Tracking Genetic Evolution of Avian Influenza Viruses

Frank Wong
Team Leader – Agent Characterization

OIE Seminar, WAVLD, Saskatoon, 15-18 June 2015
CSIRO Australian Animal Health Laboratory

One of the world’s largest laboratories for the safe handling and containment of animal diseases
- Viral diseases of livestock and zoonoses
- Diagnosis, surveillance and research
- BSL3/4 large animal facility (1000 m²)
- BSL3 insectary
- Small animal facility and farm facility

OIE Reference Laboratory for multiple diseases
OIE Collaborating Centre for New and Emerging Animal Diseases
OIE Collaborating Centre for Veterinary Laboratory Capacity Building
WHO Collaborating Centre for SARS

Influenza Activities:
OIE Reference Laboratory for Avian Influenza
FAO Reference Centre for Animal Influenza
Reference Laboratory for OFFLU:
- Animal Health & Food Security
- Zoonotic Influenzas & Pandemic Risks
(participates in the WHO VCM for zoonotic AIV)
How does OFFLU Lab Network contribute to the WHO VCM process?

- Focus on sharing **timely** genetic data from zoonotic influenza viruses circulating in birds (and animals) to track virus evolution and identify emergence (Asian HP-H5N1/H5Nx, HP-H7, H7N9, H9N2, novel subtypes)
- Fills crucial surveillance gap where human health sector does not have access to human isolates
- Collate associated epidemiological, outbreak, and sample metadata
- Key labs produce HI data from H5 HPAI viruses using standardised antigenic panels produced by WHO-CCs that represent the circulating lineages/clades & CVVs (consist of strain specific ferret antisera and corresponding homologous virus antigens)
- **Speed up production of human vaccines against emergent zoonotic and potentially pandemic influenza viruses**
- Assess animal influenza viruses for zoonotic potential, before spillover occurs (analysis of key genetic residues)
Emergent LP AIV (to poultry) of zoonotic concern

A(H7N9)
A(H10N8)
A(H9N2)
(1) Zoonotic A(H7N9) situation update

Human cases: (to 9 June 2015)

- 661 confirmed; 252 deaths (38% CFR)
- Reported cases generally severe illness (eg. ARS)
- >200 cases in 3rd wave (since Oct 2014)
- 3 exported human cases: 1 in Sabah, Malaysia and 2 in BC, Canada; otherwise not yet detected outside of China & its ARs.
A(H7N9) HA genetic drift

- Increasing genetic heterogeneity over the successive infection waves in humans
- Leading to separation into sub-lineages

Limitations of WHO VCM data:
- Majority are HA data; what novel reassortments could be occurring?!
- Ongoing need for more WGS from current viruses!

Source: WHO Feb 2015 VCM (HKU data)
A(H7N9) – FAO targeted risk-based surveillance in at-risk countries outside China

Total number of samples (mostly chicken) collected in at-risk countries from April 2013 to October 2014 (active & retrospective sampling)

<table>
<thead>
<tr>
<th>Country</th>
<th>Virological samples</th>
<th>Serological samples</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bangladesh</td>
<td>11333</td>
<td>2235</td>
<td>13568</td>
</tr>
<tr>
<td>Bhutan</td>
<td>780</td>
<td>4058</td>
<td>4838</td>
</tr>
<tr>
<td>Lao PDR</td>
<td>3843</td>
<td></td>
<td>3843</td>
</tr>
<tr>
<td>Myanmar</td>
<td>18827</td>
<td>2009</td>
<td>20836</td>
</tr>
<tr>
<td>Nepal</td>
<td>2204</td>
<td>798</td>
<td>3002</td>
</tr>
<tr>
<td>Viet Nam</td>
<td>33480</td>
<td></td>
<td>33480</td>
</tr>
<tr>
<td>Total</td>
<td>70467</td>
<td>9100</td>
<td>79567</td>
</tr>
</tbody>
</table>

→ Avg. 1.9%–36.3% virological samples were FluA positive per country
→ No A(H7N9) CHN detected
(2) Novel Zoonotic A(H10N8), China - Summary

- First report of A(H10N8) infection in humans in Nanchang, Jiangxi Province in Dec 2013
- 3 human cases reported from Jiangxi Province since Feb 2014
- All infected individuals had severe disease with 2 fatalities
- All cases had contact with poultry or associated contaminated environment (LBM/LPM)
- Zoonotic A(H10N8) characterised; genes of AI origin with internal genes (PB2, PB2, PA, NP, M, NS) derived from A(H9N2) viruses circulating widely in chickens in China (reassortment with H9N2 genetic backbone similar to H7N9)
- Presence of a complex picture of A(H10N8) genotype variants indicate prior extended circulation of related viruses in the regional poultry population

