UPDATE ON AVIAN INFLUENZA

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The disease = **Avian Influenza (AI)**  
The agent = **influenza A virus (IAV)**

Influenza A viruses with high pathogenicity (HPAI) and **H5 and H7** subtypes with low pathogenicity (H5/H7 LPAI) are reportable worldwide.

**Waterfowl are natural hosts for H1-H16 influenza A of avian origin**, but **not** usually HPAI.

Influenza A viruses tend to circulate within flyways seasonally and wax/wane and in multiyear cycles.

The only **HPAI** currently recognized to circulate in natural reservoir hosts emerged in domestic poultry in **Asia (goose Guangdong [GsGD] lineage H5N1)**
Avian Influenza Ecology

Over 200 avian species are susceptible hosts.
IAV can rapidly EVOLVE

- Antigenic Drift
- Antigenic Shift

- Pathotype: determined in CHICKENS
- Potential for H5/H7 to mutate from LPAI to HPAI
  - Addition of basic amino acids (AA) most common, H5 or H7
  - Accumulation of basic AA
  - Insertion of random sequence (H7)
  - Viruses with different cleavage sites may often circulate simultaneously

- Host Adaptation
  e.g. Gs/GD lineage H5N2

Mallards > Pheasants, Partridges, GF, Pekin, geese > Quail > Turkeys > Chickens

ADAPTED FROM E. SPACKMAN AND M. PANTIN-JACKWOOD SEPRL
OIE HPAI 2005-2016 Sept

Triangles = Wild bird H5 HPAI GsGD
HPAI 2014/15 Confirmed Detections

211 Commercial Flocks
21 Backyard Flocks
50,400,000 Birds Affected
6/16/15 Last Detection Reported
Network cheat sheet

- *Oldest viruses are centrally located*
- *Orientation of branch for visual only*
- *Length of branch is meaningful - indicates number of nucleotide substitutions from index case*
  - *Longer branches originating from the spine suggestive of point source or independent introduction*
  - *Shorter branches radiating from cluster suggestive of secondary or lateral spread*

**Recall:**

- *All viruses are highly similar and all >99% identical to index (oldest) detections*
- *More wild bird viruses are available from the Pacific Flyway as compared to Midwest for analysis*
Network analysis
H5Nx 5-genes

TMRCA HA gene

- icA H5 Jun 2013
- EA H5N8 Oct 2014
- EA/AM H5N2 Nov 2014
- EA/AM H5N1/N8 Dec 2014

Courtesy Lee DH, USDA ARS SEPRL
For more information refer to
http://dx.doi.org/10.3201/eid2207.160048
H5N2 Midwest First Detections

8-gene network: 17 detections spanning 5 states and 16 counties from 27 February to 20 April 2015; long branches suggest largely point source introductions with limited evidence of lateral spread.

Network analysis with DH Lee USDA/ARS/SEPRL
Mapping with USDA/CEAH

Refer to H5 September 2015 Epi and Virus Report
Phylogeny of other US H5/H7s

Use of sequencing both for rapid determination of LPAI/HPAI and lineage as well as virus characterization

Ongoing internal and external collaboration on bioinformatics
HA H7s 2015-2016

Different from H5N8 2.3.4.4

2015 BYD PA H7N7 LPAI

2016 TKY IN H7N8 HPAI/LPAI

2015 TKY CA H7N3 LPAI

Wild bird 2015-16

LBM/BYD
COMM
WILD

1971 TKY OR H7N3

2001 DCK PA H7N3
1995 TKY UT H7N3
1997, 2002 CKN PA H7N2
1998 QUA PA H7N2
1998 GSE NY H7N2
2001-03 PLT NJ, MA, NY H7N2
2001-02 NY, NC, VA PLT H7N2
1998 GSE NY H7N2
1998 GSE NY H7N2
2010 DCK NJ H7N3
2011 GSE NE H7N9
2014 CKN DE H7N7
2012-14 CKN MX H7N3

2015 TKY CA H7N3 LPAI

2015 BYD PA H7N7 LPAI

2016 TKY IN H7N8 HPAI/LPAI

Different from H5N8 2.3.4.4

2010 DCK NJ H7N3
2004 CKN BC H7N3
2001-03 PLT NJ, MA, NY H7N2
2001-02 NY, NC, VA PLT H7N2
1998 GSE NY H7N2
1998 QUA PA H7N2
1995 TKY UT H7N3
1997, 2002 CKN PA H7N2
1998 GSE NY H7N2
2001-03 PLT NJ, MA, NY H7N2
2001-02 NY, NC, VA PLT H7N2
1998 GSE NY H7N2
1998 GSE NY H7N2
2010 DCK NJ H7N3
2011 GSE NE H7N9
2014 CKN DE H7N7
2012-14 CKN MX H7N3

2015 TKY CA H7N3 LPAI
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