



**UNIVERSITI PUTRA MALAYSIA**

***PURIFICATION OF LONG HELICAL CAPSID OF NEWCASTLE DISEASE  
VIRUS FROM ESCHERICHIA COLI***

**YAP CHEE FAI**

**IB 2013 5**

**PURIFICATION OF LONG HELICAL CAPSID OF  
NEWCASTLE DISEASE VIRUS FROM  
ESCHERICHIA COLI**



**MASTER OF SCIENCE  
UNIVERSITI PUTRA MALAYSIA**

**2013**

**PURIFICATION OF LONG HELICAL CAPSID OF NEWCASTLE DISEASE  
VIRUS FROM *ESCHERICHIA COLI***



**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,  
in Fulfilment of the Requirements for the Degree of Master of Science**

**January 2013**

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment  
of the requirement for the degree of Master of Science

**PURIFICATION OF LONG HELICAL CAPSID OF NEWCASTLE DISEASE  
VIRUS FROM *ESCHERICHIA COLI***

By

**YAP CHEE FAI**

**January 2013**

**Chairman: Professor Tan Wen Siang, PhD**

**Institute: Bioscience**

The truncated version of nucleocapsid (N) protein of Newcastle disease virus (NDV) expressed in *Escherichia coli*, NP<sub>Δc375</sub> self-assembles into relatively long herringbone-like particles. This truncated protein is vulnerable to endogenous host cell proteases. In order to limit the degradation and improve the production yield of recombinant NP<sub>Δc375</sub>, a bioinformatics programme, PeptideCutter was used to predict the possible endogenous proteases that led to the NP<sub>Δc375</sub> degradation. The size of the degraded bands of the NP<sub>Δc375</sub> of NDV on Western blots was analyzed by using the Quantity One software to predict the potential proteases cleavage sites on NP<sub>Δc375</sub> amino acid sequence. The possible proteases that degrade NP<sub>Δc375</sub> are serine and metalloproteases. Serine and metalloprotease inhibitors, namely phenylmethylsulfonyl fluoride (PMSF) and ethylenediaminetetraacetic acid (EDTA) were therefore employed to inhibit the endogenous proteolytic activities. Combination of the mentioned protease inhibitors at their optimal concentration was found to have a synergistic effect and resulted in about 2.1-fold increase in the NP<sub>Δc375</sub> yield. When tested with enzyme-linked immunosorbent assay (ELISA), the

purified NP<sub>Δc375</sub> treated with protease inhibitors was found to retain its reactivity against chicken anti-NDV antisera. In addition, they assembled into ring-like, short and long herringbone-like structures when examined under a transmission electron microscope (TEM). These imply that both the antigenicity and the particle forming capacity of the NP<sub>Δc375</sub> were preserved after being treated with protease inhibitors.

The conventional sucrose density gradient ultracentrifugation has been stated to be tedious and time consuming in the purification of NDV N protein. With the intention of improving the purification efficiency, the recombinant NP<sub>Δc375</sub> of NDV was purified with a packed bed anion exchange chromatography (AEC) from clarified *E. coli* homogenate. Packed bed AEC permits the purification processes to be completed in a shorter duration with lesser number of unit operations than that of sucrose density gradient ultracentrifugation. There was 76.3% of NP<sub>Δc375</sub> from the clarified *E. coli* homogenate adsorbed to the anion exchanger at the optimal binding pH (pH 6). An optimal desorption of the bound NP<sub>Δc375</sub> was accomplished by applying 50 mM Tris-HCl buffer at pH 7 in the presence of 0.5 M NaCl. The purification of NP<sub>Δc375</sub> of NDV by employing a pre-packed AEC has resulted in a 51.4% recovery of NP<sub>Δc375</sub> from the clarified feedstock with a purity and purification factor of 76.7% and 6.5, respectively. The antigenicity and the self-assembly property of the purified NP<sub>Δc375</sub> were preserved throughout the whole purification process as proven by ELISA and TEM analysis, respectively. The helical structure formed was as long as 490 nm and 22-24 nm in diameter.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

