

Complete genome sequence of fowl adenovirus-8b UPM04217 isolate associated with the inclusion body hepatitis disease in commercial broiler chickens in Malaysia reveals intermediate evolution

ABSTRACT

The main aim of our study was to explore the genome sequence of the inclusion body hepatitis associated Fowl adenovirus serotype 8b (FAdV-8b) UPM04217 and to study its genomic organisation. The nucleotide sequence of the whole genome of FAdV-8b UPM04217 was determined by using the 454 Pyrosequencing platform and the Sanger sequencing method. The complete genome was found to be 44,059 bp long with 57.9% G + C content and shared 97.5% genome identity with the reference FAdV-E genome (HG isolate). Interestingly, the genome analysis using ORF Finder, Glimmer3 and FGENESV predicted a total of 39 open reading frames (ORFs) compared to the FAdV-E HG that possessed 46 ORFs. Fourteen ORFs located within the central genomic region and 16 ORFs located within the left and right ends of the genome were assigned as being the high protein-coding regions. The fusion of the small ORFs at the right end terminal specifically in ORF22 and ORF33 could be the result of gene truncation in the FAdV-E HG. The frame shift mutation in ORF25 and other mutations in ORF13 and ORF17 might have lead to the emergence of genes that could have different functions. Besides, one of the minor capsid components, pVI, in FAdV-8b UPM04217 shared the highest similarity of 93% with that of FAdV-D, while only 47% similarity was found with FAdV-E. From the gene arrangement layout of the FAdV genome, FAdV-8b UPM04217 showed intermediate evolution between the FAdV-E HG and the FAdV-D although it was apparently more similar to the FAdV-E HG.

Keyword: Genome organization; Fowl adenovirus; Evolution; Next generation sequencing; Inclusion body hepatitis