

## **CHAPTER 4**

### **Epitope Mapping of Canine Distemper Virus Phosphoprotein by Monoclonal Antibodies**

## SUMMARY

Canine distemper virus (CDV) is a member of genus *Morbillivirus* with Measles virus (MV) and Rinderpest virus (RPV), and the virus possesses six structural proteins. Phosphoprotein (P) gene encodes three different proteins, P, V and C, and is related to virus gene transcription. In Chapter 4, author produced monoclonal antibodies (MAbs) against CDV P protein in order to analyze the functions of P protein. P gene of the CDV Yanaka strain, not V nor C region, was cloned into pQE E.coli expression vector, and P protein was produced in mass culture and purified with Ni affinity column. By immunizing the expressed protein into BALB/c mice, author obtained 7 monoclonal antibodies (13Ea, 52G, 36Ba, 33Ba, 36E 42Ba, and 99Bb). Competitive binding assay revealed that they recognizing two antigenic sites of P protein. The first site was interestingly conserved in other recent field isolates and in RPVs, but not in old type CDVs nor in MVs. The second site was appeared specifically only for the Yanaka strain.

## INTRODUCTION

In negative-stranded RNA viruses, phospho (P) protein has been shown to have multiple functions. Transcription initiates at the 3' end of the genome RNA, giving the sequential synthesis of (+) strand leader (le+) RNA and then the N, P/C/V, M, F, H, and L mRNAs [Mellon, 1978; Lamb and Kolakofsky, 2001]. During genome replication, synthesis of viral RNA and encapsidation by N protein are concomitant. N protein has the capacity to self-assemble on cellular RNA to form nucleocapsid-like particle in the absence of viral RNA and viral proteins [Fooks, 1993]. Association of P protein with the soluble, monomeric form of N ( $N^0$ ) protein prevents it from binding to cellular RNA [Curran, 1995; Huber, 1991]. The  $N^0$ -P complex is the substrate used by the polymerase to initiate encapsidation of genomic RNA [Spehner, 1997]. N forms complexes with P and with the P-L complex during transcription and also during replication, in its self-assembled form [Horikami, 1992]. Structural studies show that SeV P protein is a tetramer and the oligomerization domain has a coiled coil structure which extends to aa 433 aa through part of the L protein binding domain [Tarbouriech, 2000a; Tarbouriech, 2000b]. MV P protein is also an oligomer, although the nature of the complex has not been determined [Curran, 1995; Harty and Palese, 1995; Liston, 1995]. RPV P protein is reported to have a key role in the replication of the virus in the cross species infection and pathogenicity using animal model of rabbit and recombinant viruses based on the RPV-L strain [Yoneda, 2004].

All paramyxovirus P proteins are likely to be oligomeric, containing heptads sequence repeats in the central region (approximately 340-410aa) of the molecule, characteristic of helical coiled coils [Curran, 1995]. The structure of this region of the SeV P protein has determined and is a tetrameric coiled [Tarbouriech, 2000]. The

extreme of C terminus of P is critical for nucleocapsid binding, as short SeV eliminate or dramatically decrease N-RNA. The final 50 amino acids of P protein are predicted to form a trihelical structural motif in many paramyxoviral P proteins, including MV [Curran, 1995]. Recent crystal structure of this domain from MV P protein shows it to be a compact bundle of three alpha-helices [Johansson, 2003]. For MV, the C-terminal region of P protein including the putative coiled coil and down stream sequences, can bind to the N protein [Huber, 1991; Liston, 1995; De, 2000; Longhi, 2003].

In Chapter 4, to understand the multifunction of P protein, author established and characterized monoclonal antibodies (MAbs) against CDV P protein of the CDV Yanaka strain.

## **MATERIALS AND METHODS**

### **Cells and viruses**

B95a cells and Vero cells were maintained in RPMI1640 containing 5% FCS and in DME containing 10% FCS respectively. The Onderstepoort (vaccine strain), Snyder Hill (old virulent strain), Haku93 and Hake00 [Japanese field isolates from masked palm civets, Hirama 2004] of CDV strains, the RBOK (vaccine strain) and L (lapinized strain) of RPV strains, and the Edmonston (vaccine strain) and HL (virulent strain) of MV strains were used. The Onderstepoort, Snyder Hill, RBOK, and Edmonston strains were grown in Vero cells and the others in B95a cells.

### **Production of recombinant CDV P protein**

CDV P cDNA was cloned from the CDV Yanaka strain infected cells [Wakasa, Genbank accession no. AB028914]. CDV P gene produced three kinds of viral proteins, P, V, and C [Lamb and Kolakofsky, 2001]. The V protein shares its N-terminal half (1-231 aa) with the P protein and has a different C-terminus (232-246 aa). Therefore, a DNA fragment coding C-terminal half of P protein (232 aa to 507aa) was used as the antigen. The DNA fragment was inserted into E. coli expression vector pQE30 (QIAGEN) which can produce recombinant protein as a fusion protein with histidine-tag at N-terminal. The plasmid was transformed in the M15 bacteria strain for high-yield of recombinant proteins. One-litter culture was incubated to express CDV-P at mid-log phase of growth (0.2 OD<sub>600</sub>) by addition of 1mM IPTG. After 3 hr incubation, the E. coli culture were centrifuged, pelleted and washed by PBS (-). It was lysed by lysis buffer (0.5% Triton X-100, 0.5% DOC, 5mM NaCl, 25mM Tris-HCl pH8.0) and centrifuged at 10,000xg for 30 min to remove insoluble materials. Recombinant CDV-P was found mainly in soluble

fractions. The P protein containing the N-terminal histidine tag was purified according to chapter 3. This purified recombinant P protein was provided as an antigen for generation of MAbs.

### **Generation of monoclonal antibodies**

The recombinant CDV P protein was mixed with RIBI adjuvant (Corixa) and immunized into BALB/c mice three times. Anti-CDV P antibody titer was checked by ELISA using the recombinant P protein as antigen. When high titer of P antibody in these sera was detected, mice were sacrificed, and then spleen cells were obtained and fused with myeloma PAI cells using PEG1500 (Roche) as described previously [Kohler and Milstein, 1975]. Hybridoma cells were selected by HAT (Gibco, BRL) and culture supernatants were examined by immunofluorescence (IFA) using B95a cells infected with the CDV Yanaka strain. Hybridomas with positive reaction were selected, propagated and inoculated into peritoneal cavity of BALB/c mice after pristane treatment (Sigma-Aldrich). After approximately 10 days, ascites including high titer of MAbs were collected.

### **Immunofluorescence assay (IFA)**

B95a cells were grown in 10cm plates and infected with various strains of CDV, RPV and MV. After 3 days, the cells were removed by scraper, washed once with PBS (-) and cultured in the wells of FA plates. The cells were dried up briefly and fixed in acetone for 30 min. The cells were consecutively processed for 60 min with the MAbs (diluted at 1:200) in PBS (-) washed, and then goat anti-mouse antibody- FITC conjugate in PBS (diluted at 1:500) (CAPPEL). After washing by PBS three times, imaging analysis was

performed with confocal microscopy, Fluoview FV500 system (Olympus).

### **Immunoprecipitation**

B95a cells infected with or without the Yanaka strain were radiolabelled with 3 MBq/ml [<sup>35</sup>S] methionine and cystine (DuPont NEN Research Products) for 2 hrs. The radiolabelled cells were lysed in RIPA buffer (1% Triton X-100, 1mM iodoacetamide, 0.2 U/ml of the trypsin inhibitor aprotinin, 1mM phenylmethylsulfonyl fluoride, 1% sodium deoxycholate, 0.14M NaCl, and 10mM Tris-HCl, pH 8.0). The lysate was reacted with the MAbs for 3 hrs at 4°C, followed by incubation with protein A beads (Amersham Biosciences). The beads were washed with PBS (-) three times and then loading dye was directly added. The immunoprecipitates were resolved by 10% SDS-PAGE and analyzed by BAS2000 (Fuji Film).

### **Competitive binding inhibition assay**

MAbs were purified by protein A sepharose and then biotinylated MAbs were prepared according to the manufacture procedure (Biotin labeling kit, Roche). CDV-Yanaka infected B95a cells were lysed by RIPA buffer and the lysate was spread in each well of 96-well plate. After 1 hr at 37°C, each well was blocked by PBS with 4% block ace. Each well was reacted with appropriate dilutions of non-labeled MAbs for 1 hr at 37°C and then washed five times with PBS. Each well was reacted with appropriate dilutions of each biotinylated MAbs and washed as well as described above. The detection was performed by Vectastain Elite ABC kit (Vector Laboratories). After the reaction was visualized with o-phenylenediamine and then stopped with H<sub>2</sub>SO<sub>4</sub>, the resulting optical density at 492 nm was measured with an ELISA reader (Bio-Rad).