**PENULENAN KAPSID HELIKS PANJANG VIRUS PENYAKIT SAMPAR  
AYAM DARI *ESCHERICHIA COLI***

Oleh

**YAP CHEE FAI**

**Januari 2013**

**Pengerusi: Profesor Tan Wen Siang, PhD**

**Institut: Biosains**

Versi terpotong protein nukleokapsid (N) virus penyakit Sampar Ayam (NDV) diekspres dalam *Escherichia coli*, NP<sub>Δc375</sub> gabung sendiri membentuk partikel menyerupai “herringbone” yang agak panjang. Protein terpotong ini adalah terdedah kepada protease endogenus *E. coli*. Dalam usaha untuk menghadkan degradasi dan meningkatkan penghasilan rekombinan NP<sub>Δc375</sub>, satu program bioinformatik, PeptideCutter telah digunakan untuk meramal protease endogenus potensi yang menyebabkan degradasi NP<sub>Δc375</sub>. Saiz pita NP<sub>Δc375</sub> NDV yang mengalami degradasi pada pemplotan Western telah dianalisis dengan menggunakan Quantity One software untuk meramal tapak pemotongan protease potensi pada jujukan asid amino NP<sub>Δc375</sub>. Protease potensi yang bertindak ke atas NP<sub>Δc375</sub> adalah protease serina dan protease metallo. Oleh itu, perencat protease serina dan metallo, iaitu fenilmetilsulfonil fluorida (PMSF) dan asid etilenadiaminatetra asetat (EDTA) telah digunakan untuk merencat aktiviti proteolitik endogenus. Gabungan perencat protease tersebut pada kepekatan optimum telah didapati mempunyai kesan sinergistik dan telah meningkatkan kira-kira 2.1 kali ganda hasil NP<sub>Δc375</sub>. Apabila

diuji dengan asai imunosorben bergabung enzim (ELISA), hasil penulenan NP<sub>Δc375</sub> yang telah dirawat dengan perencat protease didapati mengekalkan kereaktifannya terhadap antisera anti-NDV ayam. NP<sub>Δc375</sub> yang ditulenko juga membentuk struktur cincin dan struktur “herringbone” pendek dan panjang semasa diperiksa di bawah mikroskop elektron (TEM). Ini menunjukkan bahawa kedua-dua keantigenan dan keupayaan pembentukan partikel NP<sub>Δc375</sub> dipelihara selepas dirawat dengan perencat protease.

Pengemparan-ultra ketumpatan sukrosa konvensional adalah menyusahkan dan memakan masa dalam penulenan N protein NDV. Dengan tujuan untuk meningkatkan kecekapan penulenan, rekombinan NP<sub>Δc375</sub> NDV telah ditulenko daripada homogenat *E. coli* yang telah dijernihkan dengan mengaplikasikan sistem kromatografi pertukaran anion (AEC) pada lapisan terpadat. AEC lapisan terpadat membolehkan proses penulenan disempurnakan dalam jangka masa yang lebih singkat dengan bilangan unit operasi yang kurang berbanding dengan pengemparan-ultra ketumpatan sukrosa. Terdapat 76.3% NP<sub>Δc375</sub> daripada homogenat *E. coli* yang telah dijernihkan terjerap pada penukar anion pada pH penjerapan optimum (pH 6). Kadar elusi optimum NP<sub>Δc375</sub> terjerap tercapai dengan menggunakan larutan penimbang yang mengandungi 50 mM Tris-HCl dan 0.5 M sodium klorida (NaCl) pada pH 7. Penulenan NP<sub>Δc375</sub> NDV dengan menggunakan AEC lapisan terpadat telah membawa 51.4% pemulihan NP<sub>Δc375</sub> daripada suapan yang telah dijernihkan dengan ketulenan dan faktor penulenan 76.7% dan 6.5 masing-masing. Keantigenan dan ciri-ciri gabung sendiri NP<sub>Δc375</sub> yang ditulenko dipelihara selepas proses

penulenan seperti yang dibuktikan melalui analisis ELISA dan TEM masing-masing.

Struktur heliks terbentuk adalah sepanjang 490 nm dan berdiameter 22-24 nm.



## **ACKNOWLEDGEMENTS**

The success of this research project depends mostly on the kind guidance and support of many individuals and organizations. I wish to address my most sincere appreciations to all of them. First and foremost, I would like to express my greatest gratitude to my supervisor: Prof. Dr. Tey Beng Ti, for his valuable guidance, motivation and advice throughout the entire research and thesis writing; and also to another two members of the supervisory committee: Prof. Dr. Tan Wen Siang and Assoc. Prof. Dr. Sieo Chin Chin, for all their beneficial comments and suggestions.

Deepest thanks are also due to seniors: Wei Boon, Few Ne and Yong, who have assisted, guided and encouraged me whenever I encountered problems. I have earned a lot of priceless lab skills and ideas from them. Not forgetting, to all the members from Laboratory of Biochemical Engineering, Faculty Engineering, and Laboratory 134, Faculty Biotechnology and Biomolecular Sciences, UPM, especially Yien Yien. I would like to thank them for their earnest help and making my lab life more colorful and enjoyable. I must also express my truthful gratitude to Dr. Tan Sheau Wei and Jin Yew for their precious contribution in this study.

I wish to convey my heartfelt appreciations to my family for their endless love, care, understanding and support. Special thanks to my wonderful boyfriend, Ivan. His infinite motivation and spiritual support have toughened my mind towards research.

Last but not least, I'm grateful to the Ministry of Higher Education of Malaysia for supporting me through the Mini Budget Scheme. I'm also thankful to the Special

Graduate Research Allowance (S-GRA) provided by Universiti Putra Malaysia. I could not have accomplished this without all of them.



