

## References

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# APPENDIXES

## APPENDIXES

Appendix A: The procedure for preparation of the tissue processing

Objective	Reagent	Time (minutes)
Dehydration	80% ethyl alcohol	30
	80% ethyl alcohol	30
	95% ethyl alcohol	30
	95% ethyl alcohol	30
	100% ethyl alcohol	40
	100% ethyl alcohol	40
Clearing	xylene	30
	xylene	30
Infiltration	Melted paraffin	30
	Melted paraffin	30

Appendix B: Calculation of 50% tissue culture infectious dose (TCID<sub>50</sub>) assay  
(Behrens-Karber method)

$$\text{TCID}_{50} = 10^m$$

$$m = X_k - d/2 - (a_1 + a_2 + a_3 + \dots + a_{k-1})/n \times d$$

, and  $X_k$  = the least dilution that show CPE in all well,

$d$  = the different of fold of dilution,

$a$  = the well that show CPE in the least dilution,

$n$  = number of well in each dilution

Example

Sample 12 BR:

The sample had been isolated in 10 - fold dilution. First dilution was  $10^{-1}$  and the last was  $10^{-7}$  and had 3 wells per one dilution.

After 48 hours, it showed CPE from dilution  $10^{-1}$  until dilution  $10^{-4}$  for all 3 well and at dilution  $10^{-5}$  showed CPE only 2 well.

In this case,  $X_k = -4$

$$d = 1$$

$$(a_1 + a_2 + a_3 + \dots + a_{k-1}) = 2$$

$$n = 3$$

$$m = X_k - d/2 - (a_1 + a_2 + a_3 + \dots + a_{k-1})/n \times d = -4 - 1/2 - 2/3 \times 1$$

$$= -5.167$$

$$\text{TCID}_{50} = 10^{-5.167}$$

$$\text{TCID}_{50} / \text{ml} = 1.48 \times 10^5$$

### Appendix C: The sequences of the samples

The nucleotide sequence of P gene from Thai isolated CDV

#### Sample 1IN

Sequence 390 BP; 117 A; 67 C; 125 G; 81 T; 0 other;

```

AAGAGGTAA GGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA 60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG 120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTCGGCCTT AAACCAGACA 180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA 240
GAAATGTGGGGATTAAGAAAAGGGATGGGATGACTCTGCAGTCCCACACAATCCCGAAG 300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CACATGGAATGGGGATAGTTGCTGGATCGA 390

```

#### Sample 3IN

Sequence 390 BP; 119 A; 67 C; 124 G; 80 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA 60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG 120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTCGGCCTTAAACCAGACA 180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA 240
GAAATGTGGGGATTAAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAA 300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CACATGGAATGGGGATAGTTGCTGGATCGA 390

```



## Sample 5BR

Sequence 390 BP; 120 A; 67 C; 123 G; 80 T; 0 other;

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA	60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG	120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA	180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA	240
GAAATGTAGGGATTAAGAAAAGGGATGGGAAGACTCTGCAGTTCCACACAATCCCGAAA	300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT	360
CACATGGAATGGGGATAGTTGCTGGATCGA	390

## Sample 12BR

Sequence 390 BP; 116 A; 67 C; 126 G; 81 T; 0 other;

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA	60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG	120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA	180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA	240
GAAATGTGGGGATTAAGAAAAGGGATGGGATGACTCTGCAGTTCCACACAATCCCGAAG	300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGACCGGAGAGAGGTCAGCCT	360
CACATGGAATGGGGATAGTTGCTGGATCGA	390

## Sample 14BR

Sequence 390 BP; 117 A; 67 C; 125 G; 81 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA 60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG 120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCCGGCCTTAAACCAGACA 180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA 240
GAAATGTGGGGATTAAGAAAAGGGATGGGATGACTCTGCAGTCCCACACAATCCCGAAG 300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CACATGGAATGGGGATAGTTGCTGGATCGA 390

