



***TRANSCRIPTOME PROFILE OF 28-4+ INTRAEPITHELIAL  
LYMPHOCYTE NATURAL KILLER CELLS OF CHICKEN INFECTED BY  
VIRULENT INFECTIOUS BURSAL DISEASE VIRUS***

**BOO SOOK YEE**

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**By**

**BOO SOOK YEE**

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

**December 2019**

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## **DEDICATION**

*This thesis is dedicated  
to my husband and parents  
for their endless love and support*



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

**TRANSCRIPTOME PROFILE OF 28-4<sup>+</sup> INTRAEPITHELIAL LYMPHOCYTE  
NATURAL KILLER CELLS OF CHICKEN INFECTED BY VIRULENT  
INFECTIOUS BURSAL DISEASE VIRUS**

By

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**December 2019**

**Chairman : Associate Professor Noorjahan Banu Binti Mohamed Alitheen, PhD**  
**Faculty : Institute of Bioscience**

Infectious bursal disease (IBV) caused by infectious bursal disease virus (IBDV), has been infecting chicken flocks for more than fifty years exerting a considerable economic impact to the global poultry industry. The virus infection response by chicken natural killer (NK) cells has been inadequately studied due to the limited monoclonal antibodies that are available. Development of 28-4 monoclonal antibody has allowed the identification of chicken intraepithelial lymphocytes (IEL) NK cells. However, the role of IEL-NK cell and its involvement in initiating the innate immune response in fighting the very virulent IBDV (vvIBDV) are still unknown. Therefore, the objective of this study was to identify the transcriptome profile of uninfected CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells and identify the differential expressed genes and small RNAs (sRNAs) in response to vvIBDV infection at 1 and 3 days post infection (dpi). In this study, the chicken was infected by 10<sup>3</sup> mean egg lethal dosage (ELD<sub>50</sub>) of vvIBDV strain 0081 for 1 and 3 days. The CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells were isolated from duodenum of the infected chicken. Then, the total RNA was isolated from CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells and used for library preparation, mRNA and sRNA sequencing, and followed by differential expression and pathway analysis. The RNA sequencing (RNA-Seq) result was validated by NanoString and sRNA sequencing result was validated by RT-qPCR. A total of 12,141 genes were expressed in uninfected chicken IEL-NK cells and most of the genes with high expression are involved in metabolic pathway whereas most of the low expressed genes involved in cytokine-cytokine receptor pathway. There is a total of 1,115 and 1,266 genes differentially expressed (DE) at 1 and 3 dpi respectively. The DE genes at 1 dpi mainly involved in DNA replication, cell cycle, apoptosis whereas the DE genes at 3 dpi involved in inflammation, antiviral response and interferon stimulation. For sRNA sequencing, there are 35 and 16 sRNAs were differentially expressed at 1 and 3 dpi, respectively. The SNORD101, gga-miR-222a and gga-miR-221-3p were up-regulated on Day 1 and 3 whereas gga-miR-30a-50, gga-miR-142-5p, gga-miR-32-5p and gga-miR-146b-5p were down-regulated on both days.

Meanwhile, *GAPDH* and *YWHAZ* were the most stably expressed genes in the chicken CD3<sup>-</sup>/28.4<sup>+</sup> IEL-NK cells infected by vvIBDV according to the RT-qPCR result. In conclusion, the immunity of chicken CD3<sup>-</sup>/28.4<sup>+</sup> IEL-NK cells was suppressed at 1 dpi and the proliferation of NK cells was an act of a preparation step for the defense against virus at 2 or 3 dpi. At 3 dpi, the innate immune response was activated as several genes involved in inflammation, antiviral response and recruitment of NK cells to infected area were up-regulated. This is the first study which examined the whole transcriptome profile of chicken NK cells towards IBDV infection, which provides a better insight into the early immune response of chicken NK cells.



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

**KAJIAN EKSPRESI GEN MENGENAI TINDAK BALAS IMUN INAT SEL LIMFOSIT INTRAEPITHELIAL PEMBUNUH SEMULAJADI AYAM 28-4<sup>+</sup> TERHADAP VIRUS PENYAKIT BURSAL BERJANGKIT YANG SANGAT VIRULEN**

