Follow-up report No. 2

Report Summary
Name of sender of the report: Dr. John Clifford
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Place: Deputy Administrator

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Washington 20250

Date submitted to OIE: 13/02/2015

Disease: Highly pathogenic avian influenza

Cause Agent: Highly pathogenic avian influenza virus

State of report: 13/02/2015

Date of start of the event: 16/01/2015

Date of start of the event: 16/01/2015

Date of pre-confirmation of the event: 16/01/2015

Serotype(s): H5N1

Country or zone: A zone or compartment

Clinical signs: No

Number of outbreaks: submitted = 1, Draft = 0

Outbreak Details

<table>
<thead>
<tr>
<th>State</th>
<th>Number of Outbreaks</th>
<th>County</th>
<th>Unit Type</th>
<th>Location</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Start Date</th>
<th>End Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>WA</td>
<td>-</td>
<td>Whatcom</td>
<td>Not applicable</td>
<td>Whatcom County</td>
<td>48.796</td>
<td>-121.866</td>
<td>16/01/2015</td>
<td></td>
</tr>
</tbody>
</table>

Species: Green-winged Teal (Anas carolinensis)

Measuring units: Animals

Susceptible: No applicable

Cases: No applicable

Deaths: No applicable

Destroyed: No applicable

Slaughtered: No applicable

AFFECTED POPULATION: Wild American green-winged teal duck

Outbreak summary: Total outbreaks = 1 (Submitted)

Species: Green-winged Teal

Susceptible: No applicable

Cases: No applicable

Deaths: No applicable

Destroyed: No applicable

Slaughtered: No applicable

Epidemiology

Epidemiological comments:

As part of the increased AI surveillance of wild birds (performed by testing hunter harvested birds), another Eurasian H5 clade 2.3.4.4 virus has been identified through whole genome sequencing of the virus isolate. Introduction of the Eurasian (EA) H5N8 virus into the Pacific Flyway sometime during late 2014 has allowed mixing with North American (AM) lineage viruses and generated new combinations with genes from both EA and AM origin (or “reassortant” viruses) such as the EA/AM H5N2-reassortant detected in Canada and the United States. Such findings are not unexpected as the EA-H5N8 virus continues to circulate. A novel EA/AM H5N1-reassortant clade 2.3.4.4 was isolated from an American green-winged teal in Whatcom County, Washington. This H5N1 subtype is different from strain circulating in Asia. The gene constellation is as follows: Eurasian lineage genes (PB2, H5, NP, MP >99% identical to A/gyrfalcon/WA/41088/2014 H5N8); North American lineage genes (PB1 (98% identical to A/Northern pintail/Washington/40964/2014 H5N2), PA, N1, NS of North American LPAI wild bird lineage. The HA cleavage site is compatible with strains that are highly pathogenic.

As of 12 February 2015 there are no new occurrences of novel EA/AM H5N1.

This novel HPAI EA/AM H5N1-reassortant virus has NOT been found in commercial poultry anywhere in the United States.

Source of the outbreak(s) or origin of infection:
• Contact with wild species

Measures applied

No Control Measures

Animals treated: Vaccination Prohibited

No: Yes

Future Reporting
The event is continuing. Weekly follow-up reports will be submitted.