

Molecular detection and phylogenetic analysis to evaluate the evolutionary pattern of VP1 gene sequence of recent duck hepatitis A virus (DHAV) isolate and assessment of new genotyping emerging in Egypt.

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Abstract:

Duck hepatitis A virus (DHAV) is an *Avihepatovirus A* which consider one of the most serious threatening viral pathogens influencing duck rearing in Egypt until now, with disastrous economic effects on duck industries' not only at local level but also worldwide. In this study, suspected DHAV samples (n=10) were collected from commercial flocks and backyard rearing from different localities in Kaliobyia province from September 2020 to January 2021. The infected flocks were showing high mortality and nervous signs without history of previous vaccination against DHAV. Hemorrhagic liver samples were prepared from recently died (7 to 15) day old ducklings. Trials for isolation of the virus on SPF-ECEs using allontic route showed stunting, subcutaneous hemorrhage, and yellowish discoloration of liver with necrotic foci in the inoculated embryos. Then, viral isolates were undergone molecular identification using RT-PCR targeting 5' UTR and VP1 gene which revealed amplicon size 250 bp and 880 bp respectively for positive DHAV isolates. The positive isolate was further subjected to sequencing of the partially amplified VP1 gene and phylogenetic analysis was performed in relation to the Egyptian DHAV strains, vaccinal strain and other sequences available on the GenBank. Our results revealed that this new DHAV isolate was more homologous and genetically related to emerging DHAV genotype 3 which recently identified in Egypt. The studied vaccinal strain using in vaccination against the virus was out of grouping. Consequently, further serological studies to update the nature of future vaccine strains for successful preventive strategies would be urgent.

Keywords; Duck hepatitis A virus, isolation, VP1 gene, phylogenetic analysis, genotype 3