Sources: (1) Chen H et al, 2014, Clinical and epidemiological characteristics of a fatal case of avian influenza A H10N8 virus infection : a descriptive study. The Lancet. Published online February 5, 2014 http://dx.doi.org/10.1016/S0140-6736(14)60111-2;
Emergent novel H5-HP AIV of zoonotic concern

Clade 2.3.4.4 A(H5Nx)
eg. zoonotic A(H5N6)
Distribution of reported notifiable avian influenza events/outbreaks from Feb 2013 to Feb 2015

Includes WAHID entries
2014-2015!

CDC: No human bird flu cases, but keep an eye out

H5N6 man CHN
H5N8 poultry KOR
H5N2 poultry USA
H5N6 Poultry CHN
Eurasian H5N1 (>15 years)

Rapid intercontinental spread of emergent Eurasian clade 2.3.4.4 H5Nx HPAI (2014-2015)

KOR/JPN H5N8 cluster (2014). Reassortants with some H5N2 internals & H3N8-NA. >15mill poultry deaths in Rep KOR; ongoing poultry outbreaks.

H5N8 EUR

H5N8 & H5N1/H5N2 N.Am. >47mill poultry deaths in USA

H5N8 JPN

VNM/14 H5N1 cluster (2014). Detected by active LBM surveillance

GD CHN/LAO H5N6 cluster (2013-2015); 1 human case. Reassortant with 2.3.2.1 H5N1 internals and H6N6-NA(trunc). Ongoing poultry detections in CHN and LAO.

CHN/KOR H5N2 & H5N8 cluster (2011-2014). Reassortants with some H11N9 internals & mix of LPAI N2/N8-NA.

SCH CHN/VNM H5N6 cluster (2014-2015); 2 human cases. Reassortant with 2.3.2.1 H5N1 internals and H6N6-NA. Ongoing poultry detections in CHN and VNM.

Novel Eurasian Clade 2.3.4.4 H5 HPAI – Summary
Regional Spread of novel H5N6 HPAI 2014

AIVs circulating in domestic duck populations, SE China

- H5Nx HPAI clade 2.3.4.4
- H5N1 HPAI clade 2.3.2.1b
- H6N6 LPAI

Mixing in LBMs leading to novel reassortants in mixed poultry

- HA
- NA

Export to neighboring countries via poultry trade movement

Novel H5N6 LBM/LPM in South-East China since 2013

Novel H5N6 Lao PDR/Vietnam 2014
A(H5N6) Lao PDR – antigenically divergent

Reference antigen:

<table>
<thead>
<tr>
<th>Clade</th>
<th>2.3.4</th>
<th>2.3.4</th>
<th>2.3.4</th>
<th>2.3.2.1</th>
<th>2.3.2.1b</th>
<th>2.3.2.1a</th>
<th>2.3.2.1c</th>
<th>2.3.2.1a</th>
<th>2.3.2.1a</th>
<th>2.3.2.1a</th>
<th>2.3.2.1a</th>
</tr>
</thead>
<tbody>
<tr>
<td>JWE/HK/1038/06</td>
<td>2.3.4</td>
<td>80</td>
<td>80</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DK/Laos/3295/06</td>
<td>2.3.4</td>
<td>&lt;40</td>
<td>160</td>
<td>80</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Anhui/1/05</td>
<td>2.3.4</td>
<td>&lt;40</td>
<td>320</td>
<td>320</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CM/HK/5052/07</td>
<td>2.3.2.1</td>
<td>&lt;40</td>
<td>40</td>
<td>80</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BS/HK/1161/10</td>
<td>2.3.2.1b</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>80</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DK/VNM/NCVD-2848/13</td>
<td>2.3.2.1c</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CK/BGD/15205/12</td>
<td>2.3.2.1a</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>40</td>
<td>80</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ENV/BGD/15121/12</td>
<td>2.3.2.1a</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DK/BGD/19097/13</td>
<td>2.3.2.1a</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CK/BGD/42010/12</td>
<td>2.3.2.1a</td>
<td>&lt;40</td>
<td>40</td>
<td>40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/DK/VNM/NCVD-1584/12</td>
<td>2.3.2.1c</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>40</td>
<td>80</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/DK/VNM/NCVD-129-7/11</td>
<td>2.3.2.1b</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Test antigen:

<table>
<thead>
<tr>
<th>Clade</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
<th>2.3.4.6</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/CK/Laos/LPQ001/14(H5N6)</td>
<td>2.3.4.6</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/DK/Laos/LPQ002/14(H5N6)</td>
<td>2.3.4.6</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/CK/Laos/XBY003/14(H5N6)</td>
<td>2.3.4.6</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/DK/Laos/XBY004/14(H5N6)</td>
<td>2.3.4.6</td>
<td>&lt;40</td>
<td>&lt;40</td>
<td>40</td>
<td>&lt;40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Antigenically unrelated to older 2.3.4 H5N1 reference viruses; >30 aa differences in HA1 subunit

Concerns for diagnostic serodetection and coverage of current vaccine virus candidates for pandemic preparedness
Spread of novel Eurasian H5N8 & Eurasian/American(Intercontinental) H5N2 HPAI in North American Poultry

• First ever introduction of Eurasian H5 HPAI into Nth America
• Wholly Eurasian Clade 2.3.4.4 H5N8
• Mixed-IC Clade 2.3.4.4 H5N2 with Nth Am LPAIV PB1, NP and N2 genes.
• Mixed-IC H5N1 with Nth American LPAIV PB1, PA, N1 and NS genes.
• Largest HPAI poultry outbreaks in USA
• No human infections

Summary

• A(H7N9) has provided a new awareness of the zoonotic potential of LPAI of miscellaneous subtypes circulating in poultry (difficult to detect as no clinical signs in birds)...eg. alerted to detection and concerns over recent China A(H10N8) human cases

• Increased interest in A(H9N2) host infection dynamics and genome mechanics

• Over 2013-2015, several new reassortant HPAI viruses of divergent Eurasian clade 2.3.4.4 H5-HA lineage with different NA subtypes have emerged and spread globally, threatening both poultry-dependant livelihoods and human health

• OFFLU formulating assistance strategy for at-risk & affected countries in the region to implement AI surveillance to enable early detection of incursion or spread of H5N6 (SE Asia) and other novel HPAI viruses
Importance of Whole Genome Surveillance of AIV (facilitated by NGS Approach)

- Tracking genetic drift of all gene segments
- Identification of endemic vs. exotic origins
- Identification of novel genomic reassortants
- Identification of genetic markers for zoonotic potential
NGS applications at CSIRO-AAHL

NGS capabilities: on-site Illumina MiSeq (in secure facility) and external access

Research
- Animal Influenza virus genome dynamics and evolution
- Bluetongue virus landscape genomics
- Urbanisation and disease emergence - pathogen distribution and dynamics
- Virus discovery and characterisation
- Mosquito anti-viral immune pathways

Disease outbreak investigation
- Unresolved veterinary diagnoses

Exotic disease response
- Foot-and-mouth disease

Surveillance
- OIE/FAO OFFLU network – rapid avian influenza characterization
Two approaches to MiSeq NGS of AIV samples

(i) Random/non-target biased amplified libraries:

Based on random amplification primers from Palacios et al. 2007. EID. 13, No. 1. DOI: 10.3201/eid1301.060837

(ii) Influenza specific amplified libraries:


Target specific

Random/”shotgun”
## Random approach – lower coverage

<table>
<thead>
<tr>
<th>Sample</th>
<th>Subtype</th>
<th>details</th>
<th>Index1/2</th>
<th>Number of reads</th>
<th>% mapped to ref AIV genome</th>
</tr>
</thead>
<tbody>
<tr>
<td>06-01614-1</td>
<td>A/Silver Gull/Tasmania/349/2006 (H13N6)</td>
<td>0801-21-1630 P3AF HA1:?</td>
<td>N701/S501</td>
<td>2984926</td>
<td>32.5</td>
</tr>
<tr>
<td>12-01051-11</td>
<td>A/Peking Duck/NSW/33/2012 (H4N6)</td>
<td>1204-05-2011 P2AF HA 1:16</td>
<td>N704/S501</td>
<td>960022</td>
<td>63.2</td>
</tr>
<tr>
<td>12-01056-10</td>
<td>A/Turkey/NSW/10/2012 (H9N2)</td>
<td>1204-16-1010 P1AF HA 1:128</td>
<td>N705/S501</td>
<td>2415106</td>
<td>0.9</td>
</tr>
<tr>
<td>12-03121-5</td>
<td>A/chicken/NSW/12-03121-5/2012 (H7N7)</td>
<td>Pass 1 A/F</td>
<td>N706/S501</td>
<td>2087684</td>
<td>1.9</td>
</tr>
</tbody>
</table>

