



Pathological and Molecular Biological Studies on
Canine Distemper

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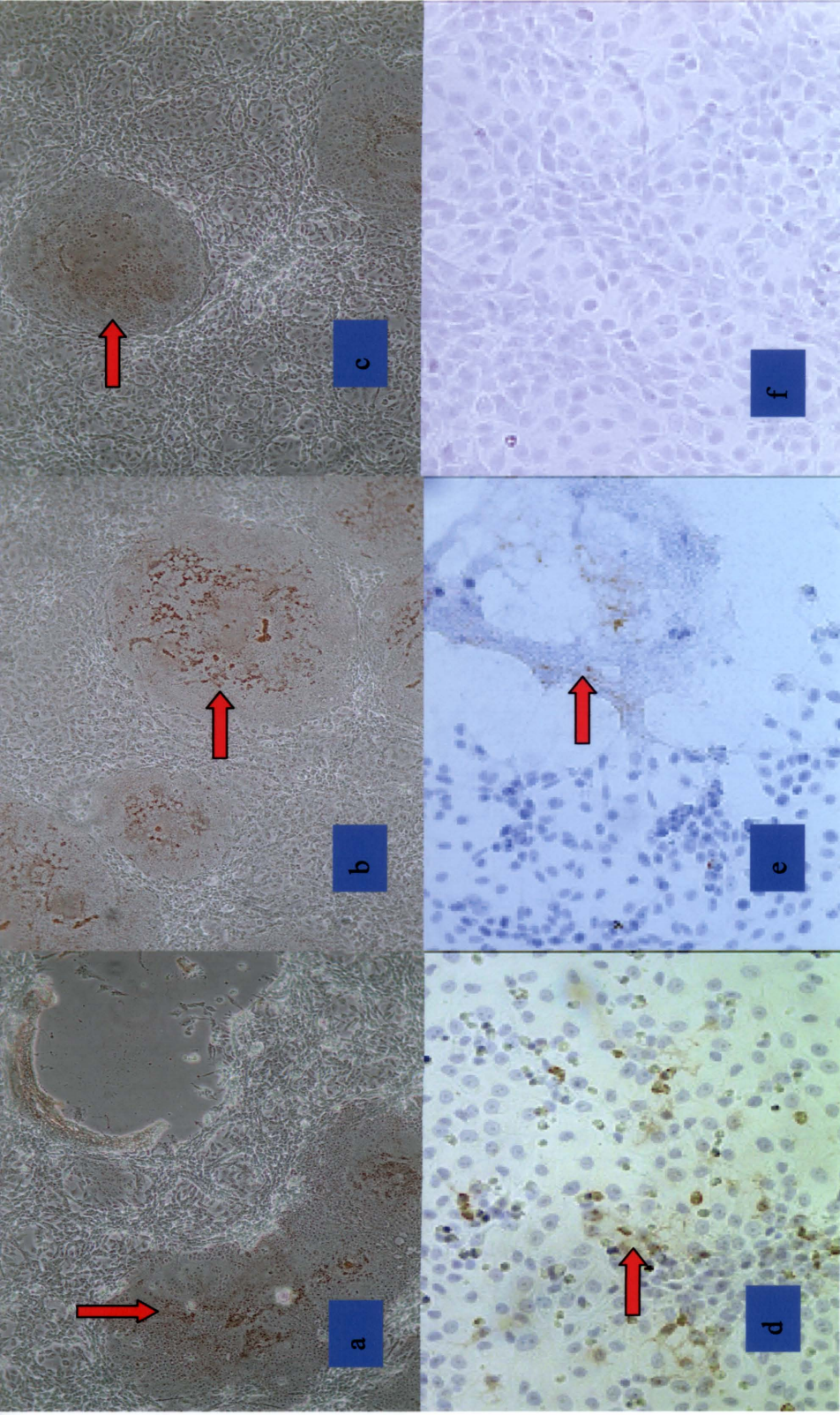


Fig. 1. The distribution of CDV antigens in Vero-DST cells and Vero cells. CDV antigens were detected by immunohistochemistry. Positive CDV antigens were demonstrated by brown color (arrows). Vero-DST cells at 24 hr post inoculation (hpi) with strains MD77 (a), at 36 hpi with Onderstepoort (b) and at 72 hpi with KDK1 (c). Vero cells at 48 hpi with strains MD77 (d), Onderstepoort (e) and KDK1 (f). Photographs a, b and c were taken by contrast phase microscope (x 10). Photographs d, e and f were taken by light microscope (x 20).

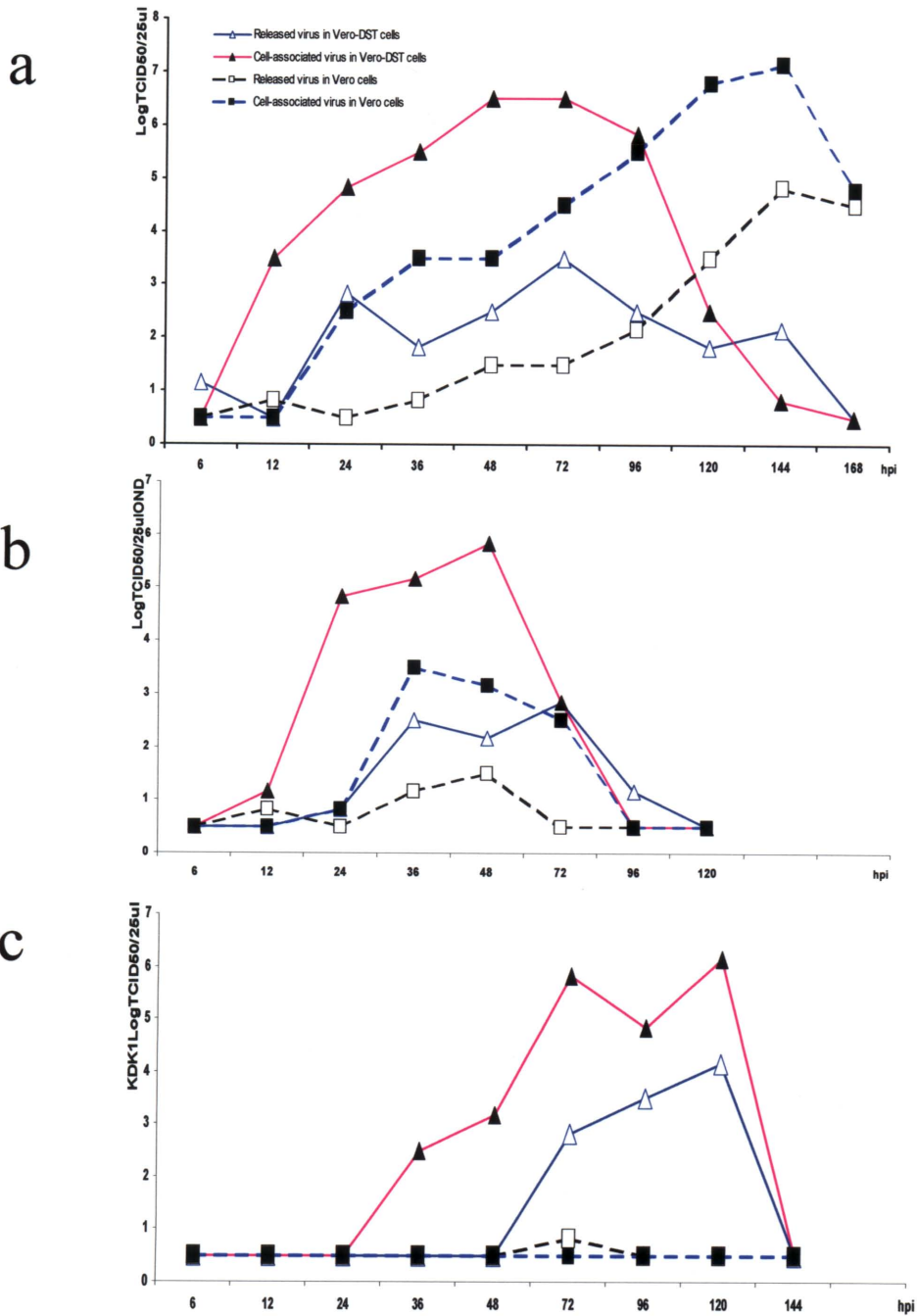


Fig. 2. Growth curves of strains MD77 (a), Onderstepoort (b) and KDK-1 (c) in Ver0-DST cells and Ver0 cells

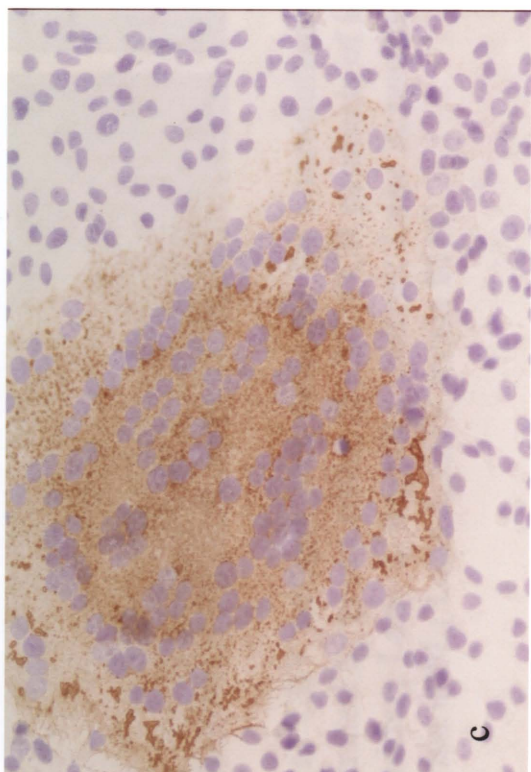
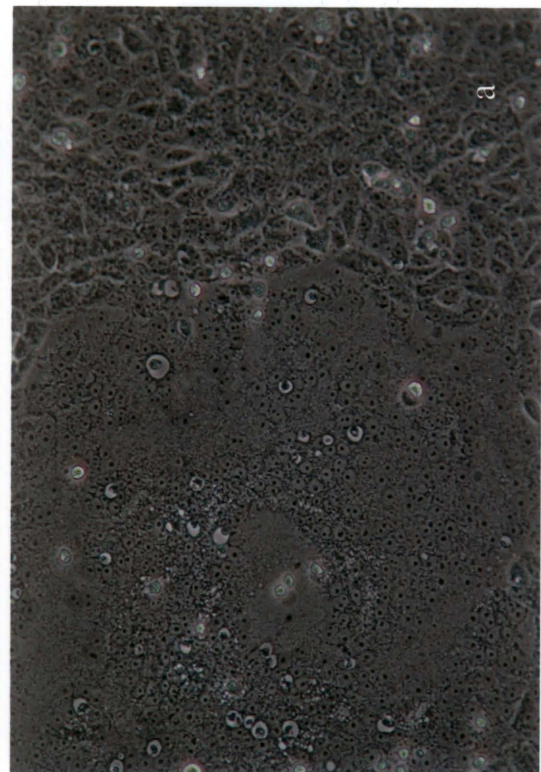
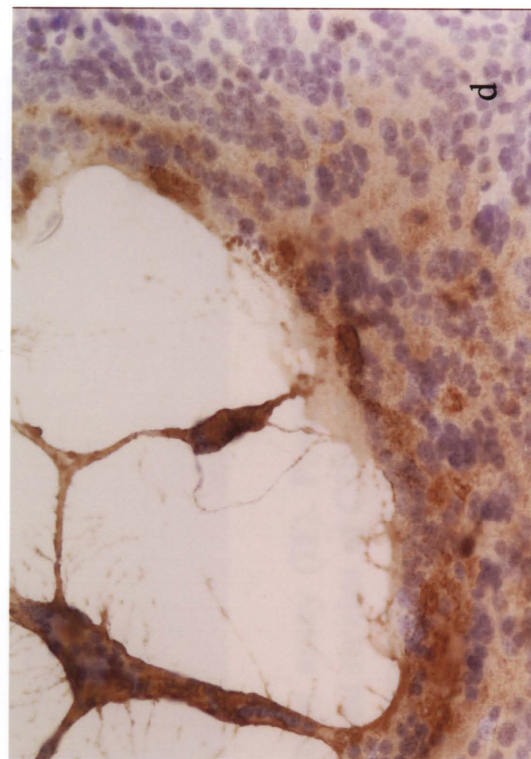
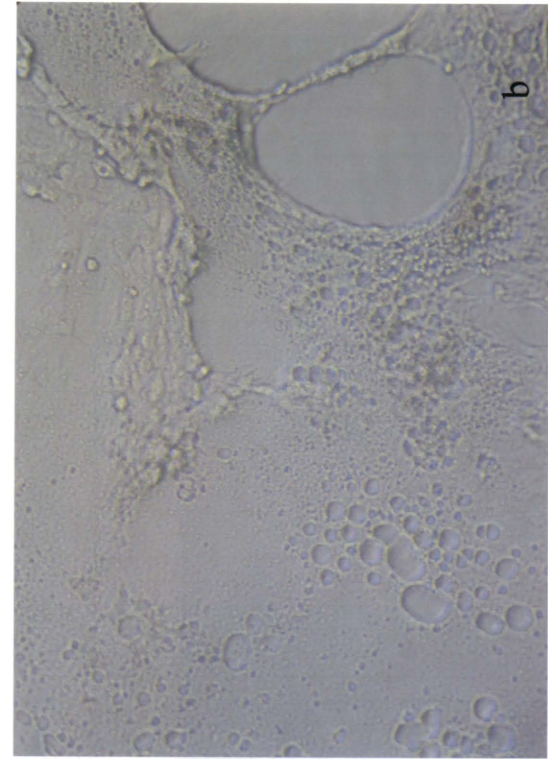


