

# **UNIVERSITI PUTRA MALAYSIA**

ISOLATION, IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF FELINE CORONAVIRUS IN MALAYSIA

AMER KHAZAAL SALIH AL-AZAWY

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## ISOLATION, IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF FELINE CORONAVIRUS IN MALAYSIA



Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, In Fulfilment of the Requirement for the Degree of Doctor of Philosophy

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# DEDICATED WITH LOVE AND GRATITUDE TO: THE SPIRIT OF MY FATHER AND MOTHER

MY BELOVED WIFE...JINAN, WHO WAS THE SOURCE OF INSPIRATION, UNDERSTANDING AND ENCOURAGEMENT THROUGHOUT MY STUDY

LOVING SONS, YESSER AND HYDER LOVING DAUGHTERS, SARAH AND RAZ FOR THEIR ENDLESS PATIENCE AND UNDERSTANDING

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirements of the degree of Doctor of Philosophy

# ISOLATION, IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF FELINE CORONAVIRUS IN MALAYSIA

By

AMER KHAZAAL SALIH

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Chairman:Associate Professor Siti Suri Arshad, PhDFaculty:Faculty Veterinary Medicine

Feline infectious peritonitis virus (FIPV) and feline enteric coronavirus (FECV) are coronaviruses causing disease in cats. FIPV is a highly fatal and immune-mediated pyogranulomatous disease, whereas FECV is asymptomatic and a subclinical or mild enteric infection. Both FIPV and FECV are further subdivided into serotypes I and II.

Cases of FIP occur in young and adult cats with varying degree of severity. In Malaysia, Feline coronavirus (FCoV) is prevalent where 100% of cats in catteries developed antibodies against the feline coronavirus. However, 84% of cats kept in catteries and shelters, were found to have viral genome of feline coronavirus in their feces. FIP is believed to be mutated from FECV and the virus has tropism towards the macrophages. Although many cats can be infected with FCoV, only 10% will develop FIP disease. There is no effective vaccine to control the disease because immunized cats are found to be more susceptible to infection than unvaccinated cats due to the antibody-dependent enhancement (ADE) phenomena. Although the FCoV is prevalent in Malaysia, the virus causing the disease has not been characterized and serotype. The study was conducted to isolate, identify, characterize and type the local feline coronavirus. The local isolates and two reference strains of FCoV were compared with respect to their biological properties, morphology and genome homology. A total of 42 cats clinically suspected of having FIP disease were obtained during the 4 years period (2007-2010) and were designated as UPM1C/07 to UPM42C/10. Affected cats showing respiratory distress with distended abdominal cavity were sampled. Ascites fluid or tissues from cat dying from FIP were screened for FCoV by a one-step reverse transcriptase polymerase chain reaction (RT-PCR) assay and adapted in Crandell feline kidney (Crfk) and Felis catus whole foetus (Fcwf-4) cell cultures. About 95% (40/42) of them were positive by virus isolation and confirmed by RT-PCR. Upon infection into two cell lines, infected cells showed cytopathic effect (CPE) characterised by giant cells, ballooning and detachment of infected cells. Fcwf-4 cell line provides more suitable growth conditions for local Representative of three FCoV isolates namely the UPM5C/O8, isolate FCoVs. UPM11C/08 and UPM24C/09 were clone purified by limiting dilution and were used for subsequent studies. Identification of the virus isolates was conducted by indirect immunofluorescent (IIF), indirect immunoperoxidase (IIP), haematoxylin and eosin staining (H&E) and transmission electron microscope (TEM). The study showed that FCoV multiply in the cytoplasm of infected cells. The virus particles possessed the characteristic of coronavirus with spherical shapes and surrounded by club shaped peplomers indicative of typical coronavirus.

The determination of the serotypes of local FCoV and their phylogenetic relatedness was performed by analyzing their S gene region using published primers. Following

analyses, 97.5% and 2.5% of local FCoV isolates belonged to serotypes I and II, respectively. Phylogenetic analysis performed on selected 12 FCoV type I local isolates on the S region showed that the homology amongst them ranged from 92.3-100% and decreased to 90% with reference viruses. Whereas the local FCoV type II has 97.5-99% homology with reference strains. Malaysian FCoV isolates fall in 3 clusters where 2 clusters comprise most of type I which are closer to the USA, Netherlands, UK, Japan and Taiwan isolates, and third cluster comprises the type II which is in the group of reference viruses of USA and Italy.