Oleh

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Penyakit bursal berjangkit (IBD) yang disebabkan oleh virus penyakit bursal berjangkit (IBDV) telah menjejaskan ekonomi industri ayam selama 50 tahun. Penyelidikan yang berkaitan dengan tindak balas sel pembunuh semulajadi (NK) terhadap jangkitan virus dalam ayam adalah terhad kerana antibodi monoklonal yang sasar pada sel NK di ayam adalah terhad. Penghasilan antibodi monoklonal 28.4 telah membenarkan pengenalpastian untuk sel limfosit intraepitelium (IEL) NK dalam ayam. Walau bagaimanapun, peranan dan penglibatan untuk IEL-NK sel dalam tindak balas imun semula jadi di ayam selepas dijangkiti dengan IBDV amat virulen (vvIBDV) adalah tidak diketahui. Objektif kajian ini adalah untuk mengenalpasti profil transkrip untuk sel IEL-NK 28.4<sup>+</sup> / CD3<sup>-</sup> dalam ayam yang tidak dijangkiti dan mengenalpasti gen dan RNA yang kecil (sRNAs) yang di ekspresi berbeza sebagai tindak balas terhadap vvIBDV selepas dijangkiti selama satu and tiga hari. Ayam berjangkit dengan vvIBDV UPM0081 menggunakan dos mematikan telur sebanyak 10<sup>3</sup> selama satu dan tiga hari. Sel CD3<sup>-</sup>28.4<sup>+</sup> IEL-NK ayam telah terpencil dari bahagian duodenum untuk ayam yang dijangkiti. Selepas itu, jumlah RNA telah dikeluarkan dari CD3<sup>-</sup>28.4<sup>+</sup> IEL-NK sel ayam dan digunakan untuk persediaan perpustakaan, penjujukan RNA (RNA-Seq) dan sRNA diikuti dengan analisis perbezaan transkrip dan laluan. Keputusan RNA-Seq telah disahkan oleh NanoString dan keputusan penjujukan sRNA telah disahkan oleh tindak balas rantaian polimer masa sebenar. Sebanyak 12,141 gen telah dinyatakan di sel CD3<sup>-</sup>28.4<sup>+</sup> IEL-NK yang tidak dijangkit. Kebanyakan gen dengan ekspresi tinggi terlibat dalam laluan metabolik manakala gen yang ekspresi rendah terlibat dalam laluan reseptor sitokin. Gen yang berjumlah 1,115 dan 1,266 ada perbezaan ekspresi pada hari yang pertama dan ketiga selepas berjangkit dengan vvIBDV. Gen dengan perbezaan ekspresi pada hari yang pertama terlibat dalam replikasi DNA, kitaran sel dan apoptosis manakala gen dengan perbezaan ekspresi pada hari yang ketiga terlibat dalam keradangan, tindak balas antivirus dan rangsangan interferon. Kajian dari

penjujukan sRNA menunjukan 35 dan 16 sRNAs dengan perbezaan ekspresi selepas berjangkit dengan vvIBDV selama satu dan tiga hari. Transkripsi gen untuk SNORD101, gga-miR-222a dan gga-miR-221-3p telah dipertingkatkan sedangkan transkripsi gen untuk gga-miR-30a-50, gga-miR-142-5p, gga-miR-32-5p dan gga-miR-146b-5p telah dikurangkan selepas berjangkit dengan vvIBDV selama satu dan tiga hari. Sementara itu, GAPDH dan YWHAZ adalah gen yang paling stabil untuk digunakan sebagai gen rujukan di CD3<sup>+</sup>28.4<sup>+</sup> sel pembunuh semulajadi di ayam berdasarkan hasil dari tindak balas rantaian polimer masa sebenar. Kesimpulannya, imuniti untuk CD3<sup>+</sup>28.4<sup>+</sup> sel pembunuh semulajadi di ayam ditindas pada hari yang pertama selepas berjangkit dengan vvIBDV. Percambahan sel NK bertindak sebagai langkah persediaan untuk pertahanan terhadap virus bagi hari yang kedua or ketiga. Selepas dijangkiti selama tiga hari, tindak balas keimunan inat telah diaktifkan kerana transkripsi gen yang terlibat dalam keradangan, tindak balas antivirus dan penghantaran sel NK ke kawasan yang dijangkiti telah dipertingkatkan. Ini adalah kajian pertama yang memeriksa keseluruhan profil transkrip untuk sel CD3<sup>+</sup>28.4<sup>+</sup> IEL-NK dalam ayam yang dijangkiti dengan vvIBDV dan kajian ini memberikan pengetahuan yang lebih mendalam berkenaan tindakbalas imun awal oleh sel NK ayam.