Fig. 3. Recent isolated CDV caused cytopathic effects in Vero-DST cells (a,b). CDV antigens were detected by immunohistochemistry (c,d). Positive CDV antigens were demonstrated by brown color. Photographs a and b were taken by contrast phase microscope (x 10). Photographs c and d were taken by light microscope (x 20).

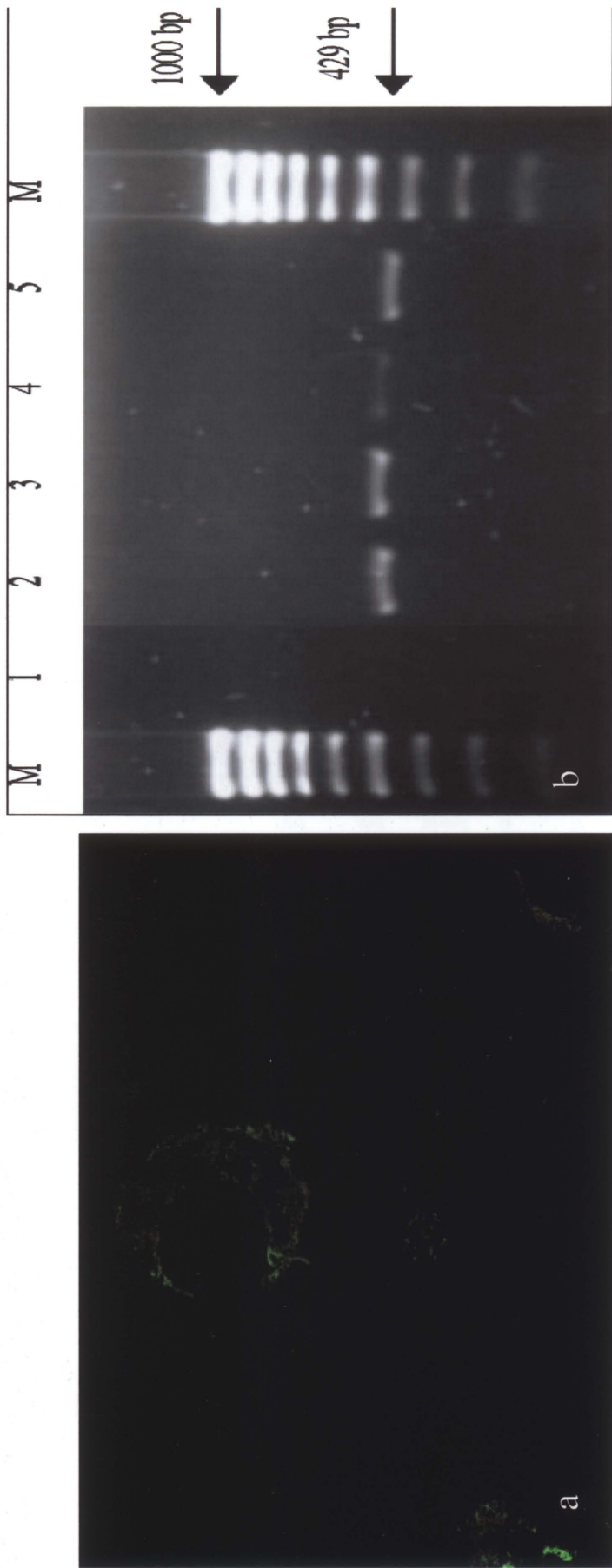


Fig. 4. (a) CDV antigen was detected by immunofluorescent assay (IF). Positive CDV antigens were demonstrated by green color; (b) RT-PCR products of isolated strains of CDV: Lane M, marker 100 bp DNA Ladder; Lane 1, negative control; Lane 2, positive control; Lane 3, CDV strain 007Lm; Lane 4, CDV strain 009L; Lane 5, CDV strain 011C.

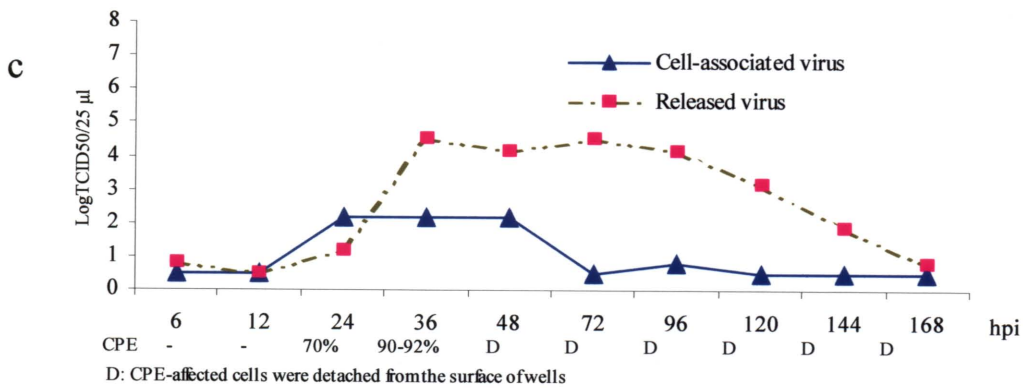
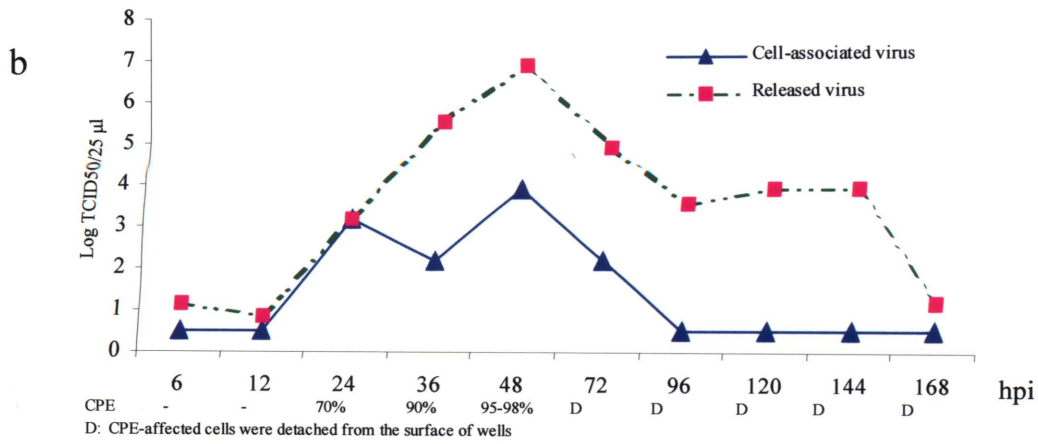
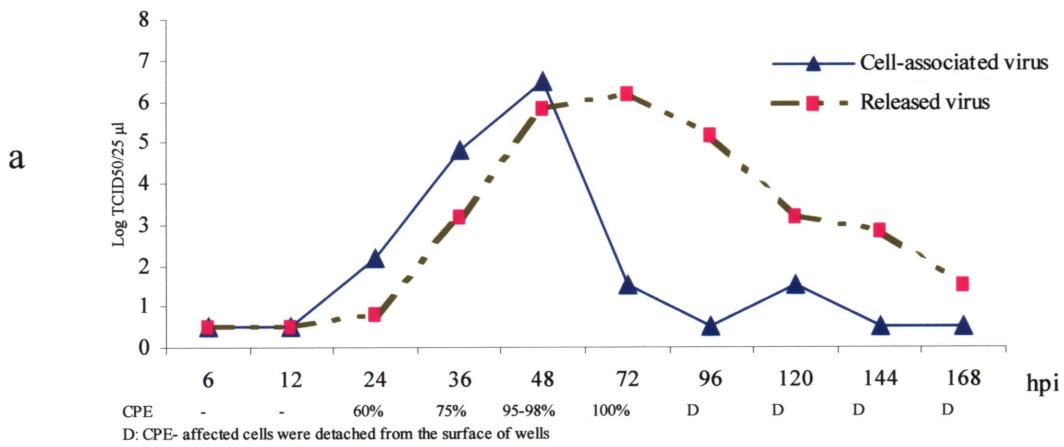


Fig. 5. Growth curves on Vero-DST cells of isolated CDV strains (a) 007Lm, (b) 009L, and (c) 011C.

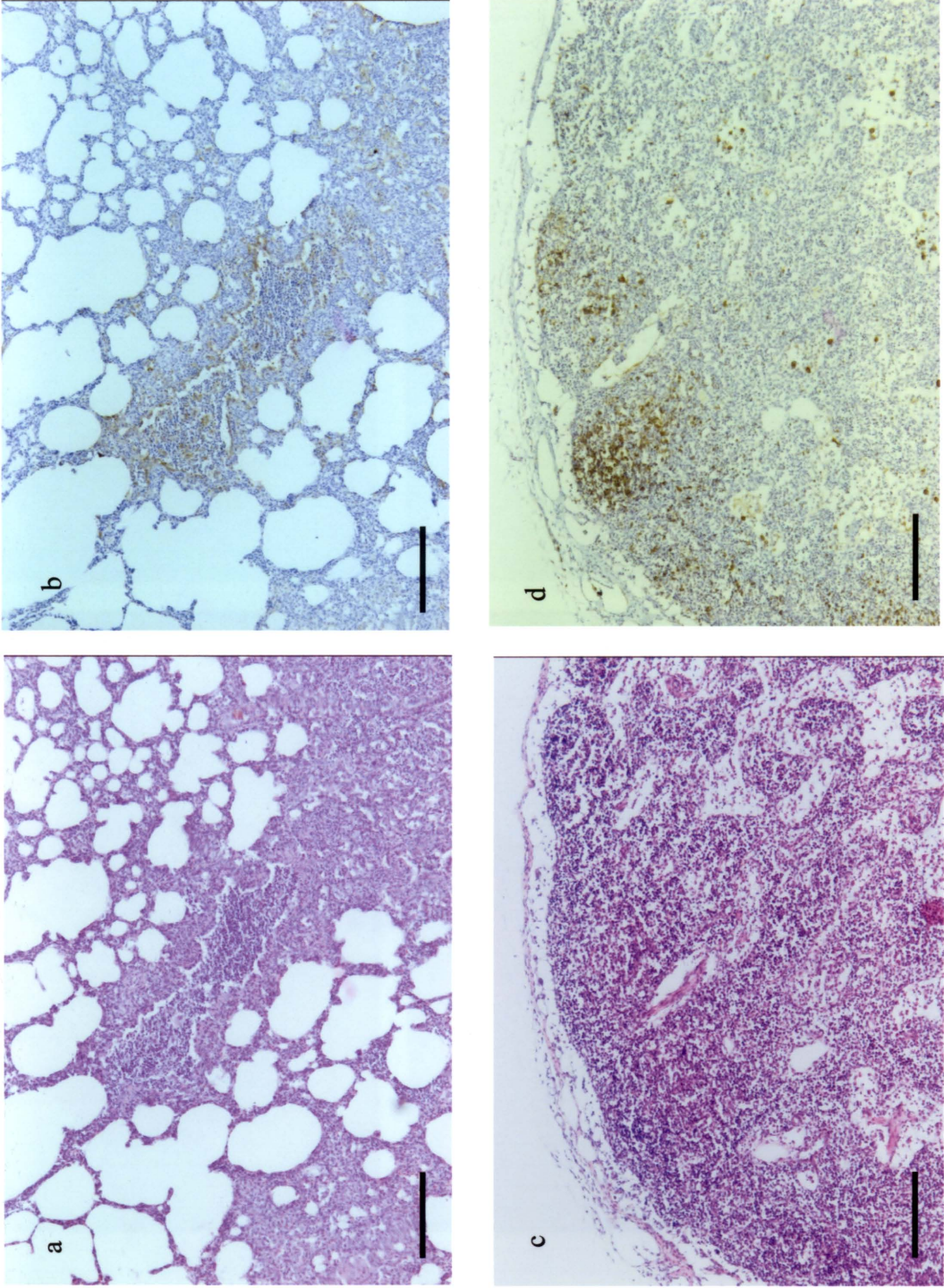


Fig. 6a. Characteristic histopathological lesions of canine distemper from dog 6. Lung with broncho-interstitial pneumonia (a,b), pulmonary lymph node with lymphocyte depletion(c,d). (Staining:a,c: haematoxylin and eosin; b,d: immunohistochemical labeling for CDV; bar = 200 um)