## Targeted approach – good coverage

<table>
<thead>
<tr>
<th>Sample</th>
<th>INFLUENZA</th>
<th>1PB2</th>
<th>2PB1</th>
<th>3PA</th>
<th>4HA</th>
<th>5NP</th>
<th>6NA</th>
<th>7MP</th>
<th>8NS</th>
<th>total reads mapped</th>
<th>Unused Reads</th>
<th>total reads</th>
<th>% mapped</th>
</tr>
</thead>
<tbody>
<tr>
<td>13-02584-11</td>
<td>H1N1 (swine)</td>
<td>42638</td>
<td>46768</td>
<td>76078</td>
<td>114941</td>
<td>146765</td>
<td>205344</td>
<td>269440</td>
<td>276646</td>
<td>1178613</td>
<td>14279</td>
<td>1192892</td>
<td>99</td>
</tr>
<tr>
<td>13-02811-01</td>
<td>H7N2 (avian)</td>
<td>206825</td>
<td>264123</td>
<td>175424</td>
<td>354129</td>
<td>203819</td>
<td>211921</td>
<td>340376</td>
<td>442134</td>
<td>2198751</td>
<td>27479</td>
<td>2226230</td>
<td>99</td>
</tr>
<tr>
<td>13-02929-08</td>
<td>H7N2 (avian)</td>
<td>158877</td>
<td>455092</td>
<td>240399</td>
<td>500652</td>
<td>455776</td>
<td>292247</td>
<td>813838</td>
<td>809431</td>
<td>3726297</td>
<td>47309</td>
<td>3773606</td>
<td>99</td>
</tr>
<tr>
<td>13-02509-01</td>
<td>H1N1 (swine)</td>
<td>207579</td>
<td>234983</td>
<td>260933</td>
<td>344552</td>
<td>352719</td>
<td>524774</td>
<td>778886</td>
<td>670936</td>
<td>3375361</td>
<td>29057</td>
<td>3404418</td>
<td>99</td>
</tr>
<tr>
<td>13-01599-01-01</td>
<td>H7N9 (wild bird)</td>
<td>247297</td>
<td>407299</td>
<td>147937</td>
<td>341147</td>
<td>388474</td>
<td>68368</td>
<td>796649</td>
<td>467251</td>
<td>3479729</td>
<td>135809</td>
<td>3615538</td>
<td>96</td>
</tr>
<tr>
<td>13-02465-63</td>
<td>H7N9</td>
<td>335347</td>
<td>248091</td>
<td>227443</td>
<td>460191</td>
<td>387513</td>
<td>387529</td>
<td>599367</td>
<td>498795</td>
<td>3144271</td>
<td>68585</td>
<td>3212856</td>
<td>98</td>
</tr>
</tbody>
</table>
NGS in animal health - issues

• Data sharing
  – Disease reporting and impacts on trade
  – IP and data ownership
• Presence of agent vs presence of disease
  – Sequences vs viable pathogen
  – Non-pathogenic variants
• Tests fit for purpose
  – Diagnostic sensitivity and specificity
  – Validation for targeted surveillance, presumptive diagnosis, confirmatory diagnosis
• Quality assurance and traceability
  – ISO accreditation
  – Standardisation of methodologies
  – Quality control
  – Proficiency testing
• Baseline host sequence data
  – Multitude of species (particularly aquatics)
• Global animal disease information system
• Facilitates access to regional and global disease information
• Early warning and response to trans-boundary and high impact diseases

How to maximise use of your AIV sequences
Linking virus genetic data with disease information
Original article

The EMPRES-i genetic module: a novel tool linking epidemiological outbreak information and genetic characteristics of influenza viruses

Filip Claes\textsuperscript{1,\dagger}, Dmitry Kuznetsov\textsuperscript{2,\dagger}, Robin Liechti\textsuperscript{2,\dagger}, Sophie Von Dobschuetz\textsuperscript{2}, Bao Dinh Truong\textsuperscript{1}, Anne Gleizes\textsuperscript{2}, Daniele Conversa\textsuperscript{1}, Alessandro Colonna\textsuperscript{1}, Ettore Demaio\textsuperscript{1}, Sabina Ramazzotto\textsuperscript{1}, Fairouz Larfaoui\textsuperscript{1}, Julio Pinto\textsuperscript{1}, Philippe Le Mercier\textsuperscript{2}, Ioannis Xenarios\textsuperscript{2,*} and Gwenaelle Dauphin\textsuperscript{1,*}

\textsuperscript{1}Animal Health Service, Food and Agriculture Organization of the United Nations (FAO), Viale delle Terme di Caracalla, 10532 Rome, Italy and
\textsuperscript{2}Vital-IT/Swiss-Prot Groups, SIB, Swiss Institute for Bioinformatics, Quartier Sorge, 1015 Lausanne, Switzerland

