

O1210 Avian influenza surveillance: LPAI and HPAI H5Nx viruses in northern Eurasia: 2005-2019

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Background: Wild aquatic birds migrate to and congregate in Asian wetlands and lakes for breeding and molting. Major wild aquatic bird migration routes overlap in Asian part of Russia, connecting this broad geographic area to the wintering grounds of Eurasia and Africa. The unique ecosystem of these territories has been implicated and plays a crucial role in the geographical dispersal of the virus as it was shown by HPAI H5N1 spreading in 2005–2010 and in 2014–2015.

Materials/methods: The specimens were tested for AIV, then isolates were characterized by standard methods.

Results: During AIV surveillance in wild bird population in Asian part of Russia in 2005–2019 more than 11000 avian samples were collected and screened according to the standard protocols. All samples were collected from the various sites located at the studied territory, such as Novosibirsk region, Tuva region, Russian Far East. In total, more than 200 LPAI viruses and 50 HPAI H5Nx were isolated. In winter 2017–2018 clade 2.3.4.4. HPAI H5N2 were registered in Central Russia. The LPAI viruses were further subtyped as H1N1, H3N8, H4N6, H5N3, H8N4, H11N9. In summer and autumn of 2016, several outbreaks were reported at Uvs-Nuur Lake on the border of Russia and Mongolia and in Novosibirsk region and then spread to the west to European countries. In winter 2017–2018 the virus re-emerged to Central Russia and caused poultry outbreaks. All isolated viruses, which caused outbreaks, belong to novel highly pathogenic avian influenza viruses of subtype H5N8, clade 2.3.4.4. The H5N8 viruses were found to be reassortant with other avian influenza viruses in waterfowl and shorebirds of Northern Eurasia. We conducted the pathogenic potential assessment of the viruses with molecular-biological analysis and animal models. In this study we have shown circulation of different Avian Influenza viruses in Russia in 2005–2019.

Conclusions: The report contains more detailed comparative virological, molecular, pathogenic characteristics of viruses with emphases at HPAI H5N8. This study demonstrates the need for ongoing surveillance to detect new variants of influenza viruses and facilitate prevention of outbreaks.

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