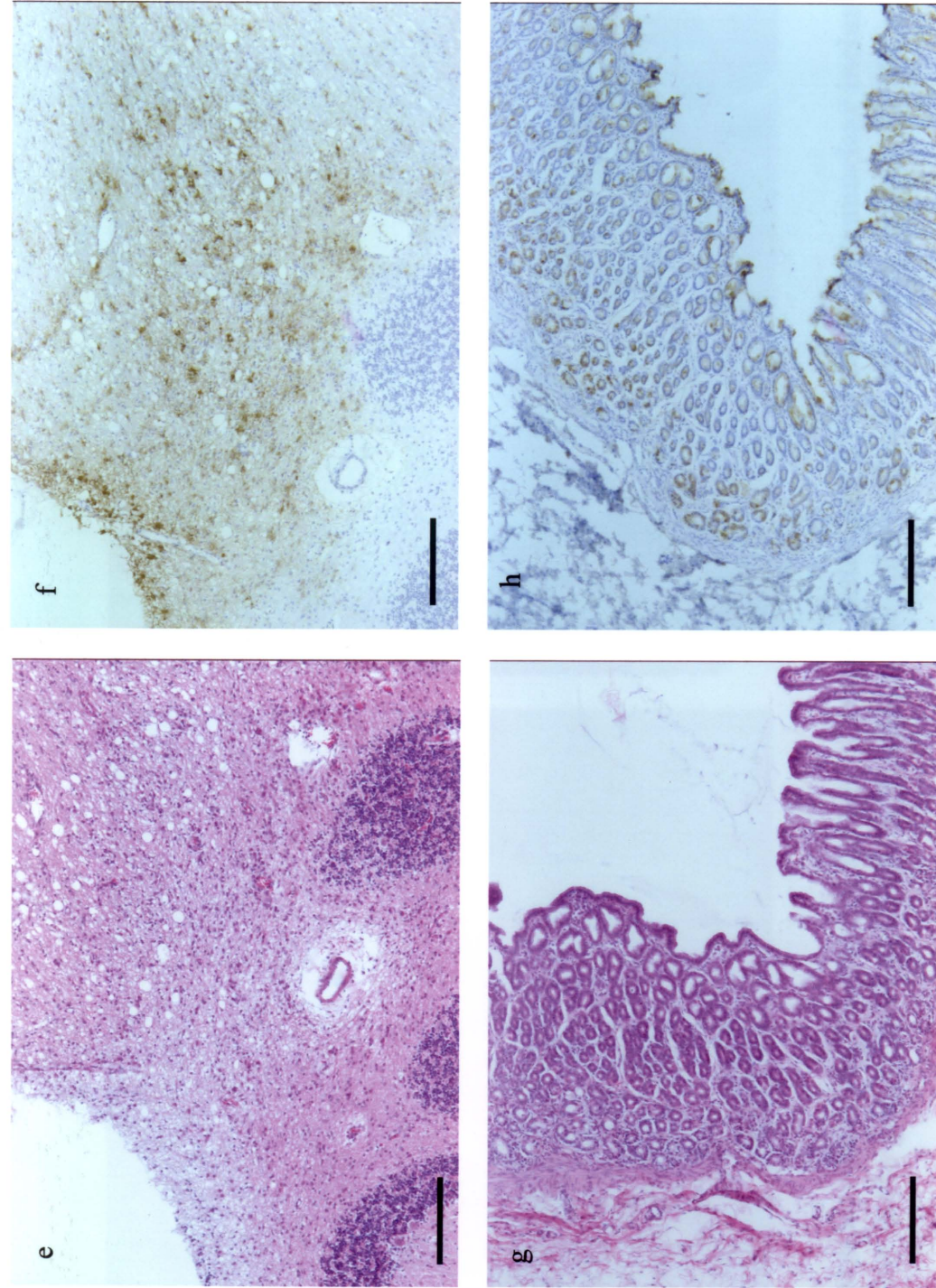


Fig. 6b. Characteristic histopathological lesions of canine distemper from dog 6. Cerebellum with non-suppurative encephalitis(e,f); stomach with mild diffuse degeneration with some inclusion bodies (g,h). (Staining:e,g: haematoxylin and eosin; f,h: immunohistochemical labeling for CDV; bar = 200 um)

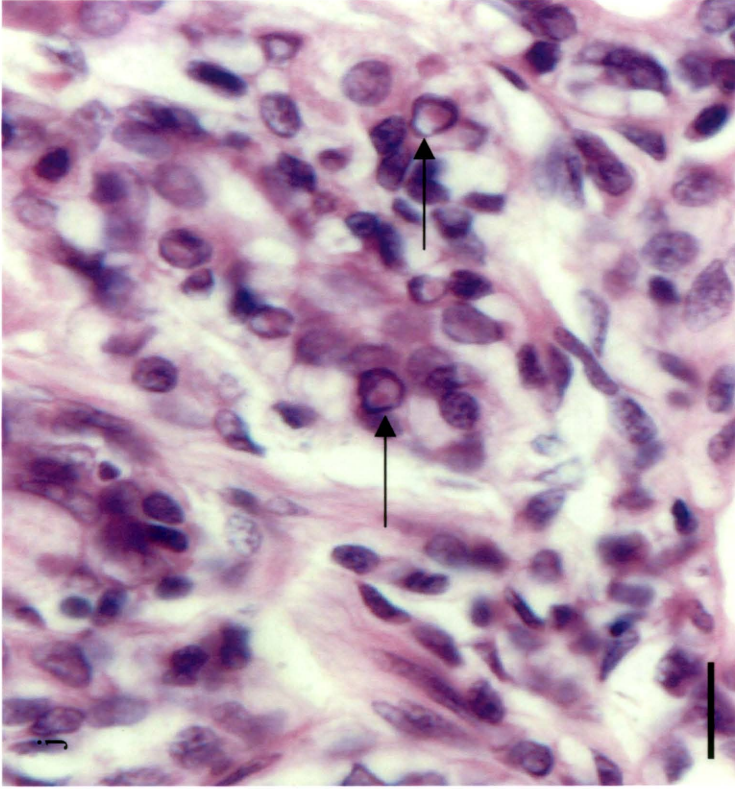
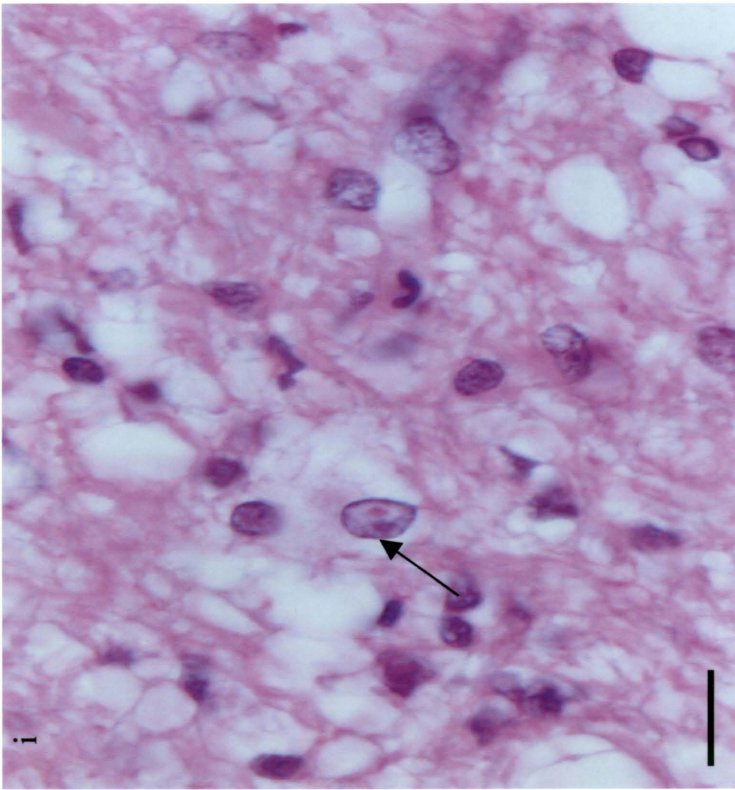


Fig. 6c. Characteristic histopathological lesions of canine distemper from dog 6. Intranuclear inclusion bodies (arrow) in the glial cells of cerebellum (i) and in the epithelial cells of gastric glands (j). HE stain; bar= 20 um.

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Vaccine 1:AAGAGGTTAAGGGAATGGAAGATGCTGCCAGTCTCGTGGTACCTGCAGGCCACTGTCCGGA 60
Ac96I 1:.....C.....A.....G.....A... 60
P94S 1:.....A.T..A.....A.....G.....A... 60
S124C 1:.....C.....A.....G.....A... 60
007Lm 1:.....C.....A.....G.....A... 60

Vaccine 61:ATCGAGGATTCGAGAGAGGAGGAAGGCCCTTGATGATAGCACTGAGGATTCTGGCGAAG 120
Ac96I 61:..... 120
P94S 61:..... 120
S124C 61:.....C..... 120
007Lm 61:.....A..... 120

Vaccine 121:ATTATTCCGAAGGAAATGCTTCACTAACTGGGGATATTCTTTTCGGCCTTAAACCCGGACA 180
Ac96I 121:.....G..... 180
P94S 121:.....G..... 180
S124C 121:.....G..... 180
007Lm 121:.....G..... 180

Vaccine 181:SAGCAGCTGATGTGAGCATGCTGATGGAGGAAATTAAGTGTCTACTCAGGACAAAGCA 240
Ac96I 181:....G.....G.....G.....G.....A..... 240
P94S 181:....G.....G.....G.....G.....A..... 240
S124C 181:....C.....C.....C.....C.....A..... 210
007Lm 181:....C.....C.....G.....G.....T. 240

Vaccine 241:GAAATGTAGGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTTCCCCACATAATCCCGAAG 300
Ac96I 241:....G.....A.....T.....C..... 300
P94S 241:....G.....A.....T.....C..... 300
S124C 241:....G.....A.....T.....C..... 300
007Lm 241:....G.....G.....C.....C..... 300

Vaccine 301:GTAAGACAAGGGATCCGGAGTGTGGATCCATTAAAAAGGGCACAGAAAGGTCAGTCT 360
Ac96I 301:....GA.....G.A.G.....C.. 360
P94S 301:....CA.....G.A.C.....C.. 360
S124C 301:....GA.....C.....G.....C.. 360
007Lm 301:....G.....G.....G.A.....C.. 360

Vaccine 361:CACAATGGAATGGGGATAGTTCCTGGATCGA 390
Ac96I 361:..... 390
P94S 361:..C..... 390
S124C 361:..... 390
007Lm 361:..... 390

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Fig. 7. Nucleotide sequence of a 390bp gene fragment of strains P94S, Ac96I, S124C and 007Lm compared with that of the vaccine strain. Dots (.) indicate identity.