In conclusion, this is the first detailed study on isolated local feline coronavirus in an attempt to adapt the viruses in *vitro* and characterize them. About 95% (40/42) of cats that were naturally infected with feline coronavirus have the viral genome in their body excretion. The isolated viruses were adaptable in cell culture and induce of cytopathic effect. FCoV type I was highly prevalent amongst the local cats.

Key word: Feline coronavirus, Crfk, Fcwf-4, Indirect immunofluorescent, Indirect immunoperoxidase, H&E, RT-PCR, Phylogenetic analysis.

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## PENGASINGAN, PENGENALPASTIAN DAN PENCIRIAN MOLEKUL KORONAVIRUS KUCING DI MALAYSIA

Oleh

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Virus kucing berjangkit peritonitis (FIPV) dan koronavirus kucing enterik (FECV) adalan penyebab penyakit kucing. FIPV menyebabkan pyogranulomatous penyakit yang sangat fatal dan imun-pengantara, manakala FECV berupa asimptomatik dan jangkitan enterik subklinikal atau ringan. Kedua-dua FIPV dan FECV terbahagi kepada serotip I dan II. Kes-kes FIP berlaku pada kucing muda dan dewasa dengan pelbagai tahap keterukan. Di Malaysia, FCoV tersebar luas di mana 100% daripada kucing dalam catteri didapati mempunyai antibodi terhadap koronavirus kucing. Walau bagaimanapun, kucing di catteri dan tempat perlindungan, 84% didapati mempunyai genom virus koronavirus kucing dalam najis mereka. FIP dipercayai bermutasi dari FECV dan virus mempunyai tropisma pada sel makrofaj. Walaupun banyak kucing boleh dijangkiti dengan FCoV, hanya 10% akan mendapat penyakit FIP.Tiada vaksin yang berkesan untuk mengawal penyakit kerana kucing yang menerima imunisasi lebih terdedah

kepada jangkitan daripada kucing tak vaksin disebabkan oleh fenomena ADE.Walaupun FCoV adalah lazim di Malaysia, virus yang menyebabkan penyakit ini tidak di ciri dan serotip. Kajian ini telah dijalankan untuk mengasing, menciri dan menaip koronavirus kucing tempatan. Isolat tempatan dan dua strain rujukan daripada FCoV dibanding dengan merujuk kepada sifat-sifat morfologi biologi, dan homologi genom. Sebanyak 42 kucing berpetanda klinikal yang disyaki mempunyai penyakit FIP diperolehi semasa tempoh 4 tahun (2007-2010) dan telah dijujukkan sebagai UPM1C/07 hingga UPM42/10. Kucing berpenyakit menunjukkan masalah pernafasan dengan perut buncit disampel. Cecair ascites atau tisu dari kucing yang mati sebab FIP di saring untuk FCoV dengan esei RT-PCR dan disesuai dalam sel kultura Crfk dan Fcwf-4. Kira-kira 95% (40/42) sampel positif dengan pengasingan virus dan disahkan oleh RT-PCR. Jangkitan kepada sel menunjukkan kesan cytopathic (CPE) yang dicirikan oleh sel gergasi, membulat dan tanggal. Fcwf-4 sel didapati lebih sesuai untuk percambahan FCoVs dalam mengasingkan isolate tempatan. Tiga FCoV klon UPM5C/08, UPM11C/08 dan UPM24C/09 yang ditulenkan secara pencairan terhad telah digunakan untuk pengkajian berikutnya. Pencirian isolat virus telah dijalankan melaui teknik immunopendafloran tidak langsung (IIF), immunoperoxidase secara tidak langsung (IPP), H & E dan TEM. Kajian menunjukkan bahawa FCoV membiak di dalam sitoplasma sel yang dijangkiti. Zarah virus mempunyai pencirian koronavirus dengan bentuk sfera dan dikelilingi oleh peplomers. . Penentuan serotip FCoV tempatan dan filogenetik keberhubungan mereka dilakukan dengan menganalisis rantau gen S. Berikutan analisis filogeni, 97.5% dan 2.5% daripada FCoV tempatan adalah serotip I dan II masingmasing. Filogenetik analisis yang dilakukan ke atas 12 FCoV tempatan pada rantau S menunjukkan bahawa homologi di kalangan mereka antara 92.3-100% dan menurun