```

## Sample 15BR

Sequence 390 BP; 115 A; 69 C; 126 G; 80 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA 60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACTGAGGATTCTGGCGAAG 120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCCGGCCTTAAACCAGACA 180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240
GAAATGTGGGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CCCATGGAATGGGGATAGTTGCTGGATCGA 390

```

## Sample 16BR

Sequence 390 BP; 116 A; 66 C; 126 G; 82 T; 0 other;

AAGAGGTTAAGGGAATCGAAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTA	60
ATCGAGGATTCGAGAGAGGAGAAGGAAGCTTTGATGATAGCACTGAGGATTCTGGCGAAG	120
ATTATTCCGGGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA	180
GAGCGGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCA	240
GAAATGTGGGGATTAAGAAAAGGGATGGGATGACTCTGCAGTCCCACACAATCCCGAAG	300
GTAAGACAGAGGATCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT	360
CACATGGAATGGGGATAGTTGCTGGATCGA	390

## Sample 270 BR-homogenate

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA	60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG	120
ATTATTCCGAGGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA	180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA	240
GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG	300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT	360
CACATGGAATGGGGACAGTTGCTGGATCGA	390

## Sample 270 LU-homogenate

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA 60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240
GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CACATGGAATGGGGACAGTTGCTGGATCGA 390

```

## Sample 270 LI-homogenate

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA 60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240
GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360
CACATGGAATGGGGACAGTTGCTGGATCGA 390

```

## Sample 270 SP-homogenate

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA 60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGACAGTTGCTGGATCGA 390

## Sample 270 SP-isolate (without CPE)

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA 60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGACAGTT GCTGGATCGA 390

## Sample 270 BR-isolate (with CPE)

Sequence 390 BP; 118 A; 72 C; 124 G; 76 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA   60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGAT TCTGGCGAAT   120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA   180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA   240
GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG   300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT   360
CACATGGAATGGGGACAGTTGCTGGATCGA                                     390

```

## Sample 270 LU-isolate (with CPE)

Sequence 390 BP; 118 A; 72 C; 125 G; 75 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAATA   60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG   120
ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA   180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA   240
GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG   300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT   360
CACATGGAATGGGGACAGTTGCTGGATCGA                                     390

```

## Sample 290 BR-homogenate

Sequence 390 BP; 117 A; 71 C; 126 G; 76 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA 60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGATAGTT GCTGGATCGA 390

## Sample 290 LI- homogenate

Sequence 390 BP; 117 A; 71 C; 126 G; 76 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA ..60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGATAGTTGCTGGATCGA 390

## Sample 290 LN- homogenate

Sequence 390 BP; 117 A; 71 C; 126 G; 76 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA 60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGATAGTTGCTGGATCGA 390

## Sample 290 SP- homogenate

SQ Sequence 390 BP; 117 A; 71 C; 126 G; 76 T; 0 other;

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA 60  
 GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG 120  
 ATTATTCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA 180  
 GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA 240  
 GAAATGTAAGGATTCAGAAAAGGGATGGGAAGACTCTGCAGTCCCACACAATCCCGAAG 300  
 GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT 360  
 CACATGGAATGGGGATAGTTGCTGGATCGA 390



Sample 290 SP- isolate (without CPE)

Sequence 390 BP; 116 A; 71 C; 126 G; 77 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA   60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG   120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA   180
GAGCAGCTGTTGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA   240
GAAATGTAAGGATTGAGAAAAGGGATGGGAAGACTCTGCAGTCCACACAATCCCGAAG   300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT  360
CACATGGAATGGGGATAGTTGCTGGATCGA                                     390

```

Sample 290 SP-isolate (without CPE)

Sequence 390 BP; 117 A; 71 C; 126 G; 76 T; 0 other;

```

AAGAGGTTAAGGGAATCGAAGACGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCGATA   60
GTCGAGGACTCGAGGAAGGAGAAGGAAGCCTTGATGACAGCACTGAGGATTCTGGCGAAG   120
ATTATCCGAGGGAAATGCTTCATCTAACTGGGGATATTCTTTCGGCCTTAAACCAGACA   180
GAGCAGCTGATGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAGGACAAGCA   240
GAAATGTAAGGATTGAGAAAAGGGATGGGAAGACTCTGCAGTCCACACAATCCCGAAG   300
GTAAGACAGGGGAGCCGGAGTGTGGATCCATTA AAAAGGGCACAGGAGAGAGGTCAGCCT  360
CACATGGAATGGGGATAGTTGCTGGATCGA                                     390

