

Session 06

Theatre 4

Epidemiological factors associated with variation of the HA, NA, and NS genes of H5N1 highly pathogenic avian influenza viruses isolated from birds in Romania in 2005-2007

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Molecular characterization studies of a diverse collection of avian influenza viruses (AIVs) have demonstrated that AIVs' greatest genetic variability lies in the HA, NA and NS1 genes. The objective here was to quantify the association between epidemiological factors and pairwise nucleotide variation in the HA, NA, and NS1 genes of 70 isolates of highly pathogenic avian influenza (HPAI) H5N1 collected from October 2005 to December 2007 from birds in Romania. A mixed binomial Bayesian regression model was used to quantify the probability of nucleotide variation between isolates and its association with epidemiological factors. As expected for the three target genes, a higher probability of nucleotide differences (ORs>1) was found between: those viruses sampled from places at greater geographical distances from each other; viruses sampled over greater periods of time; and viruses derived from different species. However, a lower probability of nucleotide differences (OR<1) was detected in comparison of isolates from birds of different orders for the NA gene, compared to the HA and NS1 genes. The study quantifies the dynamics of evolution of H5N1 HPAI virus in bird populations, and will be useful in predicting the most likely genetic distance for any of the three gene segments of viruses that have not yet been isolated or sequenced based on space, time, and host species during the course of an epidemic