kepada 90% dengan virus rujukan. Manakala jenis II FCoV tempatan mempunyai homologi 97.5-99% dengan strain rujukan. Isolat FCoV Malaysia terbahagi dalam 3 kelompok dimana 2 kelompok terdiri daripada jenis I yang kebanyakannya berasal dari Amerika Syarikat, Belanda, UK, Jepun dan Taiwan, dan kelompok ketiga terdiri daripada jenis II yang dalam kumpulan virus rujukan Amerika syarikat dan Itali. Kesimpulannya, ini adalah kajian tempatan pertama yang terperinci mengenai koronavirus kucing dalam usaha untuk mengasingkan, penyesuaian vitro dan pencirian. Kira-kira 95% (40/42) kucing yang dijangkiti secara semulajadi mempunyai genom koronavirus kucing dalam perkumuhan badan mereka. Virus terpencil menyesuaikan diri dalam sitoplasma sel dan meransang kesan sitopatik.

Kata kunci: koronavirus kucing, Crfk, Fcwf-4, immunofluorescent tidak langsung, immunoperoxidase tidak langsung, H & E, RT-PCR, analisis filogenetik.

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I certify that a Thesis Examination Committee has met on 13 December, 2011 to conduct the final examination of Amer Khazaal Salih Alazawy on his Doctor of philosophy thesis entitled "ISOLATION, IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF FELINE CORONAVIRUS IN MALAYSIA" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U. (A) 106] 15 March 1998. The Committee recommends that the student be awarded the Doctor of Philosophy.

Members of the Thesis Examination Committee were as follows:

### Y. Bhg. Professor Tengku Azmi bin Tengku Ibrahim, PhD

Faculty of Veterinary Medicine Universiti Putra Malaysia (Chairman)

### Associate Professor Dr. Hassan b Hj Mohd Daud, PhD

Faculty of Veterinary Medicine Universiti Putra Malaysia (Internal Examinar)

#### Associate Professor Dr. Jasni bin Sabri, PhD

Faculty of Veterinary Medicine Universiti Putra Malaysia (Internal Examinar)

## Y. Bhg. Professor Peter J.M. Rottier, PhD

Department of Infections Diseases and Immunology Veterinary University Utrecht University (External Examiner) Netherlands

### SEOW HENG FONG, PhD

Professor and Deputy School of Graduate Studies Universiti Putra Malaysia

Date:

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

# Siti Suri Arshad, PhD

Assoc. Prof Faculty of Veterinary Medicine Universiti Putra Malaysia (Chairman)

## Mohd Hair Bejo, PhD Professor Faculty of Veterinary Medicine Universiti Putra Malaysia (Member)

## Abdul Rahman Omar, PhD Professor Faculty of Veterinary Medicine Universiti Putra Malaysia (Member)

## **BUJANG BIN KIM HUAT, PhD**

Professor and Dean School of Graduate Studies Universiti Putra Malaysia

Date:

## **DECLERATION**

I declare that the thesis is my original work except for 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 any other institution.



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- 6.3 Screening of FCoVs adapted cell culture isolates to detect FCoV type I
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Reference virus type II FECV 79-1683; Lane 6: Reference virus type II FIPV DF2.