```

## The nucleotide sequence of H gene from Thai isolated CDV

Sample 270 BR-isolate (with CPE)

Sequence 1824 BP; 545 A; 376 C; 393 G; 510 T; 0 other;

ATGCTCTCCTACCAAGACAAGGTGGGTGCGTTCTACAAGGATAATGCAAGAGCTAATTCA 60  
 TCCAAGCTGCCCTTAGTGACAGAAGAGCAAGGGGCAGGAGACCACCTTATTTGCTGTTT 120  
 GTCCCTTCATCCTACTGGTTGGAATCATGGCCTTGCTTGCTATCAC'TGGAGTTAGATTT 180  
 CATCAAGTATCAACTAGCAATATGGAATTTAGCAGATTGCTGAAAGAGGATATGGAGAAA 240  
 TCAGAGGCCGTACATCACCAGGTCATAGATGCTTGACACCGCTATTCAAATTTATTGGA 300  
 ATGAGATTG GGTACGGTT GCCACAAAAA CTAACGAGA TCAAACAATT TATCCTTCAA 360  
 AAGACAAACT TCTTCAATCCGAACAGGGAATTCGACTTCCGCGATCTCCACTGGTGCATT 420  
 AACCCACCTAGTAAGATCAAGGTGAATTTACTAATTACTGCGATACAATTGGGATCAGA 480  
 AAATCTATTGCATCAGCAGCAAATCCCATCCTTTTATCAGCACTCTCCGGAGGCAGAGGT 540  
 GAGATATCCGACCATAGAGATGCAGTGGAGCTACTACTTCAGTAGGCAG-AATTTTCCCC 600  
 CTATCAGTATCTTTGTCCATGTCTTTGATCTCAAGAAAATCAGAGATAATCAGTATGATA 660  
 ACCGCTATCTCGGACGGAGTGTATGGTAAAACCTTATTTGCTAGTGCCTGATTATATTGAA 720  
 GGGGAGTTTCGACACGCAGAAGATTGAGTCTTTGAGGTAGGGTTCATCAAACGGTGGCTA 780  
 AATGACATGCCACTACTCCAGACAACCAATTATTTGGTCTCCAGAGAATTCCAAAGCT 840  
 AAAGTATGTAATATAGCAGTGGGCGAGTTGACACTGGCTTCCCTTGTGTAGATGAGAGC 900  
 ACTGTATTGTTATATCATGACAGCAATGGTTCACAAGATGGTATCTTGGTAGTGACGCTG 960  
 GGAATATTTGGGGCAACACCTATGGATCAAGTTGAAGAGGTGATACCTGTCGCTCACTCA 1020  
 TCCGTAGAAAAAATGCATATAACAAATCACCGTGGGTTTCATAAAAGATTCAATAGCAACC 1080  
 TGGATGGTGCCTGTATTGGTCTCTGAGAAACAAGAACAAGAATTGTCTGGAGTCG 1140  
 GCTTGTCAAAGAAAATCCTACCCTATGTGTAACCAAACGTCATGGGAACCCCTTTGGAGGA 1200  
 GGACAGTTGCCGTCGTATGGACGGTTGACATTACCTCTAGATCCAAGCATTGACCTTCAA 1260  
 CTTAACATATCTTTACAAACGGTCCGGTTATACTGAATGGAGACGGTATGGATTATTAT 1320  
 GAAAGCCCA TTTTGGACT CGGATGGCTTACCATTCTCCTAAGAACGGGACAGTCCTT 1380  
 GGACTGATAAACAAAGCAAGTAGAGGAGACCAATTCAGTGTAGTCCCCCATGTGTTGACA 1440  
 TTTGCGCCCAGGGAATCAAGTGGAAATTGTTATTTACCTA TTCAAACATCCCAAATTATG 1500  
 GATAAGGATGTCCTTACTGAGTCCAATTTAGTGGTGTGCCTACACAGAATTTTAGATAT 1560  
 GTCATAGCAACATATGACATATCCCGGGACGATCATGCTATTGTTTATTATGTTTATGAC 1620  
 CCAATTCGGACGATTTCTTATACGTACCCATTAGACTAACTACCAAGGGTAGGCCTGAT 1680  
 TTCCTAAGGATTGAATGTTTTGTGTGGGATGACGATTTATGGTGTACCAATTTTATCGA 1740  
 TTCGATGCTGACATCACCAACTCTACAACCAGTGTGAGAATTTAGTCCGTATAAGATT 1800  
 TCATGTAACCGTTCAAACCTTGA 1824

