

Summary

In this study the prevalence of circulating respiratory viruses AIV, ND and IBV were investigated in 86 broiler chicken flocks from Fayoum, Beni-Suef, EL-Menia and Qaliobia governorates during 2012 through winter season of 2014 using rRT-PCR. Clinical signs and lesions varied according to the infecting virus strain, the immune status of the flock and number of infecting pathogens. Mortality rates in the flocks under investigation ranged from 1 to 47%. The highest mortality was observed in mixed infection. IBV followed by H9N2 AIV were found to be more prevalent. 72, 53, 22 and 7 flocks were found positive to IBV, AIV-H9, AIV-H5 and vNDV, respectively. Mixed infection was prevalent in flocks under investigation 66.3% (57/86 flocks) while single infection of different viruses was found in 33.7% (29 flocks). The most common mixed infection was AIV-H9 with IBV (36 flock) representing 63 and 41.9 % of mixed infected and total investigated flocks, respectively. Mortality rates after single infection with vNDV, IBV, AIV-H9 and AIV-H5 viruses ranged from 8 to 13, 1 to 19, 3 to 20 and 2 to 30%, respectively. The immune status and age of birds at time of field challenge, the hygienic conditions in the farm as well as the role of secondary bacterial agent had a great effect on the mortality rates in such flocks.

Partial sequence of S1 glycoprotein hyper variable region 3 revealed that isolates of this study were related to variant group of IBV, four isolates were closely related to each other and to recent Egyptian isolates and also related to the Israeli isolate IS/885. On the other hand, IB/Ck/Eg/BSU-FA-KB23/2013 was quite distant from the other 4 isolates. Variant strains carry multiple mutations at the virus neutralizing epitopes.

Phylogenetic analysis of the F gene revealed that five NDV isolates are velogenic. Isolates were found closely related to each other and to recent Egyptian isolate and all of them belong to genotype VIIId (lineage 5d class II).

H5N1 and H9N2 AIVs co-circulated and virus pathogenicity even within subtype varied greatly. All H5N1 isolates obtained in the current study are genetically related to each other and to recent Egyptian strains which belonged to clade 2.2.1. The cleavage site of HA of H5 viruses contained polybasic amino acids motif: P_QG_ER_RR_RK_KR a marker of pathogenicity. Variations in proposed antigenic sites and receptor binding sites of the HA genes were observed. On the other hand Egyptian H9N2 HA gene showed lower rate of mutations and the collected strains were genetically related to each other, also related to recent Egyptian and Middle East circulating H9N2 strains, which belonged to G1-like lineage group. Mutations at various positions of the HA genes were detected in both AIV subtypes.

The pathogenesis of single and mixed infection with AIV-H9 or IBV mixed including both classical and variant field IBV as well as 4/91 vaccinal strain was experimentally evaluated. All groups receiving mixed infection, AIV-H9 with either field or vaccinal (4/91) IBV strain, showed more severe respiratory signs and P.M in trachea, thymus, air sacs than did the single virus infected groups. Renal damage was noticed in groups infected with variant IBV or 4/91 vaccine. Mortality as well as duration and level of virus shedding was high in AIV-H9 / IBV (Field and 4/91 strain) mixed infection than single infection thus adding another evidence of the role of IBV in increasing severity and mortality of AIV-H9 in birds.