

Establishment and Lineage replacement of H6N2 influenza viruses in domestic ducks in southern China (2000 – 2007)

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Multiple reassortant events between different subtypes of endemic avian influenza viruses have increased the genomic diversity of influenza viruses circulating in poultry in southern China. Gene exchange from the natural gene pool to poultry has contributed to this increase in genetic diversity. However, the role of domestic ducks as an interface between the natural gene pool and terrestrial poultry in the influenza ecosystem has not been well defined. Here we phylogenetically and antigenically analyzed 206 H6 viruses isolated from domestic ducks from 2000 to 2007 in southern China which contains the largest population of domestic ducks in the world. Three distinct H6 lineages were identified. Group 1 contained the majority of isolates with a single internal gene complex and was endemic in domestic ducks in Guangdong from the late 1990's to 2005. Group 2 was derived from reassortment events in which the surface genes of Group 1 viruses were replaced by novel H6 and N2 genes, which appeared in 2004 and gradually replaced the Group 1 viruses and became the predominant H6N2 variant after 2005. Epidemiological and genetic findings also show that the Group 2 viruses started to disseminate from the coastal regions to inland provinces and was also introduced into terrestrial poultry. The Group 3 H6 viruses represent part of an influenza gene pool that undergoes frequent gene exchange with different subtypes. Our study revealed that gene exchanges between viruses from domestic duck and migratory duck occurred throughout the surveillance period. These findings suggest that domestic duck in southern China mediate the interaction of viruses between different gene pools and facilitate the generation of novel influenza variants circulating in poultry.