UPDATE: USDA Influenza A Virus Surveillance Program in Swine

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Data Disclaimers:

1. Surveillance is voluntary, passive, and for the most part anonymous.

2. No measure of disease prevalence by:
   - time
   - location
   - subtype

3. State-level data summaries are not disclosed externally beyond internal state stakeholders.
Update:

1. Regional reports
2. Program analysis/review
3. Budget
4. Program efficiencies
5. Data
   - National/Regional
   - Phylogenetic analysis
Regional IAV-S reports for Industry:

1. Report development and content:
   • 2014 USAHA with NPB, NPPC, and AASV
   • 2015 AASV meeting with AASV Influenza committee
   • Mock-up review

2. AASV Influenza Committee

3. FY 2015 Industry IAV-S reports (status)
   • 1st, 2nd, and 3rd quarter reports completed and undergoing clearance requirements before distribution
   • 4th quarter report – data in by end of November for report development
   • Planned distribution via posting to a USDA website and email to NPB, NPPC, and AASV for sharing
Program analysis:

1. Request from NPPC for IAV-S program review/analysis to determine program value
2. Approved by APHIS administrator
3. Internal analysis - APHIS’ PPD, Program Assessment & Analysis group
   • Achievements and likely outcomes generated
   • Collect / analyze program, cooperator and key stakeholder views on current and desired future of IAV-S surveillance in the U.S.
   • Identify / analyze IAV-S surveillance cost factors & develop forward projections
Program analysis:

4. External analysis
   - Technical epidemiologic review
   - Overall surveillance design, sampling efficiency, sample selection and submission process, sampled populations, representativeness of data
   - Recommendations for process improvement and system efficiencies

5. With stakeholder collaboration will consider program revisions based on analyses results / budget
Budget:

1. Initial funding through Health and Human Services (HHS) during pH1N1 outbreak
   • No year funding (use until money is spent)
2. Funds expected to expire in FY 2016
   • Once funds expended, absorbed under APHIS appropriated funding at some level
   • FY 2015 spending above expectations, working on adjustments to conserve funding (more later)
Program efficiencies:

• **Efficiencies implemented in June 2014**
  • Goal - increase # of virus isolates from samples tested
  • Evaluation:
    • CEAH-NSU analysis of samples submitted and resulting isolates
    • Presented and approved by the NAHLN technical working group, implemented June 2014
  • Efficiency:
    • CT cutoff values established for further program testing
      • CT < 35 for Nasal swabs and Lung; CT < 30 for OF
    • Limit the number of Oral Fluid samples to 5 per accession (total of 10 samples allowed per accession)
    • Reminder of ways for novel findings to be included in the program
Impact: June 2014 program modifications:

Comparing data from 11 months prior to the change with data from 11 months after the change, the # VI Attempted decreased, but average percent of successful VI’s increased by 13.00%
Program efficiencies:

Efficiencies implemented in Feb 2015

- Situation: NVSL immediately propagates all viruses that are shipped to the repository and stores until requested
- Goal: Refine use of resources
- Efficiency: NVSL influenza virus propagation of:
  - Viruses that are going into full genomic sequencing (16 viruses per month selected by NVSL based on multiple characteristics)
  - Viruses identified by research, academic, or public health partners upon request.
- Impact: potential delay (2-4 weeks) in getting a virus that is not already grown out
Program efficiencies:

Efficiencies under discussion:

• **Situation:** Increase in NAHLN testing in 2015

• **Goal:**
  • Judicious use of funds while continuing to meet program objectives and stakeholder needs

• **Evaluation:**
  • Input received from diagnostic laboratories
  • CEAH-SDA analysis of impact from reduction in CT cutoff values
  • Presented to the NAHLN Technical Working Group in early July - No concerns voiced
Program efficiencies:

Proposed efficiencies:

• Reminder:
  • Only accessions meeting program case definition of *pigs exhibiting ILI*
  • Limit 10 samples/accession, no more than 5 OF samples / accession

• Suggestions proposed by diagnostic laboratories:
  • Implement a more targeted approach to sample selection
  • Adjustments in testing algorithm
    • New CT cutoff values for further testing
    • Lung/Nasal CT < 30; OF CT <25

• For future consideration: discontinuation of the Matrix gene sequencing
  • The pandemic Matrix gene is the only Matrix gene found since Jan, 2015
  • NVSL can continue to monitor the Matrix gene through monthly WGS
Phylogenetic Analysis

The Pay-off

• Continuing cooperative agreements with Dr. Amy Vincent and her lab at ARS-NADC
  • Phylogenetic analysis of Genbank sequences from USDA IAV-S surveillance data
  • Testing novel influenza viruses in swine

• Same caveats apply regarding representativeness of sample set

• Regional phylogenic work highlighted in regional reports
  • Some of the phylogenic analysis information that is provided in reports data will be shared in this presentation
Regional Map for Influenza A in Swine

Data

Regions
- Region 1
- Region 2
- Region 3
- Region 4
- Region 5

Regions:
- Region 1
- Region 2
- Region 3
- Region 4
- Region 5
USDA IAV-S Surveillance


