Genetic and replication analysis of highly virulent Feline Calicivirus isolate, KS-2019

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Feline calicivirus (FCV) is a non-enveloped, positive-sense RNA virus belonging to the genus *Vesivirus* within the family *Caliciviridae*. Typically, FCV infection in cats causes upper respiratory symptoms and oral ulcers with high morbidity and low mortality. However, over the past 20 years, there have been many reports of highly fatal diseases caused by virulent systemic (VS) FCV. In 2019, a feline patient exhibiting acute onset of illness with a high fever, anorexia, swollen legs and neck was presented to the Kansas State University Veterinary Health Center. Subsequent histology and laboratory testing confirmed VS FCV infection. FCV was isolated from the tissue in Crandell Reese Feline Kidney (CRFK) cells and designated as KS-2019. In this study, the full-length sequencing analysis and investigation of replication characteristics of FCV KS-2019 were conducted. The multiple sequence alignment and phylogenetic analysis using the VP1, VP2 and LC proteins of KS-2019 showed that there is approximately 80% amino acid homology between KS-2019 and other reported FCV strains and there is no evidence of phylogenetic clustering of VS FCV strains. The replication characteristics of KS-2019 in CRFK cells were determined by conducting the single-cycle replication assay and compared to those of Urbana strain, a prototype non-VS FCV strain. Single-cycle replication assay revealed that KS-2019 strain has higher virus yields in comparison to Urbana strain, which is consistent with previous reports with VS FCV strains. Further studies are undergoing to assess individual viral entry events including virus attachment, endosome entry, and endosomal escapes to determine which step is responsible for the increased replication of KS-2019 in cell culture.