

# **UNIVERSITI PUTRA MALAYSIA**

# DEVELOPMENT OF A RECOMBINANT GENOTYPE-MATCHED LIVE ATTENUATED VACCINE AGAINST GENOTYPE VII NEWCASTLE DISEASE VIRUS

**MUHAMMAD BASHIR BELLO** 

IB 2018 29



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**MUHAMMAD BASHIR BELLO** 

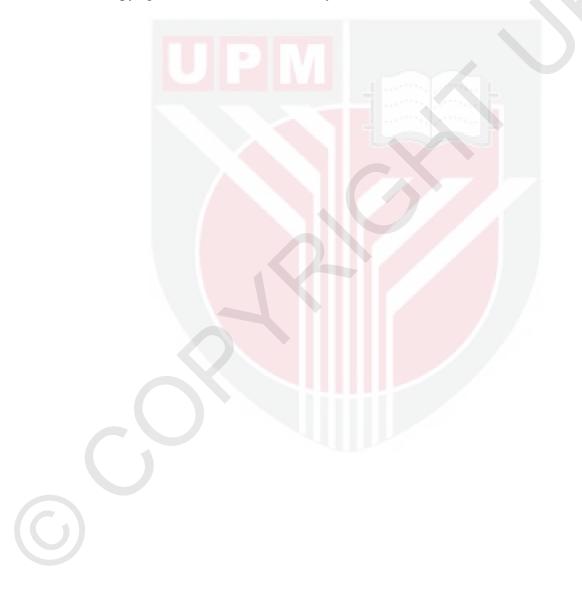
Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfillment of the Requirements for the Degree of Doctor of Philosophy

May 2018

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## **DEDICATION**

This thesis is dedicated to my beloved parents, Dr. Bello Muhammad Tambuwal and Hajiya Fatima Bello Tambuwal, for their endless love and prayers. May Allah's blessings continue to be with them in this world and the here after.



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy

## DEVELOPMENT OF A RECOMBINANT GENOTYPE-MATCHED LIVE ATTENUATED VACCINE AGAINST GENOTYPE VII NEWCASTLE DISEASE VIRUS

By

#### **MUHAMMAD BASHIR BELLO**

Chairman : Abdul Rahman Omar, DVM, PhD Faculty : Bioscience

Newcastle disease is a highly contagious viral disease of birds considered as one of the most important militating factors against poultry production all over the world. Current control strategies against the disease rely on the use of vaccines developed more than six decades ago. Although those vaccines are still effective by virtue of the fact that all Newcastle disease viruses (NDV) belong to the same serotype, they neither provide a complete protection in commercial chickens, nor do they block the replication and shedding of the virulent virus following infection with genotype VII NDV. Phylogenetically, the vaccines are classified as either genotype I or II, and are evolutionarily divergent from genotype VII isolates which have been the most predominantly circulating NDV strains in Malaysia and many parts of the world for the past 20 years. Therefore in the present study, reverse genetics technology was applied to genetically attenuate the pathogenicity of a recently isolated virulent Malaysian NDV strain IBS025/13. First and foremost, in silico nucleotide substitutions were made on the complete genome sequence of NDV strain IBS025/13, in order to modify the fusion protein (F) cleavage site of the virus from the virulent polybasic (RRQKRF) to avirulent monobasic (GRQGRL) amino acid motifs. Unique MluI and SgrDI enzyme sites were also created at the P-M junction in order to facilitate future expression of foreign genes using the NDV backbone. The modified full length sequence (15.2 kb) was then entirely synthesised (GenScript, USA), subcloned into pOLTV5 transcription vector under the transcriptional control of T7 promoter and then named pOLTV5-mIBS025. Furthermore, expression plasmids for the NDV's minimum replication machinery (NP, P and L genes) were constructed in pCIneo mammalian expression vector and named pCIneo-NP, pCIneo-P and pCIneo-L respectively. These constructs, collectively referred as helper plasmids, were later tested for functionality in reverse genetics experiments using minigenome rescue system. Next, baby hamster kidney (BHK-21) cells stably expressing T7 RNA