## **RESULTS**

### **Production of Recombinant P Protein derived from the CDV Yanaka strain.**

CDV P gene produced three kinds of viral proteins, P, V, and C [Lamb and Kolakofsky, 2001], and the P protein (507 aa) is expressed from the largest ORF in the P mRNA (Fig. 1A). The V protein (299 aa) shares its N-terminal half with the P protein and has a different C-terminus. To produce P protein specific antibodies, we prepared a DNA fragment coding C-terminal region of P protein of the CDV Yanaka strain (232 aa to 507aa). The DNA fragment was inserted into E.coli expression vector which recombinant protein was expressed as a fusion protein with histidine tag at N-terminal. E.coli transformed with the plasmid produced recombinant P protein in soluble form and by single-step affinity purification procedure using nickel chelating column. The purified protein was shown with an expected molecular weight of approximately 21 kDa and obtained at high yield (Fig. 1B). The purified CDV-P protein was applied for the generation of antibodies.

### **Establishment of CDV-P MABs against CDV P protein**

Author immunized the recombinant CDV P protein in mice and fused their splenocytes to myeloma cells to establish hybridomas. After first screening by ELISA using recombinant CDV-P protein, 205 positive-colonies were obtained. Following screening by ELISA using lysate of B95a cells infected with the CDV Yanaka strain, author selected seven clones, 13Ea, 52G, 36Ba, 33Ba, 36E 42Ba, and 99Bb, which hybridoma cells were propagated well and their supernatant showed high reactivities to P protein of the CDV Yanaka strain. In analyses of IFA and immunoprecipitation, positive reactivity of all of the MABs reacted with B95a cells infected with the CDV Yanaka strain



was observed and specific 72kDa-bands were visualized respectively (Fig. 2). Although immunoprecipitation by some anti-N MAbs was respected to be co-precipitated due to N-P interaction [Orvell, 1985; Sugiyama, 1989], none of the related proteins was precipitated by all the anti-P MAbs (Fig. 2). No MAbs reacted with V and C proteins of the CDV Yanaka strain transiently expressed in COS1 cells (data not shown). These results indicate that the MAbs specifically react with P protein of the CDV Yanaka strain.

### **Characterization of MAbs**

Antigenic sites recognized by the 7 MAbs were determined by a competitive binding inhibition assay using the lysate of B95a cells infected with the CDV Yanaka strain (Table 1). The analysis revealed that the MAbs recognized in two different epitopes of P protein. MAb 13Ea, 52G, 36Ba, 42Ba, and 99Bb reacted one epitope (site I), and 33Ba and 36E another (site II).

### **Reactivity of the MAbs against Morbilliviruses**

The 7 MAbs were examined for their antigenic specific reactivity against morbillivirus strains; the CDV Onderstepoort, CDV-Snyder Hill, CDV-Haku 93 and Haku 00, RPV-RBOK, RPV-L, MV-Edmonston and MV-HL strains (Table 2). New field isolates of CDV, the CDV Haku93 and Haku00 strains, showed reactivity to the MAbs recognizing antigenic site I, 13Ea, 52G, 36Ba and 99Bb, but they did not react with the MAbs for site II, 33Ba and 36E. Unexpectedly, all of the MAbs did not react with both of old type CDV strains; the Onderstepoort and Snyder Hill strains.

All MAbs did not show positive reactivity with any of MV infected cells. Interestingly, MAbs for site I reacted with RPV infected cells except MAb 99Bb. The P

protein of RPVs probably conserved the antigenic site I, but some genetic alteration might cause minor differences of antigenicity which is responsible for the MAb 99Bb recognition.

## DISCUSSION

In this study, author produced the specific region (321-507aa coding) recombinant P protein of the CDV Yanaka strain by E.coli and established seven hybridomas producing MAbs against the protein. The seven MAbs recognized two antigenic epitopes (site I and II). Orvell and colleagues reported that the established MAbs against whole P protein of the CDV Convac strain had 6 epitopic groups in 22 MAbs [Orvell, 1985]. P protein in RNP is proposed to form tetramers with helical coiled coils in the central region (approximately 340-410aa) and with a compact bundle of three alpha-helices for N-binding at the C-terminal region (457-507aa of MV) [Kingston, 2004]. The tetrameric P protein structurally penetrates to L protein at the central region of P protein and thus the region is masked due to interaction of L protein. Thus by the screening method of IFA using CDV infected B95a cells, it is speculated that MAbs recognized N-binding region are more selective than L-binding region. All the anti-P MAbs did not induce to co-precipitate CDV-N-proteins. This result suggests that the antigenic region of the MAbs might locate at the region of N-P interaction.

Sequence alignment of the P protein of the Yanaka strain with that of the Onderstepoort strain showed 94% identity [Genbank accession, Yanaka: AB028914; Onderstepoort: AF378705]. Highly conserved regions were preferentially located in the C-terminal half corresponding to the recombinant P protein and were 96% identical to each other. Although the P gene sequences of Haku93 and Haku00 were not determined, those of H proteins showed more than 98% similarity to the Yanaka strain, indicating high similarity also for P protein. On the other hand, the amino acid identities between the CDV Yanaka strain and other morbilliviruses are only 44.3% (MV Edmonston) and 46.0% (RPV-RBOK). Curiously, the MAbs, 13Ea, 52G, 36Ba and 42Ba,

reacted with the RPV-RBOK and RPV-L strains but neither the CDV Onderstepoort nor Snyder Hill strains, probably recognizing a conformation-dependent epitope. This result may be explained by previous study that one anti-CDV-P MAb is found with reactivities of the CDV Onderstepoort and Convac strains but not the CDV Rockborn strain. And another study also showed that one anti-MV-M MAb cross-reacted with the CDV Convac and RPV RBOK strains but not the CDV Onderstepoort strain, and another MAb reacted with only the RPV RBOK strain but not the CDV Convac and Onderstepoort strains [Sheshberadaran, 1986]. All proteins consist of both functional highly conservative regions and non-functional variant regions. These facts raise a possibility that one of the conservative regions in P protein was evolutionally changed independently, and then a common epitopic structure in P proteins abiogeneticly appeared in both the CDV Yanaka and PRV strains.

In this study, MAbs of P protein of CDV Yanaka atrain established in this study should be useful for functional study of P protein.

## FIGURE LEGENDS

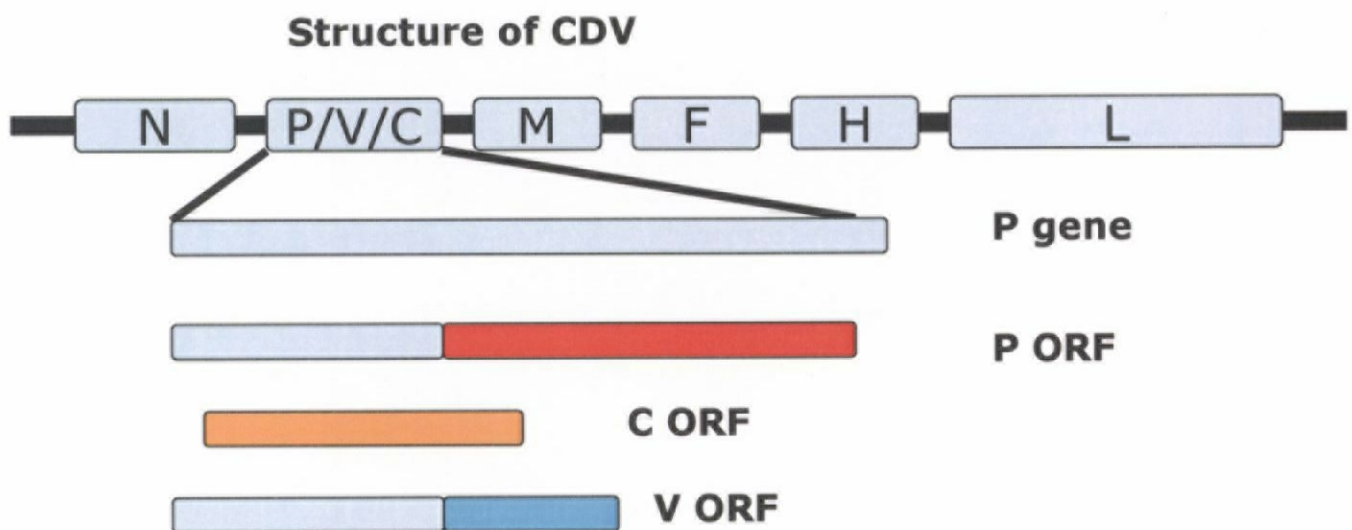
Fig. 1 Expression of recombinant P protein. (A) Scheme of CDV-P gene. CDV P gene produced three kinds of viral proteins, P, V, and C. (B) Silver staining (left) and western blot analyses (right) are shown. The P protein containing the N-terminal histidine-tag purified with NTA resin column was observed as a single band (arrow). 1. E.coli, 2. prepurification, 3. purified CDV-P protein.

