Emerging Infectious Diseases: Avian influenza and MERS

Malik Peiris

School of Public Health; The University of Hong Kong

Novel viral pathogens continue to emerge to threaten human health, those transmitted by the respiratory route being the most concerning. At present, MERS coronavirus (MERS-CoV), avian influenza (AI) viruses and Nipah are causes of concern. MERS-CoV is endemic in dromedary camels and causes zoonotic infections in the Middle-East. Many of these zoonotic infections appear to be mild and unrecognized but some can lead to chains of human transmission, especially within health care facilities, a few being sustained for many months and leading to hundreds of human cases. This highlights the importance of consistent implementation of good basic infection control practices. Mild or asymptomatic infections appear to be commoner than previously appreciated, severe disease being typically associated with older age and other underlying diseases. The virus is genetically diverse and widespread in camels across the Middle East and parts of Africa, but for reasons yet unclear, human zoonotic disease apparently remains confined to the Middle East. Although genetically diverse, MERS-CoV remains antigenically homogenous. Repeated MERS outbreaks are reminiscent of the emergence of SARS in late 2002 and are a cause for major public health concern. Low pathogenic avian influenza A/H7N9 is now entrenched across multiple provinces in China and threatens to spill over into adjacent countries. Among avian viruses, it is unique in being able to efficiently infect the human conducting airways, transmit efficiently to humans with a large unrecognized iceberg of infection, and exhibits some (albeit inefficient) airborne transmission in ferrets, a marker of potential for transmissibility between humans. Highly pathogenic avian influenza (HPAI) A/H5N1 continues to be entrenched in poultry in Asia and Egypt. Recently, clade 2.3.4.4 HPAI H5 has reassorted to generate H5N8, H5N6, H5N3 and other subtypes in Asia, of which H5N6 has zoonotically infected humans. A/H5N8 has adapted to transmit via long range bird migration and has spread to Europe and North America. Further reassortment of A/H5N8 with North American lineage avian viruses led to the emergence of HAPI H5N2 viruses which caused major outbreaks in poultry in North America, though without evidence of human infections. Enhancing preparedness for dealing with these emerging viral threats requires early detection of novel pathogens, risk-assessment of zoonotic pathogens and pre-emptive preparedness. The understanding of common pathways of virus emergence can lead to strategies for “prevention at source”.