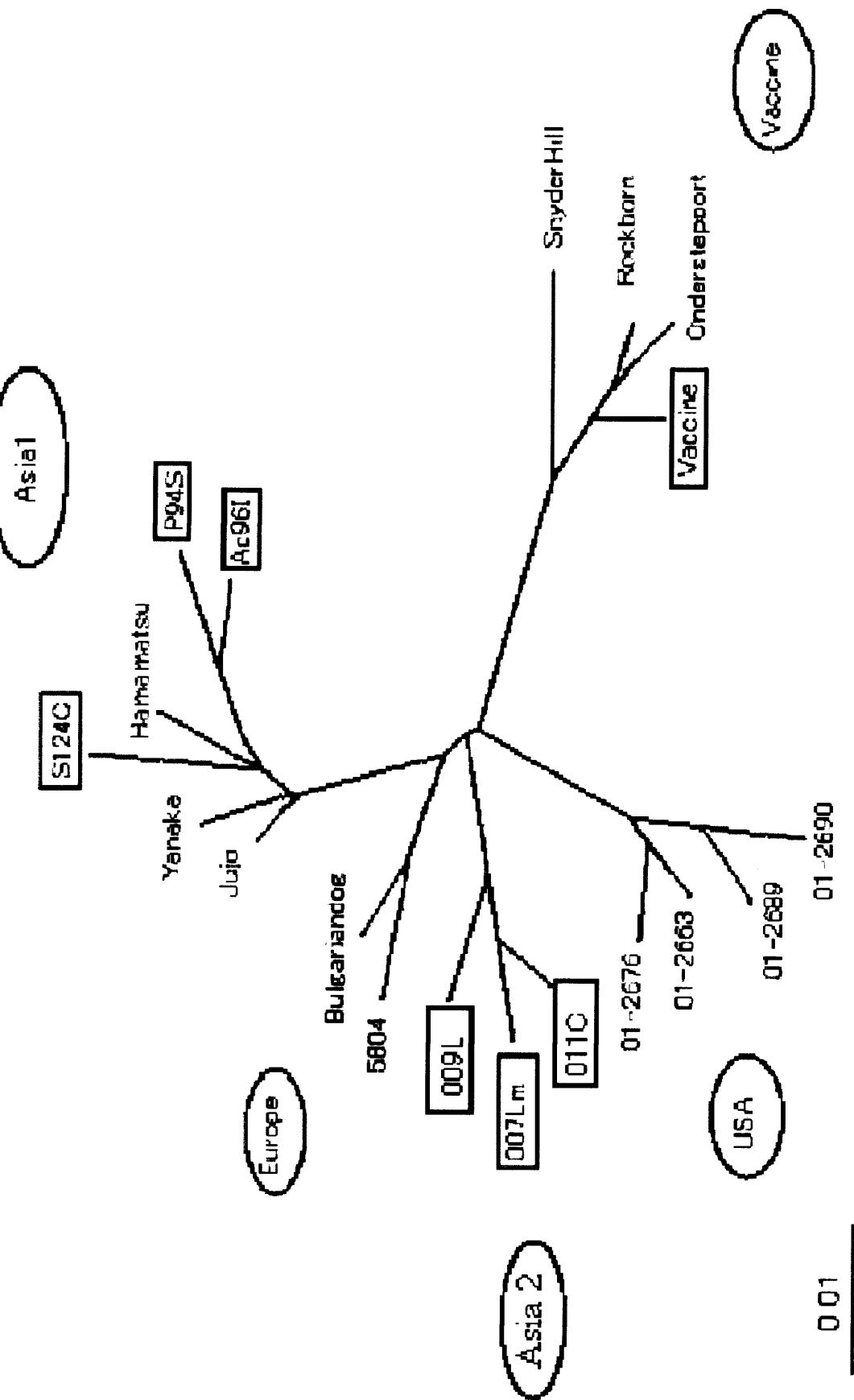


Fig. 8. Phylogenetic analyses of CDV strains based on the nucleotide sequence of 390 bp gene fragments. The names of new isolates from vaccinated dogs and the vaccine strain are in square boxes. The bootstrap values indicate the number of times that each branching was found in 100 bootstrap analyses. Branch lengths indicate phylogenetic distances calculated from distance matrices of nucleotide sequences.

Onderstepoort 1: MLSYQKVGAFYKDNARANSIKLSLVTEEHGRRPPYLLFVLLILLVGLALLAITGVR 60
 Vaccine 1: 60
 Ac96I 1:S.....Q.....I..... 60
 P94S 1:S.....Q.....I..... 60
 S124C 1:S.....Q.....I..... 60
 O07Lm 1:S.....Q.....A..... 60

 Onderstepoort 61: HOVSTNMEFSRLKEDMEKSEAVHHQVIDVLTPLFKIIGEIGLRPQKLNKQFILQ 120
 Vaccine 61: 120
 Ac96I 61: 120
 P94S 61: 120
 S124C 61:N..... 120
 O07Lm 61: R.....V..G...D.L.....M..... 120

 Onderstepoort 121: KTNFFNPNREFDFRDLHUCINPPSKVKWFTNYCESIGIRKAIASAANPILLSALSGRS 180
 Vaccine 121: 180
 Ac96I 121: ..K.....I.....DTV.VK.S.....I.....A.G 180
 P94S 121: ..K.....I.....DTV.VK.S.....I.....A.G 180
 S124C 121:I.....DTV.VK.S.....I.....A.G 180
 O07Lm 121:I.....DA..V..S.....G 180

 Onderstepoort 181: DIFPHRCGATTSVGKVFPLSVLSMSLISRTSEINMLTAISDCVYGKTYLLVPDDIE 240
 Vaccine 181:Y.....R.....G.....N.M.....Y.. 240
 Ac96I 181:Y.....R.....M.....Y.. 240
 P94S 181:Y.....R.....L.....Y.. 240
 S124C 181:Y.....R.....K.....S.....Y.. 240
 O07Lm 181:Y.....R.....K.....S.....Y.. 240

 Onderstepoort 241: REFDTQEI RVFEIGFIKRWLDMPLLQTTNYMVL PENS KAKVCTI AVGELT LASLCVEES 300
 Vaccine 241:P..... 300
 Ac96I 241: G...S.K.....T.....D.. 300
 P94S 241: G...S.K.....T.....D.. 300
 S124C 241: G...S.K.....T.....D.. 300
 O07Lm 241:K..... 300

 Onderstepoort 301: TVLLYHDSGSDGILVVTLGIFWATPMDHIEEVI PVAHPSMEKIHI TNHRGFIKDSIAT 360
 Vaccine 301: 360
 Ac96I 301: ..N.....G.....QV.....I...V.R.....V. 360
 P94S 301: ..N.....G.....QV.....I...V.R.....V. 360
 S124C 301: I.....N.....G.....QV.....I...V.R.....V. 360
 O07Lm 301: ..N...S.....G...NQV.....V.R.....V.. 360

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Understepoort 361:UMVPALASEKQEEQKGCLESACQRKTYPMCNQTSWEFFGGRQLPFSYGRLLTLPDASVDLQ 420
Vaccine 361:.....V.V.....N.....S.....G.....P.I... 420
Ac96I 361:.....V.V.....N.....S.....G.....P.I... 420
P94S 361:.....V.V.....N.....S.....G.....P.I... 420
S124C 361:.....V.V.....N.....S.....G.....P.I... 420
007Lm 361:.....V.Q..G..N.....S.....V.....I... 420

Understepoort 421:LNISFTYGPVILNGDGM DYESP LLNSGWL TIPPKNGTIVGLINKAGRGDQFTVLP HVL T 460
Vaccine 421:.....V.V.....N.....S.....G.....P.I... 480
Ac96I 421:.....V.V.....N.....S.....G.....P.I... 480
P94S 421:.....V.V.....N.....S.....G.....P.I... 480
S124C 421:.....V.V.....N.....S.....G.....P.I... 480
007Lm 421:.....V.V.....N.....S.....G.....P.I... 480

Understepoort 481:FAPWESSGNCYLP IQTSQI I DRDVL IESNI VVLP TQSFR YRVIATYD ISRS DHA I VVYVD 540
Vaccine 481:.....R.....M.K..T..L..N.....G.....D. 540
Ac96I 481:.....R.....M.K..T..L..N.....G.....D. 540
P94S 481:.....R.....M.K..T..L..N.....G.....D. 540
S124C 481:.....R.....M.K..T..L..N.....G.....D. 540
007Lm 481:.....R.....M.K..T..L..N.....V.....EN..... 540

Understepoort 541:PIRTISYTHPFRLTTKGRPDFLR IECFVDDNLWCHQFYRFEADIANSTTSVENLVRIF 600
Vaccine 541:.....Y.....D.....N..T..... 600
Ac96I 541:.....Y.....D.....N..T..... 600
P94S 541:.....Y.....D.....N..T..... 600
S124C 541:.....Y.....D.....N..T..... 600
007Lm 541:.....Y.....D.....S..T.....D..... 600

Understepoort 601:SCNR---
Vaccine 601:.....SKP..... 604
Ac96I 601:.....SKP..... 604
P94S 601:.....SKP..... 607
S124C 601:.....SKP..... 607
007Lm 601:.....SKP..... 607

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Fig. 9. Deduced H protein amino acid sequences of CDV strains P94S, Ac96I, S124C and 007Lm compared with those of the vaccine strain and other reference strains from Genbank. Potential N-linked glycosylation sites are boxed. Dots (.) indicate identity. The major hydrophobic region is overlined.

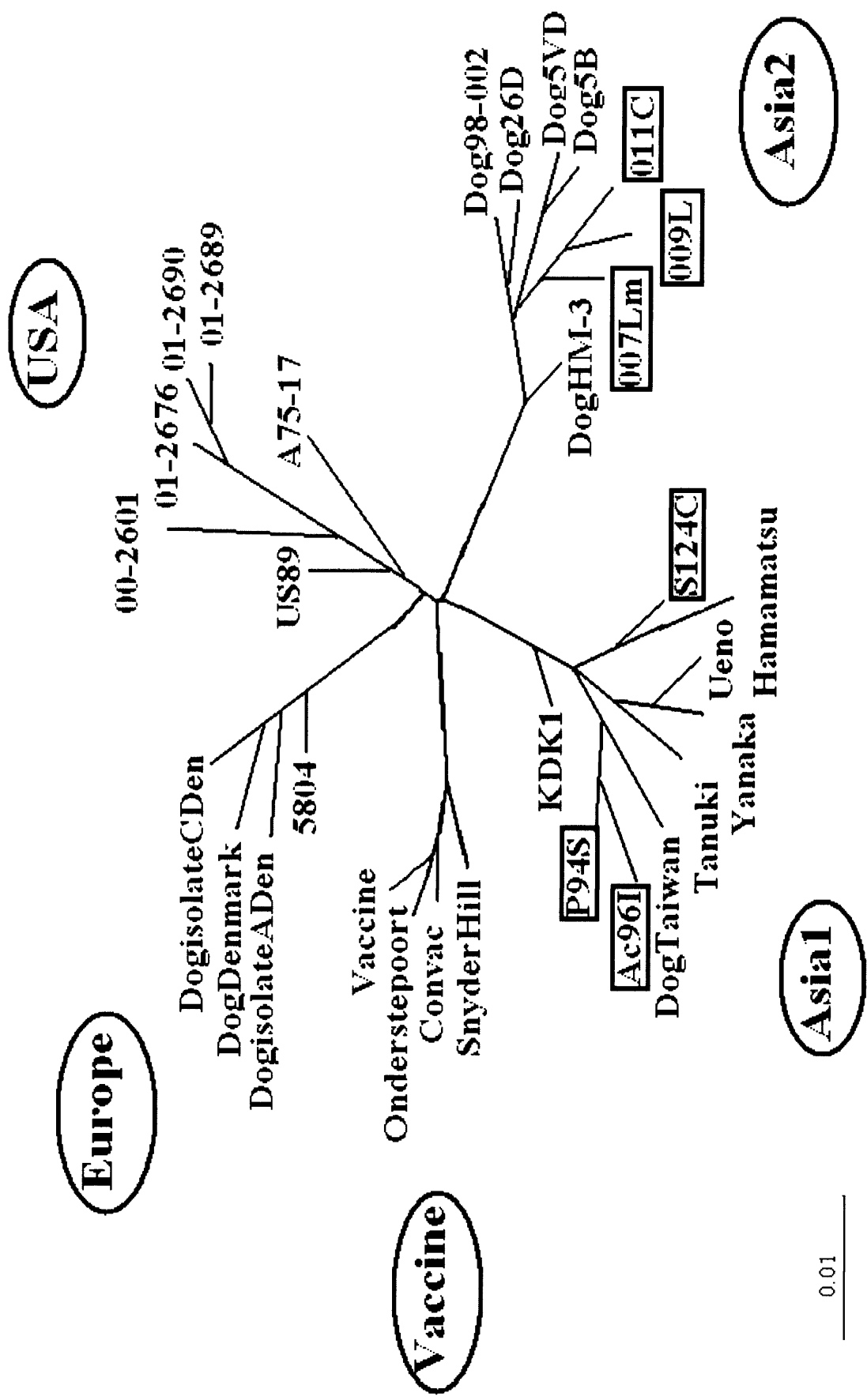


Fig. 10. Phylogenetic tree of amino acid sequences of the coding regions of CDV H proteins. The names of new isolates from vaccinated dogs and the vaccine strain are in square boxes. The bootstrap values indicate the number of times that each branching was found in 100 bootstrap analyses. Branch lengths indicate phylogenetic distances calculated from distance matrices of deduced amino acid sequences.

