

## Follow-up report No.2

Report reference: , Reference OIE : 17191, Report Date : 13/02/2015, Country : United States of America

### Report Summary

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<b>Animal type</b>	Terrestrial	<b>Date of report</b>	13/02/2015
<b>Disease</b>	Highly pathogenic avian influenza	<b>Date of start of the event</b>	16/01/2015
<b>Causal Agent</b>	Highly pathogenic avian influenza virus	<b>Date of pre-confirmation of the event</b>	16/01/2015
<b>Serotype(s)</b>	H5N1	<b>Date of last occurrence</b>	2004
<b>Reason</b>	Reoccurrence of a listed disease	<b>Diagnosis</b>	Laboratory (advanced)
<b>Country or zone</b>	a zone or compartment	<b>Clinical signs</b>	No
<b>Number of reported outbreaks</b>	submitted= 1, Draft= 0		

### Outbreak details

State	Number of outbreaks	County	Unit Type	Location	Latitude	Longitude	Start Date	End Date:
WASHINGTON-other report - submitted	-	Whatcom	Not applicable	Whatcom County	48.796	-121.866	16/01/2015	
Species	Measuring units	Susceptible	Cases	Deaths	Destroyed	Slaughtered		
Green-winged Teal:Anatidae(Anas carolinensis)	Animals	...	...	...	...	...		
Affected Population	Wild American green-winged teal duck							

### Outbreak summary: Total outbreaks = 1 (Submitted)

Species	Susceptible	Cases	Deaths	Destroyed	Slaughtered
Green-winged Teal					

### 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	
<b>Animals treated</b>	<b>Vaccination Prohibited</b>
No	Yes

### Future Reporting



## Outbreak maps