Sample 270 LU-isolate (with CPE)

Sequence 1824 BP; 544 A; 378 C; 392 G; 510 T; 0 other;

ATGCTCTCCTACCAAGACAAGGTGGGTGCCTTCTACAAGGATAATGCAAGAGCTAATTCA	60
TCCAAGCTGCCCTTAGTGACAGAAGAGCAAGGGGGCAGGAGACCACCTTATTTGCTGTTT	120
GTCCTTCTCATCCTACTGGTTGGAATCATGGCCTTGCTTGCTATCACTGGAGTTCGATTT	180
CATCAAGTATCAACTAGCAATATGGAATTTAGCAGATTGCTGAAAGAGGATATGGAGAAA	240
TCAGAGGCCGTACATCACCAGGTCATAGATGTCTTGACACCGCTATTCAAAATTATTGGA	300
GATGAGATTGGGTTACGGTTGCCACAAAACTAAACGAGATCAAACAATTTATCCTTGAA	360
AAGACAAACTTCTTCAATCCGAACAGGGAATTCGACTCCGCGATCTCCACTGGTGCATT	420
AACCCACCTAGTAAGATCAAGGTGAATTTTACTAATTACTGCGATAACAATGGGATCAGA	480
AAATCTATTGCATCAGCAGCAAATCCCATCCTTTTATCAGCACTCTCCGGAGGCAGAGGT	540
GACATATCCCACCATAACAGATGCAGTGGAGCTACTACTCAGTAGGCAGAATTTTCCC	600
CTATCAGTATCTTTGTCCATGTCTTTGATCTCAAGAAAATCAGAGATAATCAGTATGATA	660
ACCGCTATCTCGGACGGAGTGTATGGTAAAACCTATTTGCTAGTGCCTGATTATATTGAA	720
GGGGAGTTCGACACGCAGAAGATTGAGTCTTTGAGGTAGGGTTCATCAAACGGTGGCTA	780
AATGACATGCCACTACTCCAGACAACCAATTATTTGGTCTCCAGAGAATTCCAAAGCT	840
AAAGTATGACTATAGCAGTGGGCGAGTTGACACTGGCTTCCTTGTGTGTAGATGAGAGC	900
ACTGTATTGTTATATCATGACAGCAATGGTTCACAAGATGGTATCTTGGTAGTGACGCTG	960
GGAATATTTGGGGCAACACCTATGGATCAAGTTGAAGAGGTGATACCTGTCGCTCACTCA	1020
TCCGTAGAAAAAATGCATATAACAAATCACCGTGGGTTTCATAAAAGATTCAATAGCAACC	1080
TGGATGGTGCCTGTATTGGTCTCTGAGAAACAAGAAGAACAAAAGAATTGTCTGGAGTCG	1140
GCTTGTCAAAGAAAATCCTACCCTATGTGTAACCAAACGTCATGGGAACCCTTTGGAGGA	1200
GGACAGTTGCCGTCGTATGGACGGTTGACATTACCTCTAGATCCAAGCATTGACCTTCAA	1260
CTTAACATATCTTTTACAAACGGTCCGGTTATACTGAATGGAGACGGTATGGATTATTAT	1320
GAAAGCCCAATTTTGGACTCCGGATGGCTTACCATTCCCTAAGAACGGGACAGTCCTT	1380
GGACTGATAAAACAAAGCAAGTAGAGGAGACCAATTCAGTGTAGTCCCCCATGTGTTGACA	1440
TTTGCGCCCAGGGAATCAAGTGGAAATTGTTATTTACCTATTCAAACATCCCAAATTATG	1500
GATAAGGATGTCCTTACTGAGTCCAATTTAGTGGTGTGCCTACACAGAATTTTAGATAT	1560
GTCATAGCAACATATGACATATCCCGGGACGATCATGCTATTGTTTATTATGTTTATGAC	1620
CCAATTCGGACGATTTCTTATACGTACCCATTCAGACTAACTACCAAGGGTAGGCCTGAT	1680
TTCCTAAGGATTGAATGTTTTGTGTGGGATGACGATTTATGGTGTACCAATTTTATCGA	1740
TTCGATGCTGACATCACCAACTCTACAACCAGTGTTGAGAATTTAGTCCGTATAAGATTC	1800
TCATGTAACC GTTCAAACC TTGA	1824