Fig. 2 Immunoprecipitation by each MAb against CDV-P protein.

CDV-Yanaka infected B95a cells were labeled with  $^{35}\text{S}$ -Met and Cys, and immunoprecipitated by MAb-Protein A Sepharose. Expected size of protein bands were observed at 72kDa (indicated by arrow).

Fig. 1

A)



B)

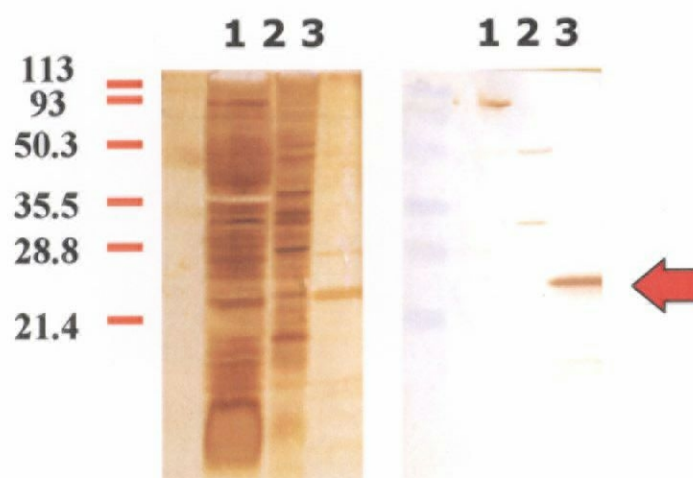
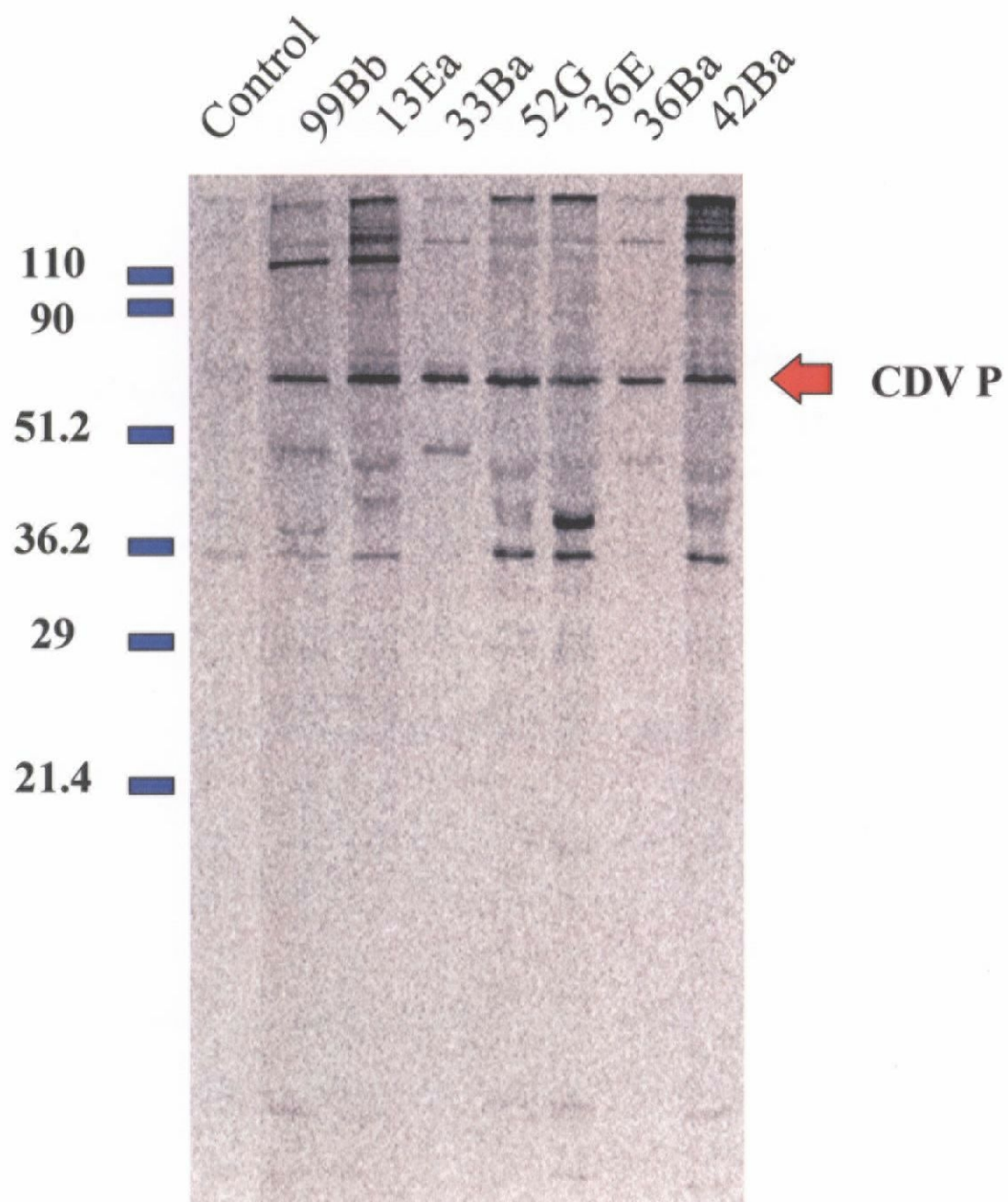


Fig. 2



**Table 1 Competitive binding inhibition assay**

Purified MAbs	Antigenic site	Biotinylated MAb						
		99Bb	13Ea	52G	36Ba	42Ba	33Ba	36E
<b>99Bb</b>	<b>I</b>	+	+	+	+	+	-	-
<b>13Ea</b>	<b>I</b>	+	+	+	+	+	-	-
<b>52G</b>	<b>I</b>	+	+	+	+	+	-	-
<b>36Ba</b>	<b>I</b>	+	+	+	+	+	-	-
<b>42Ba</b>	<b>I</b>	+	+	+	+	+	-	-
<b>33Ba</b>	<b>II</b>	-	-	-	-	-	+	+
<b>36E</b>	<b>II</b>	-	-	-	-	-	+	+

\* +: 80%< competition, -: 30%> competition



**Table 2 Immuno reactivity of anti-P MAbs with various strains of morbilliviruses**

		MAb						
		99Bb	13Ea	52G	36Ba	42Ba	33Ba	36E
<b>CDV</b>								
	<b>Yanaka</b>	+	+	+	+	+	+	+
	<b>Onderstepoort</b>	-	-	-	-	-	-	-
	<b>Snyder Hill</b>	-	-	-	-	-	-	-
	<b>Haku93</b>	+	+	+	+	+	-	-
	<b>Haku00</b>	+	+	+	+	+	-	-
<b>RPV</b>								
	<b>RBOK</b>	-	+	+	+	+	-	-
	<b>L</b>	-	+	+	+	+	-	-
<b>MV</b>								
	<b>Edmonston</b>	-	-	-	-	-	-	-
	<b>HL</b>	-	-	-	-	-	-	-

## **CHAPTER 5**

### **Characterization of CDV Genome in Viral Particle by Electron Microscopy**

## **SUMMARY**

Compared to the studies of CDV or MV genomes released in cytoplasm of infected cells, morphologic studies of them in virus particle remain unknown. In this study, author investigated the morphologic features of CDV genome packaged in viral particle by electron microscopy. The released CDV particles were prepared from culture medium by sucrose gradient ultra-centrifugation. In electron microscopic analysis, viral genome packaged in viral particle was extensively longer than predicted in length (1000 nm). Additionally, the viral genomes existed as large filamentous (LF) form and small filamentous (SF) form. By immunoelectron microscopic analysis using the monoclonal antibodies against CDV P proteins established in Chapter 4, P protein was only localized on the surface of genome as LF form of genome but not as SF form. These results suggest that multiple genomes are packaged in a single viral particle and P protein-attached filamentous structure is a natural form in infectious viral particles.