- 6.6 Sensitivity studies on RT-nPCR assay. (A) Using specific primer pairs fecv1bnf /fecv1bnr to detect the S region of FCoV type I. The primer pairs amplify the target region with PCR product of 183bp. Detection limit was done by performing nested PCR assay on ten-fold dilution of RNA extracted from FIPV NW1 type I reference virus. The 1.5 agarose gel was electrophoresed and stained with 0.5µg/ml ethidium bromide. Lane 4 NTC: Non-template control; Lane 3: 10 ng of RNA; Lane 2: 100 ng RNA; Lane 1: 1µg RNA. (B) Using specific primer pairs fecv2bnf / fecv2bnr to detect the S region of FCoV type II. The primer pairs amplify the target region with PCR product of 151bp. Detection limit was done by performing nested PCR assay on ten-fold dilution of RNA extracted from FIPV DF2 type II reference virus. The 1.5 agarose gel was electrophoresed and stained with 0.5µg/ml ethidium bromide.Lane 4: NTC: Non-template control; Lane 3: 10 ng of RNA; Lane 2: 100 ng RNA; Lane 1: 1µg RNA.
  - Sequence Identity Matrix of partial S gene of FCoV type I.
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Note: The names were truncated to maximum 5 characters. The value could be converted to percentage by multiplying it with 100.Legend: ID= identical, 1=UPM2C, 2= UPM5C, 3= UPM11C, 4= UPM13C, 5= UPM14C, 6= UPM22C, 7= UPM24C, 8= UPM25C, 9= UPM26C, 10= UPM27C, 11= UPM28C, 12= UPM35C, 13= Black, 14= UU19, 15= RM, 16= UU31, 17= UU10, 18= UCD11a, 19= UU8, 20= UU4, 21= UU7, 22= NTU2, 23= UU34, 24= FCoV/S, 25= UCD13, 26= CIJe, 27= UCD5.

6.8

6.7

Sequence nucleotide difference of partial S gene of FCoV type I. Twenty seven FCoV type I were compared: Local isolates UPM2C/07, UPM5C/08, UPM11C/08, UPM13C/08, UPM14C/09, UPM22C/09, UPM24C/09, UPM25C/09, UPM26C/09, UPM27C/09, UPM28C/09, UPM35C/10 are shaded and corresponding reference sequences from GenBank: Black, UU19, RM, UU31, UU10, UCD11a, UU8, UU4, UU7, NTU2, UU34, FCoV/S, UCD13, CIJe, UCD5. Nucleotides differences among local FCoV type I isolates 0-21, while nucleotides

difference increased to 1-29 when compare with reference sequences strains FCoV. Note: The names were truncated to maximum 5 characters. The value could be converted to percentage by multiplying it with 100.Legend: ID= identical, 1=UPM2C, 2= UPM5C, 3= UPM11C, 4= UPM13C, 5= UPM14C, 6= UPM22C, 7= UPM24C, 8= UPM25C, 9= UPM26C, 10= UPM27C, 11= UPM28C, 12= UPM35C, 13= Black, 14= UU19, 15= RM, 16= UU31, 17= UU10, 18= UCD11a, 19= UU8, 20= UU4, 21= UU7, 22= NTU2, 23= UU34, 24= FCoV/S, 25= UCD13, 26= CIJe, 27= UCD5.

- 6.9 Sequence Identity Matrix of partial S gene of FCoV type II. Six FCoV were compared: Local isolate UPM8C/08 and corresponding reference sequences from GenBank, FIPV 79- 1146, FIPV complete genome (AY994055), FIPV DF2, FIPV/E2 and CCV/NTU. The local isolate show identical in the range of 97.5-100% with FIPV 79-1146, FIPV complete genome with accession number (AY994055), FIPV DF2, FIPV/E2, but show 77.6-79% identical with CCV/NTU. Note: The names were truncated to maximum 5 characters. The value could be converted to percentage by multiplying it with 100.
- 6.10 Sequence difference count matrix of partial S gene of FCoV type II. Six FCoV type II were compared: Nucleotides difference count matrix among local isolate FCoV type II UPM8C/08 and corresponding reference sequences from GenBank, FIPV 79- 1146, FIPV complete genome (AY994055), FIPV DF2, FIPV/E2 were (2-5 nt), while nucleotides difference count matrix increased (45-48 nt) when compared with CCV/NTU.

Note: The names were truncated to maximum 5 characters. The value could be converted to percentage by multiplying it with 100.

