

**DATA INTERPRETATION CHALLENGES: THE EXAMPLE OF GENETIC AND
PATHOBIOLOGICAL CHARACTERISATION OF HPAI H5N2 AND H5N1 VIRUSES IN CANADA**

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Geographical barriers as well as with other factors have likely prevented the long range spread by migratory birds of Asian origin A/goose/Guangdong/1/1996 (H5N1) lineage viruses from Eurasia to the Americas. This changed in late November 2014 when increased mortalities on meat turkey and broiler breeder farms in the Fraser Valley of British Columbia, Canada were caused by a novel H5N2 virus. This virus possessed a gene constellation derived from Eurasian HPAI H5N8 and North American lineage wild bird origin viruses. Subsequent isolations of a wholly Eurasian HPAI H5N8 virus from a gyrfalcon, a HPAI H5N2 virus that possessed the identical gene constellation as that found in the poultry isolates from a northern pintail, and a HPAI H5N1 virus from a green-winged teal pointed to wild birds as a likely source of these viruses. All three viruses have caused outbreaks in poultry in Canada and the USA and in many of the outbreaks there is an association with wild birds. HPAI H5N2 has been responsible for the majority of the outbreaks and has the largest geographical distribution followed by HPAI H5N8 and HPAI H5N1. Phylogenetic and phylogeographic analysis can help us to understand how these viruses spread temporally and spatially, and studying their individual pathobiological characteristics in domestic poultry and wild waterfowl may help us to better understand why the HPAI H5N2 reassortant has predominated.