

Genomic Characterization of a Fowl Adenovirus Isolated from Chickens with Inclusion Body Hepatitis in Thailand Using Whole Genome Sequencing

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Abstract

Background: Inclusion body hepatitis (IBH) is a significant viral disease causing substantial economic losses in the global broiler industry due to high mortality rates and characteristic hepatic pathology. The disease is primarily caused by fowl adenovirus (FAdV), a member of the genus *Aviadenovirus*, which comprises five species (FAdV-A to E) and 12 serotypes. Despite recurring outbreaks in Thailand, comprehensive genomic data on circulating strains remain limited.

Objectives: This study aimed to isolate an FAdV strain from an affected poultry farm and utilize whole-genome sequencing (WGS) to analyze the sequences of major structural and virulence genes to identify mutations associated with its biological properties.

Methods: Liver samples were collected in 2022 from broiler chickens in Chonburi Province exhibiting clinical signs and gross lesions pathognomonic for IBH. The virus was isolated and propagated in primary chicken embryo liver (CEL) cells, with viral presence confirmed via polymerase chain reaction (PCR) targeting the *hexon* gene. The extracted viral DNA was subsequently subjected to WGS using Oxford Nanopore technology, leveraging its long-read capabilities to facilitate high-accuracy genome assembly.

Results: Phylogenetic analysis at the whole-genome level confirmed that the isolate belongs to species E, serotype 8b (FAdV-8b). In-depth genomic assessment focused on critical structural genes and virulence determinants, specifically the hypervariable regions (HVRs) of the *hexon* gene and the full-length *fiber* gene. Comparative analysis with global reference strains from GenBank revealed distinct mutation patterns and specific amino acid substitutions within these key genes, highlighting the unique genetic profile of the circulating Thai strain.

Conclusion: The genomic characterization provided by this study establishes a vital molecular epidemiological foundation for disease surveillance and tracking viral evolution. Furthermore, these findings provide a scientific basis for selecting appropriate local candidate vaccine seeds to effectively control IBH within the Thai poultry industry.

Keywords: Fowl adenovirus, Inclusion body hepatitis, Genomic characterization, Whole genome sequencing, Nanopore sequencing

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