

Abstract

Surveillance and Molecular Epidemiology of Avian Influenza H9N2 Viruses Circulating in Pakistan

Muhammad Farooq Tahir

Corresponding Author:
Muhammad Farooq Tahir

Abstract

Background: Avian influenza H9N2 is highly endemic in commercial and backyard poultry in Pakistan. Its widespread circulation and high mutation rates provide a possibility of novel reassorted viruses hence posing a serious public health threat.

Objective: This study was aimed to isolate and evaluate the AI H9N2 viruses circulating in poultry as well as aquatic birds in Pakistan between 2014 and 2017.

Methods: Specimens were collected from morbid or dead birds suspected for AI H9N2 on the basis of clinical signs or post-mortem lesions brought to five poultry diagnostic laboratories in Punjab. The samples were subjected for virus isolation. The isolates then were confirmed for H and N type using PCR. Six isolates were subjected to phylogenetic analysis of Haemagglutinin gene. The results were compared with isolate reported previously from Pakistan and other regional countries for homology.

Results: 129,622 samples from 7481 poultry flocks were processed, 5.3% (399/7481) were positive for AIV H9N2. Sequence analysis showed that it had homology of 84-93% with different regional strains. Changes were seen at 24 different sites and at cleavage site at K148R and I151R in comparison to previous Pakistani isolates. Six possible glycosylation sites were observed. Neighbor joining phylogenetic tree confirmed its 93.4% homology with the isolate of Iran. The isolates were the same clade as other regional isolates and have common ancestors.

Conclusions: The prevailing H9N2 viruses in Pakistan have certain markers and elements in the HA gene that may improve its avian to human transmission. Continuous surveillance of influenza A viruses is necessary to monitor their antigenic determinants. Protocols for the AI surveillance have officially been notified by Department of Livestock & Dairy Development Department, Punjab as a result of these findings.

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