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The new insight about interspecies transmission of Iranian H9N2 influenza viruses from avian to human

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Documented cases of human infection with H9N2 avian influenza viruses first detected in 1999 in Hong Kong and China indicated that these viruses can be directly transmitted from birds to humans. In this study, we characterized the mutation in the Hemagglutinin (HA) genes and proteins that correlates with a shift in affinity of the Hemagglutinin (HA) protein from the “avian” type sialic receptors to the “human” type in 10 Iranian isolates. We delineated the genomes and receptor binding profile of HA gene of some field isolates and established their phylogenetic relationship to the other Asian H9N2 sub lineages. A total of 1200 tissue samples collected from 40 farms located in various states of Iran during 2008-2010 as part of a program to monitor Avian Influenza Viruses (AIV) infection. To determine the genetic relationship of Iranian viruses, the Hemagglutinin (HA) genes from ten isolates were amplified and sequenced (by RT-PCR method). Nucleotide sequences (orf) of the (HA) genes were used for phylogenetic tree construction. Deduced amino acid sequences showed the presence of L226 (234 in H9 numbering) in all ten Iranian isolates which indicates a preference to binding of α (2-6) sialic acid receptors, so these Iranian H9N2 viruses have the potential to infect human beings. These isolates showed high degree of homology with 2 human H9N2 isolates A/HK/1073/99, A/HK/1074/99. Phylogenetic analysis of showed that all the HA genes of the Iranian H9N2 viruses fall into a single group within a G1-like sub lineage which had contributed as donor of six internal genes to H5N1 highly pathogenic avian influenza. The results of this study indicated that all Iranian viruses have the potential to emerge as highly pathogenic influenza virus and considering the homology of these isolates with human H9N2 strains, it seems that the potential of these avian influenza isolates to infect human should not be overlooked.

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