polymerase were co-transfected with the mixture of the helper plasmids and pOLTV5mIBS025 at an optimized ratio (1:0.5:0.25:0.2µg of POLTV5-mIBS025: pCineo-NP: pCIneo-P: pCIneo-L respectively). Interestingly, a recombinant virus designated NDV mIBS025, was successfully rescued following amplification in specific-pathogen-free (SPF) embryonated eggs, as evidenced by positive hemagglutination reaction. To confirm the identity of the recombinant virus, reverse transcription polymerase chain reaction (RT-PCR) was used to amplify a partial F gene region encompassing the cleavage site. DNA sequencing of the amplicons confirmed the presence of the engineered monobasic F cleavage site. Further biological characterization indicate that the recombinant virus has completely lost its pathogenicity as determined by the mean death time (MDT) in SPF embryonated eggs (150.4 hours) and the intracerebral pathogenicity index (ICPI) (0.0) in one-day old SPF chickens. Interestingly, when the recombinant virus was sequentially passaged in SPF eggs, it was found to not only maintain the monobasic F cleavage site, but also retained its attenuated phenotype after five consecutive passages, indicating the stability of the newly acquired attenuated phenotype. Finally, when one-day old SPF chickens were immunised with either 6log10 EID<sub>50</sub> LaSota or the recombinant NDV mIBS025, a steadily increasing antibody titer was observed in both groups from 0-21 days post immunization, as determined by hemagglutination inhibition test using either genotype II or genotype VII NDV isolates as the HA antigen. Moreover, birds vaccinated with either LaSota or the recombinant NDVmIBS025 at the dose of 10<sup>6</sup> EID<sub>50</sub> were completely protected against morbidity and mortality following experimental challenge with a lethal dose of the virulent genotype VII NDV strain IBS002/11. However, while both vaccines reduced the cloacal and oropharyngeal virus shedding compared to the unvaccinated group, the recombinant NDV mIBS025 significantly reduced both the duration and load quantity of the virus shed compared to the LaSota vaccine.

In conclusion, reverse genetics has been used to generate a genotype-matched live attenuated vaccine candidate based on the recently circulating virulent NDV IBS025/13. Immunogenicity assessment indicates that the vaccine induced a high antibody titer capable of protecting chicken against the virulent genotype VII NDV challenge. The vaccine also appears to be more promising in terms of reducing the shedding of the virulent virus post challenge.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

## PEMBANGUNAAN REKOMBINAN VAKSIN HIDUP TERATENUAT PADANAN-GENOTIP TERHADAP VIRUS SAMPAR AYAM GENOTIP VII

Oleh

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Penyakit sampar ayam (ND) adalah wabak virus burung yang mudah berjangkit dan dianggap sebagai salah satu faktor menghadkan yang paling penting terhadap pengeluaran ayam di seluruh dunia. Strategi kawalan semasa terhadap penyakit ini bergantung kepada penggunaan vaksin yang dibangunkan lebih enam dekad yang lalu. Walaupun vaksin tersebut masih dianggap efektif berdasarkan fakta bahawa semua virus penyakit sampar ayam (NDV) tergolong dalam serotip yang sama, namun vaksin ini kerap gagal memberi pelindungan lengkap dalam ayam komersial, menyekat replikasi virus dan pembebasan virus yang virulen selepas dijangkiti dengan virus ND genotip VII. Secara filogenetik, vaksin ini diklasifikasikan sebagai genotip I atau II, dan secara evolusinya berlainan daripada isolat genotip VII, dimana ianya merupakan strain NDV yang paling banyak tersebar di Malaysia dan di pelbagai negara di dunia sejak 20 tahun yang lalu. Oleh itu dalam kajian ini, teknologi genetik songsang telah digunapakai untuk melemahkan kepatogenan secara genetik bagi strain NDV Malaysia (IBS025/13) yay dipencilkan baru-baru ini.

