AVIAN INFLUENZA & NEWCASTLE DISEASE ACTIVITIES

MIA KIM TORCHETTI, DVM MS PHD

SECTION HEAD - AVIAN, DIAGNOSTIC VIROLOGY LABORATORY
U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
VETERINARY SERVICES

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Overview

Part I – Year in Review
- H5/H7 status
- Test protocol and reporting

Part II – Update
- IAV and APMV-1 activity
- Test workflow
Historic global HPAI reports by subtype/year 1934-2017 (n=419; count by subtype and country)

- HPAI reported at low frequency
- Aquatic migratory birds found to be natural hosts of low pathogenic strains
- HPAI not observed in natural hosts

HPAI BY REGION N=375

- Africa
- Americas
- Asia
- Australia
- Europe
What do we know about the genesis of HPAIV from LPAIV?

ERICA SPACKMAN, MARY PANTIN-JACKWOOD, DAVID SWAYNE, DAVID SUAREZ, DARREL KAPCZYNSKI

US NATIONAL POULTRY RESEARCH CENTER

USDA-ARS, ATHENS, GA
First, what do we mean by highly pathogenic and low pathogenic?

Technically only applies to gallinaceous poultry

Highly pathogenic (HP) has always been an H5 or H7 subtype

- Other subtypes?
  - Some H4, H6 and H10 isolates (Brugh and Beck 1992; Capua et al.; Swayne et al. 1994; Wood et al. 1996) met the definition based on a IV lethality study, but not by a natural route of exposure
  - LPAIV can also cause disease, low rates of mortality, and decreases in production
Highly pathogenic: Systemic infection

Low pathogenic: Localized infection

What determines if the infection will become systemic?

- A very short protein sequence in the HA protein → the proteolytic cleavage site (PCS) – as defined for chickens

Chen, et al., Cell 95 (409-17). 1998

COURTESY OF E. SPACKMAN, ET AL, USDA NPRC, ATHENS, GA
The HA protein must be cut by an enzyme in the host cell so that the virus can replicate.

Where cleavage occurs by enzymes only in the respiratory tract or intestinal tract = LPAI

Where cleavage occurs by enzymes available in many tissues = HPAI
Why does LPAIV mutate to HPAIV in chickens and turkeys?

The mutation from LPAIV to HPAIV occurs when LPAIV circulates in chickens and turkeys.

(Courtesy of E. Spackman, et al, USDA NPRC, Athens, GA)
Can we predict which viruses will mutate?

NO...
The most sensitive and specific tools target conserved regions of the *influenza Type A* (IAV) protein or genome (e.g. matrix, nucleoprotein).

The virus pathotype is *presumptive* based upon the clinical presentation of the flock compared to the USDA [HPAI case definition](https://www.aphis.usda.gov/aphis/our-focus/poultry-and-egret/hs/hs-avian-influenza/avian-influenza-in-human-animals-and-egrets/h5n1-pennon-case-summary) and *confirmed* based upon the HA cleavage site sequence.

What do the other tests tell us?

<table>
<thead>
<tr>
<th>Target</th>
<th>HA subtype</th>
<th>NA subtype</th>
<th>pathotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>IAV AGID/ELISA</td>
<td>NP-Antibody</td>
<td>☐</td>
<td>☐</td>
</tr>
<tr>
<td>IAV HI/NI</td>
<td>HA-Antibody</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>IAV-M PCR</td>
<td>M-RNA</td>
<td>☐</td>
<td>☐</td>
</tr>
<tr>
<td>H5/H7 PCR</td>
<td>HA-RNA</td>
<td>✓</td>
<td>☐</td>
</tr>
<tr>
<td>Sequencing</td>
<td>genome</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td><em>In vivo</em> pathogenicity test</td>
<td><em>in vivo</em></td>
<td>☐</td>
<td>☐</td>
</tr>
</tbody>
</table>

✓ = test can determine  
☐ = test cannot determine
SeroLogic Test Protocol

How is the finding confirmed?

NPIP
AGID/ELISA
• Detect antibody to NP
Molecular Test Protocol

How is the finding confirmed?