6.11 Sequence Identity Matrix of partial S gene of type I and II FCoV. Twenty seven FCoVs were compared: Local isolates type I, UPM2C/07. UPM5C/08. UPM11C/08. UPM13C/08. UPM14C/09. UPM22C/09, UPM24C/09, UPM25C/09, UPM26C/09, UPM27C/09, UPM28C/09, UPM35C/10 are light shaded and corresponding reference sequences from GenBank: Black, UU19, RM, UU31, UU10, UCD11a, UU7, NTU2, UU34, FCoV/S/3b, UCD13, CIJe, UCD5 compared with type II, UPM8C/08, FIP 79-1146, FIPV DF2 are thick shaded. Local isolates type I identical amongst themselves with more 209 than 92.3-100% homologous. The degree of identity reduces to 90% when compared with reference of type I from GenBank. Whereas the homology percentage decreased to 53.6% when compared with FCoV type II.

Legend: ID= identical, 1=UPM2C, 2= UPM5C, 3= UPM11C, 4= UPM13C, 5= UPM14C, 6= UPM22C, 7= UPM24C, 8= UPM25C, 9= UPM26C, 10= UPM27C, 11= UPM28C, 12= UPM35C, 13= Black, 14= UU19, 15= UU31, 16= UU10, 17= UU7, 18= NTU, 19= UU34,

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20= UCD11a, 21= FCoVS/3b, 22= UCD13, 23= CIJe, 24= UCD5, 25= UPM8C/08, 26= FIPV 79-1146, 27= FIPV DF2.

6.12 Sequence nucleotide difference of partial S gene of FCoV isolates type I and II. Twenty seven FCoV were compared: Local isolate type I, UPM2C/07, UPM5C/08, UPM11C/08, UPM13C/08, UPM14C/09, UPM22C/09, UPM24C/09, UPM25C/09, UPM26C/09, UPM27C/09, UPM28C/09, UPM35C/10 are light shaded and corresponding reference sequences from GenBank: Black, UU19, RM, UU31, UU10, UCD11a, UU7, NTU2, UU34, FCoV/S/3b, UCD13, CIJe, UCD5 were compared with type II FCoV, UPM8C/08, FIP 79-1146, FIPV DF2 are thick shaded. Nucleotides differences among local FCoV type I isolates (0-21 nt), while nucleotides difference increased to 1-29 when compare with reference sequences FCoV type 1 from GenBank. While the range increased (137-143 nt) when compared with type II FCoV. Legend: ID= identical, 1=UPM2C, 2= UPM5C, 3= UPM11C, 4= UPM13C, 5= UPM14C, 6= UPM22C, 7= UPM24C, 8= UPM25C, 9= UPM26C, 10= UPM27C, 11= UPM28C, 12= UPM35C, 13= Black, 14= UU19, 15= UU31,

16= UU10, 17= UU7, 18= NTU, 19= UU34, 20= UCD11a, 21= FCoVS/3b, 22= UCD13, 23= CIJe, 24= UCD5, 25= UPM8C/08, 26= FIPV 79-1146, 27= FIPV DF.

- 6.13 Multiple nucleotide sequence alignment were performed using ClustalW Multiple alignment (Bioedit version 7.0.9) on the 221 bp fragment of the S gene from 12 type I Malaysian local FCoV isolates in comparison with some reference isolates retrieved from GenBank. Sequence identity is indicated by dots while dash indicates deletion. The Malaysian FCoV type I local isolates GenBank accession numbers are HQ206644, HM628778, HQ206646, HQ829849, 211 HQ829850, HQ206647, HQ206648, HQ206649, HQ206650, HQ206651, and HQ829851 respectively. The reference strains type I GenBank accession numbers are EU186072, HQ392470, FJ938051, HQ012371, HQ012371, FJ938059, FJ917519, FJ938055, FJ938054, FJ938053, DQ160294, HQ012372, AB535528, FJ917523, DQ848678 and FJ917522 respectively.
- 6.14 Multiple nucleotide sequence alignment were performed using ClustalW Multiple alignment (Bioedit version 7.0.9) on the 200 bp fragment of the S gene from type II Malaysian local FCoV isolates UPM8C/08 accession number is JF757239. The latter isolate is compared with some reference isolates retrieved from GenBank. 214 Sequence identity is indicated by dots while dash indicates deletion. The reference strains include FIPV 79-1146 (DQ010921), FIPV complete genome (AX994055), FIPV DF2 (DQ286389), and FIPV E2 (X06170).