Dengan menggunakan jujukan genom NDV IBS025/13 yang lengkap sebagai templat, penggantian nukleotida secara in silico dibuat untuk mengubah suai tempat belahan protein (F) bagi virus dari polibes virulen kepada motif asid amino monobes avirulen. Tempat enzim yang unik bagi Mlul dan SgrDl juga dibuat di persimpangan P-M bagi memudahkan pengekspresan gen asing pada masa akan datang. Jujukan yang telah diubahsuai kemudiannya disintesis sepenuhnya (GenScript, USA), disubklon ke dalam pOLTV5 di bawah kawalan transkrip promoter T7 dan seterusnya dinamakan sebagai pOLTV5-mIBS025. Tambahan pula, plasmid ekspresi untuk jentera replikasi minima NDV (gen NP, P dan L) dibina dalam vektor ekspresi mamalia pCIneo dan dinamakan pCIneo-NP, pCIneo-P dan pCIneo-L setiap satunya. Pembinaan ini, secara kolektif merujuk sebagai plasmid penbantu, kemudian diuji untuk fungsi dalam

eksperimen genetik songsang menggunakan sistem penyelamatan minigenom. Selanjutnya, sel BHK 21 secara stabil menghasilkan polimerase RNA T7 telah ditransfeksi bersama dengan campuran plasmid pembantu dan pOLTV5-mIBS025 pada nisbah optimum. Menariknya, virus rekombinan NDV mIBS025, telah berjaya diselamatkan berikutan amplifikasi di dalam telur embrio yang bebas patogen (SPF), seperti yang dibuktikan oleh reaksi hemaglutinasi positif. Untuk mengesahkan identiti virus rekombinan, tindak balas rantai polimerase transkripsi berbalik (RT-PCR) telah digunakan untuk amplifikasi separa gen F yang merangkumi tapak belahan. Penjujukan DNA amplikon mengesahkan kehadiran tapak belahan monobasik F yang direka. Pencirian biologi lebih lanjut menunjukkan bahawa virus rekombinan telah hilang secara keseluruhan patogeniknya seperti yang ditentukan oleh masa kematian purata (MDT) di dalam telur embrio SPF (150.4 jam) dan indeks kepatogenan intracerebral (ICPI) (0.0) dalam ayam SPF berusia satu hari. Menariknya, apabila virus rekombinan secara beransur-ansur dipindahkan dalam telur SPF, ia didapati hanya mengekalkan tapak pemisahan monobasik F, tetapi juga mengekalkan fenotipnya yang dilemahkan selepas lima pemindahan berturut-turut, menunjukkan kestabilan fenotip dilemahkan. Seterusnya, apabila ayam SPF yang sudah berusia satu hari diimunisasi dengan LaSota atau rekombinan NDV mIBS025, titer antibodi yang semakin meningkat diperhatikan dalam kedua-dua kumpulan dari 0-21 hari selepas imunisasi, seperti yang ditentukan oleh ujian penghambatan penghemaglutinatan menggunakan genotip II atau genotip VII NDV asingan sebagai antigen HA. Tambahan lagi, ayam yang diyaksin dengan samaada LaSota atau rekombinan NDV mIBS025 dilindungi sepenuhnya terhadap morbiditi dan mortaliti berikutan halangan eksperimen dengan dos virulen genotip VII NDV strain IBS002/11 yang membawa maut. Walau bagaimanapun, semasa kedua-dua vaksin mengurangkan virus kloakal dan orofarinks dibebaskan berbanding dengan kumpulan yang tidak divaksinkan, NDV rekombinan mIBS025 dengan ketara mengurangkan kedua-dua jangkamasa dan jumlah kuantiti virus yang dibebaskan berbanding dengan vaksin LaSota.

Kesimpulannya, genetik songsang telah digunakan untuk menghasilkan calon vaksin hidup yang dilemahkan secara padanan genotip berdasarkan NDV IBS025/13 yang baru tersebar. Penilaian menunjukkan bahawa titer antibodi tinggi yang disebabkan oleh vaksin ini mampu melindungi ayam terhadap ancaman genotip VII NDV yang virulen. Vaksin ini dilihat lebih terjamin dari segi mengurangkan halangan selepas pembebasan virus yang virulen.

#### ACKNOWLEDGEMENTS

In the name of Allah, the most compassionate, the most merciful. All praises are due to the almighty Allah for giving me the strength, courage and patience to undertake this research and complete it successfully. I give thanks to Him for His immeasurable blessings throughout my life. Without those blessings, all my life achievements would not have been possible.