## INTRODUCTION

Paramyxoviruses have a single-stranded non-segmented negative-sense RNA genome of between 15 and 19kb in length [Lamb and Kolakofsky, 2001]. The RNA genome is packaged with the viral nucleoprotein (N) within a helical nucleocapsid. *Mononegavirales* use this N-RNA complex (here after referred to as the nucleocapsid) as a template for both transcription and replication. These reactions are carried out by the RNA-dependent RNA polymerase (L) in conjunction with the phosphoprotein (P). The morphology of nucleocapsid is considered as one of the defining features of the *Paramyxoviridae* and is described as having a 'herringbone' appearance when imaged under a transmission electron microscope. The nucleocapsid, rather than naked genomic RNA, is the template for replication and transcription [Emerson, 1987]. The nucleocapsid is packaged in viral particle with viral glycoproteins and then released from the cells. Compared to the nucleocapsid in the intracellular environment, its morphologic structure in viral particle has not been well-investigated. Although the nucleocapsid penetrates cytoplasm after the infection, it is not clear how adequate morphologic structure of nucleocapsid is packaged in a viral particle in order to start transcription and replication immediately and where P and L proteins are localized in viral genome for transcription and replication.

In this study, to investigate morphologic structure of packaged CDV genome in viral particle, author purified CDV particles from culture medium by sucrose gradient ultra-centrifugation, and performed electron microscopic analysis. Furthermore, author determined localization and distribution of CDV P protein in the genome by immunoelectron microscopy using the MAbs against CDV P protein established in Chapter 4.

## **MATERIALS AND METHODS**

### **Cells and viruses**

B95a cells, which were derived from a marmoset B-lymphoblastoid cell line were maintained in RPMI1640 containing 5% FCS. The CDV Yanaka strain was isolated in Japan from a dog clinically diagnosed with distemper [Gemma 1996b].

### **Electron microscopic analysis**

B95a cells were infected with the CDV Yanaka strain at a MOI of 0.1, and 2 days later the cells were fixed in 2% formaldehyde and 2.5% glutaraldehyde in 0.1 M phosphate buffer (pH7.3) for 1 hr. The cells were post-fixed in 1% osmium in the phosphate-buffer for 1 hr, dehydrated and embedded in Epon (TAAB). Fifty  $\mu\text{m}$  of ultra thin sections were prepared by ultra microtome (Leica) and stained with 2% Urinaly acetate in 70% Ethyl alcohol and lead citrate. The sections were examined with 1200EX electron microscope (Jeol). Culture medium collected from B95a cells infected with the CDV Yanaka strain was concentrated by filtration system (Centricon filter, pore size of 100K, Millipore). The concentrate was applied to sucrose bed at the dense between 20% and 60% and separated by centrifugation with 25,000 x g for 2 hr. Virus particle-including band was purified by desalting column in order to remove the sucrose. The samples were dropped on the plastic-coated copper grids and incubated for 15 min at room temperature. The viral particles just after budding were also examined with electron microscopy (Jeol).

### **Immunoelectron microscopic analysis**

The purified viral particles were dropped on the plastic-coated copper grids and

incubated as described above. After blocking with 3% gelatin in PBS (-) for 1 hr, the sample was incubated with anti-CDV P MAb (36Ba), CDV-N MAb (6H) or CDV-M polyclonal antibody [Uema, 2005] for 1 hr at room temperature. After three times washing with PBS (-), the sample was labeled by gold particle-protein A (Amersham Bioscience) for 1 hr. After several wash by 0.05M phosphate buffer, grids were post-stained by 2% phosphotungstic acid. Immunoelectron microscopic analysis was demonstrated by 1200EX (Jeol).

## **RESULTS**

### **Electron microscopic analysis of CDV Yanaka infected B95a cells**

In previous electron microscope studies, viral formation or budding of CDV or MV was characterized in Vero cells or Hela cells [CDV: Narang, 1982; MV: Nakai, 1969; Oyanagi, 1971]. Initially, author investigated how viral particle of CDV released from CDV-Yanaka infected B95a cells (Fig. 1AB). Viral particles near the surface of a cell are clearly visible. One spherical viral particle was observed near the cell (Fig. 1A a) and other particles have attached to the cells and the interior of the particle was continuous with the cytoplasm (Fig. 1A b, c). The shedding of viral particles was always accompanied with extensive spiking. On the other hand, nucleocapsid regularly aggregated in cytoplasm (Fig. 1B, NC). These results agreed with the previous studies [Dubois-Dalcq, 1987].

### **Electron microscopic analysis of structure of CDV genome in virus particle**

To investigate the genomic structure packaged in the virus particle of the CDV Yanaka strain, released viral particles from B95a cells infected with the virus were concentrated and separated by sucrose gradient centrifugation. The virus particle and its genome were observed under electron microscope (Fig. 2). As expected, the viral particle displayed a relatively homogenous population of spherical particles with a diameter of around 200nm (Fig. 2AB), as described previously [Lamb and Kolakofsky, 2001]. Typical nucleocapsid strands of CDV genome were also clearly seen. Unpackaged genome was observed probably due to disruption of the virus particle (Fig. 2C). Partially, a smaller diameter of nucleocapsid string was observed (Fig. 2C arrow). Based on the scale bar (100 nm), the length of the genomes was estimated. The genome length in a

viral particle was estimated to be more than 2000-3000 nm in length. Since the size of a single genome of paramyxovirus described as approximately 1000 nm in length previously [Lamb and Kolakofsky, 2001], the possibility that multiple genomes are packaged in a single virus particle was raised.

### **Immunoelectron microscopic analysis of CDV genome by anti-N, P and M antibodies**

Using each antibody against P, N or M protein of the CDV Yanaka strain, its localization and distribution on the CDV genome was observed by immunoelectron microscopy. The genomes reacted with the CDV-P MAb, CDV-N MAb or CDV-M polyclonal antibody. The antibody reaction was visible as black dots. The genome in unfixed viral particle was not able to react with the antibodies, because the viral membrane probably interfered with these reactions. Under the electron microscopy, the viral genomes with filamentous structure apparently consisted of two forms with diameters of approximately 80 nm and 20 nm. Author designated large filamentous (LF) and small filamentous (SF) genome (Fig. 3, Fig. 4B). The diameter of typical paramyxovirus genome was described as 18 nm [Lamb and Kolakofsky, 2001], corresponding to the SF genome. Anti CDV P MAb reacted with only LF genome but not SF genomes, and the reaction to the LF genomes occurred over the whole strings (Fig. 3A-C). Anti-N MAb reacted with both LF and SF genomes, implying that the strings are nucleocapsids (Fig. 4A, B). The analysis using anti-M antibody was also carried out. M proteins existed interspersely (Fig. 5 A, B) and thus did not attach to the genome.



## DISCUSSION

In this study, author shows that viral genome packaged in a viral particle was extensively longer than previous predicted size. Additionally, the viral genomes existed as two forms, LF form and SF form. By immunoelectron microscopic analysis, P protein was only localized on the surface of genome of LF form but not SF form.

A paramyxovirus produces pleomorphic particles with diameters ranging from 120 to over 300 nm [Waterson, 1965; Nakai, 1969; Lund, 1984]. The cargo space of the particles is speculated to vary from  $3 \times 10^5$  to  $>10^7$  nm<sup>3</sup>. Considering that the diameter and length of the virus genome are 20 and 1000 nm, respectively, particles should be able to accommodate from one to >30 genomes. Actually, particle sedimentation and ultraviolet inactivation studies indicate that the pleomorphic particles of parainfluenza viruses often incorporate more than one genome [Hosaka, 1966; Dahlberg, 1969] and previous studies of recombinant MV demonstrated that multiple heterogenous genomes are packaged stably in a virus particle and the particles are produced in standard infection at no expense to infectivity [Rager, 2002]. This electron microscopic analysis shows that a lot of both packaged and unpackaged viral genomes were extremely longer than the expected length of virus genome. This result suggests that packaging of multiple genomes generally occurred in many virus particles and thus the multiple genomes can effectively start to induce the transcription and replication in infected cells.

Our observation showed that the two forms with various diameters of genomes existed. The SF form was closely identical to the general morphology shown in previous studies in MV [Nakai, 1969]. On the other hand, as observed by immunoelectron microscopic analysis with anti-P and anti-N antibodies, LF form seemed to be based on SF form as a helical core and covered with P proteins together with N proteins. This

result seems that the filamentous structure covered with P proteins is a natural form in viral particle, possibly for the rapid start of transcription and replication. In case of extensive expression of N proteins at the condition without genomic RNA, filamentous string structure is known to be formed which is similar to the SF form [Schoehn, 2004]. Taken together, newly synthesized viral genome is rapidly coiled and simultaneously covered by N proteins, and then the virus genome covered with N and P proteins may functionally start transcription and replication.

## FIGURE LEGENDS

Fig. 1 Electron microscope of B95a cells infected with the CDV Yanaka strain. The cells were stained with 2% Urinayl acetate in 70% Ethyl alcohol and examined by electron microscopy. (A) Cells infected with CDV-Yanaka. Arrow heads indicate viral particles released from the surface of the infected cells. (B) Intracellular feature of infected cells. Nucleocapsid (NC) aggregates in cytoplasm.

