Ecology and host range of avian influenza viruses

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High pathogenicity avian influenza is a fatal infectious disease of poultry, which has now spread worldwide, causing extensive damage to poultry and wildlife. The causative agent, high pathogenicity avian influenza virus (HPAIV), is mainly introduced into Japan via bird migration; therefore, it is important to monitor the virus among wild birds for the control of the disease. Accordingly, we have monitored the HPAIV through active and passive surveillance using fecal samples of migratory ducks and carcasses of dead wild birds. As a result, we found that while HPAIV was not predominant in wild birds until around 2014, many wild birds were found dead with HPAIV and carried the virus to Japan during the winter of 2016-2017. In 2022, we demonstrated HPAIV infections during the mass mortality event in a crow flock in a public garden in Sapporo, Hokkaido. During the event, we also isolated HPAIVs from a fox and a raccoon dog found in the same garden. This was the first case of HPAIV isolation from mammals in Japan. As a result of continued monitoring of HPAIVs in the same garden, H5N5 subtype HPAIVs, which had previously been detected only locally in Western Russia and Northern Europe, were isolated from crows in Hokkaido, suggesting that the virus was introduced to Japan from Europe across the Eurasian continent. Furthermore, we experimentally inoculated various HPAIVs into crows, sparrows, and black rats and found that crows and sparrows are highly susceptible to HPAIV infection, although there are differences among virus strains.

The receptor of influenza viruses is a sialic-acid-containing glycans. These receptors have been largely classified into two types based on the linkage of the terminal sialic acid and the penultimate galactose: Siaα2-6Gal (human-type) and Siaα2-3Gal (avian-type). The binding specificity of viruses to the avian or human receptors is one of the major factors that define their preference for hosts. We focused on the difference in susceptibility to influenza viruses between ducks and chickens and clarified that the difference in susceptibility is related to the difference in glycan structures in the avian receptor. After the findings, we promoted the interdisciplinary research between veterinary microbiology and glycoscience, focusing on the structural diversity of avian influenza virus receptors. As a result, we demonstrated the importance of the structural diversity of avian-type receptors as a determinant of the susceptibility to avian influenza viruses in turkeys, foxes, and raccoon dogs. Following the report of HPAIV infections in dairy cattle in the United States in 2024, we also revealed that various avian-type receptors are distributed in the bovine mammary gland, the target tissue for virus infection.

Assessing the risk of avian influenza virus infection in wildlife is extremely important from the perspective of elucidating the route of virus invasion into poultry flocks and conservation medicine. Therefore, it will be necessary to continue to monitor virus invasion in wildlife, analyze the receptor specificity of isolated viruses, and clarify the distribution of receptors in various animals in order to understand the risk of virus infection in each species.