With a deep sense of gratitude, I express my sincerest appreciation to the chairman my supervisory committee in person of Prof. Dr. Abdul Rahman Omar, whose mentoring style has widened my horizon of intellectuality. The knowledge, skills and experience I acquired in his laboratory are what continue to place me on a pedestal among my contemporaries. He is a simple, gentle and humble supervisor everyone would love to work with. His words on the first day I met him will never be forgotten. He said 'Bashir, if you walk to me, I will run to you'. Despite his busy schedule as the Director, Institute of Bioscience (IBS), he was always there for me whenever I needed him. His moral support and encouragement kept me moving during the hardest moments of my research journey. I appreciate all the contacts he made with experts around the world to make my research a successful one. I remain ever indebted to him for being a great teacher and mentor.

I am immensely grateful to my co-supervisors Prof. Datin Paduka Khatijah Yusoff, Prof. Dr. Mohd Hair-Bejo, Prof. Datin Paduka Aini Ideris and Dr. Ben P.H Peeters, for all the useful suggestions offered to make my research a success. Dr. Ben P.H Peeters has particularly offered invaluable troubleshooting tips at various steps of the experiments. He also constructively reviewed my manuscripts and polished my writing skills. Likewise Prof. Khatijah Yusoff, a very intelligent paramyxovirologist, provided all the necessary assistance to see the success of my research. I equally feel highly honoured for the invaluable insights from Prof. Datin Paduka Aini ideris and Prof. Dr. Mohd Hair-Bejo especially during my PhD comprehensive examination. To all of them, I say a very big thank you.

I want to extend my special appreciations to my beloved parents, Dr. Bello Muhammad Tambuwal and Hajiya Fatima Bello Tambuwal. Their endless prayers, love and moral as well as financial supports have always been my strength at all the stages of my studies. I pray to God almighty to infinitely bless them and reward them with jannatul firdaus. I equally appreciate my dearest uncle Dr. F. M Tambuwal, who trained me from childhood to date and from whom I continue to learn basic principles of life. May Allah reward him abundantly. Let me also acknowledge all my siblings especially Abdulsalam, Abdulrahman, late Mahmud, Mariya, Amina, Aisha, Saadatu, Yusuf, Ibrahim and the rest, for their patience, sacrifices and prayers throughout my studies.

My wonderful friends equally deserve a special acknowledgement. Top most on the list is Abdulazeez Musa, a true friend that continued to take care of my mother while I was away for studies in Malaysia. I also appreciate the prayers and goodwill messages from Abdulsalam Isiaku, Ibrahim Rice, Murtala ADC, Dr. Mubarak, Nafiu Lawal, Bashir Garba, Adamu Abdul, Jamilu Wudil and so many others too numerous to mention. I specially thank Dr. Danmaigoro for his assistance in some statistical analysis of my data. Mal Mamman Attahiru, a humble personality of iconic proportion, will never be forgotten for his friendship and usual goodwill messages. I also want to extend bundles of gratitude to Dr. Faruku Bande for his suggestions and keen interest in my research progress throughout the studies. Drs. Elina and Kavitah are also appreciated for their help during the infancy of my research. To all of them, I remain ever grateful.

I also appreciate the Scholarship division, Ministry of Higher Education Malaysia for paying my tuition fees and providing me with monthly stipends from the 4<sup>th</sup> to 6<sup>th</sup> semester of my studies. Without this support, my study would not have been a smooth one. I am really grateful. Bundles of thanks also go to the management of my institution, Usmanu Danfodiyo University Sokoto, for providing me the study leave to enable me pursue a PhD degree. My special regards also go to Prof. A. A. Magaji (Dean of Vet. Medicine), Dr. M. B. Abubakar, Dr. B. R. Alkali, Prof. A. I Daneji, Prof. A. U. Junaidu and indeed all my teachers for their amazing support and encouragements throughout my studies.

I cannot afford to ignore the mention of my lab mates together with whom we celebrated our success and mourned our challenges. They Include Dilan, Mostafa, Daniel, Khanh, Sadiya, Omar, Umar, Iswadi, Suwaiba, Zahiah, Rohaya and my very good friend Oday. Our stress relieving discussions in the student's room after exhaustive lab work still remain fresh in my memories. I equally appreciate the motivation from my lab bench neighbour, Chawyee, who always reminds me that success comes with hard work. Special regards also go to the well-mannered Sakinah Yusoff for being a trustworthy sister and a good friend. I also profusely give thanks to my gentle friend Faiz, for his assistance in translating the thesis abstract into bahasa melayu. The staff of the Laboratory of Vaccines and Immunotherapeutics are equally appreciated for creating a favourable working atmosphere. I thank them all.

