

The Impacts of Avian Influenza Virus NS1 proteins on Viral Compatibility and Immune Response



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Date and time

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11:00 ~ 12:00

Venue

東京農工大学 府中キャンパス
50周年記念ホール
Memorial Hall
(Alumni 50th Anniversary Hall)
Fuchu Campus, TUAT

Abstract

Avian influenza virus (AIV) could possibly cause severe diseases in poultry worldwide. From 1985, H6N1 AIV was the dominant enzootic subtype in the chicken farms of Taiwan until the initial outbreak of a low pathogenic avian influenza (LPAI) H5N2 virus in 2003; thereafter, this and other LPAIs have been sporadically detected. In 2015, the outbreak of three novel H5Nx of highly pathogenic avian influenza (HPAI) emerged and devastated Taiwanese chicken and waterfowl industries. The mechanism of variation in pathogenicity among these viruses is unclear, but, in light of the many biological functions of viral non-structural protein 1 (NS1), including interferon antagonist and host range determinant, we hypothesized that NS genetic diversity contributes to AIV pathogenesis. To determine the impact of NS1 variants on viral infection dynamics, we established a reverse genetics system with the genetic backbone of the enzootic Taiwanese H6N1 for generation of reassortant AIVs carrying exogenous NS segments of three different Taiwanese H5N2 strains. Among the reassortant viruses, we observed distinct cellular distributions of NS1. Moreover, exchange of the NS segment significantly influenced growth kinetics and induction of cytokines (IFN- α , IFN- β , and TNF- α) in a NS1- and host-specific manner. The impact of NS1 variants on viral replication appears related to their synergic effects on viral RNA-dependent RNA polymerase activity and IFN response. With these approaches, we revealed that NS1 is a key factor responsible for the diverse characteristics of AIVs in Taiwan.



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