TRACKING THE GENETIC EVOLUTION OF AVIAN INFLUENZA VIRUSES AND RELATED CHALLENGES

Frank Wong[1,3], Vicky Stevens[1], and Gwenaelle Dauphin[2,3]

[1]CSIRO Australian Animal Health Laboratory, Private Bag 24, East Geelong, VIC. 3219, Australia
Tel.: +61-3 5227.5056; frank.wong@csiro.au
[2]Animal Health Service, Food and Agriculture Organization of the United Nations (FAO), Rome, Italy
[3]World Organisation for Animal Health (OIE)/FAO Network of Expertise on Animal Influenza (OFFLU)

Avian influenza A viruses (AIV) pose serious disease threats to domestic poultry and wild birds worldwide, and present a continually evolving zoonotic risk. H5N1 highly pathogenic avian influenza (HPAI) remains endemic in poultry in many Asian and African countries along with sporadic spillover infections in humans. Zoonotic infections by other AIV subtypes, including H7N9, H9N2 and H10N8, that are of low pathogenicity to poultry have also been increasingly reported in recent years. Asian clade 2.3.4.4 H5N1 HPAI viruses have also gained the capacity to stably reassort with various non-N1 subtype AIV, resulting in the emergence of novel HPAI genotypes that have spread to many countries in East and South-East Asia, Europe and North America. Such H5N6 subtype viruses have caused recent human infections in China and affected poultry in Laos and Vietnam, and novel H5N2 and H5N8 viruses with an apparent improved adaptation to transmission by wild migratory waterfowl have emerged with unprecedented rapid distribution to different regions of the globe. Although there has not yet been human cases recorded, both HPAI subtypes have had record-breaking devastating impacts on local commercial poultry industries and affected wild and domestic birds since their emergence over 2014. The increasing reports of novel viruses by inter-subtype genomic reassortments have increased awareness of the spectrum of AIV subtypes and genotypes that have the potential to impact animal health and present new potential zoonotic and pandemic risks. The diversity of the pathogenic AIV genetic pool has also reinforced the importance of maintaining vigilance in virus surveillance of domestic and wild bird populations alike. Current demand for accurate and cost effective whole genome and subpopulation analyses of influenza viruses for disease investigations and zoonotic risk assessments have been facilitated by the availability of affordable benchtop next generation sequencing (NGS) technologies, although diagnostic challenges and limitations remain. In addition to the increased computational demands for handling NGS analysis for agent characterisation, there has been recognition of the need for comprehensive and integrated harmonised approaches to archiving and assessing pathogen and disease outbreak data. The EMPRES-i platform with genetic module developed by the FAO allows epidemiological information from reported animal influenza events to be coordinated and linked to available genetic and other virus metadata. An update on current global AI events due to recently emergent AIV genotypes, the application of NGS and whole genome approaches to their diagnostic and epidemiological characterisation, and animal influenza outbreak and virus data management strategies are presented.