



HOKKAIDO UNIVERSITY

Title	Studies on epidemiology and control of H5 high pathogenicity avian influenza virus in Japan
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学位論文内容の要旨
Abstract of the dissertation

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Studies on epidemiology and control of H5 high pathogenicity avian influenza virus in Japan
(日本における H5 高病原性鳥インフルエンザウイルスの疫学および制御に関する研究)

This study assessed the epidemiology, evolution, and transmission dynamics of clade 2.3.4.4b H5 HPAIV, with a focus on repeated introductions into Japan in recent years. By integrating molecular, pathogenic, and phylodynamic analyses, this thesis aimed to clarify viral diversity, transmission pathways, and potential control measures to mitigate HPAIV outbreaks in poultry through enhanced biosecurity.

In Chapters I and II, multiple genetically distinct H5 HPAIVs detected in Japan during winters 2022–2024 were characterized. Based on HA gene analyses, these viruses were classified into four subgroups (G2a, G2b, G2c, and G2d), each associated with distinct geographic origins, including Europe, Northeast Asia, North Asia, and Northwest America. These findings suggest that Japan may serve as a hub for multiple independent viral introductions from different regions each winter. Despite their genetic diversity, all subgroups retained high pathogenicity in chickens. Differences in disease severity between broiler and layer chickens indicated variation in host susceptibility. Antigenic analyses showed that recent clade 2.3.4.4b viruses remain antigenically similar and show limited divergence from strains circulating over the past decade, indicating minimal antigenic drift and low selective pressure on the HA surface glycoprotein.

In Chapter III, phylodynamic analyses provided insights into the geographic origins and host transmission routes of H5N1 HPAIVs circulating in Japan from 2021 to 2025. Distinct

introduction patterns were observed among subgroups: G2c viruses were primarily linked to Northeast Asia, whereas G2b viruses originated in both Northeast and North Asia. The G2d subgroup initially shared a common ancestor with viruses detected in Northwest America and North Asia, but later shifted toward Northeast Asian origin. Interspecies transmission analyses indicated that waterfowl in the family Anatidae, and possibly raptor species, play key roles in viral dissemination within Japan. In contrast, poultry and several wild bird species, including crows, charadriiformes, and cranes, typically act as terminal hosts. However, repeated annual viral incursions appear to have altered transmission dynamics, enabling spillover from hosts previously considered terminal to other avian species.

In Chapter IV, gaseous ClO₂ was evaluated as a biosecurity intervention. Exposure to low concentrations of gaseous ClO₂ (0.05 ppmv) for 5 minutes effectively inactivated aerosolized H5 HPAIV under *in vivo* conditions, providing near-complete protection for chicks against HPAIV infection. Although maintaining stable concentrations of gaseous ClO₂ in large environments can be challenging, targeted applications in ventilation systems or at enclosed farm entry points may offer a practical approach to reducing the risk of viral introduction into poultry facilities.

In summary, this thesis provides a comprehensive assessment of the epidemiology, evolution, and transmission dynamics of clade 2.3.4.4b H5 HPAIV in Japan. The integration of molecular, pathogenic, and phylodynamic data underscores the importance of continuous surveillance for monitoring viral evolution, assessing emerging risks, and enabling timely interventions. Furthermore, the demonstrated efficacy of gaseous ClO₂ supports its use as an additional biosecurity measure, contributing to improved control strategies for HPAIV in Japan and other affected regions.