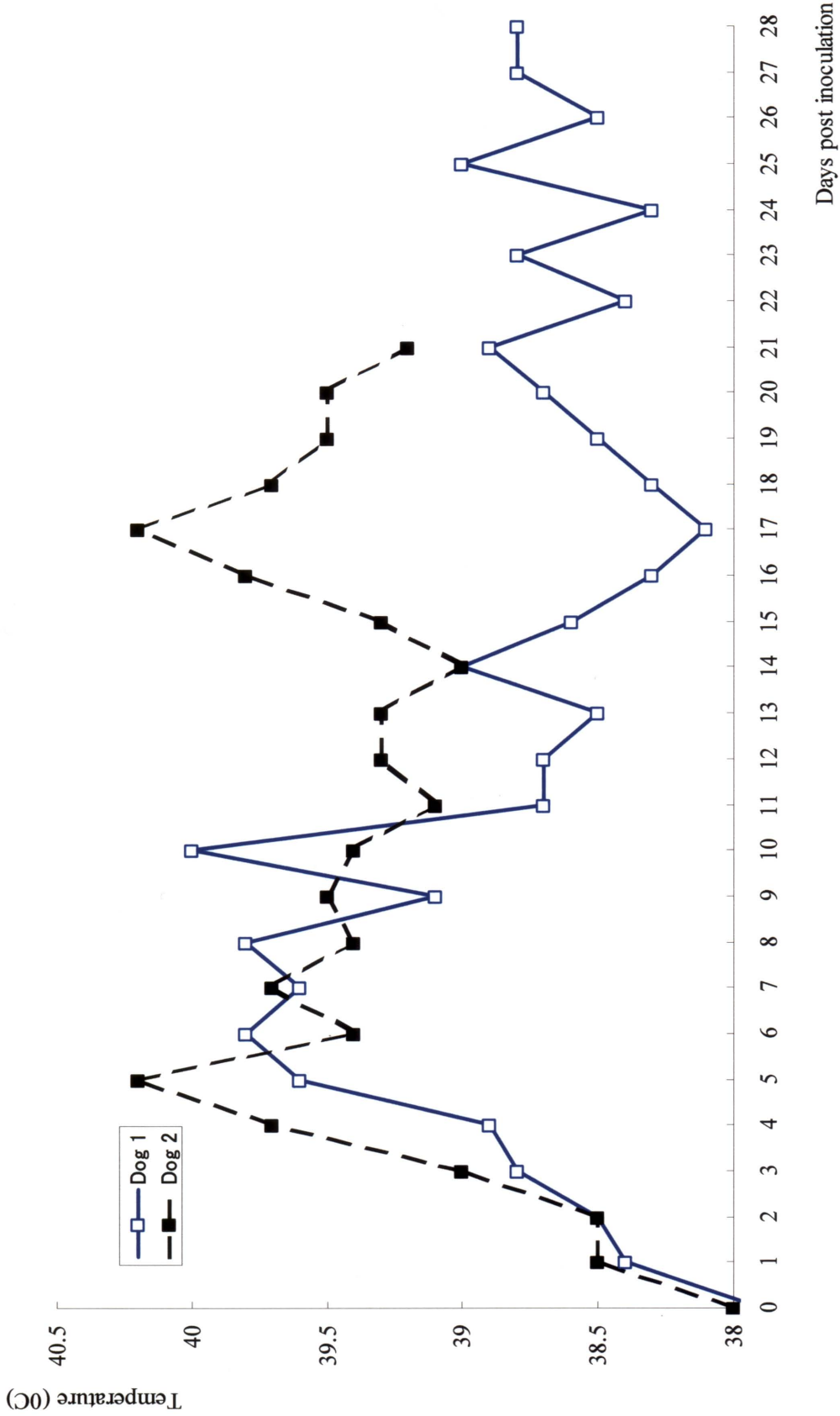


Fig. 11. Rectal temperatures of the two dogs after inoculation

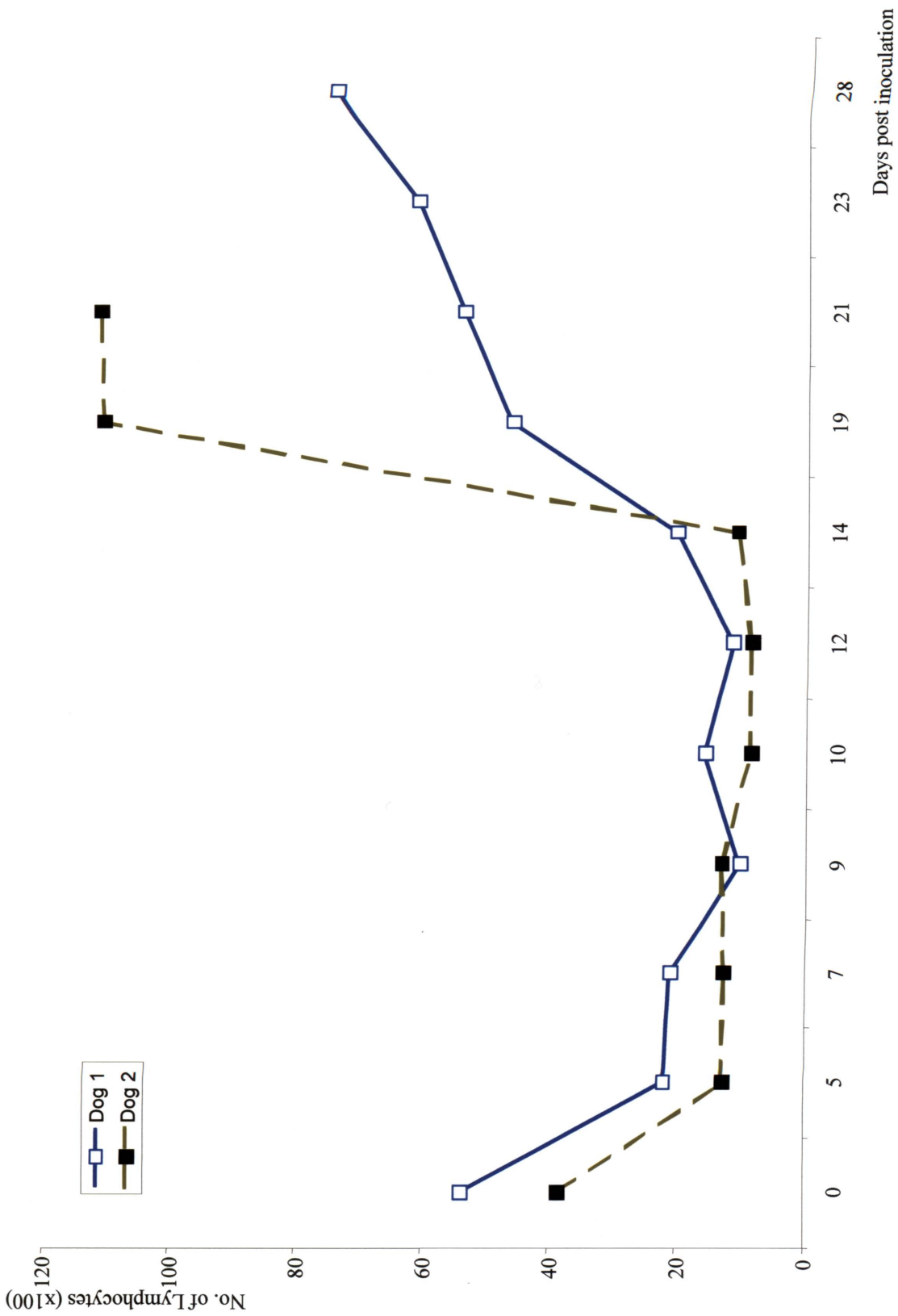


Fig. 12. Numbers of lymphocytes in the bloods of the two dogs after inoculation

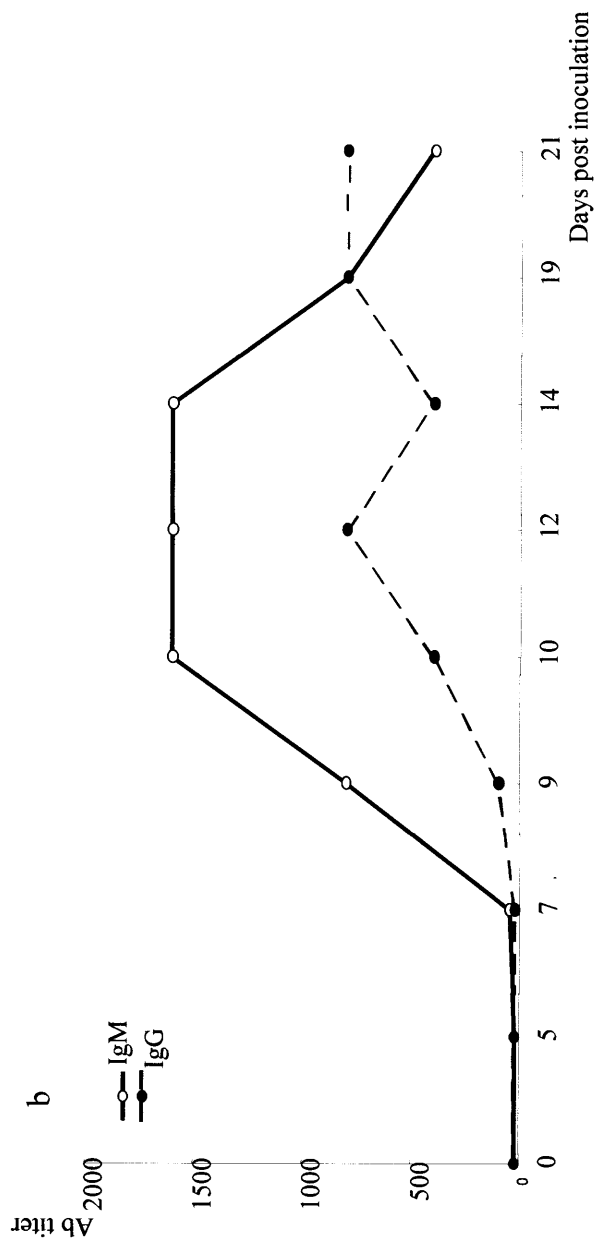
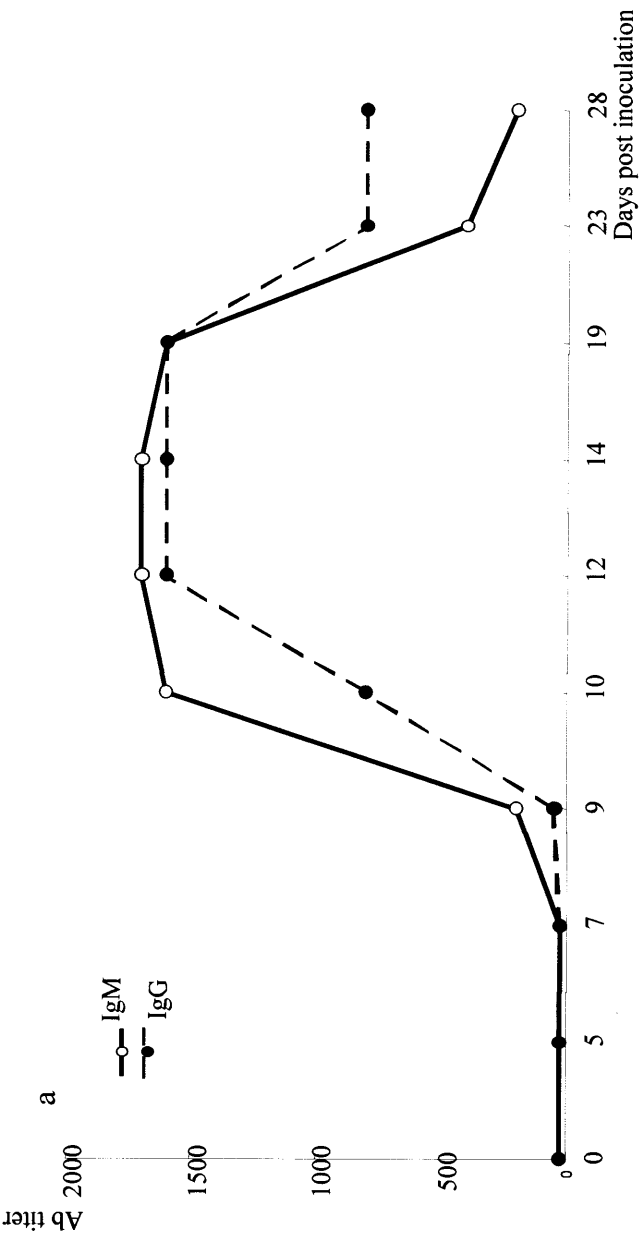