NAHLN lab
rRT-PCR

- FluA (M)
- Subtype (H)
How Test Results Contribute to Flock Status*

**Subtype:**
H5 or H7

- **Clinical presentation**
- **NAHLN lab**
- **NVSL**

**Pathotype:**
Low or highly pathogenic

- **Clinical presentation**
- **NAHLN/NPIP lab**
- **NVSL**

*Avian influenza-affected flock based upon non-negative antigen results or antibody detection at a NAHLN or NPIP lab.

**Notations:**
- **Cannot determine**
- **Presumptive** by rRT-PCR
- **Confirmed** by molecular test or serology (HI/NI)
- **Confirmed** by virus sequence and/or in vivo testing

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* (Avian influenza)
## Reporting...simplified

<table>
<thead>
<tr>
<th>Test confirmed</th>
<th>Sector</th>
<th>International Reporting</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPAI or LPAI as confirmed by virus sequence &amp;/or isolation</td>
<td>HPAI – any</td>
<td>Immediate</td>
</tr>
<tr>
<td></td>
<td>LPAI – all except BYD</td>
<td></td>
</tr>
</tbody>
</table>
## 2016-17 Poultry Events

<table>
<thead>
<tr>
<th>Date</th>
<th>State</th>
<th>Surv stream</th>
<th>Subtype (AM=North American)</th>
<th>Outcome</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jan-16</td>
<td>IN</td>
<td>Commercial turkeys</td>
<td>HPAI/LPAI H7N8, first H7N8 HPAI detection</td>
<td>Limited spread, mutation to HPAI occurred at a single site</td>
</tr>
<tr>
<td>Apr-16</td>
<td>MO</td>
<td>Commercial turkeys</td>
<td>LPAI H5N1</td>
<td>Single premises with no further spread</td>
</tr>
<tr>
<td>Jun-16</td>
<td>NJ, NY, PA</td>
<td>LBM - primarily Muscovys</td>
<td>LPAI H5N2</td>
<td>Traced to single distributor/source flock</td>
</tr>
<tr>
<td>Mar-17</td>
<td>TN, AL, KY, GA</td>
<td>Commercial chickens and backyards</td>
<td>LPAI AM H7N9 HPAI in TN only</td>
<td>Multiple point source LPAI introductions; HPAI mutation occurred at a single location with lateral spread to one site</td>
</tr>
<tr>
<td>Mar-17</td>
<td>WI</td>
<td>Commercial turkeys</td>
<td>LPAI H5N2</td>
<td>Single premises with no further spread; unrelated to H5N2 from LBM</td>
</tr>
<tr>
<td>Apr-17</td>
<td>ID</td>
<td>Backyard duck</td>
<td>LPAI H5N2</td>
<td>Single premises with no further spread; unrelated to other recent H5N2</td>
</tr>
</tbody>
</table>
2016 January: AM H7N8

- Turkeys in Indiana – initial detection in response to clinical signs.
- LPAI>HPAI mutation occurred in a single flock.
- Data from a highly similar wild bird virus collected in KY 11/2015 (6/8 genes) allows estimate for both the timing and likely location of introduction, and is supported by epidemiologic data.
2017 March: AM H7N9

- Commercial chickens and backyard flocks – initial detection in response to clinical signs.
- LPAI>HPAI mutation occurred once (later during circulation) with a single event of secondary spread.
- Data from a highly similar wild bird virus collected in WY 9/2016 (8/8 genes) allows estimate for timing and frequency of introductions, and is supported by epidemiologic data.
- More than one independent introduction.

H2N2 in Northeast LBMS since 2014

<table>
<thead>
<tr>
<th>LBM H2N2</th>
<th>2015</th>
<th>2016</th>
<th>2017</th>
</tr>
</thead>
<tbody>
<tr>
<td>CT</td>
<td>3</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>MA</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>NJ</td>
<td>7</td>
<td>13</td>
<td>6</td>
</tr>
<tr>
<td>NY</td>
<td>8</td>
<td>5</td>
<td>80</td>
</tr>
<tr>
<td>PA</td>
<td>3</td>
<td>0</td>
<td>21</td>
</tr>
<tr>
<td>RI</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>
H7N2 in Cats at NYC Shelter

Rare bird flu strain infects 45 cats in single Manhattan shelter and may have spread to recently adopted felines