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The genetic diversity of Asian isolates of canine distemper virus and their characterization in Hamster cell lines

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Canine distemper virus (CDV) is an enveloped virus with a negative-stranded RNA genome. Together with Measles virus (MV) and Rinderpest virus, it belongs to the morbilliviruses which form a serologically related genus in the family paramyxoviridae. CDV primarily affects dogs, but infections of other terrestrial carnivores have been reported. During our study on the molecular characterization of hemagglutinin (H) and fusion (F) protein genes in a mouse retrovirus vector we found that hamster cell lines might be susceptible to CDV infection. To confirm the propagation of various CDV strains in HmLu and BHK hamster cells, 13 field strains that were classified as Asia 1 and Asia 2 based on the deduced amino acid sequence of H protein were passaged in hamster cells and the cytopathic effect (CPE) were observed. In this study, eleven of 13 strains grew in HmLu cells and 12 of 13 strains grew in BHK cells with apparent CPE of cell fusion in the last stage of infection. Two strains and a strain of Asia 1 group could not grow in HmLu and BHK cells, respectively. This study demonstrates at the first time that hamster cells can propagate the majority of Asian field isolates and the two hamster cell lines are useful to characterize the field isolates biologically.

To know the adaptation process of Asia 2 isolates of CDV in HmLu cells, the adapted viruses were tested for their infectivity to HmLu cells. Three types of infectivity improvement were observed in the re-infection of adapted viruses to HmLu cells; strong, weak and unaffected improvements. To know molecular basis of this phenomenon, nucleotide sequencing of original and adapted Asia 2 isolates were carried out.

As results, following aspects were revealed. (1) The F proteins or the F genes of Asia 2 isolates had an extra sequence upstream of the usual N-terminal or 5'-end position in comparison to other CDV strains of Asia 1, European, American and vaccine strain (Onderstepoort). (2) Full sequencing of original Asia 2 isolates revealed four genotypes basing on the sequences of F gene, L gene and H-L intergenic region. (3) Full sequencing of adapted Asia 2 isolates revealed amino acid changes in the F, P and M genes. In the F gene, two types of amino acid changes were suggested to be correlated to the strong improvement (characteristic amino acid change in cytoplasmic tail region of F protein) and to the unaffected improvement (amino acid changes in regions outside heptad repeats (HRA and HRB)) of infectivity to HmLu cells. The amino acid changes or nucleotide changes in both P and M genes were suggested to be correlated to the weak improvement of infectivity.

Biography

Dr. Serageldeem Sultan received his Ph.D. degree in virology with the Professor Kazushige Kai at Yamaguchi University (2010). His primary field is virology with research emphasis on construction of retrovirus vectors to elucidate the relationship between Hemagglutinin (H) and Fusion (F) genes using various combinations of Asian isolates of CDV. He has recently entered the developing field of molecular virology research. He published the first description of Asian isolates in Hamster cell lines in the October 2009, issue of *Acta veterinaria scandinavica*. After that I described the diversity of F genes among Asian isolates in the October 2009, issue of virology journal.