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This thesis was submitted to the Senate of 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

$\mu\text{L}$	Microlitre
$\mu\text{M}$	Micromolar
AIV	Avian Influenza virus
ALV-J	Avian Leukosis virus J
ANOVA	One-way analysis of variance
BCL	Base calling
BCR	B-cell receptor
<i>BF</i>	Bursa of Fabricius
<i>BM-DC</i>	Bone marrow-derived dendritic cell
<i>bp</i>	Base pairs
BRSV	Bovine respiratory syncytial virus
BSL-2	Biosafety level-2
CASP	Caspase
CCL	CC chemokine ligand
cDNA	Complementary deoxyribonucleic acid
chBM-DCs	Bone marrow-derived DCs
<i>CHIR</i>	Chicken Ig-like receptors
<i>CRD</i>	Carbohydrate recognition domain
<i>CRT</i>	Cyclic reversible termination
$C_q$	Threshold cycle
CTLD	C-type lectin-like domain
CV%	Coefficient of variation percentage

DC	Dendritic cell
DE	Differential expressed
DEPC	Diethyl Pyrocarbonate
DNA	Deoxyribonucleic acid
ddNTP	Dideoxynucleotide triphosphates
dNTP	Deoxynucleotide triphosphates
dpi	Day-post-infection
dsDNA	Double-stranded deoxyribonucleic acid
dsRNA	Double-stranded RNA
DTT	Dithiothreitol
ELD <sub>50</sub>	Mean Egg Lethal Dosage
FDR	False discovery rate
FFPE	Formalin-Fixed Paraffin-Embedded
<i>gDNA</i>	Genomic DNA
GEO	Gene Expression Omnibus
GO	Gene Ontology
HPgV	Human Pegivirus
HS	High sensitivity
HT1 buffer	Hybridization buffer
HTLV	Human T-cell lymphotropic virus
HVT	Herpes virus of turkey
<i>IACUC</i>	Institutional Animal Care and Use Committee
IBD	Infectious bursal disease
IBDV	Infectious bursal disease virus

<i>IBS</i>	Institute of BioScience
<i>Icx</i>	Immune complex
IDT	Integrated DNA Technologies
IEL-NK	Intraepithelial lymphocytes-natural killer
<i>IELs</i>	Intraepithelial lymphocytes
IFITs	Tetratricopeptide repeats
IFNAR	Interferon alpha receptor
IFNGR	Interferon gamma receptor
IFN-I	Type I interferons
IFN- $\gamma$	Interferon-gamma
IgM+	Immunoglobulin M
Igs	Immunoglobulins
<i>IHC</i>	Immunohistochemistry
IL	Interleukin
IPNV	Infectious pancreatic necrosis virus
ISGs	IFN-stimulated genes
ITIM	Immunoreceptor tyrosine-based inhibitory motifs
ITSM	Immunoreceptor tyrosine-based switch motifs
JAK-STAT	Janus activated kinase-signal transducer and activation of transcription
KEGG	Kyoto Encyclopedia of Genes and Genomes
KIRs	Killer cell immunoglobulin-like receptors
LPS	Lipopolysaccharide
M value	Expression stability value



<i>MACS</i>	Magnetic Activated Cell Sorting
<i>MAPK</i>	Mitogen-activated protein kinase
<i>MCM</i>	Minichromosome maintenance
<i>MDA</i>	Maternal-derived antibodies
<i>MHC</i>	Major histocompatibility complex
<i>miRNA</i>	microRNA
<i>MNC</i>	Mononuclear cell
<i>mRNA</i>	Messenger ribonucleic acid
<i>NaOH</i>	Sodium hydroxide
<i>NCBI</i>	National Centre for Biotechnology Information
<i>NDV</i>	Newcastle disease virus
<i>NFκB</i>	Nuclear factor-κB
<i>ng/μL</i>	Nanogram/microlitre
<i>NGS</i>	Next-Generation Sequencing
<i>NK</i>	Natural killer
<i>NKC</i>	Natural killer gene complex
<i>nM</i>	Nanomolar
<i>NO</i>	Nitric oxide
<i>nts</i>	nucleotides
<i>ORFs</i>	Open reading frames
<i>PAGE</i>	Polyacrylamide gel electrophoresis
<i>PARP</i>	Poly(ADP-ribose) polymerase
<i>PBS</i>	Phosphate buffer saline
<i>PCA</i>	Principal Component Analysis

