

## ***Hexon Gene Loop 1 Region Phylogeny of Fowl Adenoviruses Associated with Inclusion Body Hepatitis in Broiler Chickens in Sri Lanka***

S.A.S. Indunika, P.G.A.S Palkumbura, T.A. Gunawardana, R.R.M.K.K. Wijesundera, A.W. Kalupahana\*

*Department of Veterinary Pathobiology, Faculty of Veterinary Medicine and Animal Science,  
University of Peradeniya  
\*anilwkalupahana@yahoo.com*

Inclusion body hepatitis (IBH) is an acute disease in 3–7week broiler chickens, caused by Fowl adenoviruses (FAdVs) of the genus *Aviadenovirus*, family *Adenoviridae*. FAdV-D (serotypes 2, 3, 9, and 11) and FAdV-E (serotypes 6, 7, 8a, and 8b) mainly target the liver of the infected bird causing IBH. Our previous study detected, serotypes 8b and 11 from the North-Western Province (Kurunagala and Kuliyaipitiya) and serotype 8b from the Central Province (Gampola). The objective of this study is to determine the hexon gene loop 1 (L1) region based phylogenetic relationship of these serotypes. The sequencing data from the serotypes were analysed by Basic Local Alignment Search Tool N (BLASTN) against sequences in the GenBank database. The results revealed that FAdV 8b isolate from Kurunagala had 98.75% sequence homology to a FAdV isolated from South Africa (HQ117899.1), and, 98.63% and 98.52% nucleotide homology to FAdVs isolated in France (MK572865.1) and India (MH379248.1) respectively. The FAdV 8b isolate from Gampola had a 99.19% sequence similarity to a FAdV reported from France (MK572865.1), 99.07% to a Canadian FAdV (JN112373.1) and 98.96 % to a South African FAdV (HQ117904.1). The FAdV 11 isolate from Kuliyaipitiya had a 99.88% sequence similarity to a FAdV found in Japan (LC650578.1), 99.77% to a FAdV in Trinidad and Tobago (MG676334.1) and 99.77% to a Saudi Arabian FAdV (MK995483.1). The pairwise sequence comparison of the two FAdV 8b isolated from Kurunagala and Gampola revealed 99% sequence similarity to each other. This study suggests that genetically close related FAdV 8b serotype had been circulating in the two different geographically distant provinces in Sri Lanka. Sequencing of recently isolated FAdV serotypes from these two provinces is on-going.

**Keywords:** Broiler, Fowl Adenovirus, Inclusion Body Hepatitis, Phylogeny, Serotype

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