Lastly, I want to appreciate my wife, Aisha and three children, Ahmad, Khadija and Mahmud, whose companionship served as a 'shock absorber' during the most stressful days of my research. They have all been incredibly supportive throughout the period of this study. May Allah continue to shower His blessings upon them till eternity.

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

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# LIST OF ABBREVIATIONS

	μl	Microlitre
	Aa	Amino Acid
	APMV	Avian Paramyxovirus
	BEI	Binary ethylenimine
	ВНК	Baby Hamster kidney
BLAST		Basic Local Alignment Search Tool
	bp	Base pair
	BSA	Bovine Serum Albumin
	CAT	Chloramphenicol acetyl transferase
	cDNA	Complementary DNA
	CMI	Cell-mediated immunity
	CMV	Cytomegalovirus
	DAPI	4',6-diamidino-2-phenylindole
	DNA	Deoxyribonucleic Acid
	dpc	Days post challenge
dpv	dpv	Days post vaccination
dsRNA	dsRNA	Double strand deoxyribonucleic acid
	Е	Glutamic acid
	EDTA	Ethylene-diamine-tetraacetic Acid
	EGFP	Enhanced green fluorescent protein
	ELD <sub>50</sub>	50% Mean egg lethal dose
	ELISA	Enzyme-linked immunosorbent assays

F Fusion protein F0 Fusion protein 0 F1 Fusion protein fragment 1 F2 Fusion protein fragment 2 Foot and mouth disease virus **FMDV** GALT Gastrointestinal associated lymphoid tissue GE Gene end GFP Green fluorescent protein GIT Gastrointestinal tract GS Gene start HA Hemagglutination Hammerhead ribozyme Hamrz HDVrz Hepatitis delta virus ribozyme Hep-2 Human epitheloid carcinoma 2 HI Hemagglutination inhibition HIV TAT Human Immunodeficiency virus trans-activator of transcription Hemagglutinin-Neuraminidase HN HVT Herpes virus of turkeys Infectious bursal disease IBD ICPI Intracerebral pathogenicity index IFAT Immunofluorescence antibody test Interferon IFN Ig Immunoglobulin IGR Inter genic resions

IRES	internal ribosome entry site
ITU	Independent transcription unit
IVPI	Intravenous pathogenicity index
K	Lysin
L	Large protein
LAMP	Loop mediated isothermal amplification
LB	Luria bertani
LIC	Ligation independent cloning
LND	Lentogenic Newcastle disease
М	Matrix protein
MAB	Monoclonal antibody
MCS	Multiple cloning site
MDT	Mean death time
MEGA	Molecular evolutionary genetics analysis
МНС	Major histocompatibility complex
MLT	Mean lethal dose
MND	Mesogenic Newcastle disease
mRNA	Messenger RNA
MVA	Modified vaccinia Ankara
NCBI	National center for biotechnology information
ND	Newcastle disease
NDV	Newcastle disease virus
NDV mIB025	Genetically modified recombinant Newcastle disease virus IBS025/13

NP	Nucleocapsid protein
NSNS	Negative sense nonsegmented virus
NVND	Neurotropic velogenic Newcastle disease
OE-PCR	Overlap extension polymerase chain reaction
OIE	Office international des epizooties
ORF	Open reading frame
Р	Phophoprotein
PAMPs	Pathogen associated molecular patterns
PBMC	Peripheral blood mononuclear cells
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
Pol-1	RNA polymerase 1
pOLTV5- mIBS025	Full length clone of modified Newcastle disease virus antigenome strain IBS025
Q	Glutamine
R	Arginine
rAF-GFP	Recombinant NDV AF2240 strain expressing GFP
RE	Restriction endonuclease
rHVT	Turkey herpesvirus-based recombinant Vaccine
RIG-1	Retinoic acid inducible gene 1
RNA	Ribonucleic acid
RNP	Ribonucleoprotein
rpm	Revolutions per minute
RT	Reverse transcription

RT-PCR	Reverse transcription-polymerase chain reaction
SEAP	Secreted alkaline phosphatase
SPF	Specific-pathogen-free
STAT	Single transducer and activator of transcription
TAE	Tris-acetate-EDTA
Us	Uracil
UTR	Untranslated regions
VG/GA	Villegas-Glisson/University of Georgia
VLP	Virus-like particle
VVND	Viscerotropic velogenic Newcastle disease