85,559 Samples (not Graphed)
24,040 Accessions
8,748 Positive Accessions
2,898 Accessions with viral isolates
5,537 Accessions subtyped
### USDA IAV-S Surveillance

<table>
<thead>
<tr>
<th>Region</th>
<th>Swine tested</th>
<th>Accessions</th>
<th>Positive accessions</th>
<th>Accessions with viral isolates</th>
<th>Accessions subtyped</th>
</tr>
</thead>
<tbody>
<tr>
<td>Region 1</td>
<td>7.66%</td>
<td>8.97%</td>
<td>5.04%</td>
<td>16.69%</td>
<td>11.92%</td>
</tr>
<tr>
<td>Region 2</td>
<td>54.56%</td>
<td>57.04%</td>
<td>52.07%</td>
<td>59.05%</td>
<td>52.63%</td>
</tr>
<tr>
<td>Region 3</td>
<td>10.34%</td>
<td>5.45%</td>
<td>2.52%</td>
<td>8.84%</td>
<td>7.07%</td>
</tr>
<tr>
<td>Region 4</td>
<td>21.06%</td>
<td>20.53%</td>
<td>32.10%</td>
<td>12.06%</td>
<td>20.60%</td>
</tr>
<tr>
<td>Region 5</td>
<td>0.47%</td>
<td>0.99%</td>
<td>0.48%</td>
<td>0.42%</td>
<td>0.66%</td>
</tr>
<tr>
<td>Unknown</td>
<td>5.91%</td>
<td>7.02%</td>
<td>7.80%</td>
<td>2.95%</td>
<td>7.13%</td>
</tr>
</tbody>
</table>
Regional breakdown of accessions in FY 2015 YTD

~7% of accessions submitted to USDA did not have a state location associated with them

~1% of accessions come from Region 5
Regional Subtypes deposited in Genbank (2 year Window)

Virus Type by Region

Number of swine isolates

H1N1  H1N2  H3N1  H3N2  mixed

Region1  Region2  Region3  Region4  Region5

Regional breakdown of submitted subtypes FY 2015 Q3

<table>
<thead>
<tr>
<th>Region</th>
<th>H3N1</th>
<th>H3N2</th>
<th>H1N1</th>
<th>Mixed</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Region 1</td>
<td>6%</td>
<td>28%</td>
<td>36%</td>
<td>30%</td>
<td>412</td>
</tr>
<tr>
<td>Region 2</td>
<td>5%</td>
<td>32%</td>
<td>38%</td>
<td>25%</td>
<td>1604</td>
</tr>
<tr>
<td>Region 3</td>
<td>3%</td>
<td>44%</td>
<td>27%</td>
<td>44%</td>
<td>144</td>
</tr>
<tr>
<td>Region 4</td>
<td>5%</td>
<td>44%</td>
<td>33%</td>
<td>18%</td>
<td>707</td>
</tr>
<tr>
<td>Region 5</td>
<td>5%</td>
<td>42%</td>
<td>58%</td>
<td>17%</td>
<td>12</td>
</tr>
<tr>
<td>Region Unknown</td>
<td>8%</td>
<td>29%</td>
<td>46%</td>
<td>0%</td>
<td>116</td>
</tr>
</tbody>
</table>

Region 1 (n = 412) | Region 2 (n = 1604) | Region 3 (n = 144) | Region 4 (n = 707) | Region 5 (n = 12) | Region Unknown (n = 116)
H1 phylo-cluster by Region

Number of swine isolates

Region1 Region2 Region3 Region4 Region5

alpha beta delta1 delta2 gamma pandemic

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Region 1 – FY 2015 Q3

Percentage of HA and NA combinations

<table>
<thead>
<tr>
<th>HA type</th>
<th>NA type</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>H3.1V-A</td>
<td>N1.Classical</td>
<td>0</td>
</tr>
<tr>
<td>H1.pandemic</td>
<td>N1.Pandemic</td>
<td>0</td>
</tr>
<tr>
<td>H1.gamma</td>
<td>N2.1998</td>
<td>30-40</td>
</tr>
<tr>
<td>H1.delta2</td>
<td>N2.2002</td>
<td>0</td>
</tr>
<tr>
<td>H1.delta1</td>
<td></td>
<td>0</td>
</tr>
</tbody>
</table>

Total HA & NA combinations – 299
Region 2 – FY 2015 Q3

Percentage of HA and NA combinations

Total HA & NA combinations – 857
Region 3 – FY 2015 Q3

Total HA & NA combinations – 87
Region 4 – FY 2015 Q3

Total HA & NA combinations – 187
Region 5 – FY 2015 Q3

Percentage of HA and NA combinations

Total HA & NA combinations – 2
Summary:

• Influenza A in swine continues to be dynamic/unstable
• Genomic analysis of collected data continues
• Minor modifications have been made to improve efficiencies in the program
• Working to provide regional reporting of IAV-S data to all stakeholders
• The USDA IAV-S Surveillance Program is currently undergoing an internal and external analysis to help direct the future of the program
Thanks to the USDA IAV-S Team

- **USDA-STAS**
  - Beth Lautner
- **CEAH**
  - Celia Antognoli
  - Sara Ahola
  - Marta Remmenga
  - Linde Bischak
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  - Tari Moody
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