

Development of a Risk Factor Surveillance System for Conservation of Endangered Bird Species and Studies on the Risk for their Population Reduction Due to Avian Influenza Virus Infection and a Countermeasure against the Risk

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[Abstract]

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This project consisted of four subthemes. In subtheme 1, we established an efficient isolation technique for highly pathogenic avian influenza viruses (HPAIVs) from environmental water. In addition, we experimentally infected three species of wild ducks that share the habitat of endangered bird species. We found that the ducks shed the virus without any symptoms after HPAIV infection, and had the virus in multiple organs. This indicates that the ducks could be a natural source of infection for endangered species. In subtheme 2, we evaluated detection procedures for HPAIV genes and antigens, and showed that they were effective. We also evaluated the therapeutic potential of the anti-influenza drug Baloxavir marboxil using HPAIV-infected chickens and found that it had therapeutic effects. The concentration of antiviral active substance after administration of the drug was different between ducks and white-tailed eagles, indicating the need to determine the appropriate dosage for each bird species. In subtheme 3, we experimentally infected white-tailed sea eagles, an endangered species. HPAIV intranasally infected was detected systemically, and was continued to be detected in oral swabs for about a week. This indicates that infected eagles have a high potential for non-contact transmission of the virus to other individuals. We also examined whether disinfectants used in livestock farms could be used to decontaminate water but these efforts were unsuccessful. Other methods of disinfection need to be developed. In subthemes 1 and 3, many HPAIVs were isolated from environmental water samples, indicating that water could be used to monitor viruses in the environment. In subtheme 2, we isolated the first HPAIV detected in Japan in the winter of 2020-2021 in a fecal survey in Hokkaido. Our ability to isolate the virus prior to the domestic epidemic made it possible to alert poultry farms to HPAIV. In subtheme 4, we established a method to evaluate the susceptibility of endangered bird species to HPAIV infection without the need to experimentally infect live birds. The method was based on comparing the expression level of the Mx gene in cultured cells after HPAIV infection. Mx expression was found to increase significantly in avian species that are relatively resistant to HPAIV infection, while it did not increase significantly in susceptible avian species. These results indicate that the expression of Mx may be a useful indicator of the susceptibility of each bird species to HPAIV infection.

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