Fig. 2 Electron microscope of released viral particles of the CDV Yanaka strain. (A, B) CDV-virions. Filamentous genome is packaged in the virion. (C) Naked genome of CDV. Arrow head indicates small filamentous genome.

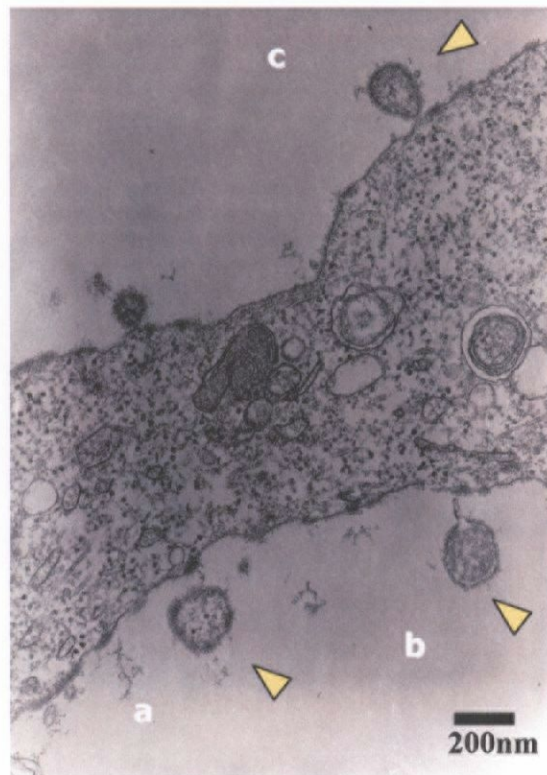
Fig. 3 Immunolectron microscope of CDV genome by anti-CDV P antibody (A-C). Arrow head indicates small filamentous genome (B, C).

Fig. 4 Immunolectron microscope of CDV genome by anti- CDV N antibody (A, B). Arrow head indicates small filamentous genome.

Fig. 5 Immunolectron microscope of CDV genome by anti- CDV M antibody (A, B).

Fig. 1

(A)



(B)

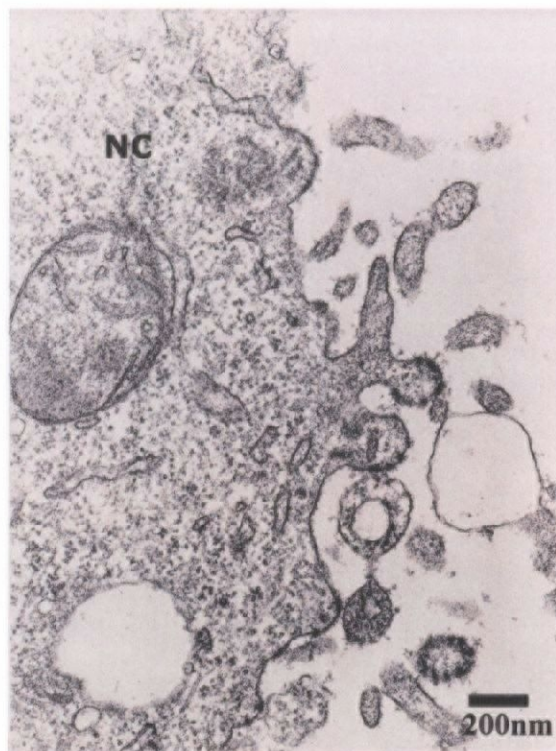
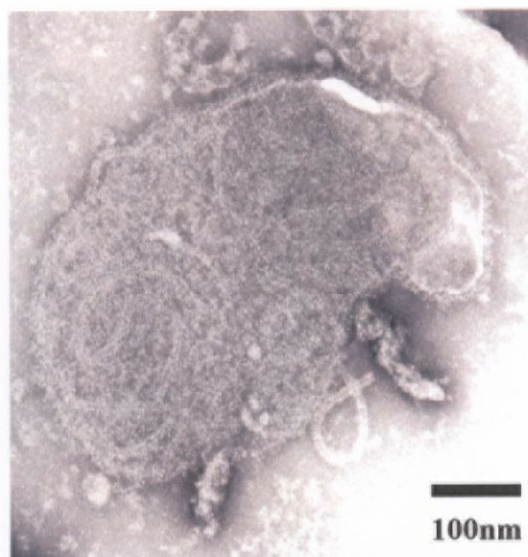
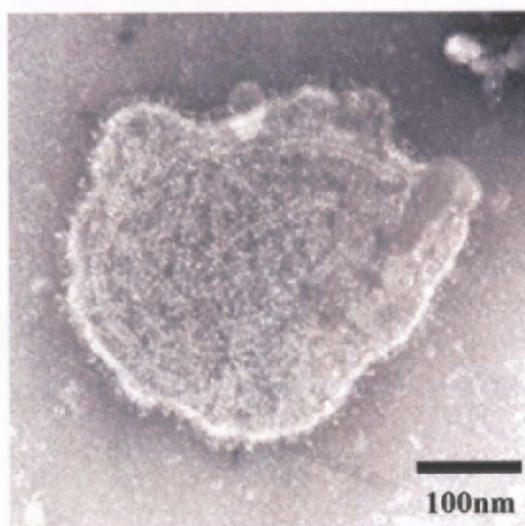


Fig. 2

(A)



(B)

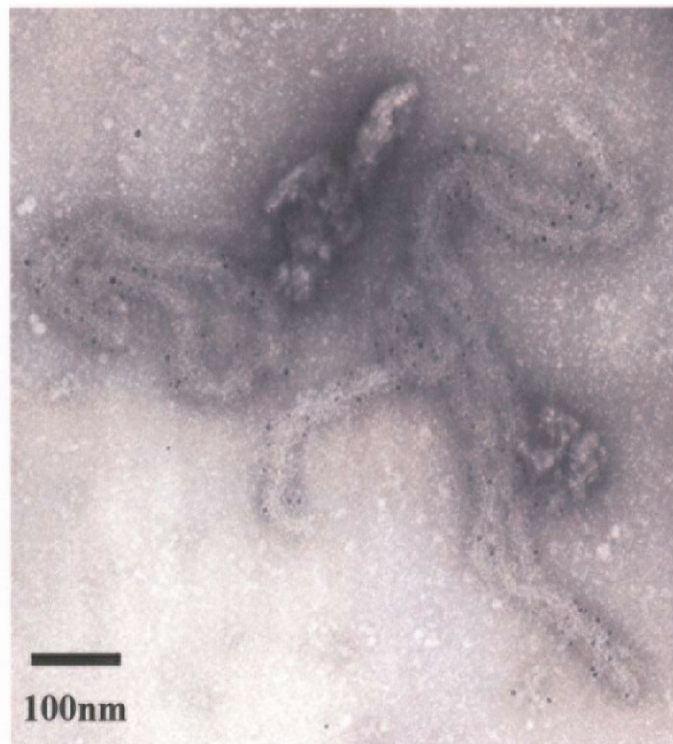


(C)

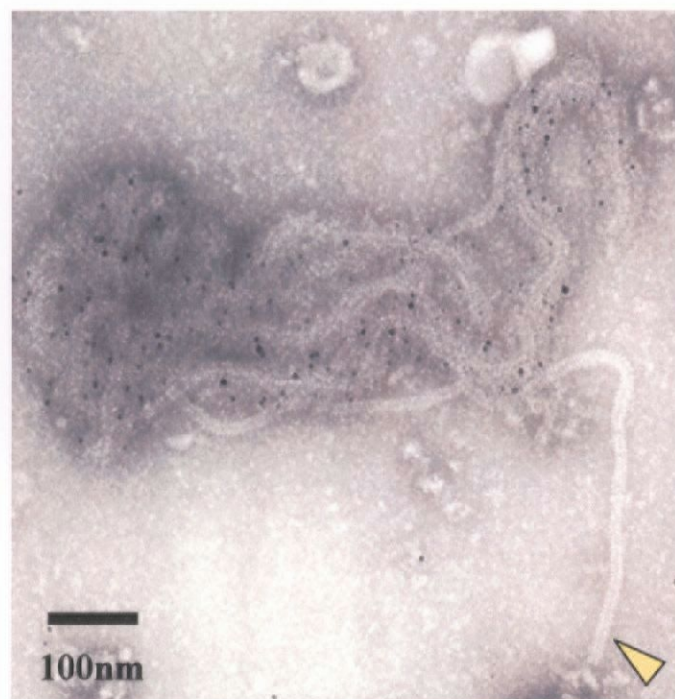


Fig. 3A, B

(A)