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### **CHAPTER 1**

#### **INTRODUCTION**

### 1.1 General background

Newcastle disease is a highly contagious viral disease of birds considered as one of the most important militating factors against poultry production across the globe. It has a worldwide distribution and is associated with significant economic losses in the global poultry industry (Alexander, 2001). It is also included in the World Organisation of Animal Health (OIE) List A diseases. The aetiology of the disease is Newcastle disease virus (NDV), an avian paramyxovirus type-1 (APMV-1) which is a member of the genus Avulavirus in the family *Paramyxoviridae*. The virus is enveloped and has a nearly 15.2 kb non-segmented genome, made up of six genes in the order 3' NP-P-M-F-HN-L 5'. With the exception of the P gene which can undergo RNA editing to give rise to two additional non-structural proteins, V and W (Steward *et al.*, 1993), all the genes are transcribed into a single mRNA that encodes a single structural protein namely the Nucleocapsid protein (NP), Phosphoprotein (P), Matrix protein (M), Fusion protein (F), Hemagglutinin-neuraminidase protein (HN) and Large protein (L) (Yusoff and Tan, 2001).

To date, all strains of NDV are grouped into one serotype. However, their genetic diversity is enormous. Information from the available literature reveals two major schemes used to classify NDV isolates on the basis of their genomic characteristics. The first system, proposed by the Aldous group, classifies the NDV isolates into lineages (I-VI) and their respective sublineages (Aldous et al, 2003). The other classification scheme proposed by Ballagi-Pordány et al. (1996), divides the NDV isolates broadly into class I and class II with several genotypes and subgenotypes in each class. All class I isolates uniquely have a genome length of 15,198 bp and are distributed worldwide in wild birds. More so, apart from a single isolate that caused devastating outbreak in Ireland around the early 1990s (Alexander et al., 1992), all class I strains are usually avirulent in chicken (Kim et al., 2007). On the other hand, the class II viruses which have been extensively studied constitute both the virulent and avirulent strains. Usually, their total genome length is either 15,186 bp for genotypes isolated before 1960 (early genotypes) or 15,192 bp in the case of late genotypes that were isolated after 1960 (Czeglédi et al., 2006) although some recently isolated strains were shown to have a total genome size of 15,186 bp (Satharasinghe et al., 2016). Interestingly, a more comprehensive criteria for NDV classification was recently adopted in order to bring an end to the confusion created by simultaneous usage of the two schemes of NDV taxonomy (Diel et al., 2012). Based on this unified system of classification, NDV isolates are grouped into class I, with only one genotype and class II having up to 18 genotypes (Snoeck et al., 2013). Importantly, all members of class II genotypes I and II, with the exception of a neurotropic virulent chicken strain, isolated in 1948 in the United States, are of low virulence in chicken (Miller et al. 2010). Indeed most of the popular commercially available ND vaccines such as

LaSota, B1 and VGGA are derived from these genotype II isolates (Dimitrov *et al.* 2016). Genotypes III to XVIII are however mostly composed of strains that are highly pathogenic in chicken.

Traditionally, the NDV isolates are classified into lentogenic, mesogenic and velogenic pathotypes using indices such as the mean death time (MDT) in 9 to 10days old embryonated chicken eggs, intracerebral pathogenicity index (ICPI) in 1 day old chicks and intravenous pathogenicity index (IVPI) in 6 weeks old chicken (OIE, 2008). Usually, the lentogenic isolates are considered non virulent because they neither cause any clinical disease in adult birds nor do they kill chicken embryo even after 90 hours of propagation. In contrast, the velogenic strains are associated with high mortality in chicken and can kill chicken embryo in less than 60 hours post inoculation (Alexander and Parsons, 1986). The mesogens are of intermediate virulence usually causing respiratory disease of moderate severity in chicken. In addition to these in vivo pathogenicity tests, the amino acid composition of the F protein cleavage site is used as a molecular marker for NDV virulence (Ganar et al., 2014; Panda et al., 2004). The F protein is normally synthesised in an inactive form, F<sub>0</sub>, and is activated via cleavage by certain host cell proteases into two fragments, F1 and F2 linked by disulphide bonds (de Leeuw et al., 2005). Virulence of NDV strains is defined by the presence of a multiple basic amino acid residues (lysine or arginine) between positions 112 to 116 and a phenylalanine residue at position 117 on the fusion protein. Isolates with this type of cleavage site are easily cleavable by intracellular furin-like proteases ubiquitously distributed in many chicken organs, explaining the widespread multisystemic lesions associated with the virulent strains of NDV. On the contrary, avirulent NDV strains have a monobasic amino acid residue at the fusion protein cleavage site and can only be activated by trypsin like extracellular proteases mostly present in the respiratory and gastrointestinal systems (Wang et al., 2017).