OpenFlu database

\textsuperscript{SIB} Swiss Institute of Bioinformatics
The genetic module takes advantage of:

- **Existing EMPRES-i tools and functions**: spatial mapping, graphs, export of information and interfaces with other databases (e.g. GLiPHA)

- **OpenFluDB phylogenic tools** already developed, e.g. Sequence Similarities Maps (SSM)
### Disease Event Details

#### General Info
- **Disease Event ID**: 173557
- **Reporting date**: 15/10/2004
- **Observation date**: 15/10/2004

#### Location
- **Region**: Asia
- **Admin 1 (Country)**: Suphanburi (Thailand)
- **Locality**: Suphanburi
- **Lat/Long**: 14.69922 / 99.89504

#### Disease
- **Status**: Confirmed
- **Disease**: Influenza - Avian
- **Serotype**: H5N1 (HPAI)
- **Source**: National authorities

#### Species affected
- **Type**: Domestic
- **Class**: Mammal
- **Species**: dogs

#### Laboratories
- **Disease Tested**: Influenza - Avian
- **Species**: dogs

#### Genetic Information
- **Type/Subtype**: H5N1
- **Isolate Name**: A/H5N1/Thailand-Suphanburi/KU-08/04
- **Isolates (OpenFlu)**: HA, MP, NA, NP, NS, PA, PB1, PB2
- **Key Mutations (Isolates (OpenFlu))**: PB21-62M2, NS1

---

**Definition of links**

**Export to XLS**
Sequence record

A/duck/Vietnam/7/2010

OpenFlu Isolate ID: OFL_ISL_50557
Name and synonyms: A/duck/Vietnam/7/2010
Type/subtype: A/H5N1
H5 Clade ID: 1.1.2
Sample collection date: 2010-02-17
Host: Animal - Anas sp. - Duck
Location: Viet Nam
First submission: 2011-03-17
Last update: 2011-11-08

Authors
Sequence submitter: public domain

Epidemiological properties
Empres-i disease event id: 160397

Computed annotations
Protein name: HA
Numbering on the reference sequence: 329
Numbering on the reference sequence: 330
RRKRR
High Pathogenicity: 1
Multibasic cleavage site: 1

action segment length OpenFlu acc DDBJ/EMBL/GB sequence and info

gene HA
incomplete CDS
117 nucleotides missing at 5' end
01 nucleotides missing at 3' end

0001 gttctgttta cacatgcca agacactca gaaagcgc aatacggaa
0051 gctcttgac ctatgtgga tttggcttc aatatttga gattgtgtg
0101 tgcgttagc gttttcggc aacccagt gtgtcgatgt catctggtg
0151 ccagatgt ctatatagt ggagaggcc atccagctca atgcctcctg
0201 ttctccgga gtttccaaa ctgatgaa atgggaca ctctgggca
0251 gataaaacc ttttggag aattgagta ttcgaagaag ttctttgccc
0301 actcagac cctctgcggg gtgtccgct gcctcctc accagggc
0351 gctcttttt ttcԲaғaг ttttsgtct tttttttaag aacagtcst

complete CDS in bold
download in fasta format
Virus information

Other sources (information tracking, FAO projects)

Peer-reviewed publications

Sequence and meta data

Outbreak-isolate link

Selected virus meta data

Epi data

Selected Epi meta-data
eg. In Asia – ~20,000 H5N1 HPAI outbreaks have been recorded since 2004
However only ~400 of the outbreaks linked to virus sequences in databases
Customizable cluster information – eg. distribution of particular H5N1 clades

OUTBREAKS DATA – Influenza – Avian, Asia (H5N1 HPAI) – Clade information

Outbreaks

- Clade 1 and derived
- Clade 2.1 and derived
- Clade 2.2 and derived
- Clade 2.3 and derived
- Clade 2.3.2 and derived
FLU EMPRES-i Summary

- Centralized platform for disease events that offers multiple species/subtype/strain surveillance
- Surveillance (IRD-EMPRES-i) can be customizable to needs and constraints
- Linkage of epi/virus information and alignment of information across global flu databases
- Monitoring of virus circulation: outbreaks and isolates
- Useful for molecular epi and contributes to risk assessments
Acknowledgements

FAO HQ, Rome:
Gwenaelle Dauphin, Filip Claes, Sophie Dobschuettz

FAO Regional office for Asia/Pacific, Bangkok:
Wantanee Kalpravidh, Subhash Morzaria

OFFLU Network Reference Laboratories and Regional National Animal Health Laboratories

AAHL Diagnosis Surveillance & Response Group

www.offlu.net