Complete Genome Sequence of Feline Panleukopenia Virus Strain HRB-CS1, Isolated from a Domestic Cat in Northeastern China

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Here, we report the complete genome sequence of feline panleukopenia virus (FPLV) strain HRB-CS1, isolated from a dead domestic cat showing enteric symptoms in China in 2014. The genome of HRB-CS1 was sequenced and analyzed, which will help to understand the genetic characteristics and evolution of FPLV in China.

In this study, FPLV strain HRB-CS1 was isolated from a dead domestic cat with enteritis in Heilongjiang province, northeastern China, in 2014, and the full-length genome was sequenced and analyzed. The samples were treated and inoculated with a Crandell-Rees feline kidney (CRFK) cell monolayer as previously analyzed. The samples were treated and inoculated with a recombinant virus between FPLV and CPV and was the same as the China isolate strain FPLV XJ-1 (1).

Furthermore, compared with the CPV-b strain, the genome of HRB-CS1 had a 60-nt insertion in the 3′ untranslated region (UTR), which was similar to FPLV 193/70, FPLV CU-4, and MEV Abashiri. However, some other CPV and MEV strains with a 3′ UTR available in GenBank kept a different pattern of deletion. The function was not clear, and further study should be carried out.

Nucleotide sequence accession number. The genome sequence of FPLV strain HRB-CS1 has been deposited in GenBank under the accession number KP280068.

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REFERENCES


