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**NORTH-EASTERN ASIA
AS A MODERN GENETIC SUBGROUP GENERATION CENTER
FOR HIGHLY PATHOGENIC AVIAN INFLUENZA A / H5 VIRUSES
(*ORTHOMYXOVIRIDAE, INFLUENZAVIRUS A*)**

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Hemagglutinin type 5 of highly pathogenic avian influenza A (HPAI) virus (*Orthomyxoviridae, Influenzavirus A*), which is distributed nowadays all over the world and is the main epizootic threat for poultry as well as wild birds, was appeared in the South Chinese province of Guangdong. This hemagglutinin of prototype A/goose/Guangdong/1/1996 (H5N1) strain changing many times during genetic shifts and generating new genetic subgroups participated in various reassortations; it still circulates and evolves.

New genetic subgroups are formed every winter of Northern Hemisphere when the virus is forced to change to avoid collective immunity in dense populations of overwintering birds. In spring, migrating birds introduce small amounts of new viral subgroups into nesting areas in Northern Eurasia. Even these small amounts of new subgroup origin are enough to amplify in the non-immune juvenile bird populations and accumulate in noticeable amounts closer to the autumn – to the new periods of the migration of wild birds. This natural process takes place annually and is the basis for the emergence of new genetic subgroups.

Starting from the winter of 2013–2014, the center for the formation of new genetic subgroups shifted from South–Eastern to North–Eastern Asia. During referred overwintering period HPAI/H5N8/2.3.4.4 subgroup was appeared in the Korea Peninsular. In autumn 2014 one of the genotype, <D3>, belonging to HPAI/H5N8/2.3.4.4 was found throughout the migration routs of wild birds in Republic of Sakha (Yakutia) (A/wigeon/Sakha/1/2014), the Netherlands, Germany, great Britain and Italy; migration of birds to the East initiated the epizootic process in Japan, in the North direction – in the North America, where genotypes HPAI/H5N8/2.3.4.4/<AmN1> and <AmN2> were formed as result of reassortation with American variants. In the next overwintering period it was the North–Eastern Asia where new genotypes of HPAI/H5N8 and HPAI/H5N6 were appeared.

Monitoring of influenza A virus in the Far East allows detecting the wide penetration of new variants into Northern Eurasia. Such monitoring is conducting nowadays in the frame of the Network Project of Russian Scientific Foundation “Forecasting of Avian Influenza spreading in Russia and Japan for prevention and control: Involvement of East Asian – Australasian Flyway in genetic migration and reassortment of influenza virus” N 17-44-07001.