDTs from **Class I to Class II**
  - Add “**special controls**” to ensure device safety and effectiveness
    - Set minimum clinical performance criteria for sensitivity and specificity
    - Identify appropriate comparator tests for new assays
    - Accuracy assessed by manufacturers **each year** and when **novel strain emerges**

- **When will this happen?**
- **Possible impacts:**
  - Better tests? Fewer tests?
Rapid Influenza Diagnostic Tests

*It gets even better…*

**Molecular Results in Minutes!**

- Novel isothermal amplification technology
- Amplification of target NA at a single temperature
- Results in ~15min
- Point-of-care testing
Next Generation Sequencing (NGS)

Impact on influenza diagnostics and surveillance

Broad Applications

- Current focus on Food-borne diseases STDs, HIV
- Pathogen identification
- Antiviral/drug susceptibility
- Molecular epidemiology
- Host-pathogen interactions

- Immediate impact on influenza diagnosis and surveillance not clear at present

Update on Ongoing Efforts to “Right-Size” Influenza Virologic Surveillance
Influenza Virologic Surveillance

**Goals**

- Provide situational awareness
- Detect novel or reassortant viruses
- Inform vaccine strain selection
- Detect and monitor antiviral resistance
Influenza Virologic Surveillance Right Size Project

• How much influenza surveillance is really needed? What is the “right size”?
• Do we need more or less laboratory testing?
• How do we know the surveillance data we have provides an accurate picture of what is really happening? Is it representative of the all populations and influenza activity?
• The resulting Roadmap helps jurisdictions evaluate where we are, where we want to get to, and how to get there.

Right Size Roadmap Executive Summary
**Right Size Roadmap**

**Roadmap** to achieve an effective virologic surveillance system:

**Requirements**: define state and national virologic surveillance needs, and associated functional requirements of state and local public health laboratories.

**Implementation Guidance/toolkit** for CDC, state and local health departments and public health laboratories.

**Sample Size Calculators** to determine effective sample size needed to detect/monitor key virologic surveillance objectives.
Right Size Influenza Virologic Surveillance Requirements

- Sampling (sample size and representativeness)
- Laboratory Testing
- Data Management
- Partnerships and Communications
- Quality Systems (performance metrics, benchmarks)
- Surge (outbreaks, novel events, pandemics)
- Financial Resources

Requirements developed based on multiple engagements over 2 years of stakeholder (epi and lab) input.
Right Size Roadmap

Key First Year Efforts...

- Opening dialogue with states to help with Roadmap implementation
- “Using Alternative Data for Influenza Virologic Surveillance”
- Development of sample size calculators
- Roadmap Implementation Checklists
- Right-size Example Practices, Resources and Tools
- Communications Toolbox
Using Alternative Data for Influenza Virologic Surveillance(I)

• **What is Alternative Data**
  
  *Alternative data is *existing virologic data* from *non-public health laboratory sources* that can be used to supplement public health laboratory testing data for *improved situational awareness*.*

• **Include data from PCR(preferred) or RIDTs**

• **Benefits to surveillance:**
  
  • Enhance influenza seasonal situational awareness
  • Identify positives during low prevalence
  • Detect potential geographic clusters
  • Detect institutional outbreaks
Using Alternative Data for Influenza Virologic Surveillance(II)

- **Type and frequency of data collection**
  - Aggregate data (# tested and # positive)
  - Weekly collection
  - Test methods used
  - Consider requesting other RVP data as well

- **Request specimens for follow-up as needed**

- **Cautions:**
  - Be aware of test used by data submitters
  - Be mindful of biases
  - Time /resource intensive to set up submitter networks
Using Alternative Data for Influenza Virologic Surveillance (III)

Things to consider for success

• No one being compelled to change virologic surveillance practices
• Communication/Coordination among partners is critical
• What level of data is readily available?
  • What can PH reasonably ask for? What can clinical labs provide?
• Need to ensure detection/reporting/submission of novel viruses
• Technology advances vs. performance/interpretation
  • Ongoing monitoring of diagnostic test performance
  • Impact on surveillance
Remember Pandemic Preparedness??

www.cdc.gov/mmwr/preview/mmwrhtml/rr6306a1.htm?s_cid=rr6306a1_w
2014 Influenza Update