Duck viral hepatitis (DVH) is an acute and fatal disease of young ducklings characterized by rapid transmission and damages. The most important agent of DVH is duck hepatitis virus 1 (DHV-1). The effective control of DVH was achieved by active immunization of 1-day-old ducklings with an attenuated DHV-1 virus vaccine. However, the attenuated virus might reverse to virulence. In this study, a DHV-1 strain, Du/CH/LBJ/090809, was identified and its genomic sequences were determined. The genome of Du/CH/LBJ/090809 is composed of 7,692 nt excluding poly A and the virus was clustered into genotype A by comparing with other referenced DHV-1 strains. Du/CH/LBJ/090809 could lead to 30% mortality of 10-day-old specific pathogen free (SPF) ducklings. The virus was passaged serially in SPF chicken embryonated eggs and three viruses, passage 16 (P16), P29 and P40, were selected for genomic analysis. P29 and P40 were used to evaluate the attenuation in duckling by inoculating the virus to 10-day-old SPF ducklings. Results of vaccination-challenge assay showed that the inactivated virus P40 could evoke protection against the pathogenic parent virus. Nucleotide and amino acid sequences of the genomes of Du/CH/LBJ/090809, P16, P29 and P40 were compared. Changes both in nucleotides and amino acids, which might be contributed to the decreasing in virulence by chicken embryo-passaging of DHV-1, were observed. We speculated that these changes might be important in the adaption and attenuation of the virulent virus. Additionally, strains obtained in this study will provide potential candidate in the development of vaccines against DHV-1.

Key words: duck hepatitis virus 1, pathogenicity, attenuation, mutant site