An Update on Aspects of Feline Immunodeficiency Virus in Taiwan

Bi-Ling SU, Hui-Wen CHANG, Chao-Nan LIN, Victor Fei PANG, Ling-Ling CHUEH, *Chian-Ren JENG

Graduate Institute of Veterinary Medicine, School of Veterinary Medicine, National Taiwan University, Taipei 10617, Taiwan, ROC
Veterinary Hospital, College of Bio-Resources and Agriculture, National Taiwan University, Taipei 10617, Taiwan, ROC

ABSTRACT To determine the prevalent subtypes of feline immunodeficiency virus (FIV) in the domestic cat population in Taiwan during 2005-2006, the variable V3-V5 region of the envelope (env) gene was amplified by a nested PCR from the samples of whole blood of 18 FIV antibody positive cats. The blood samples were collected from animals in the animal shelters and from clinical cases in the Veterinary Hospital at National Taiwan University. Within the 18 serum positive samples, 12 samples were successful amplified by PCR. After sequencing and phylogenetic analysis of PCR products, 11 samples were clustered within group of subtype C, which is consistent with previous reports. However, the remaining one sample was grouped within subtype B; this is the first time this subtype has been identified in Taiwan. This observation suggests the need of a more comprehensive epidemiological survey before appropriately evaluation of the use of FIV vaccine in Taiwan. [Su BL, Chang HW, Lin CN, Pang VF, Chueh LL, *Jeng CR. Taiwan Vet J 35 (3): 167-173, 2009. *Corresponding author TEL: 886-2-2362-1965, FAX: 886-2-2366-1475, E-mail: crjeng@ntu.edu.tw]

Key words: feline immunodeficiency virus, subtype, Taiwan

INTRODUCTION

Feline immunodeficiency virus (FIV) is an important pathogen of domestic cats and is present worldwide. FIV is a member of the Retroviridae family, genus Lentivirus, and its infection in cats has been associated with acquired immunodeficiency syndrome (AIDS)-like disease [1,6].

The genome of FIV is comprised of three main structure genes, including gag, pol, and env. The viral env gene shows significant sequence diversity in comparison with the regions of the gag and pol [12]. The sequence variation of the FIV env gene is considered to be useful in understanding the evolution and origin of FIV. Based on their env gene sequences, FIV isolates have been classified into five distinct subtypes, A, B, C, D, and E [2]. Subtypes A and B are predominant in North America, Europe, and Japan [8,13,17]; subtype C has been reported predominantly in Canada [17]; subtypes D and E have been reported in Japan [8] and Argentina [15], respectively. In Taiwan, the overall FIV positive rate reported has varied from 2.5%, to