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Marek's Disease in Egyptian Turkeys: Molecular Characterization of the Causative Virus and A Novel Phylogentic Classification System

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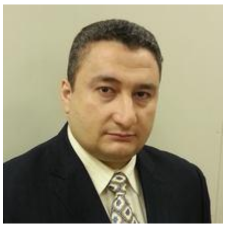
Abstract

Marek's disease (MD) is an oncogenic viral disease that causes severe economic losses in chickens and rarely in turkeys. MD is caused by Gallid herpesvirus 2 (GaHV-2), which is a member of genus Mardivirus, family Herpesviridae. Among 200 genes identified in the genome of GaHV-2, meq gene was intensively studied for its role on viral virulence, oncogenicity, and diversity. Meq gene sequences were frequently exploited in phylogenetic analysis of GaHV-2 strains identified in many countries worldwide. However, no integrated system was proposed for phylogenetic classification of GaHV-2 strains worldwide. In this study, turkeys from two commercial Egyptian farms were presented with signs of dullness, dehydration and emaciation. Gross examination has revealed grayish white soft masses in the majority of internal organs, and diffuse enlargement in sciatic nerve. Diffuse infiltration of pleomorphic neoplastic cells with hyperchromatic and mitotic activities was observed by histopathological examination of internal organs and sciatic nerve fibers. All lymphoma cells were characterized as T- lymphocytes of CD3+ phenotype by immunohistochemistry. PCR was utilized to identify the viral cause of the suspected lymphoproliferative disease. GaHV-2 was identified in all samples using two PCR systems targeting partial sequence of ICP4 gene and the complete meq gene sequence. All samples were negative for avian leucosis and reticulendotheliosis viruses. Sequence analysis of meq gene has classified turkey strains as relevant to the Egyptian strains identified in chicken in 2012. All Egyptian strains showed unique amino acid substitutions; A88T, T139A, E263D, whereas turkey strains also displayed an additional unique site E54K. A universal system for phylogenetic analysis of GaHV-2 strains was proposed using the entire sequence of meq gene. This system indicated separation of GaHV-2 strains into 4 clusters. The vaccine strains were all grouped in cluster 2. The Indian and Japanese strains identified in 2010 and 2011 were members of cluster 3, while most of the classical American strains belonged to cluster 4. Cluster 1 was further divided to three sub-clusters (1.1-1.3). In conclusion, GaHV-2 was identified in turkeys for the first time in Egypt and Africa. A universal system for phylogenetic classification of GaHV-2 was established using GaHV-2 strains selected on temporal, spatial, pathological, and taxonomic bases.

Biography:



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Speaker Publications:

1. Al-Qudari, Ahmed & Amer, Haitham & Abdo, Ayman & Hussain, Zahid & Al-Hamoudi, Waleed & Alswat, Khalid & Almajhdi, Fahad. (2015). Surface Gene Variants of Hepatitis B Virus in Saudi Patients. Saudi journal of gastroenterology: official journal of the Saudi Gastroenterology Association. 22. 10.4103/1319-3767.167186.
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