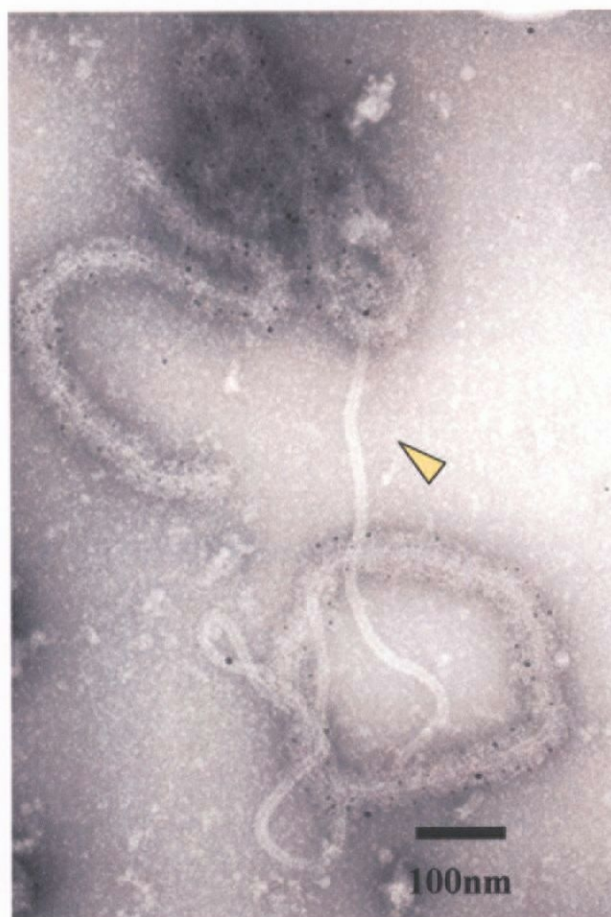
(B)



**Anti-P MAb**



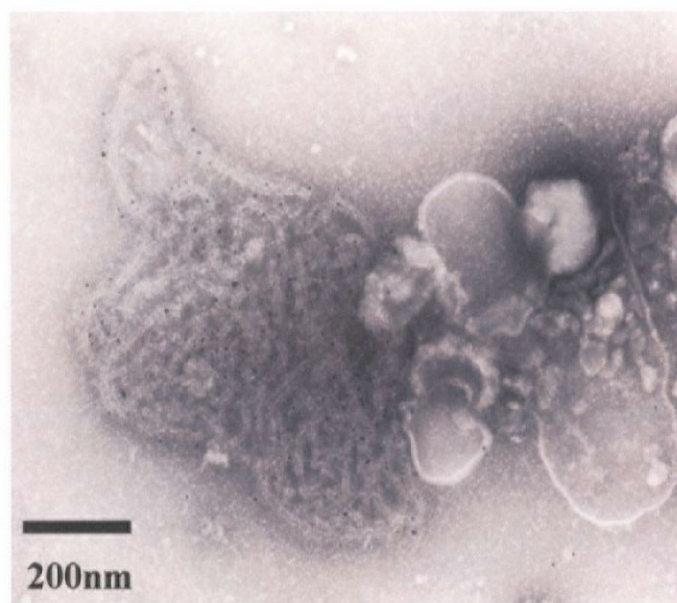
Fig. 3C



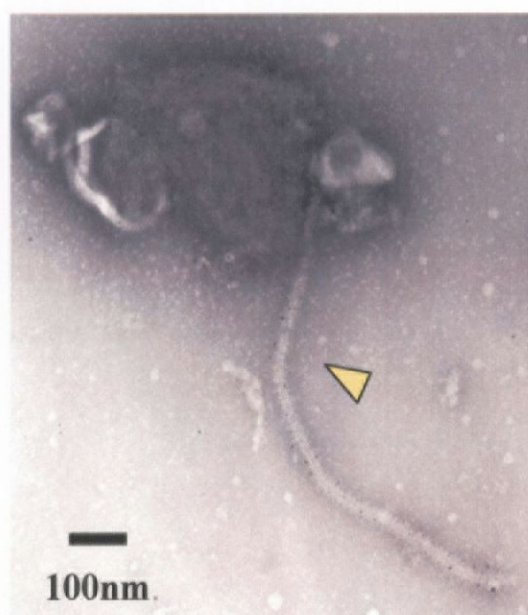
**Anti-P MAb**

Fig. 4

(A)



(B)

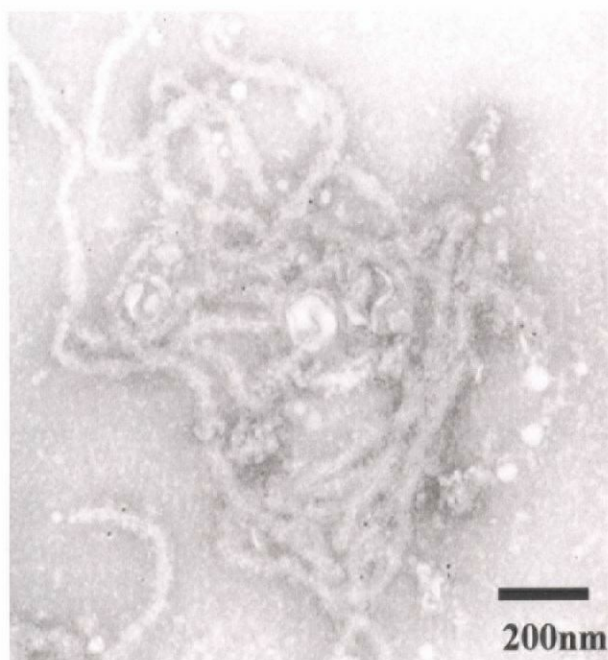


**Anti-N MAb**



Fig. 5

(A)



(B)



**Anti-M MAb**

## **CONCLUSION**

Mononegavirus with reverse genetics system is a useful tool not only to analyze factors involved in pathogeny, tissue tropism and viral transcription and replication, but also to generate recombinant vaccines, gene expression vectors and gene delivery vectors. Using the CDV reverse genetics system, the author aimed in this thesis to understand the mechanism of CDV propagation and spread in dog hippocampus and to develop the therapeutic CDV vectors and leishmania polyvalent vaccine based on CDV. In addition, author also aimed to obtain the fundamental information of genomic structure of CDV to study the biological characteristics of infection and replication.

In Chapter 1, the author analyzed the mechanism of CDV propagation and spread in dog hippocampal slices by using recombinant CDV expressing enhanced green fluorescence protein (EGFP-CDV). The CDV infection and propagation mainly occurred in cornu ammonis regions. Neurons are more effectively infected with the EGFP-CDV than astrocytes and oligodendrocytes. The EGFP-CDV was observed to transport from a neuron to the other through synapses, and a part of synapses of infected neuron mediated the transmission. The viral envelop proteins F and H were distributed in the whole neurons but M protein is mainly located at soma and partially at dendrites and synapses. Electron microscopic analysis demonstrated that ribonucleocapsid protein (RNP) is sorted to synaptic terminals and viral particles were visualized at extrasynaptic regions. These data suggest that CDV may be transmitted to synapses of neurons via extrasynaptic regions. This study shows that CDV is available for long-term transduction of neurons as a delivery vector.

In chapter 2, the author constructed a recombinant CDV expressing dog superoxide dismutase 1 (SOD1) and characterized the effect of recombinant CDV. Since

oxidative stress is thought to be a main cause of neurological disorders in mammals, development of delivery system of the antioxidant enzymes to target cells is important for an effective therapy. A recombinant virus, SOD1-CDV, was successfully rescued, which was confirmed to express SOD1 in a marmoset B cell line, B95a. The size of CPE caused by the recombinant CDV and its growth kinetics were comparatively similar to the parental strain. Western blot analysis revealed that the exogenous dog SOD1 (17kDa) was co-expressed with the endogenous marmoset SOD1 (19kDa) in the infected B95a cells. In nitroblue tetrazolium assay, the increased SOD activity in SOD1-CDV infected cells was shown. These results indicate that SOD1-CDV is expected to produce functional SOD1 in infected cells and the recombinant CDV is considered to be useful as a delivery viral vector.

In Chapter 3, the author displayed recombinant CDVs for use as effective polyvalent vaccine candidates against CDV and *Leishmania* infections. Two recombinant CDVs expressing *Leishmania* antigens, a homologue to eukaryotic thiol-specific antioxidant protein (TSA) and a homologue of a yeast stress-inducible protein 1 (LmSTI1) were successfully rescued (TSA-CDV and LmSTI1-CDV). Dogs immunized with the TSA-CDV, LmSTI1-CDV or the mixture of TSA-CDV, LmSTI1-CDV and LACK-CDV did not show observable clinical signs of infection. The dogs were challenged with *Leishmania major* intradermally in the ears. Nodules appeared in the ears of control dogs at 10 days after the challenge and then enlarged. Most significant protective effects were found in the dogs inoculated with the mixture of TSA-CDV, LmSTI1-CDV and LACK-CDV in all stages of *leishmania* infection. The results indicate that the recombinant CDV with *Leishmania* antigens could induce protective immunity in the inoculated dogs against both CDV and *Leishmania* infections. This study shows

that the recombinant CDVs are powerful tools for the prevention of leishmaniasis epidemics.

