

Molecular and phylogenetic analysis of hemagglutinin (HA) and neuraminidase (NA) genes of H9N2 avian influenza viruses isolated from vaccinated broiler chickens in Iran in 2011

Abstract

H9N2 avian influenza outbreaks have been one of the major problems of poultry industry in Iran. A vaccination program has been implemented to control disease since 1988, but some outbreaks continued to occur in several broiler flocks. In this study four strains which were isolated in 2011 from vaccinated broiler flocks with a history of respiratory illness were sequenced. Sequence analysis HA and NA genes indicated that all strains isolated in this study shared nucleotide homologies of 91.3% to 92.4% and 90.4% to 91.1% with the vaccine strain for HA and NA genes, respectively. Extra potential glycosylation sites could be observed in HA and NA genes of current isolates versus vaccine strain. Molecular analysis of all four isolated strains showed KSSR motif of cleavage site in the HA genes, while it is RSSR for typical strains in Iran. Phylogenetic analysis of HA and NA genes showed that all strains isolated in this study fell into the same subgroup and they belong to A/Quail/HongKong/G1/97 H9N2 lineage but in comparison with vaccine strain they had some deviation in the decade and fell into different subgroup. Other changes included loss, addition and variation in predicted epitope in HA and NA genes of field strains. These results suggest that the commercial vaccine genetically is not enough coordinated with current viruses in region. Therefore, constant evaluation of important genes induced immunity and vaccine efficiency in protection against these strains would be essential.