

Immediate notification report

Report reference: REF OIE 16771, Report Date: 16/12/2014, Country : United States of America

Report Summary

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Animal type	Terrestrial	Date of report	16/12/2014
Disease	Highly pathogenic avian influenza	Date of start of the event	10/12/2014
Causal Agent	Highly pathogenic avian influenza virus	Date of pre-confirmation of the event	15/12/2014
Serotype(s)	H5N2	Date of last occurrence	2004
Reason	Reoccurrence of a listed disease	Diagnosis	Laboratory (advanced)
Country or zone	a zone or compartment	Clinical signs	Yes
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- (this report - submitted)	-	Whatcom	Not applicable	Whatcom County	48.9	-122.48	10/12/2014	
Species	Measuring units	Susceptible	Cases	Deaths	Destroyed	Slaughtered		
Northern Pintail: Anatidae(Anas acuta)	Animals		
Affected Population	Wild pintail ducks							

Outbreak summary: Total outbreaks = 1 (Submitted)

Species	Susceptible	Cases	Deaths	Destroyed	Slaughtered
Northern Pintail					

Epidemiology

Epidemiological comments

As a precaution and in response to the recent HPAI outbreak in Canada, surveillance of poultry premises and of wild bird mortality events was enhanced by the USDA, and State personnel along the United States - Canadian Border. Through this surveillance, highly pathogenic avian influenza (HPAI) H5 was identified in wild birds. Two serotypes were identified on enhanced surveillance, both with amino acid sequence at the HA cleavage site consistent with HPAI, H5N8 and H5N2. H5N8 was identified in a captive wild gyrfalcon that was fed hunter killed wild birds from Whatcom County, Washington and H5N2 was identified in a wild pintail duck also from Whatcom County, Washington. Preliminary analysis suggests this H5N2 is similar to the HPAI identified in the current Canadian outbreak. Based upon sequence attempt from a virus isolate, an avian influenza subtype H5 of Eurasian lineage (partial HA 98% similarity to A/bean goose/Korea/H40/2014) and N2 of US wild bird lineage (partial NA 98% similarity to A/American green-winged teal/California/HKWF609/2007); the amino acid sequence at the hemagglutinin cleavage site is consistent with highly pathogenic avian influenza (HPAI).

Preliminary data suggests that these virus strains (H5N2 and H5N8) may be related with the H5N8 strain potentially representing the progenitor; however further analysis is needed. Neither of these viruses has been found in any poultry in the United States. These H5N8 and H5N2 detections involve only wild birds. Further investigation and characterization of the HPAI viruses is ongoing.

Source of the outbreak(s) or origin of infection

• Unknown or inconclusive

Measures applied

No Control Measures

Animals treated	Vaccination Prohibited
No	Yes

Diagnostic test results

Laboratory Type	Name of Laboratory	Species	Test Type	Date Results Provided	Result
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Laboratory Type	Name of Laboratory	Species	Test Type	Date Results Provided	Result
National laboratory	National Veterinary Services Laboratories (NVSL)	Northern Pintail	real-time reverse transcriptase/polymerase chain reaction (RRT-PCR)	15/12/2014	Positive
National laboratory	National Veterinary Services Laboratories (NVSL)	Northern Pintail	virus isolation	15/12/2014	Positive
National laboratory	National Veterinary Services Laboratories (NVSL)	Northern Pintail	haemagglutination (HA) test	15/12/2014	Positive
National laboratory	National Veterinary Services Laboratories (NVSL)	Northern Pintail	gene sequencing		Pending

Future Reporting

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

Outbreak maps

