

Follow-up report No.7

Report reference: , Reference OIE : 17530, Report Date : 15/04/2015, Country : United States of America

Report Summary

Name of sender of the report	Dr John Clifford	Telephone	(1-202) 799-7146
Position	Deputy Administrator	Fax	(1-202) 799-7146
Address	Room # 317-E	Email	John.Clifford@aphis.usda.gov
	Jamie L. Whitten Federal Building 1400 Independence Ave, SW Washington, DC 20250 Washington 20250	Date submitted to OIE	15/04/2015

Animal type	Terrestrial	Date of report	15/04/2015
Disease	Highly pathogenic avian influenza	Date of start of the event	16/01/2015
Causal Agent	Highly pathogenic avian influenza virus	Date of 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= 2, 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	15/04/2015
Species	Measuring units	Susceptible	Cases	Deaths	Destroyed	Slaughtered		
Green-winged Teal:Anatidae(Anas carolinensis)	Animals		
Affected Population	Wild American green-winged teal duck							

State	Number of outbreaks	County	Unit Type	Location	Latitude	Longitude	Start Date	End Date:
WASHINGTON- (this report - submitted)	-	Whatcom	Not applicable	Whatcom County	48.9131	-122.5976	05/03/2015	
Species	Measuring units	Susceptible	Cases	Deaths	Destroyed	Slaughtered		
American wigeon:Anatidae(Anas americana)	Animals		
Affected Population	Wild bird surveillance.							

Outbreak summary: Total outbreaks = 2 (Submitted)

Species	Susceptible	Cases	Deaths	Destroyed	Slaughtered
Green-winged Teal					
American wigeon					

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 was 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, NI, NS of North American LPAI wild bird lineage. The HA cleavage site is compatible with strains that are highly pathogenic.

As of 15 April 2015 there was one new occurrence in wild birds 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.

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 was 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 15 April 2015 there was one new occurrence in wild birds 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.

- Contact with wild species

Source of the outbreak(s) or origin of infection

- Contact with wild species

Measures applied**No Control Measures****Animals treated**

No

Vaccination Prohibited

Yes

Diagnostic test results

Laboratory Type	Name of Laboratory	Species	Test Type	Date Results Provided	Result
National laboratory	National Veterinary Services Laboratories (NVSL)	American wigeon	real-time reverse transcriptase/polymerase chain reaction (RRT-PCR)	05/03/2015	Positive
National laboratory	National Veterinary Services Laboratories (NVSL)	American wigeon	virus sequencing	05/03/2015	Positive

Future Reporting

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

Outbreak maps

