

Genetic analysis of feline panleukopenia virus (FPLV) from cats in Korea

Seok-Young Jeoung, So-Jeo Ahn, Doo Kim*

*Department of Veterinary Internal Medicine, School of Veterinary Medicine,
Kangwon National University, Chunchon 200-701, Korea*

Purpose: In this study, we attempted to detect FPLV from cats with clinical signs of FPLV and to perform a molecular study on FPLV isolated from domestic cats in Korea.

Materials and Methods: The 7 fecal specimens of cats with clinical signs of FPLV were collected from 2003 to 2007. DNA was extracted from specimens and PCR was carried out to detect VP2 gene. The VP2 gene was characterized by direct DNA sequencing and their phylogenetic tree was constructed.

Results: 5 FPLV were obtained from unvaccinated 5 cats. Sequence alignment analyses showed that there were different silent mutations and few coding changes in the VP2 gene. Alignment of VP2 gene of Korean isolates with those of other FPLV strains isolates from Argentina, Australia, China, France, Japan, Russia, Taiwan, and USA showed that nucleotide and amino acid similarity ranged from 99.3 to 99.9 and 99.3 to 100%, respectively. In the phylogenetic tree obtained from nucleotide sequence, Korean strains form a close cluster with chinese and Japanese strains.

Conclusion: Our findings support the worldwide spreading of FPLV and provide information to understand the evolution of molecular variants of FPLV in Korea.

Key words: feline panleukopenia virus, Korea, VP2 gene, phylogeny.

* Corresponding author: kimdoo@kangwon.ac.kr