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OFFLU statement on outbreak of H5N1 high pathogenicity avian influenza in Newfoundland, Canada

The recent detection of an H5N1 high pathogenicity avian influenza (HPAI) virus in Newfoundland, Canada represents the first identification of goose/Guangdong/1/96-lineage (Gs/GD/96) H5 HPAI virus in the Americas since June 2015. This is cause for concern for wild birds, zoological collections, and poultry in the Americas[1]. Some east coast states of the United States of America (USA) are home to very large poultry populations that could be at risk of exposure and outbreaks in the next few months. This finding raises concerns about the potential of this virus becoming established in the Americas within migratory and resident birds.

Epidemiological information on the HPAI outbreak is limited. It involved an exhibition farm in St John's on the Avalon Peninsula and resulted in the death of 360 of 409 mixed species of birds (layers, geese, ducks, silkie hens, peafowl, turkeys) kept on the farm. Full genome sequence of the virus were obtained from nine clinical samples collected from the infected premise. Based on BLAST analysis all eight gene segment of the virus are Eurasian origin. The virus has been confirmed as a clade 2.3.4.4b H5N1 virus, phylogenetically all eight gene segments of the virus are related to 2.3.4.4b clade H5N1 virus currently circulating widely in wild birds and poultry in Europe. The outbreak commenced on 9 December 2021. This is the first time that a clade 2.3.4.4b virus within the goose/Guangdong/1/96-lineage (Gs/GD/96) has been detected in the Americas. The remaining birds in the farm were depopulated and the Canadian authorities are continuing investigations, including additional testing of wild birds and poultry in the area.

High pathogenicity Gs/GD/96-lineage H5 virus was last introduced to North America in late 2014 and caused the largest animal health emergency in the USA during 2015. That virus arrived from Asia across the Bering Strait, belonged to clade 2.3.4.4c, and, initially, affected birds on the west coast of Canada and the USA. The current Newfoundland outbreak represents a new introduction of a different, but phylogenetically related, high pathogenicity virus. This virus lineage has shown to be capable of being carried over long distances by migratory birds, based on experiences from Eurasia and Africa.

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[1] See https://wahis.oie.int/#/report-info?reportId=45054 and https://inspection.canada.ca/animal-health/terrestrial-animals/diseases/reportable/avian-influenza/statement/eng/1640207916497/1640207916934

It has been recognised for some time that, although avian influenza viruses tend to be classified into North American and Eurasian lineages, viral genes and, on occasions, whole viruses can cross the Atlantic divide (Dusek *et al.* 2014). The introduction of a Gs/GD/96-lineage H5 HPAI via this route was considered possible previously (Sims *et al*. 2017). We postulate that a wild bird introduction might have occurred in the current outbreak (direct or indirect), although other pathways cannot be ruled out. If this is the result of wild bird introduction, experiences from Eurasia suggest that rapid and wide dispersal of virus could occur. There are few poultry in the Maritime provinces of Canada, which means there is a limited population of susceptible poultry that could provide a warning of wider transmission of the virus by wild birds.

We urge all countries in the Americas and Caribbean to increase surveillance of wild birds and poultry for any evidence of infection with this virus, and, also, advise poultry producers and keepers of other types of birds to implement stricter biosecurity measures until more information becomes available.

References

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