

Follow-up report No.1

Report reference: , Reference OIE : 17125, Report Date : 03/02/2015, Country : United States of America

Report Summary

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Animal type	Terrestrial	Date of report	03/02/2015
Disease	Highly pathogenic avian influenza	Date of start of the event	16/01/2015
Causal Agent	Highly pathogenic avian influenza virus	Date of pre-confirmation of the event	16/01/2015
Serotype(s)	H5N1	Date of last occurrence	2004
Reason	Reoccurrence of a listed disease	Diagnosis	Laboratory (advanced)
Country or zone	a zone or compartment	Clinical signs	No
Number of reported outbreaks	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 2 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

Outbreak maps