### 1.2 Statement of research problem

Although, the conventional commercially available vaccines such as LaSota and B1 developed more than 60 years ago, have been offering a promising level of protection against ND for decades, several studies indicate that their protective efficacy against the current wave of ND outbreaks is suboptimal (Miller *et al.*, 2013; Miller *et al.*, 2007). Evidences from molecular epidemiological studies indicate that the most predominantly circulating strains of NDV in Southeastern Asian countries belong to genotype VII (Liu *et al.*, 2007; Tan *et al.*, 2010), and they are known to be responsible for the recently recorded outbreaks of ND including those occurring among the farms that vaccinated their birds using the conventional genotype II vaccines. One of the major driving forces for the occurrence of ND outbreaks among the vaccinated birds is the genotype mismatch between the conventional vaccine strains and the circulating field strains. Based on nucleotide and amino acid sequence alignment, the surface glycoproteins (F and HN) of genotype VII NDV are highly divergent from those of the conventional genotype II vaccine strains (Xiao *et al.*, 2012; Zhang *et al.*, 2014). Thus the sequence variation between the field and vaccine strains might be responsible

for the suboptimal protection of genotype II vaccinated chicken against genotype VII NDV challenge.

No doubt, genotype VII isolates are currently the most disastrous NDV isolates. They are responsible for the on-going fourth ND panzootic and have manifested the potentials to become the fifth panzootic viruses by continuously emerging in new hosts and geographical areas (Miller *et al.*, 2015). They have also been shown to defy the current control strategies using the conventional genotype II vaccines. According to the records of the Malaysian Department of Veterinary Services, genotype VII NDV outbreaks (reported cases) are increasing exponentially, from 5 in 2009 to 153 in 2011. Even more recently, genotype VII NDV outbreaks have been recorded in different parts of Malaysia (Satharasinghe *et al.*, 2016; Aljumaili *et al.*, 2017) where they were associated with devastating economic losses in the national poultry industry. This therefore, highlights the need to improve the current vaccination strategy.

The fact remains the conventional genotype II vaccines when correctly administred at the right dose could still protect against clinical disease and mortality due to ND. However, they often fail to completely block virus shedding post challenge among the vaccinated birds (Miller et al., 2007). This means that the profile of humoral immune response induced by those vaccines might only protect against clinical signs but not virus replication in the vaccinated birds, presumably due to amino acid substitutions in some neutralising epitopes in the vaccine strain. Consequently, when the vaccinated bird is infected with genotypically distinct NDV isolate, the birds replicate and shed the virulent virus into the environment, posing a potential risk to naive birds in the vicinity. Indeed, live viruses have been reported in cloacal and nasopharyngeal swabs obtained from birds vaccinated with those conventional vaccines (Choi et al., 2013). Moreover, depending on the environmental factors and the presence of other concurrent infections, these conventional vaccines may cause disease symptoms in vaccinated birds. These problems, to say the least, underscore the need for the development of genotype-matched ND vaccines which are closely related to the prevailing genotypes and therefore offer a better protection with greater safety by significantly reducing virus shedding post challenge among the vaccinated birds.

