

Ecology of Avian Influenza Viruses in Siberia (pp. 83-160)

Wild aquatic birds represent major reservoirs of the influenza A virus gene pool, from which novel influenza viruses can emerge to infect other avian and mammalian species, including humans. These avian hosts have long been considered the natural reservoir for low pathogenic avian influenza viruses (AIVs) that, in some occasions, can evolve in poultry to become highly pathogenic (HP) AIVs posing a risk for animal and public health. However, changes in viral ecology have been recently observed with the possibility of perpetuation of HPAIVs in the aquatic bird reservoir. Siberia is of great importance in influenza A virus ecology. After a short reproductive season, huge numbers of wild aquatic birds move from different subarctic breeding sites and congregate in pre-migration staging areas of Siberian wetlands. Major intra-and inter-continental bird flyways overlap in these breeding and/or molting grounds where water birds from different wintering regions of the world are brought together, thus providing the influenza A virus gene pool for the possible emergence of novel reassortant viruses. Moreover, in the context of the global ecology of influenza A viruses, Siberian wetlands play a crucial role in the geographical dispersal of the virus, as shown by the HPAI H5 infections, which have spread since the early 2000s via migratory birds from Asia towards Europe, Africa, Middle East and, more recently, North America. Here we consider ecological interactions that take place within the vast region of Siberia among the avian reservoir hosts and viral populations, and the environment they utilize. We also consider ecological drivers which, in the context of the current global change, can modulate in this Asian portion of Russia the influenza A virus circulation and spill-over from wild bird reservoirs to different avian and/or mammalian hosts.