

ONE HEALTH SEMINAR SERIES

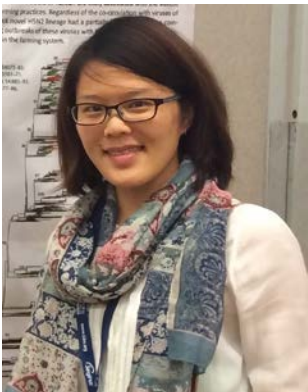
INTENSIVE POULTRY PRODUCTION AND THE ECOLOGY AND EVOLUTION OF INFLUENZA VIRUSES IN TAIWAN

Ecosystem of avian influenza viruses (AIV) has been shaped by intensive poultry production systems, resulting in the emergence and outbreaks of zoonotic AIVs such as H7N9, H10N8 and highly pathogenic Asian H5Nx AIVs in China and worldwide. Taiwan, an important stopover site on a migratory flyway and an island containing high density of poultry populations, has recently suffered from repeated outbreaks caused by H5 AIVs of multiple lineages in poultry. Taiwan also reported the world's first known H6N1 AIV infections in a human and a canine, from a lineage enzootic in chickens (TW H6N1). The increased influenza activity in Taiwan might be attributable to the development and encroachment of intensive poultry farms into natural habitats, increasing the contact between wild and domestic birds. Yet, the relevant findings are incomplete due to the lack of systematic investigation.

To expand our knowledge of AIVs in poultry in Taiwan, evolutionary and molecular analysis was performed on the full genomes of 141 and 586 AIVs from 14,602 chicken and 6,585 duck swabs collected from a live poultry market in Taiwan between December 2012 and May 2014. Full genomes of 95 archived AIVs isolated during 2005-11 at the same market and 34 goose samples collected in 2015 at farms were also included in the analysis.

Results showed that various low pathogenic and clade 2.3.4.4 of Asian H5Nx AIVs were mainly introduced by wild birds from neighbouring regions to Taiwan and frequently exchanged genes with local AIVs, resulting in diverse virus genotypes in domestic ducks. A unique low pathogenic H5N2 AIV lineage (TW H5N2) were found to become persistent and prevalent (47.8%) in domestic ducks in Taiwan. Distinct to AIVs from wild waterfowl, TW H5N2 viruses showed elevated evolutionary rates in genes, a partially fixed gene constellation and enhanced binding to both avian- and human-type receptors, which was likely attributable to a large number of densely populated birds on farms. Almost all chicken isolates belonged to either TW H6N1 or its reassortant Mexico/94-like H5N2 AIVs (Mex-like H5N2), which likely emerged and became enzootic in chickens through vaccination. These two AIV lineages were later found in domestic ducks, implying the bridging role of domestic ducks between aquatic wild waterfowl and terrestrial poultry. Molecular signatures favouring mammalian infections were found in proteins of multiple AIV lineages in poultry in Taiwan, revealing the zoonotic potential of these viruses. This study demonstrates that the intensive poultry production systems might affect the genetic diversity and evolutionary characteristics of AIVs in poultry, particularly domestic ducks, which have posed risks to veterinary and human public health in Taiwan. Strengthened surveillance of AIVs in domestic and wild birds is mandatory for making effective disease control strategies to prevent future emergence of novel AIVs in this region.

ABOUT THE SPEAKER



Dr. Pei-Yu Huang received her PhD from the School of Public Health at the University of Hong Kong (HKU) focusing on the evolutionary and ecological genomic research of avian influenza viruses in poultry in Taiwan. She received her master degrees in Veterinary Science at the University of Liverpool and in Animal Science at the National Taiwan University where she has developed strong interests in zoonotic pathogens and veterinary public health. In between, she obtained immunological knowledge during her research in vaccine development industry. Being experienced in bioinformatics, epidemiology, molecular biology and immunology, Pei-Yu believes that multidisciplinary One Health approach is the way forward for controlling the zoonotic diseases. Currently she is a postdoctoral fellow in the School of Biological Sciences at HKU focusing on the genomic research of host-pathogen interactions in avian species.

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TYB-2-G02, G/F, Block 2
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ALL ARE WELCOME

ENQUIRIES

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