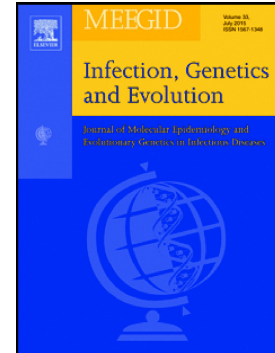


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Isolation and molecular characterization of a virulent systemic feline calicivirus isolated in China

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Abstract

In this study, a virulent systemic (VS) feline calicivirus (FCV) strain, SH, was isolated from a household cat with severe systemic clinical signs, and its full-length genome was determined and analyzed. Through immunofluorescence assays (IFA) and western blotting assays, we found that FCV SH strain, like other isolates, can stably proliferate in Crandell feline kidney (CRFK) cells. Moreover, the typical morphology of FCV particles, with a diameter of about 35 nm, was observed using electron microscopy. The full-length genome of FCV strain SH was sequenced and determined to be 7,704 nucleotides (nt) in length with a 5'-terminal untranslated region (UTR) of 19 nt and a 3'-terminal UTR of 67 nt. Three open reading frames (ORF1, ORF2, and ORF 3) were found within the genome, coding for a polypeptide, a capsid precursor (VP1) and a minor structural protein (VP2), respectively. Amino acid sequence comparison revealed diversity (from

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