This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfillment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

**Tan Wen Siang, PhD**

Professor

Faculty of Biotechnology and Biomolecular Sciences

Universiti Putra Malaysia

(Chairman)

**Sieo Chin Chin, PhD**

Associate Professor

Faculty of Biotechnology and Biomolecular Sciences

Universiti Putra Malaysia

(Member)

**Tey Beng Ti, PhD**

Professor

School of Engineering

Monash University

(Member)

---

**BUJANG BIN KIM HUAT, PhD**

Professor and Dean

School of Graduate Studies

Universiti Putra Malaysia

Date:

## **DECLARATION**

I declare that the thesis is my original work except for the quotations and citations, which have been duly acknowledged. I also declare that it has not been previously, and is not concurrently, submitted for any other degree at Universiti Putra Malaysia or at any other institution.

**YAP CHEE FAI**

Date: 8 January 2013

## TABLE OF CONTENTS

	Page
<b>ABSTRACT</b>	ii
<b>ABSTRAK</b>	iv
<b>ACKNOWLEDGEMENTS</b>	vii
<b>APPROVAL</b>	ix
<b>DECLARATION</b>	xi
<b>LIST OF TABLES</b>	xv
<b>LIST OF FIGURES</b>	xvi
<b>LIST OF ABBREVIATIONS</b>	xviii
 <b>CHAPTER</b>	
<b>1 INTRODUCTION</b>	1
<b>2 LITERATURE REVIEW</b>	
2.1 Newcastle disease virus (NDV)	6
2.1.1 Virion structure	7
2.1.2 Viral genome	9
2.1.3 Nucleocapsid (N) protein of Newcastle disease virus (NDV)	10
2.1.4 Purification approach	11
2.2 Proteolytic degradation of recombinant protein in <i>E. coli</i>	12
2.2.1 Bacterial protease	13
2.2.2 Bioinformatic tools for endogenous protease and cleavage site identification	14
2.2.3 Protease inhibitor	15
2.3 Column chromatography	16
2.3.1 Mode of operation	17
2.4 Ion exchange chromatography (IEC)	18
2.4.1 Principle of IEC operation	19
2.4.2 The stationary phase	20
2.4.3 Adsorption	22
2.4.4 Elution	24
2.4.5 Applications of IEC	25
2.5 Current research interest	25
<b>3 IMPROVEMENT OF THE YIELD OF LONG HELICAL STRUCTURE OF RECOMBINANT NUCLEOCAPSID PROTEIN OF NEWCASTLE DISEASE VIRUS</b>	
3.1 Introduction	27
3.2 Materials and methods	29
3.2.1 Identification of potential proteases and their possible cleavage sites using bioinformatics programme	29
3.2.2 Cultivation of <i>E. coli</i>	29
3.2.3 Modulation of proteolytic degradation of the recombinant N protein of NDV	30

3.2.4	Sucrose gradient ultracentrifugation	30
3.2.5	Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western blotting	31
3.2.6	Protein quantitation	31
3.2.7	Enzyme-linked immunosorbent assay (ELISA)	32
3.2.8	Electron microscopy	32
3.3	Results and discussion	34
3.3.1	Identification of molecular mass of the degraded NP <sub>Δc375</sub>	34
3.3.2	Determination of potential protease cleavage sites on amino acid sequence	36
3.3.3	Identification of potential proteases and their possible cleavage sites using bioinformatics programme	37
3.3.4	Effects of PMSF concentrations on the yield of NP <sub>Δc375</sub>	40
3.3.5	Effects of EDTA concentrations on the yield of NP <sub>Δc375</sub>	41
3.3.6	Effects of single and combined supplementation of protease inhibitors on the yield of NP <sub>Δc375</sub>	42
3.3.7	ELISA	44
3.3.8	Electron microscopic analysis	45
3.4	Conclusion	46
<b>4</b>	<b>PURIFICATION OF LONG HELICAL CAPSID OF NEWCASTLE DISEASE VIRUS FROM <i>ESCHERICHIA COLI</i> USING ANION EXCHANGE CHROMATOGRAPHY</b>	
4.1	Introduction	47
4.2	Materials and methods	49
4.2.1	Materials	49
4.2.2	Feedstock preparation	49
4.2.3	Sucrose gradient ultracentrifugation	50
4.2.4	Anion exchange chromatography	50
4.2.5	Optimization of binding and elution of NP <sub>Δc375</sub>	51
4.2.6	Dynamic binding capacity	52
4.2.7	Protein analysis and quantitation	53
4.2.8	Enzyme-linked immunosorbent assay (ELISA)	53
4.2.9	Electron microscopy	54
4.2.10	Calculations	54
4.3	Results and discussion	57
4.3.1	Effects of binding pH	57
4.3.2	Dynamic binding capacity	60
4.3.3	Effects of elution pH	61
4.3.4	Effects of elution ionic strength	62
4.3.5	Purification of NP <sub>Δc375</sub> by pre-packed SepFast™ Supor Q column	64
4.3.6	ELISA	67
4.3.7	Electron microscopy analysis	69
4.4	Conclusion	70

<b>5</b>	<b>GENERAL CONCLUSION AND FUTURE PERSPECTIVES</b>	
5.1	General conclusion	71
5.2	Future perspectives	74
<b>REFERENCES</b>		76
<b>APPENDICES</b>		90
<b>BIODATA OF STUDENT</b>		94
<b>LIST OF PUBLICATION</b>		95