In Chapter 4, the author produced monoclonal antibodies (MAbs) against CDV P protein in order to analyze the functions of P protein. P gene of the CDV Yanaka strain, not V nor C region, was cloned into pQE E.coli expression vector, and P protein was produced in mass culture and purified. By immunizing the expressed protein into BALB/c mice, author obtained 7 monoclonal antibodies (13Ea, 52G, 36Ba, 33Ba, 36E 42Ba, and 99Bb). Competitive binding assay revealed that they recognized two antigenic sites of P protein. The first site was interestingly conserved in other recent field isolates and in RPVs, but not in old type CDVs nor in MVs. The second site was appeared specifically only for the Yanaka strain. MAbs of P protein of the CDV Yanaka strain established in this study should become a useful tool for functional study of P protein.

In Chapter 5, the author investigated the morphologic features of CDV genome packaged in viral particle by electron microscopy. The released CDV particles were prepared from culture medium by sucrose gradient ultra-centrifugation. In electron microscopic analysis, viral genome packaged in viral particle was extensively longer than predicted in length (1000 nm). Additionally, the viral genomes existed as large filamentous (LF) form and small filamentous (SF) form. By immunoelectron microscopic analysis using the MAbs against CDV P proteins established in Chapter 4, P protein was only localized on the surface of genome as LF form of genome but not as SF form. These results suggest that multiple genomes are packaged in a single viral particle and P protein-attached filamentous structure is a natural form in infectious viral particles.

These finding described in this thesis supplied invaluable knowledges of CDV infection tropism in dog' brain and morphologic features of the genome, and showed

high availability of the recombinant CDV as a novel viral vector for gene therapies and polyvalent vaccines.

## **ACKNOWLEDGMENTS**

I would like to express my gratitude to everyone who has contributed to this thesis, in particular to:

Professor Chieko Kai (Laboratory Animal Research Center, Institute of Medical Science, The University of Tokyo, Tokyo) for invaluable support, critical encouragement and excellent scientific advice.

Lecturer Kyoko Tsukiyama-Kohara (Laboratory Animal Research Center, Institute of Medical Science, The University of Tokyo, Tokyo), for excellent scientific and technical advice.

Research Associate Ryuichi Miura (Laboratory Animal Research Center, Institute of Medical Science, The University of Tokyo, Tokyo), for excellent scientific and technical advice.

Research Associate Yoneda Misako (Laboratory Animal Research Center, Institute of Medical Science, The University of Tokyo, Tokyo), for excellent scientific and technical advice.

Research Associate Sagara Hiroshi (Laboratory of molecular structure analysis, Division of Fine Morphology, Fine Morphology Laboratory, The University of Tokyo, Tokyo), for encouragement, and excellent scientific and technical advice.

Lecturer Endo Yasuyuki (Laboratory of Internal Medicine, Department of Veterinary Medicine, Faculty of Agriculture, Kagoshima University, Kagoshima, Kagoshima), for encouragement.

Dr. Kentaro Fujita (Department of Molecular Genetics and Microbiology, State University of New York at Stony Brook, New York, USA), for excellent scientific and technical advice.

The colleagues of all members, of Laboratory Animal Research Center,



Institute of Medical Science (The University of Tokyo, Tokyo), in particular to: Dr. F. Kobune, Dr. Kanai, F. Ikeda, Y. Goto, A. Takenaka, Dr. A. Nuntaprasert, Dr. K. Togashi, Dr. H. Sato, Dr. Y. Katakai, Dr. T. Kuraishi, Dr. Y. Fukushima, Dr. A. Watanabe, Dr. Y. Inoue, Dr. K. Hirabayashi, Dr. Y. Muto, R. Sato, T. Katsuo, M. Tomoeda, Y. Sakuma, R. Takehara, Y. Okamoto, M. Seto, M. Katayama, K. Iwasaki, M. Kurita, M. Doki, M. Uema, M. Shiotani, T. Seki, K. Hirama, T. Nishi, M. Kanai, M. Izumi, M. Hoshi, C. Imai, T. Takano, M. Funabashi, M. Masuda, T. Kubota, K. Saito, M. Awakuni, K. Fukumoto, M. Huang, R. Fukaya, H. Uema and T. Kidokoro for many technical advices and refreshing time.

All of my friends in Institute of Medical Science (The University of Tokyo, Tokyo), in particular to: Dr. T. Ijyuin and Dr. H. Sasaki in Division of Biochemistry, Department of Cancer Biology, Dr. K. Masubuchi, Yamamoto, M. Fujimoto, Y. Yamauchi, Dr. M. Watanabe and Dr. M. Murakami in division of genetics, T. Miyasaka and M. Goto in division of oncology, Dr. Matsumura in Division of Cellular and Molecular Biology, Department of Cancer Biology; Prof. Y. Nakamura, Dr. Oguro, Dr. Fujiwara, H. Sato, C. Colin, Hara, Ms. Takada, H. Kodama and Y. Watanabe in Division of Molecular Biology, Dr. T. Kurita in Division of Molecular and Developmental Biology, T. Kimori and M. Shiraishi in Laboratory of molecular structure analysis, Division of Fine Morphology, department of Basic Medical Sciences; H. Iwai, Nagai, M. Suzuki, A. Ishijima, A. Yoshii, in Division of Bacterial Infection, T. Noda, M. Muramoto, T. Fujii and Dr. Takada Division of Virology department of Microbiology and Immunology; Urano and Minoshima in Division of Hematopoietic Factors (Chugai), M. Sakaki in Division of Stem Cell Regulation (Amgen), Donation Laboratories; Prof. Yoshida, Y. Nakatake, T. Shiota in Laboratory of Gene Expression and Regulation, K. Kagiwada in Laboratory of Cell Biology, Center for Experimental Medicine; M. Handa, E. Suzuki and M. Sato in Inspection room, Prof. Tani,

M. Kasui, H. Yokokawa and S. Suzuki in Division of Molecular Therapy, The Advanced Clinical Research Center and K. Y. Kamata in Coop for many advices and encouragements.

All animals for my studies for their lives. Particularly, smart beagle sisters: Pinokio, Bobby, Michael, Bull, Mask, Shack, Boss, Black, Chappy, Chibi and Boo.

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## **ABSTRACT IN JAPANESE**

## 論文の内容の要旨

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## 論文題目

Application of recombinant CDVs as leishmania vaccine and delivery vector

(組換えイヌジステンパーウイルスのリーシュマニアワクチンおよびデリバリーベクターとしての応用)

ジステンパーはイヌにおける代表的なウイルス性伝染病で、呼吸器系、消化器系、中枢神経系で病変が診られる致死率の高い疾病として知られている。原因となるイヌジステンパーウイルス (CDV) は麻疹ウイルス、牛痘ウイルスなどと共に、パラミクソウイルス科 (Paramyxoviridae) モービリウイルス属 (Morbillivirus) に分類される。最近まで CDV が属する一本鎖マイナス鎖 RNA ウイルス (モノネガウイルス) では、ゲノム cDNA クローンから感染性ウイルスを作出することができなかった。しかし、1994 年に狂犬病ウイルスにおいて初めて感染性ウイルス作出系 (リバースジェネティクス系) が開発され、著者らの研究グループも 1999 年に世界で初めて CDV リバースジェネティクス系の開発に成功した。リバースジェネティクス系により、ウイルス構成遺伝子の欠失や交換、変異の導入や外来遺伝子の挿入を行った組換えウイルスの作出が可能になった。その結果、性質の異なるウイルス株での遺伝子解析の比較だけではわからなかった、病原性の決定機序や特異的な宿主を決定する機構等のウイルス学上重要な問題の解明に大きく寄与することとなった。さらに、液性免疫だけではなく細胞性免疫を誘導する優れた特性を生かしたウイルスベクターの開発やその応用も盛んに進められている。

本研究ではまず、蛍光蛋白 EGFP (Enhanced green fluorescent protein) 発現組換え CDV を用いて、イヌ海馬における CDV の感染動態の解析を行った (第1章)。次に CDV デリバリーベクターへの応用例として、CDV リバースジェネティクス系により抗酸化酵素 Superoxide dismutase 1 (SOD1) 発現組換えウイルスを作出し、その評価を行った (第2章)。そして、リーシュマニア感染症に対する2価ワクチンベクターとして、リーシュマニア抗原発現組換え CDV を作出し、イヌに対する感染実験を行いその有効性を検討した (第3章)。また、CDV の基礎的な研究として、CDV P 蛋白のモノクローナル抗体を作出し、その性状の解析を行った (第4章)。最後に CDV ゲノムの性状を電子顕微鏡下での解析から新たな知見が得られたのでその報告も行った (第5章)。