Fig. 13. Titers of anti-CDV IgG and anti-CDV IgM antibodies of dog 1(a) and dog 2 (b).

Asia2	007Lm	1: MLSYQDKVGAFYKDNARANSS	KL	SLVTEE	QGGRRPPYLLFVLLILLV	GILALLAIAGVRF	60
	009L	1:					60
	011C	1:					60
	Ac96I	1:				I. T.	60
Asia1	P94S	1:				I. T.	60
	S124C	1:				I. T.	60
	007Lm	61: RQVSTSNVEFGRLKDDLEKSEAVHHQVMDVLTPLFKIIGDEIGLRLPQKLNEIKQFILQ					120
	009L	61:					120
	011C	61:					120
	Ac96I	61: H. M. . S. E. M. I.					120
	P94S	61: H. M. . S. E. M. I.					120
	S124C	61: H. M. . S. ENM. I.					120
	007Lm	121: KTNFFNPNREFDFRDLHUCINPPSKIKVNF					180
	009L	121:					180
	011C	121:				P.	180
	Ac96I	121: . . K.			TV. K.	I. A.	180
	P94S	121: . . K.			TV. K.	I. A.	180
	S124C	121:			TV. K.	I. A.	180
	007Lm	181: DIFPPYRCSGATTSVGRVPLSVLSMSLISKTSEIISMLTAISDGVYGKTYLLVPDYIE					240
	009L	181:			K.	E.	240
	011C	181:				E.	240
	Ac96I	181:			G. N. N. M.		240
	P94S	181:			R. N. M.		240
	S124C	181:			R. LN.		240
	007Lm	241: REFDTQKIRVFEIGFIKRWLNDMPLLQTTNYMVLPENSKAKVCTIAVGELTLASLCVDES					300
	009L	241:					300
	011C	241:					300
	Ac96I	241: G. . . S.				T.	300
	P94S	241: G. . . S.				T.	300
	S124C	241: G. . . S.				T.	300
	007Lm	301: TVLLYHDS	NGS	QDSILVVT	LGIFGATPMNQVEEVIPVAHPSVERIHITNHRGFIKDSVAT		360
	009L	301:			QHRX.		360
	011C	301:					360
	Ac96I	301:			NG.	D. I. IV.	360
	P94S	301:			NG.	D. I. IV.	360
	S124C	301: I.			NG.	D. I. IV.	360
	007Lm	361: UMVPALVSEQQEGQKNCLESACQRKSYPMONQTS					420
	009L	361:					420
	011C	361:					420
	Ac96I	361: V. . . . K. . E.				G. P.	420
	P94S	361: V. . . . K. . E.				G. P.	420
	S124C	361: V. . . . K. . E.				G. P.	420

(Continue)

Asia2 {	007Lm	421:	LNIS	FTYGPVILNGDGMDYYENPLLD	SGWLTIPP	KNGT	ILGLINKASRGDQFTVTPH	VLT	480
	009L	421:	480
	011C	421:	480
Asia1 {	Ac96I	421:	S	V	480
	P94S	421:	S	V	480
	S124C	421:	S	V T	480
	007Lm	481:	FAPRESSGNCYLP	IQTSQIMDKDVL	TESNLVVLPTQ	NFRYV	VATYDISREN	HAIVYYVYD	540
	009L	481:	540
	011C	481:	540
	Ac96I	481:	I GD	540
	P94S	481:	I GD D
	S124C	481:	I GD M
	007Lm	541:	P	IRTISY	TYPFRLTTKGR	PDFLR	IECFVWDDDL	WCHQFYRFES	DI
	009L	541:
	011C	541:
	Ac96I	541:	AN N
	P94S	541:	AN N
	S124C	541:	AN L
	007Lm	601:	SC	NRS	KP	607
	009L	601:	607
	011C	601:	607
	Ac96I	601:	607
	P94S	601:	607
	S124C	601:	607

584-586

Fig. 14. Deduced H protein amino acid sequences of CDV strains of Asia 1 group (P94S, Ac96I and S124C) compared with those of Asia 2 group (007Lm, 009L and 011C). Potential N-linked glycosylation sites are boxed. Dots (.) indicate identity. The major hydrophobic region of Asia 1 group is doubly overlined. The major hydrophobic region of Asia 2 group is boldly overlined.

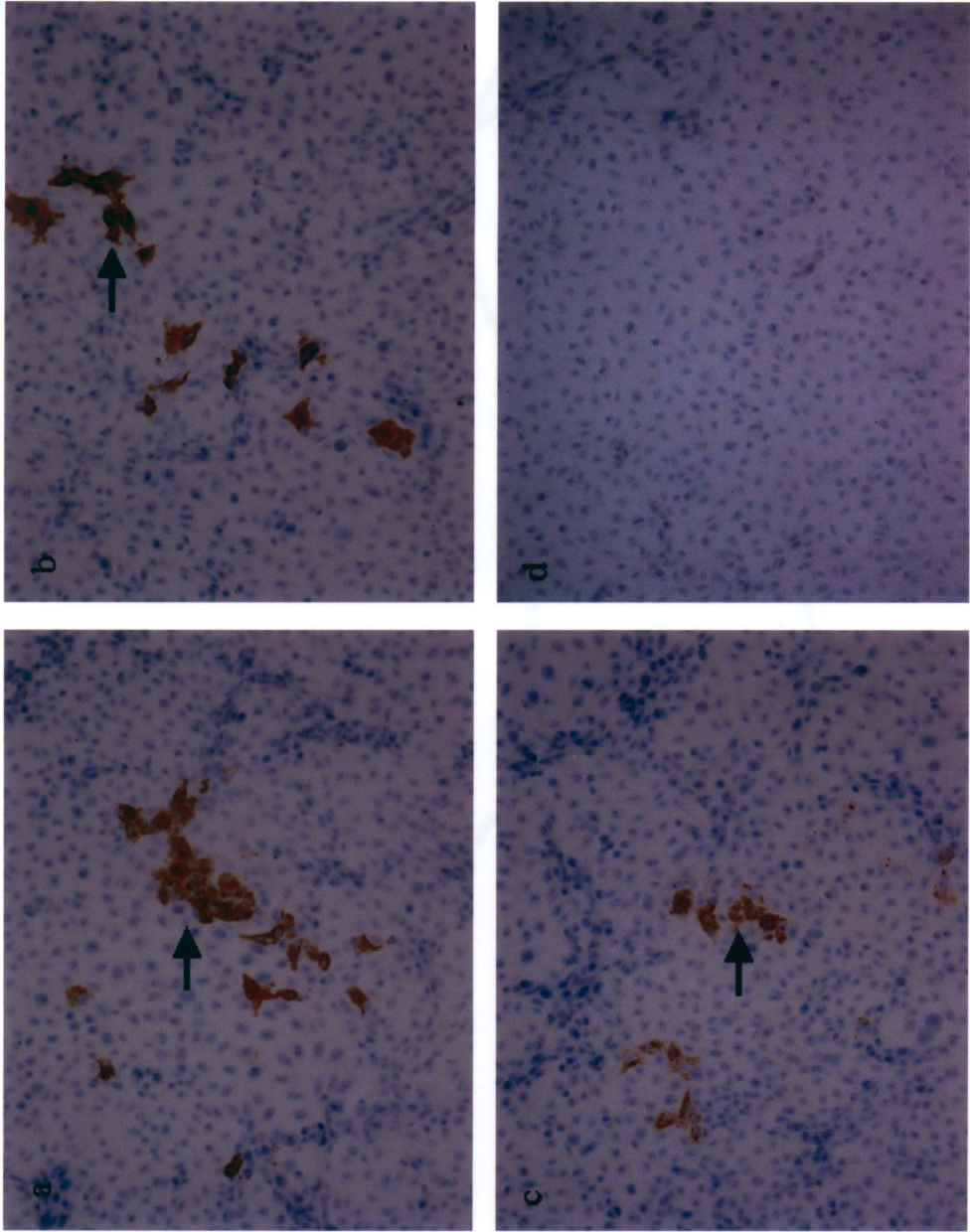


Fig. 15. CDV antigens were detected by immunocytochemistry in Vero cells infected with strains 007Lm (a), 009L (b) and 011C (c) at 24 hpi. Positive CDV antigens are shown in brown color (arrows). Vero cells were not infected with CDV as a negative control (d) at 24 hpi. Photographs were taken by light microscope. (x 20).