### **1.3** Justification

With the advent of reverse genetics system for NDV, numerous genetic manipulations ranging from individual genes mutations to complete swapping of some genes with other identical homologues have been accomplished (Peeters *et al.*, 2001). Indeed, rationally designed vaccines with greatly enhanced safety and protective efficacy have been generated within a relatively short period of time. Hu *et al.* (2011) used reverse genetics technique and attenuated a highly virulent genotype VII NDV by mutating the F protein cleavage site of the virus. The resulting recombinant virus, when used to vaccinate birds, was found to effectively protect them against virulent NDV challenge 3-4 weeks post-immunization. More so, compared to the birds vaccinated with LaSota vaccine, virus shedding among the birds vaccinated with this recombinant vaccine was

significantly lower. Similarly, Xiao *et al.* (2012) recovered a stably attenuated virus from a highly virulent isolate by changing the virulent F protein cleavage site motif "<sup>112</sup>RRQKRF<sup>117</sup>" into an avirulent motif "<sup>112</sup>GRQGRL<sup>117</sup>". The recombinant virus also reduced the challenged virus shedding in the vaccinated animals compared to the LaSota vaccine. This therefore confirms the speculation by Miller *et al.*, (2007) that genotype matched vaccines not only effectively prevent mortality and morbidity due to ND challenge, they also substantially reduce virus shedding among the vaccinated animals.

Recently, a highly virulent NDV strain designated IBS025/13, was isolated from a vaccinated commercial broiler flock in Malaysia. The virus, which has the total genome length of 15,186 bp, was shown to be a naturally recombinant NDV with its entire NP and greater parts of its P genes derived from genotype II while the M, F, HN and L genes were all derived from genotype VII. It has the typical velogenic fusion protein cleavage site with multiple basic amino acid residues and high ICPI index of 1.69 (Satharasinghe *et al.*, 2016). In addition, tissue tropism studies have shown that the virus equally has high tropism in both respiratory and gastrointestinal systems (Satharasinghe, 2016). It also grows to a high titre in chicken embryonated eggs, making it a good candidate for vaccine development. Using reverse genetics technology, it is possible to attenuate the virulence of this virus without tempering with its unique tissue tropism characteristics. This way, a highly effective genotype-matched vaccine with the potential of enhanced ND control can be developed.

#### 1.4 Research hypothesis

Recombinant genotype-matched live attenuated Newcastle disease vaccine is completely protective in chicken and is more effective in reducing cloacal and oropharyngeal virus shedding compared to the conventional LaSota vaccine, following challenge with lethal dose of genotype VII NDV.

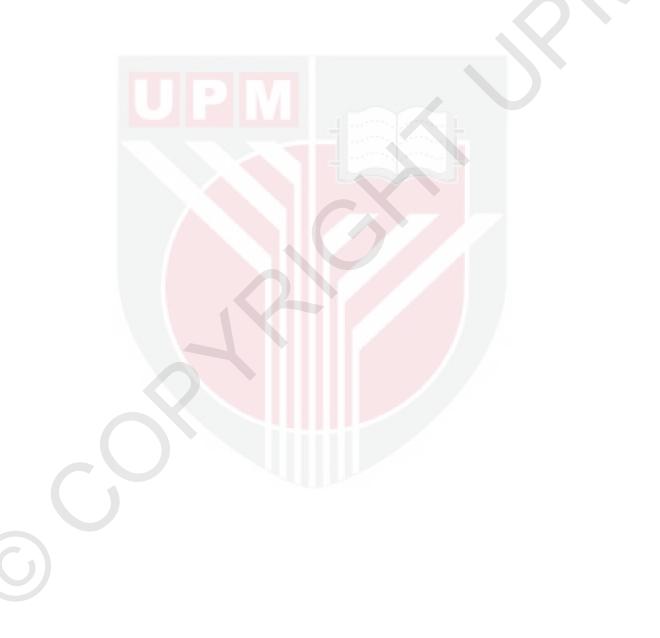
### 1.5 Main objective

The main objective of this work was to develop an effective genotype matched live attenuated Newcastle disease vaccine using reverse genetics technology.

#### **1.6** Specific objectives

- 1. To construct and express functional helper plasmids for the recovery of modified NDV strain IBS025/13 (mIBS025).
- 2. To design, synthesise and rescue a recombinant attenuated NDV mIBS025 entirely from cloned cDNA.

- 3. To biologically characterize the genetic stability and pathogenicity of the recombinant NDV mIBS025, in specific-pathogen-free embryonated eggs and one-day old chicks
- 4. To evaluate the protective immunity and safety induced by the recombinant virus (mIBS025) against challenge with virulent genotype VII NDV isolate in specific-pathogen-free chicken.



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