The amino acid sequence of H gene from Thai isolated CDV

Sample 270 BR-isolate (with CPE)

SEQUENCE 608 AA; 68349 MW; 2028098 CN;

MLSYQDKVGAFYKDNARANSSKLPLVTEEQGRRPPYLLFVLLILLVGIMALLAITGVRF  
HQVSTSNMEFSRLLKEDMEKSEAVHHQVIDVLTPLFKIIGDEIGLRPQKLNEIKQFILQ  
KTNFFNPNREFDFRDLHWCINPPSKIKVNFTNYCDTIGIR KSIASAANPILLSALS GGGRG  
DIFPPYRCSGATTSVGRIFPLSVLSMSLSIRKSEIISMITAISDGVYGKTYLLVPDYIE  
GEFDTQKIRVFEVGFIKRWLNDMPLLQTTNYLVLPENSKAKVCTIAVGELTLASLCVDES  
TVLLYHDSNGSQDGILVTLGIFGATPMDQVEEVIPVAHSSVEKM HITNHRGFIKDSIAT  
WMVPVLVSEKQEEQKNCLESACQRKSYPMCNQTSWEPFGGGQLPSYGR LTLPLDPSIDLQ  
LNISFTNGPVILNGDGMDYYESPILDSGWLTIPPKNGTVLGLINKASRGDQFTVPHVLT  
FAPRESSGNC YLPIQTSQIM DKDVLTESNL VVLP TQNFRY VIATYDISRD DHAIVVYYVD  
PIRTISYTY FRLTTKGRPDFLRIECFW DDLWCHQFY FDADITNST SVENLVRIRF  
SCNRSKP\*

Sample 270 LU-isolate (with CPE)

SEQUENCE 608 AA; 68349 MW; 2028098 CN;

MLSYQDKVGAFYKDNARANSSKLPLVTEEQGRRPPYLLFVLLILLVGIMALLAITGVRF  
HQVSTSNMEFSRLLKEDMEKSEAVHHQVIDVLTPLFKIIGDEIGLRPQKLNEIKQFILQ  
KTNFFNPNREFDFRDLHWCINPPSKIKVNFTNYCDTIGIRKSIASAANPILLSALS GGGRG  
DIFPPYRCSGATTSVGRIFPLSVLSMSLSIRKSEIISMITAISDGVYGKTYLLVPDYIE  
GEFDTQKIRVFEVGFIKRWLNDMPLLQTTNYLVPENSKAKVCTIAVGELTLASLCVDES  
TVLLYHDSNGSQDGILWTLGIFGATPMDQVEEVIPVAHSSVEKM HITNHRGFIKDSIAT  
WMVPVLVSEKQEEQKNCLESACQRKSYPMC NQTSWEPFGGGQLPSYGR LTLPLDPSIDLQ  
LNISFTNGPVILNGDGM DYYESPILDSGWL TIPPKN GTVLGLINKASRGDQFTVPHVLT  
FAPRESSGNCYLPIQTSQIMDKDVLTESNLVWLPTQNFRYVIATYDISRDDHAIVYYVD  
PIRTISYTPFRLTTKGRPDFLRIECFWDDDLWCHQFYRFADITNSTTSVENLVRIRF  
SCNRSKP\*

## BIOGRAPHY

Miss Na taya Charoenvisal was born on May 17, 1979 in Bangkok, Thailand. She graduated with Bachelor Degree of Veterinary Sciences (DVM) in academic year 2006 from the Faculty of Veterinary sciences, Chulalongkorn University. She was a candidate of graduated program of Veterinary Pathology, Department of Pathology, Chulalongkorn University. She appointed the scholarship as an exchange student for 1 year (April 2006 – April 2007) from the Japan Student Services Organization (JASSO) to study and done research work in Department of Veterinary Pathology, Faculty of Agriculture, University of Miyazaki, Japan.

