

Genetic diversity of fowl adenovirus serotype 8b isolated from cases of inclusion body hepatitis in commercial broiler chickens

ABSTRACT

Inclusion body hepatitis (IBH) is a devastating disease of chickens caused by Fowl adenovirus (FAdV) and molecular studies of hexon gene is important for classification of FAdV isolates, epidemiology of IBH infection and development of effective control strategy. The objective of the study was to molecularly characterize FAdV isolates obtained from the field outbreaks of IBH in broiler chicken from 2017 to 2019. Liver and gizzard samples named UPM1701, UPM1801, UPM1802, UPM1901 and UPM1902 were collected and processed for FAdV detection and characterization by PCR. Swollen, necrotic and haemorrhagic liver; erosion of koilin layer of gizzard and enlargement of the proventriculus were observed. The samples were positive for FAdV with 98% to 100% identical to serotype 8b reference strains based on NCBI Blast. Thirty-one nucleotide changes that produced 10 amino acid substitutions were observed in L1 loop region of UPM1701, UPM1901 and UPM1902 isolates. All isolates clustered together with FAdV 8b reference strains and shared common ancestor with UPM1137E2 and UPM04217. Gizzard erosion in FAdV 8b infection is not common and coinciding with mutations indicate evolving novel pathogenicity. These mutations could have effect on the epidemiology of IBH and be useful in designing effective prevention and control strategy.

Keyword: Fowl adenovirus; Inclusion body hepatitis; Serotype 8b; Hexon; Substitutions