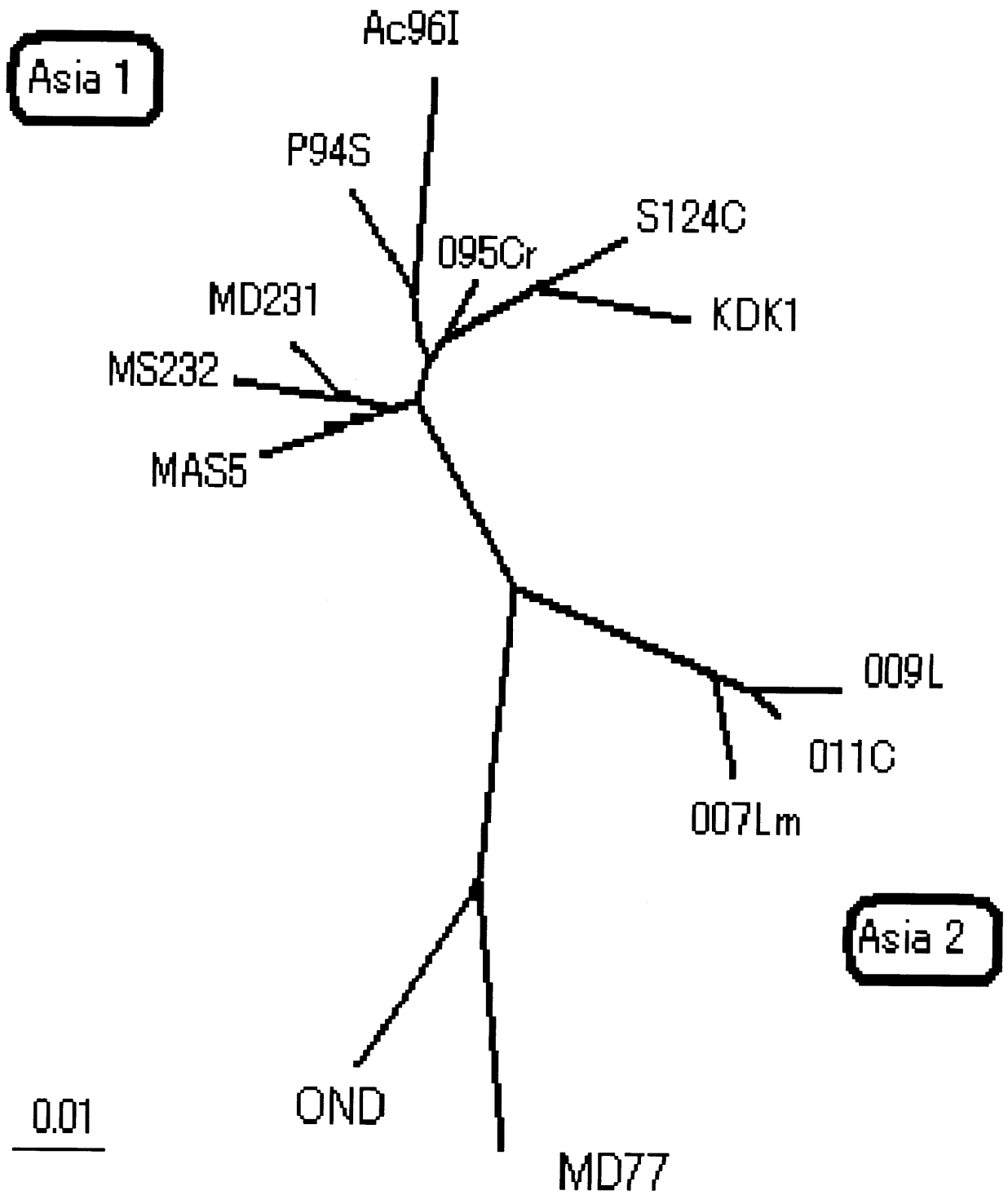


Fig. 16. Phylogenetic tree based on the nucleotide sequences of 390 bp gene fragments of CDV strains.

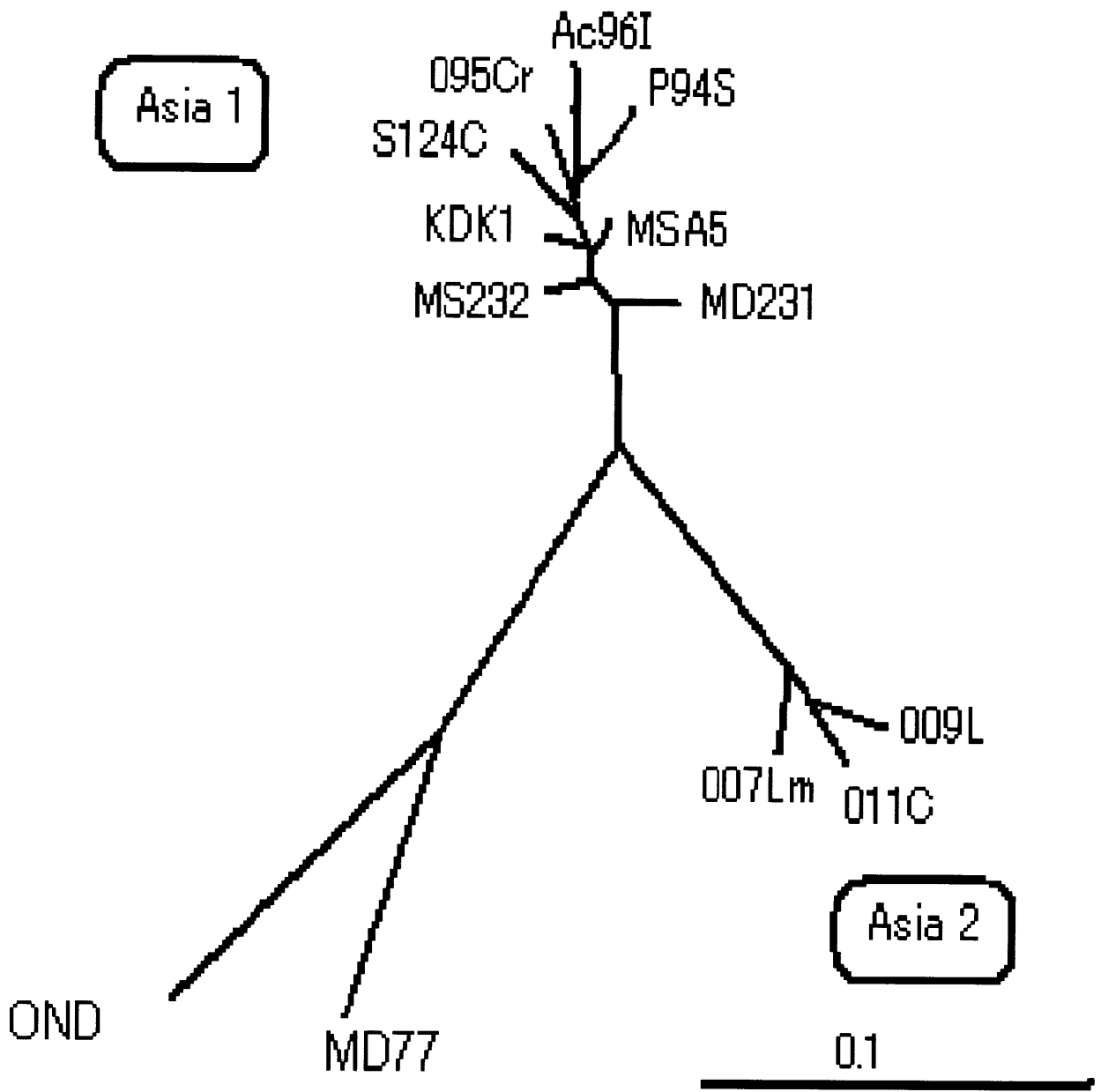


Fig. 17. Phylogenetic tree based on the amino acid sequences of the coding regions of CDV H protein.

P94S	1:	MLSYQDKVGFYKDNAR	NS	SKLSLVTEEQGRRPP	YLLFVLLILLIGILALLAITGVRF	60
Ac96I	1:	60
S124C	1:	60
MD231	1:V.....	60
MS232	1:	60
MAS5	1:	60
O95Cr	1:	60
KDK1	1:	60
OO7Lm	1:V.....A.....	60
OO9L	1:V.....A.....	60
O11C	1:V.....A.....	60
MD77	1:P.....H.....V.....S.....I.....	60
OND	1:P.....T.....GH.....V.....	60
P94S	61:	HQVSTSNMEFSRLLKEDMEKSEAVHHQVIDVLTPFKIIGDEIGLRLPQKLNEIKQFILQ				120
Ac96I	61:	120
S124C	61:N.....	120
MD231	61:T.....M.....	120
MS232	61:	120
MAS5	61:	120
O95Cr	61:	120
KDK1	61:	120
OO7Lm	61:	R.....	V.....G.....	D.....L.....M.....	120
OO9L	61:	R.....	V.....G.....	D.....L.....M.....	120
O11C	61:	R.....	V.....G.....	D.....L.....M.....	120
MD77	61:	K.....Y.....F.....	120
OND	61:	120
P94S	121:	KTKFFNPREFDFRDLHUCINPPSKIKVNF	TI	NYCDTVGVKKS	IASAANPIILSALSGARG	180
Ac96I	121:	180
S124C	121:N.....	180
MD231	121:V.....	180
MS232	121:L.....V.....	180
MAS5	121:	180
O95Cr	121:	180
KDK1	121:	180
OO7Lm	121:AI.....R.....	180
OO9L	121:AI.....R.....	180
O11C	121:AI.....R.....	180
MD77	121:I.....IR.....	180
OND	121:TV.....ESI.....IR.....A.....	180
P94S	181:	DIFPPYRCGATTSVGRVFLSVLSMSLISRTSEI	INMLTAISDGMYGKTYLLVPDYIE			240
Ac96I	181:G.....N.....	240
S124C	181:L.....	240
MD231	181:V.....	240
MS232	181:V.....	240
MAS5	181:V.....	240
O95Cr	181:V.....	240
KDK1	181:V.....	240
OO7Lm	181:K.....S.....	240
OO9L	181:K.....S.....	240
O11C	181:K.....S.....	240
MD77	181:K.....S.....	240
OND	181:H.....K.....TL.....T.....A.....V.....	240
P94S	241:	GEPDSQKIRVFEIGFIKRWLNDMPLLQTTNYMVL	PETSKAKVCTIAVGELTLASLCVDES			300
Ac96I	241:	300
S124C	241:	300
MD231	241:H.....	300
MS232	241:	300
MAS5	241:	300
O95Cr	241:T.....R.....	300
KDK1	241:	300
OO7Lm	241:	R.....	T.....N.....	300
OO9L	241:	R.....	T.....N.....	300
O11C	241:	R.....	T.....N.....	300
MD77	241:	R.....	T.....E.....N.....	300
OND	241:	R.....	T.....R.....E.....KN.....	300
P94S	301:	TVLLYHDS	NGS	ONGILVVTLGIFGATPMDOVEEVIPIAHPS	VERIHITNHRGFIKDSIVT	360
Ac96I	301:	360
S124C	301:	360
MD231	301:D.....V.....	360
MS232	301:V.....	360
MAS5	301:V.....	360
O95Cr	301:	360
KDK1	301:W.....	360
OO7Lm	301:DS.....N.....	360
OO9L	301:DS.....QHRXN.....	360
O11C	301:DS.....N.....	360
MD77	301:D.....R.....D.....E.....VS.....M.....K.....	360
OND	301:S.....D.....W.....HI.....V.....MKK.....	360

P94S	361:WMVPLVSEKQEEQKNCLESACORKSYPMGN	NOTSWEPPFGGGQLPSYGRLTLPLDPSIDQ	420	
Ac96I	361:.....	420	
S124C	361:.....	420	
MD231	361:.....A.....	420	
MS232	361:.....A.....	420	
MASS	361:.....A.....	420	
O95Cr	361:.....	420	
KDK1	361:.....A.....	420	
OO7Lm	361:.....A...Q.G.....V.....A.....	420	
OO9L	361:.....A...Q.G.....V.....A.....	420	
O11C	361:.....A...Q.G.....V.....A.....	420	
MD77	361:.....A.A.....G.....T.....A.V.....	420	
OND	361:.....A.A.....G.....T.....A.....R.....A.V.....	420	
P94S	421:LNISFTYGPVILNGDGMDDYESPLLD	SGULTIPPENGTIVLGLINKASRGDQFTVTPHVL	480	
Ac96I	421:.....	480	
S124C	421:.....T.....	480	
MD231	421:.....	480	
MS232	421:.....	480	
MASS	421:.....	480	
O95Cr	421:.....	480	
KDK1	421:.....S.....	480	
OO7Lm	421:.....N.....I.....	480	
OO9L	421:.....N.....I.....	480	
O11C	421:.....N.....I.....	480	
MD77	421:.....N.....IF.....I.Q.....	480	
OND	421:.....N.....D..IS.....G.....L.....	480	
P94S	481:FAPRESSGNCYLP	IQTSQIMDKDVLTESNLVVLPTQNF	RYVIATYDISRGDHAIVVYVDD	540
Ac96I	481:.....Y.	540
S124C	481:.....M.....	YG 540
MD231	481:.....K.....	Y. 540
MS232	481:.....	Y. 540
MASS	481:.....	Y. 540
O95Cr	481:.....	Y. 540
KDK1	481:.....	YG 540
OO7Lm	481:.....V.....EN.....	Y. 540
OO9L	481:.....V.....EN.....	Y. 540
O11C	481:.....V.....EN.....	Y. 540
MD77	481:.....G.....I.R..I.....S.....N.....Y. 540	
OND	481:.....I.R..I..I.....SI.....S.....Y. 540	
P94S	541:PIRTISYTPFRLITKGRPDFLRIE	CFVWDDDLWCHQFYRFEANITINST	TSVENLVRIRF	600
Ac96I	541:.....L.....	600
S124C	541:.....I.....	600
MD231	541:.....V.....	600
MS232	541:.....	600
MASS	541:.....	600
O95Cr	541:.....S.....R.....	600
KDK1	541:.....	600
OO7Lm	541:.....SD.....D.....	600
OO9L	541:.....SD.....D.....	600
O11C	541:.....SD.....D.....	600
MD77	541:F..F.....N.....Y.....A.....	600
OND	541:.....L.....N.....D.A.....	600
P94S	601:SCNRSKP			607
Ac96I	601:.....			607
S124C	601:.....			607
MD231	601:.....			607
MS232	601:P.....			607
MASS	601:.....			607
O95Cr	601:.....			607
KDK1	601:.....			607
OO7Lm	601:.....			607
OO9L	601:.....			607
O11C	601:.....			607
MD77	601:.....			607
OND	601:.....			604

Fig. 18. Deduced H protein amino acid sequences of 10 new isolates of CDV. Potential N-linked glycosylation sites are boxed. Dots (.) indicate identity. The major hydrophobic region is overlined.

