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Biological diversity of avian influenza viruses in birds circulating in the Asian part of RussiaMarina Gulyaeva A^{1,2}, Sharshov K A¹, Sobolev I A², Yurlov A K³ and Shestopalov A¹¹Research Institute of Experimental and Clinical Medicine-RAS, Russia²Novosibirsk State University, Russia³Institute of Systematics and Ecology of Animals-RAS, Russia

The disease of animals and humans, called influenza, is caused by representatives of the family of Orthomyxoviruses. The waterfowl and shorebirds are supposed to be a natural reservoir of the most subtypes of AIV. The territory of Western Siberia is located in the center of Eurasia and is intersected by three main bird migratory routes, pathways from Europe, Africa, Asia and Oceania. The study of the biological diversity of AIV in wild birds at the territory of Western Siberia was carried out in 2007-2018. 3,375 samples were collected from birds of 8 orders. 285 strains of AIV (including HPIV) were isolated from the material, collected from Anseriformes. During the period from 2007 to 2018, the percentage of viruses in the Anseriformes varied from 5.6% to 20%. The order of the Charadriiformes is characterized by lower percentage of virus isolation. In our study, the percentage of AIV isolation from this species was 1.4%. Phylogenetic analysis of the M gene of all isolated AIV strains showed that they belong to the classical avian-like viruses. All viruses on the phylogenetic tree of the M gene are located chaotically, which indicates the persistence of various variants of the M gene in the wild bird population of Western Siberia. Thus, Western Siberia plays an important role in the persistence of avian influenza viruses, their evolution and geographical distribution in the Eastern Hemisphere.

mgulyaeva@gmail.com