

Detection and phylogenetic analysis of H4N2 avian influenza viruses isolated from domestic waterfowl at live poultry markets in north provinces of Iran

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Abstract

Waterfowls are one of the hosts for Avian influenza virus (AIV) H4 subtypes. In fact, the importance of domestic ducks as reservoirs in the distribution of this virus has been previously proven. Also, the live poultry market could be a significant place in spreading and transmission of influenza virus among the birds and animals. Identification and molecular determination of HA and NA genes of the H4N2 avian influenza virus was isolated from this group of birds in live bird markets of Iran. From 962 cloacal samples, collected from domestic ducks and geese, the NA and HA genes sequences revealed the emergence of this virus in Iran for the first time. Phylogenetic analyses of the HA gene showed high homology to the Eurasian lineage of H4N6. On the other hand, the cleavage site of the HA genes showed a PEKQTR/GLF motif, an indicator of LPAI. Also, the NA gene showed high homology to those belonging to AIV N2 subtype. This is the first study regarding the detection and identification of AIV H4 subtypes from domestic ducks in Iran. It recommends a continuous monitoring of the avian influenza viruses in Iran in order to study the evolution and identify new strains with pandemic potential because such information will be helpful in controlling of the disease.

Key words: Avian influenza virus, H4 subtype, Domestic ducks, Phylogenetic analysis, Live poultry market

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