## 第一章：EGFP 発現CDVを用いたイヌ海馬における CDV 感染動態の解析

イヌの CDV 感染症では中枢神経系への感染が多く認められるが、中枢神経系における CDV の感染拡大様式は明らかにされていなかった。本章では、感染細胞で蛍光を発する EGFP-CDV をイヌ海馬スライスに感染させ、中枢神経系での CDV の感染動態を解析した。ピプラトームでスライス状にした海馬スライスを器官培養して3週間後にウイルス液を滴下し自然感染させた。感染動態は共焦点顕微鏡下で蛍光を指標として経時的に観察した。CDV 感染後、24 時間目には既に蛍光が観察され経時的に周囲の細胞へと伝播した。ニューロン、アストロサイト、オリゴデンドロサイトに対する特異的マーカー抗体でそれぞれ免疫染色を行ったところ、感染細胞の 80%以上がニューロンであることが明らかになった。ニューロンでの感染動態を経時的に観察したところ、シナプスを介して隣接するニューロンに感染していることがわかった。ニューロンでのウイルス膜蛋白の動態を特異抗体を用いた免疫染色で調べたところ、F と H はニューロン全体に分布しているのに対して、M は細胞体の他に一部の軸索やシナプスでのみ発現がみられた。感染3ヶ月目に海馬スライスを電子顕微鏡下で観察したところ、シナプス末端でリボヌクレオキャプシドの蓄積がみられ、更にシナプス外にウイルス粒子を観察することができた。これらの結果から、CDV は中枢神経系ではシナプス末端からシナプス外にウイルス粒子を放出し、隣接するニューロンのシナプスを介してウイルスの侵入・伝播が起こると考えられた。

## 第二章：デリバリーベクターとしての CDV の利用：抗酸化治療に向けたイヌ SOD1 発現組換え CDV の作出

酸化ストレスは神経障害の主な原因と考えられ、標的細胞への抗酸化酵素 SOD の導入は効果的な治療法の一つとして期待されている。本章では CDV リバースジェネティクス系によりイヌ SOD1 発現組換えウイルスの作出を行った。イヌ SOD1 遺伝子をクローニングし、CDV リバースジェネティクス系に従ってウイルスレスキューを行い、SOD1-CDV の作出に成功した。感染細胞での CPE の形状やウイルス増殖曲線は元株 Yanaka 株と比較し顕著な相違は認められなかった。western blot と SOD 活性測定により感染細胞で SOD 活性を持つ機能的な蛋白が十分量発現していることがわかった。第1章では、CDV はニューロンに対して高い感受性があること

が明らかになった。本章での結果から、SOD1-CDV はニューロンに感染し機能的な SOD1 を産生するデリバリーベクターとしての有用性が示唆された。

### 第三章：CDV およびリーシュマニア感染症に対する組換え CDV 二価ワクチンの開発

リーシュマニア原虫症はサシチョウバエを媒介昆虫とし、ヒトやイヌ等に感染して皮膚および内臓に重篤な病巣を形成する人獣共通感染症である。ヒトでは熱帯の発展途上国を中心に毎年 4 千万人以上の感染例が報告されている。この保有宿主ともなるイヌで感染を防ぐことはヒトリーシュマニア症の対策としても有用と考えるが、未だ有効なワクチンは開発されていない。本章では、原虫に対する有効な多価ワクチンの開発を目的として、リーシュマニア抗原を発現する組換え CDV の作出を試みた。リーシュマニア抗原として TSA, LmSTI1 を選択し、CDV リバースジェネティクス系により組換え CDV (TSA-CDV, LmSTI1-CDV) の作出に成功した。これまでに作出成功した LACK-CDV と同様、この 2 つの組換え CDV は元株 Yanaka 株と比べ、ウイルス増殖速度・CPE の形状に顕著な差異は認められなかった。特異抗体を用いた解析により、組換え CDV 感染細胞において抗原蛋白の発現が確認できた。これら組換え CDV を 6 週齢の幼犬に静脈内接種したところ、体温・リンパ球数・臨床所見においても変化がなく、組換え CDV は病原性がなく安全であることが証明できた。CDV ワクチンとしての有効性は既に LACK-CDV 接種犬が CDV 強毒株チャレンジに対して完全な抵抗性を示したことから証明している。リーシュマニアチャレンジ実験では、リーシュマニア接種後 10 週目まで、接種部位で形成される結節の大きさを指標としてリーシュマニア増殖抑制能を検討した。抵抗性誘導能は LACK-CDV で最も顕著であったが、TSA-CDV, LmSTI1-CDV, LACK-CDV を混合して接種したイヌでは結節形成の増大を抑制するのみでなく消失も早め、有効性を示した。これらの結果から、本章で作出した組換え CDV はリーシュマニア症に対する多価ワクチンとしての有効であると考えられた。

### 第四章：CDV P 蛋白に対するモノクローナル抗体による認識部位の検索

モービリウイルスゲノムは 6 つの構成遺伝子をコードし、その一つである P 遺伝子からは P、V、C の蛋白が翻訳される。P 蛋白はこれまでウイルスの転写や複製に必要であることが知られているが最近病原性の発現に関わっていることが報告されている。本章では、P 蛋白の機能解析ツールとして CDV Yanaka 株 P 蛋白に対するモノクローナル抗体を作出しその解析を行った。P と V 蛋白は一部同一のアミノ酸配列を持つため、P 特異的な領域について組換え蛋白を作出し、常法に従ってハイブリドーマを作出して、最終的に 7 つのモノクローナル抗体を得た。これら抗体間の交差反応性を調べたところ、2 つのグループ (I: 13Ea, 52G, 36Ba, 42Ba, 99Bb, II: 33Ba, 36E) に分かれた。更にモービリウイルス間での交差反応性を調べたところ、I 型は Yanaka 株と系統的に近縁なハクビシン由来 CDV Haku93 株と Haku00 株と、更に 99Bb 以外の I 型は RPV (RBOK 株, L 株) とも反応し、I 型は更に 2 つに分けられることがわかった。一方、得られた抗体は全て CDV Snyder Hill 株, Onderstepoort 株及び MV Edmonston 株, HL 株に対して反応を示さなかった。以上の結果から、P 蛋白特異的領域には少なくとも三つの抗体認識部位が存

在することがわかった。

## 第五章：CDV 粒子内ゲノムの電子顕微鏡学的解析

モービリウイルスでは、ウイルスゲノムの動態や形態学的な性状は感染細胞内に比べて、ウイルス粒子内についてはよくわかっていない。本章ではウイルス粒子内にパッケージングされた CDV ゲノムの形態学的性状について解析を行った。感染細胞から放出されるウイルス粒子を濃縮した培養液からショ糖密度勾配を用いて超遠心分離で分画し、ウイルス分画を電子顕微鏡下で解析した。ウイルス粒子に取り込まれるウイルスゲノム全長はこれまで報告されていた 1000nm よりも極めて長いものが多く観察され、一つのウイルス粒子内に複数のウイルスゲノムが取り込まれている可能性が示唆された。更にフィラメント状のウイルスゲノムは主に直径が太いタイプ（long filamentous type: LF）で、一部で、細いタイプ（small filamentous type: SF）が存在することがわかった。第4章で作出した CDV P 蛋白に対するモノクローナル抗体を用いて免疫電子顕微鏡法で解析したところ、P 蛋白は SF の表面には存在せず、一方 LF 上では全体を覆っていることがわかった。これらの結果から、ウイルス粒子内にパッケージングされたウイルスゲノムは多様な形態を構成していることが明らかになった。

本研究では、CDV リバースジェネティクス系によって作出した組換え EGFP-CDV による中枢神経系での CDV 感染動態の検索、デリバリーウイルスとして利用可能なイヌ SOD1 発現する組換え CDV の作出、更に有効な二価ワクチンウイルスとしてリーシュマニア抗原を発現する組換え CDV の有用性を示すことができた。一方将来的にはより安全で有効なウイルスベクターの開発のためにも CDV の基礎的な研究を行い、病原性やウイルス複製に関与する CDV P 蛋白に対するモノクローナル抗体を作出し、電子顕微鏡解析によりウイルス粒子内のゲノムの形態で新しい知見を得ることができた。本研究成果は、CDV の基礎的な新知見のみならずウイルスベクター開発を大きく進展させる有用な知見や成果を与えるものであると考える。