PCR	Polymerase Chain Reaction
<i>PE</i>	Phycoerythrin
<i>PF</i>	Passing filter
pg	Picogram
<i>pM</i>	Picomolar
<i>PRRs</i>	Pattern-recognition receptors
<i>PRRSV</i>	Porcine reproductive and respiratory syndrome virus
<i>PWBC</i>	Peripheral white blood cells
RCC	Reporter code count
RdRp	RNA-dependent RNA polymerase
<i>RIN</i>	RNA integrity number
ROS	Reactive oxygen species
<i>RPKM</i>	Reads per kilobase of exon per million reads
<i>RPMI</i>	Roswell Park Memorial Institute
rRNA	Ribosomal Ribonucleic acid
RT	Room temperature
RT-PCR	Reverse transcription polymerase chain reaction
RT-qPCR	Quantitative Reverse Transcription PCR
SAMHD1	Sterile alpha motif and HD-domain-containing protein 1
SBL	Sequencing by ligation
SBS	Sequencing by synthesis
SLAM	Signalling lymphocytic activation molecule
SNA	Single-nucleotide addition
snoRNA	Small nucleolar RNA

SPF	Specific-pathogen-free
SPP1	Secreted phosphoprotein 1
sRNA	Small RNA
ssDNA	Single stranded DNA
TLRs	Toll-like receptors
T <sub>m</sub>	Melting temperature
TNF- $\alpha$	Tumour necrosis factor-alpha
TNFRSF4	Tumour necrosis factor receptor superfamily member 4
UPM	Universiti Putra Malaysia
V value	Pairwise variation value
vvIBDV	Very virulent IBDV
$\mu$ g	Microgram

# CHAPTER 1

## INTRODUCTION

### 1.1 Background

Infectious bursal disease (IBD) is a contagious and immunosuppressive viral disease caused by IBD virus (IBDV), which has negative impacts on the poultry industries, causing major economic losses (Berg, 2000). IBDV is categorized as an Avibirnavirus which belongs to the Birnaviridae family, which consists of two segments of double-stranded ribonucleic acid (dsRNA) (A and B) (Müller et al., 1979a). The segment A (3.17 kb) encodes the non-structural viral protein, VP5, and a polyprotein precursor, in which after the post-translational cleavage would produce the VP2, VP3 and VP4 structural proteins (Mahgoub, 2012). The segment B which is a shorter fragment (2.8 kb) than the segment A encodes VP1, an RNA-dependent RNA polymerase (RdRp) which is involved in transcription and replication of the virus and thus, plays a critical role in determining the virulence characteristic of the virus (Coulibaly et al., 2005; Delmas et al., 2005).

IBDV isolates are categorized into subset of serotypes; serotype-1 and serotype-2. Serotype-1 is classified as highly virulent IBDV or very virulent IBDV (vvIBDV) and usually associated with typical clinical diseases such as lesion in bursal organ and even mortality, as a result of chronic infection (Mahgoub, 2012). On the other hand, serotype-2 is a low pathogenic IBDV which is commonly used as vaccine (Berg, 2000). The IBDV infection starts through the oral route, followed by viral replication inside the duodenum, caecum, and jejunum, which targets the avian immune cells for example the macrophages which capable of destroying pathogens and apoptotic cells, and the lymphoid cells at these organs (Muller et al., 1979). Afterwards, IBDV spreads to the Bursa of Fabricius (BF), an organ which IBDV rapidly replicates and attacks the undeveloped B lymphocytes, which compromises the humoral immune responses of the infected avian (Berg, 2000).

The clinical severity and mortality caused by the vvIBDV toward chicken are determined based on the existing inherited maternal antibodies, age and also genetic background for chicken (Sharma et al., 2000). Acute IBDV infections (about 2 to 3 days of incubation period) could cause the animals to be exhausted, dehydrated, prostrated, and suffered from aqueous diarrhoea as well as ruffled feathers. All these severe clinical signs lead to mortality of the chicken on the third day of infection. Any surviving chicken would recover from the infection and back to normal health condition after 5 to 7 days (Ingrao et al., 2013).

The innate immune system provides the first layer of defence against pathogen, bacteria, and virus. It is interesting to know how the chicken immune cells would

respond to the vvIBDV infection as the first three days post-infection are considered as incubation period which with faster replication of virus in affected cells (Ingrao et al., 2013). It is evident that virus infections can induce aberrant cytokine production by regulating the signalling pathway. Also, virus impacts cells of the innate immune system which express essential molecules namely pattern recognition receptors (PRRs), such as Toll-like receptors (Kimura et al., 2013). Immune cells grouped in the innate immune response are dendritic cells, macrophage and natural killer (NK) cells (Portou et al., 2015).

NK cells are a group of lymphocytes that play a critical role in the early defence against pathogens such as parasites, bacteria and viruses (Jansen et al., 2010; Lanier, 2005; Trinchieri, 1989). The primary role of NK cells is to provide an initial crucial defense against pathogens, usually within a period from 0 to 5 days while the adaptive immune system is activating (Yokoyama, 2003). NK cells secrete major inflammatory cytokines like interferon-gamma (IFN- $\gamma$ ) and tumour necrosis factor-alpha (TNF- $\alpha$ ) to activate macrophage, dendritic cells and T cells (Mandal and Viswanathan, 2015; Vivier et al., 2008). Mammalian NK cells have been intensively characterized in previous studies whereas the studies on avian NK cells are still limited (Neulen et al., 2015; Straub et al., 2013).

