

Molecular detection and characterisation of feline morbillivirus in domestic cats in Malaysia

ABSTRACT

Feline morbillivirus (FeMV), a novel virus from the family of Paramyxoviridae, was first identified in stray cat populations. The objectives of the current study were to (i) determine the molecular prevalence of FeMV in Malaysia; (ii) identify risk factors associated with FeMV infection; and (iii) characterise any FeMV isolates by phylogenetic analyses. Molecular analysis utilising nested RT-PCR assay targeting the L gene of FeMV performed on either urine, blood and/or kidney samples collected from 208 cats in this study revealed 82 (39.4%) positive cats. FeMV-positive samples were obtained from 63/124 (50.8%) urine and 20/25 (80.0%) kidneys while all blood samples were negative for FeMV. In addition, from the 35 cats that had more than one type of samples collected (blood and urine; blood and kidney; blood, urine and kidney), only one cat had FeMV RNA in the urine and kidney samples. Risk factors such as gender, presence of kidney-associated symptoms and cat source were also investigated. Male cats had a higher risk ($p=0.031$) of FeMV infection than females. In addition, no significant association ($p=0.083$) was observed between the presence of kidney-associated symptoms with FeMV status. From the 82 positive samples, FeMV RNA was detected from 48/82 (58.5%) pet cats and 34/126 (27.0%) shelter cats ($p<0.0001$). Partial L and N gene sequencing of the RT-PCR-positive samples showed 85–99% identity to the published FeMV sequences and it was significantly different from all other morbilliviruses. A phylogenetic analysis of the identified Malaysian FeMVs was performed with isolates from Japan, Thailand and China. Molecular characterisation revealed high relatedness of the Malaysian isolates with other Asian FeMVs, indicating that the virus had been circulating only within the region. Therefore, this study confirmed the existence of FeMV among domestic cats in Malaysia. The findings suggest further characterisation of the local isolates, including the whole genome sequencing and that studies at determining the direct consequences of FeMV infection in domestic cats are needed.

Keyword: Feline morbillivirus (FeMV); Molecular characterisation; N gene; L gene; Domestic cats; Malaysia