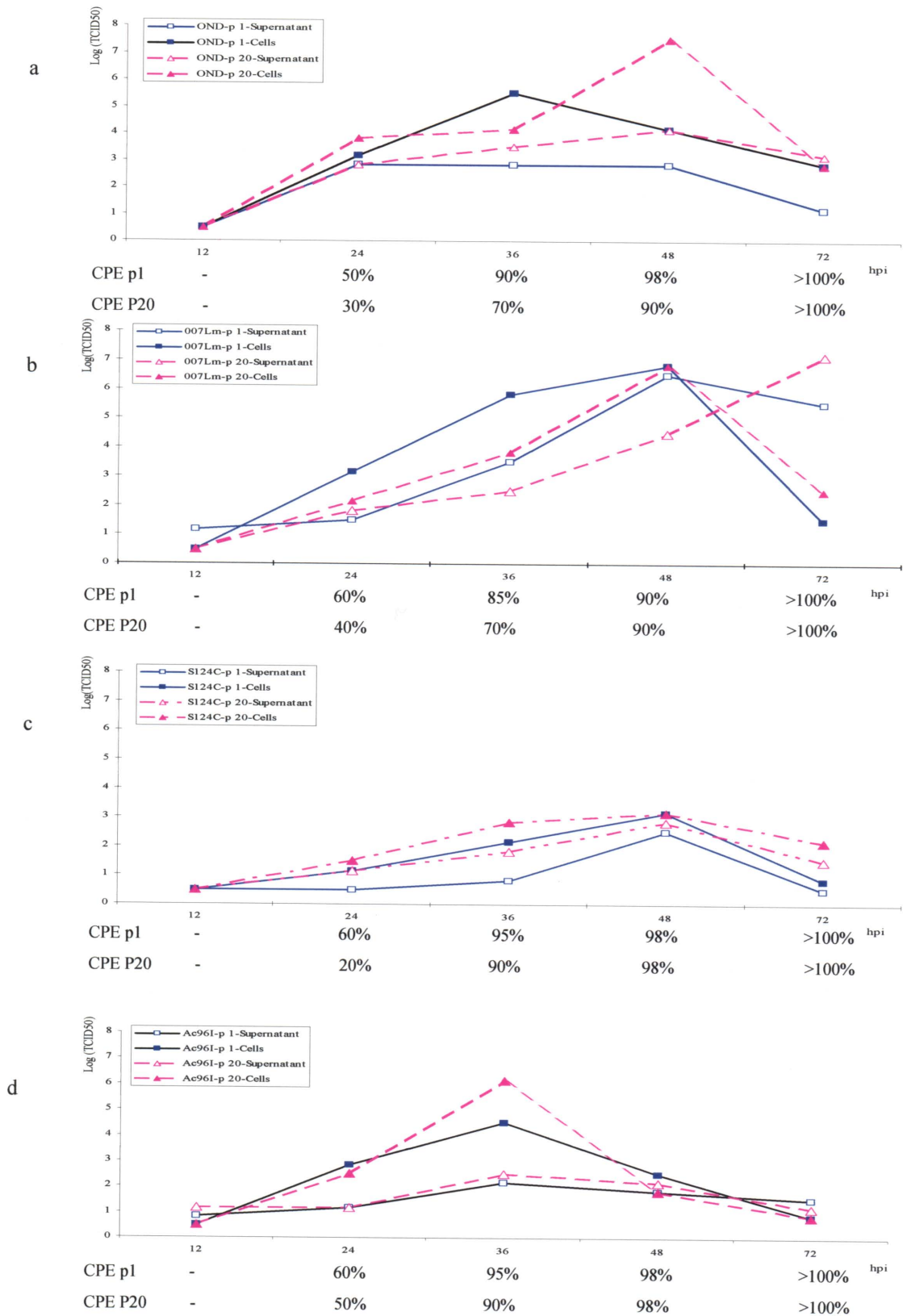


Fig. 19. Growth curves of CDV strains. (a) Onderstepoort; (b) 007Lm; (c) S124C; (d) Ac961 [original (ori) and 20 passages (20p)] in Ver0-DST cells.

OND-origin	1:MLPYQDKVGAFYKDNARANSTKLSLVTEGHGGRPPYLLFVLLILLVGLALLAITGVRV	60
OND-2Op	1:.....	60
007Lm-origin	1:..S.....S.....EQ.....A...	60
007Lm-2Op	1:..S.....S.....EQ.....A...	60
S124C-origin	1:..S.....S.....EQ.....I.....	60
S124C-2Op	1:..S.....S.....EQ.....I.....	60
Ac96I-origin	1:..S.....S.....EQ.....I.....	60
Ac96I-2Op	1:..S.....S.....EQ.....I.....	60
OND-origin	61:HQVSTSNHEFSRLLKEDMEKSEAVHHQVIDVLTPLFKIIGDEIGLRLPQKLNEIKQFILO	120
OND-2Op	61:.....	120
007Lm-origin	61:R.....V..G...D.L.....N.....	120
007Lm-2Op	61:R.....V..G...D.L.....N.....	120
S124C-origin	61:.....N.....	120
S124C-2Op	61:.....N.....	120
Ac96I-origin	61:.....	120
Ac96I-2Op	61:.....	120
OND-origin	121:KTNFFNPNREFDFRDLHUC [*] INPPSTVKV [*] NYCESIGIRKAIASAANPILLSALS [*] GGRS	180
OND-2Op	121:.....G	180
007Lm-origin	121:.....KI.....DA.V.S.....G	180
007Lm-2Op	121:.....KI.....DA.V.S.....G	180
S124C-origin	121:.....KI.....DTV.VK.S.....I.....A.G	180
S124C-2Op	121:.....KI.....DTV.VK.S.....I.....A.G	180
Ac96I-origin	121:..K.....KI.....DTV.VK.S.....I.....A.G	180
Ac96I-2Op	121:..K.....KI.....DTV.VK.S.....I.....A.G	180
OND-origin	181:DIFPPHRC [*] S [*] GATTSSVGKVFPLSVLSMSLSISRTSEVINMLTAISDGVYGKTYLLVPDDIE	240
OND-2Op	181:.....	240
007Lm-origin	181:....Y.....R.....K...I.S.....Y..	240
007Lm-2Op	181:....Y.....R.....K...I.S.....Y..	240
S124C-origin	181:....Y.....R.....IL.....Y..	240
S124C-2Op	181:....Y.....R.....IL.....Y..	240
Ac96I-origin	181:....Y.....R.....G...I.....M.....Y..	240
Ac96I-2Op	181:....Y.....R.....I.....M.....Y..	240
OND-origin	241:REFDTREIRVFEIGFIKRWLNDMPLLQTTN [*] YMLPKNSKAKVCTIAVGELTLASLCVEES [*]	300
OND-2Op	241:.....	300
007Lm-origin	241:....QK.....E.....D..	300
007Lm-2Op	241:....QK.....E.....D..	300
S124C-origin	241:G...SQK.....ET.....D..	300
S124C-2Op	241:G...SQK.....ET.....D..	300
Ac96I-origin	241:G...SQK.....ET.....D..	300
Ac96I-2Op	241:G...SQK.....ET.....D..	300
OND-origin	301:TVLLYHDSSSGSQDGILVVTLGIFWATPMDHIEEVIPVAHPSMKKI [*] HITNHRGFIKDSIAT [*]	360
OND-2Op	301:.....	360
007Lm-origin	301:....N...S.....G...NQV.....VER.....V..	360
007Lm-2Op	301:....N...S.....G...NQV.....VER.....V..	360
S124C-origin	301:..I....N...N.....G...QV...I...VER.....V..	360
S124C-2Op	301:..I....N...N.....G...QV...I...VER.....V..	360
Ac96I-origin	301:....N...N.....G...QV...I...VER.....V..	360
Ac96I-2Op	301:....N...N.....G...QV...I...VER.....V..	360

(Continue)

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OND-origin 361:WNVPALASEKQEEQKGCLESACQQRKTYPMCNQASWEPFGGRQLPSYGRLLPLDASVDLQ 420
OND-20p    361:..... 420
007Lm-origin 361:.....V..Q..G..N.....S.....T.....V.....I... 420
007Lm-20p  361:.....V..Q..G..N.....S.....T.....V.....I... 420
S124C-origin 361:.....V.V.....N.....S.....T.....G.....P.I... 420
S124C-20p  361:.....V.V.....N.....S.....T.....G.....P.I... 420
Ac96I-origin 361:.....V.V.....N.....S.....T.....G.....P.I... 420
Ac96I-20p  361:.....V.V.....N.....S.....T.....G.....P.I... 420
OND-origin 421:LNISFTYGPVILNGDGMDDYVESPLLNSGWLTIIPKDGITISGLINKAGRGDQFTVLPVHLT 480
OND-20p    421:..... 480
007Lm-origin 421:.....N..D.....N..L.....S.....T... 480
007Lm-20p  421:.....N..D.....N..L.....S.....T... 480
S124C-origin 421:.....D.....N..VL.....T.....T... 480
S124C-20p  421:.....D.....N..VL.....T.....T... 480
Ac96I-origin 421:.....D.....N..VL.....S.....T... 480
Ac96I-20p  421:.....D.....N..VL.....S.....T... 480
OND-origin 481:FAPRESSGNCYLP IQTSQIDRDVLIENIVVLPTQSI RYVIATYDISRSDHAIVYYVYD 540
OND-20p    481:..... 540
007Lm-origin 481:.....M.K..T..L.....NF..V.....EN... 540
007Lm-20p  481:.....M.K..T..L.....NF..V.....EN... 540
S124C-origin 481:.....M.K..T..L.....NF.....G...H...G 540
S124C-20p  481:.....M.K..T..L.....NF.....G... 540
Ac96I-origin 481:.....M.K..T..L.....NF.....G... 540
Ac96I-20p  481:.....M.K..T..L.....NF.....G... 540
OND-origin 541:PIRTISYTLFPRLTTKGRPDFLRIECFVWDDNLWCHQFYRFEADIANSTTSVENLVIRIF 600
OND-20p    541:..... 600
007Lm-origin 541:.....Y.....D.....S..T.....D... 600
007Lm-20p  541:.....Y.....D.....S..T.....D... 600
S124C-origin 541:.....Y.....D.....N..T..L... 600
S124C-20p  541:.....Y.....D.....N..T..L... 600
Ac96I-origin 541:.....Y.....D.....N..T..L... 600
Ac96I-20p  541:.....Y.....D.....N..T..L... 600
OND-origin 601:SCNFRNP- 606
OND-20p    601:.....- 606
007Lm-origin 601:.....SKP 607
007Lm-20p  601:.....SKP 607
S124C-origin 601:.....SKP 607
S124C-20p  601:.....SKP 607
Ac96I-origin 601:.....SKP 607
Ac96I-20p  601:.....SKP 607

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Fig. 20. Deduced H protein amino acid sequences of CDV strains. (a) Onderstepoort; (b) 007Lm; (c) S124C; (d) Ac96I (ori and 20 p) in Vero-DST cells. Potential N-linked glycosylation sites are boxed. Dots (.) indicate identity. The major hydrophobic region is overlined. The asterisk (*) is a cystein residue. Red squares indicate amino acid differences between CDV strains-ori and -20p.