



CHAPTER I

INTRODUCTION

Canine distemper is an important infectious disease in dogs, caused by Canine Distemper virus (CDV). Although many types of vaccines were developed to protect the dogs from this lethal disease but in many parts of the world including Europe, North America, South America, Africa and Asia still found dogs and other susceptible animals infected by CDV (Blixenkronne – Moller et al., 1993; Gemma et al., 1996; Carpenter et al., 1998; Headley and Graca, 2000; Prado et al., 2005; Lan et al., 2006^a; Martella et al., 2006). The factor that may cause limited effectiveness of the vaccines is viral antigenic variation (Matella et al., 2006). Researchers used nucleotide sequence of hemagglutinin glycoprotein (H) gene which was the most variable part of Morbillivirus proteins and phosphoprotein (P) gene, the highly conserved among the viruses, to compare the new isolates and vaccine strains. The results showed that the vaccines strains including Onderstepoort, Snyder hill and Rockborn were grouped in the same lineage which is differ from the new isolates of many parts of the world (Bolt et al., 1997; Carpenter et al., 1998; Mochizuki et al., 1999; Prado et al., 2005; Lan et al., 2006^a; Martella et al., 2006). This result suggested the vaccine strains had apparently disappeared in last five decades (Matella et al., 2006).

In Thailand, Keawcharoen et al. (2005) revealed 13 cases of Thai's CDV nucleotide sequences in the nucleocapsid protein (N) gene but not in the P and H gene region. The aim of study is to focus on H and P gene and compare with the strains in Genbank database. To investigate the nucleotide sequences of CDV, the viruses were isolated in Vero cell expressing Canine signaling lymphocyte activation molecules with a tag (Vero-DST), and followed by reverse transcription - polymerase chain reaction (RT- PCR) which was developed as an efficient method to detect small amounts of viruses (Elia et al., 2006). PCR products can be used for sequencing, the nucleotide sequence of H and P gene were compared with other isolates in Genbank and analyzed by percentage of homology and phylogenetic trees.