



Dr. Yoshihiro Sakoda is an Associate Professor in the Laboratory of Microbiology, Graduate School of Veterinary Medicine, Hokkaido University, Japan. After his graduation from the Faculty of Veterinary Medicine, Hokkaido University in 1994, he began his career as a researcher in the Exotic Disease Division of the National Institute of Animal Health, Japan. Subsequently, he moved to Hokkaido University as a Lecturer in 2001 and became an Associate Professor in 2007. He is an active member of the OIE Reference Laboratory for Highly Pathogenic Avian Influenza, headed by Professor Hiroshi Kida.

His main fields of interest are molecular epidemiology and pathogenesis and interspecies transmission of influenza viruses; he has been extensively involved in research in these areas. In addition, he is interested in the pathogenesis of classical swine fever and bovine viral diarrhoea viruses, as his PhD thesis was on the development of novel diagnostic methods for classical swine fever. He has contributed to the eradication of classical swine fever in Japan. Dr. Sakoda has published more than 100 peer-reviewed scientific papers in international journals.

In 2006, he was awarded the Asian Veterinary Science Prize by The Asian Association of Veterinary Schools for his research regarding highly pathogenic avian influenza. In 2008, he received the Award for Young Agricultural Researchers for the development of new diagnosis and vaccine for H5N1 highly pathogenic avian influenza from the Ministry of Agriculture, Forestry and Fisheries, Japan. In addition, it was decided that he will receive the award of the Japanese Society of Veterinary Science in 2013 for his continuous research on classical swine fever and bovine viral diarrhoea viruses.

**YOSHIHIRO
SAKODA**

Associate Professor

*Graduate School of
Veterinary Medicine
Hokkaido University
Japan*

As a member of the OIE Reference Laboratory for Highly Pathogenic Avian Influenza, he is continuously bringing tremendous zeal to the international collaboration for the control of avian influenza. He supports the diagnosis and surveillance of reference laboratories in Russia, Taiwan, Korea, Mongolia, Vietnam, Thailand, and other countries for the control of avian influenza under the umbrella of the One World, One Health concept.

GLOBAL AND NATIONAL SURVEILLANCE

of Animal Influenza to Control Highly
Pathogenic Avian Influenza

Yoshihiro SAKODA, DVM, PhD

Laboratory of Microbiology, Department of Disease Control, Graduate
School of Veterinary Medicine, Hokkaido University,

Avian influenza caused by infection with H5N1 highly pathogenic avian influenza virus (HPAIV) has spread in poultry in more than 60 countries in Eurasia and Africa since 1996, when the first outbreak occurred at a goose farm in Guangdong province in China. H5N1 HPAIV infections have become endemic in several countries and cause accidental transmissions to humans. H5N1 viruses are thus now recognized as one of the most likely candidates for the next pandemic. The widespread presence of H5N1 HPAIVs in poultry, especially in domestic ducks reared in free range, has inevitably resulted in the water-borne transmission of viruses to wild bird populations since domestic ducks and geese infected with HPAIV shed progeny viruses with feces into ponds at farms, where migratory water birds visit. In the past, such infections had been restricted to wild birds found dead in the vicinity of infected poultry farms, but it is now a concern that infections in wild birds in which HPAIV has caused mild clinical signs (e.g., ducks) could result in the spread of viruses to large areas. Infection with HPAIVs in many wild bird species at 2 water

bird parks in Hong Kong was reported in 2002 and further, more significant outbreaks in wild water birds occurred at Lake Qinghai in Western China, and Khunt and Erkhel Lakes in Mongolia in 2005. H5N1 HPAIV infections in poultry and wild birds have now spread in Asia, Europe, and Africa, and it has been suggested that the H5N1 virus could spread by migratory water birds to the west and south, since genetically closely related H5N1 viruses have been isolated in several countries since 2005. To monitor whether these HPAI viruses perpetuate in nature, virological surveillance of avian influenza has been carried out in the lakes in Japan, Mongolia, Russia, where ducks congregate on their migration path from Siberia to the south since 2001.

H5N1 highly pathogenic avian influenza virus (HPAIV) was reintroduced and caused outbreaks in chickens in 2010-2011 winter season in Japan, that had been free from highly pathogenic avian influenza (HPAI) since 2007 when HPAI outbreaks occurred and were controlled. On October 14,

2010 at Lake Ohnuma, Wakkanai, the northernmost part of Hokkaido, Japan, H5N1 HPAIVs were isolated from fecal samples of ducks flying from their nesting lakes in Siberia. Since then, in Japan, H5N1 HPAIVs have been isolated from 63 wild birds in 17 prefectures and caused HPAI outbreaks in 24 chicken farms in 9 prefectures by the end of March in 2011. Each of these isolates was genetically closely related to the HPAIV isolates at Lake Ohnuma, and those in China, Mongolia, Russia, and Korea, belonging to genetic clade 2.3.2.1. Wild water birds start migration from their nesting lakes in the northern territory to the south in the middle of August. The migratory routes of water birds are from Siberia to northern Japan via the Kamchatka Peninsula or Sakhalin Island, and to southern Japan via the Korean Peninsula or the coast of northeastern China. Our results indicate that the viruses circulating in different populations of wild migratory birds at their nesting lakes in Siberia in summer were transmitted through at least 3 different routes via China, Korea or Russia to Japan in the 2010-2011 winter season. Then, further virus spread occurred in wild birds at the resting lakes of birds in Japan by water-borne transmission or predation of carcass. Taken together, our results raise the possibility that H5N1 HPAIVs were perpetuated at the nesting lakes in Siberia before the migration of water birds to Japan.

The other serious concern is that 592 people have been infected with the H5N1 virus, 60% of whom died in 15 countries since 2004 (as of 5 March 2012). Most of the human cases (87%) are in China, Viet Nam, Indonesia, and Egypt where bird flu vaccines are used. In Egypt, 152 human cases have been reported since 1996 when vaccination to poultry started. In Thailand, 25 human cases had been reported until 2006, when the government decided to concentrate on stamping out policy without the use of vaccine for the control of avian influenza, and no human case has been reported thereafter. Unless the H5N1 HPAIVs should be eradicated from poultry in Asia, the viruses must perpetuate in the lakes where migratory water birds nest in summer in Siberia and disastrous outbreaks of HPAI must occur in each Asian country every year. We, thus, strongly propose to minimize the outbreak based on the results of global and national surveillance and eradicate immediately the H5N1 HPAIVs from Asia by stamping-out without misuse of vaccine through international collaboration under the umbrella of One World, One Health concept.