The first identified and characterised avian NK cell was a CD3<sup>+</sup>CD8 $\alpha$ <sup>+</sup> population (Göbel et al., 1994). Later, a specific mucosal NK cell population has been isolated from intestinal intraepithelial and was named intraepithelial lymphocytes-natural killer (IEL-NK) cells (Göbel et al., 2001). A monoclonal antibody known as 28-4 was developed in 2001 to specifically targeting the IEL-NK cells namely, chicken CD25 (Göbel et al., 2001; Walliser & Göbel, 2018). Notably, these chicken IEL-NK cells showed cytotoxicity towards tumour target and were expected to play an important role in mucosal immune system (Göbel et al., 2001).

There are multiple studies on the messenger ribonucleic acid (mRNA) expression profile of chicken B cells (Quan et al., 2017), macrophages (Rasoli et al., 2015), dendritic cells (Yasmin et al., 2015), and embryonic fibroblast cells (Wong et al., 2007) but the study on chicken IEL-NK cells is limited. Transcriptomic and functional evaluation of chicken NK cells are advancing at a much slower pace when compared to the mammalian NK cells due to the difference of genomic organization between chicken and human or mice and the limited choice of monoclonal antibodies. The 28-4 monoclonal antibody was being used for the isolation of IEL-NK cells isolation in Jahromi et al., (2018) study. In this study, chicken infected with the vvIBDV strain resulted in the reduced activation of the IEL-NK cells as the virus caused the down-regulation of the expression of *CD69*, *CHIR-ABI*, and *NK-lysin* receptors, especially at 1 day-post-infection (dpi). This is the first expression study on NK receptors from the isolated chicken IEL-NK cells in response to vvIBDV but notably, with limited number of genes being tested. Therefore, it is important to study the transcriptome of chicken IEL-NK cells to understand the pathways and genes involved in the chicken innate immune response following the infection by vvIBDV.

microRNAs (miRNAs) play a significant role for regulation of mRNA expression and the gene transcription, particularly in the immune cells that are involved in the defence against vvIBDV infection. Therefore, it is of great importance to understand the miRNAs expression upon infection by vvIBDV. miRNAs are small non-coding RNA molecules consisting of 21 to 25 nucleotides (nts), that are able to trigger gene silencing via translational repression or target degradation (Bartel, 2009; Eulalio et al., 2009). Based on the latest update until October 2018, there are 882 precursors and 1232 mature miRNA in miRbase 22.1 for avian. The expression of miRNA in the chicken has been shown in previous studies to be involved in several processes, such as embryo and germ cell development (Darnell et al., 2006; Hick et al., 2008; Rathjen et al., 2009; Lee et al., 2011), immune organ function (Hicks et al., 2009), and disease (Tian et al., 2012; Wang et al., 2013; Hong et al., 2014). However, there are no current reports describing the miRNA transcriptome changes associated with vvIBDV infected IEL-NK cells.

## **1.2 Problem Statements and Hypothesis**

The role of IEL-NK cell and its involvement in initiating the innate immune response in fighting the vvIBDV infection are still unknown. To understand the transcriptome changes of the IEL-NK cells, the mRNA and miRNA from the uninfected and vvIBDV-infected chickens were examined by high throughput sequencing using Illumina technology. It was hypothesized that most of the genes in cytokine-cytokine receptor interaction and Toll-like receptor signaling pathway are either activated or repressed after the vvIBDV infection at 1 and 3 dpi. The cytokines, chemokines and interferon were expected to play important roles in the innate immune response of IEL-NK cells. Lastly, miRNA could regulate the expression levels of genes as one of the strategies to defend the host in fighting against vvIBDV infection.

## **1.3 Objectives**

This is the first comprehensive study on the whole transcriptome profile in chicken CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells infected by vvIBDV by utilizing the advance technologies such as NGS and NanoString. The four specific objectives of this study are as follows:

- 1) To identify and analyse the transcriptome profile of the uninfected CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells from chickens;
- 2) To identify differential expressed genes and pathways in CD3<sup>+</sup>/28.4<sup>+</sup> IEL-NK cells in response to vvIBDV infection;
- 3) To identify miRNAs in IEL-NK cells of chickens infected by vvIBDV; and
- 4) To validate the differential expression of genes using the RT-qPCR and NanoString nCounter System.

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