- 6.15 Phylogenetic relationships determined by the S gene sequence of the local FCoV isolates type I and corresponding sequence of FCoV from GenBank. The phylogenetic trees were generated using tree top phylogenetic tree predication program (GeneBee-Molecular Biology Server) and displayed in PHYLIP format with bootstrap values. Malaysian isolates type I are located in frames A and B. Note: The names were truncated to maximum 5 characters to meet the requirement of the program.
- 6.16 Phylogenetic relationships determined by the S gene sequence of the local FCoV isolates type I and type II and corresponding sequence of FCoV from GenBank entries. The phylogenetic trees were generated using tree top phylogenetic tree predication program (GeneBee-Molecular Biology Server) and displayed in PHYLIP format with bootstrap values. Malaysian isolates type I and II are located in frame A, B and C. Note: The names were truncated to maximum 5 characters to meet the requirement of the program. Note: Malaysian isolates of FCoV type I grouping in frame A includes, UPM2C/07, UPM5C/08, UPM24C/09, UPM27/09, UPM28C/09, UPM26C/09, UPM11C/08, UPM13C/08, UPM14C/09, UPM35C/10, UPM22C/09 and frame B include UPM25C/09, while grouping of FCoV type II include UPM8C/08.
- 6.17 Unrooted Phylogenetic based on comparison of S nucleotide sequence illustrating the evolutionary relationship of FCoV types I and type II local isolates and corresponding FCoV entries from the GenBank. The tree was obtained using the neighbour-Joining algorithm on the basis of nucleotide distances. Database sequences showing the distance between type I and type II FCoV. Type II represented by one isolate UPM8C/08. While type I comprises of majority of isolates namely UPM2C/07, UPM5C/08, UPM24C/09, UPM27/09, UPM28C/09, UPM26C/09, UPM11C/08, UPM13C/08, UPM14C/09, UPM35C/10, UPM22C/09 and UPM25C/09.

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## LIST OF ABBREVIATIONS

А	Ampere
٨h	Antibody
	Antibody dependent Enhancement
aka	As know as
ΔΤΗΔ	Autoimmune Hemolytic Anemia
	Aminopontidoso N
AFN	American Type Culture Collection
ATU	Antibiotio Trypsin Vorson
hn	Antibiotic Trypsin versen
рси	Dase Fails Dritish Short Heir
	Binish Short Hall
DSA <sup>0</sup> C	Degree Celeine
CMI	Cell Mediated Immunity
CIVII	Centimetran
cm <sub>2</sub>	Centimeters
cm	Centimeter Square
CNS	Central Nervous System
CO <sub>2</sub>	Carbon Dioxide
CPE	Cytopathic Effect
Crfk	Crandell Reese Feline Kidney
CSF	Cerebrospinal fluid
DAB	3-3-Diamino Benzidine Hydrochloride
dH <sub>2</sub> O	Distilled Water
DMEM	Dulbecco Minimal Essential Medium
DNA	Deoxyribonucleic Acid
dNTP	Deoxynucleotide Itriphosphate
ds	Double Stranded
DSH	Domestic Short Hair
EDIA	Ethylen Diamine Tetra-acetate
ELISA	Enzyme-linked Immunosorbent Assay
EM	Electron Microscope
EK	Endoplasmic Reticulum
FBS	Fetal Bovine Serum
FIIC	Fluorescence Isothiocyanate
FCOV	Feline Coronavirus
FECV	Feline Enteric Coronavirus
FIP	Feline Infectious Peritonitis
FIPV	Feline Infectious Peritonitis Virus
g	Gravity
gm	Gram
h	Hours
H&E	Hematoxylin and Eosin
HIS	Hyperimmune Serum

	HRP	Horse-Radish Peroxidase
	IgG	Immunoglobulin G
	IIFT	Indirect Immunofluorescent Test
	IIPT	Indirect Immunoperoxidase Test
	i/m	Intramuscular
	i/v	Intravenous
	Kbp	Kilobase pairs
	kDa	Kilodalton
	М	Molar
	mAb	Monoclonal Antibody
	MEM	Minimum Essential Medium
	MHV	Murine Hepatitis Virus
	min	Minute
	ml	Milliliter
	mM	Millimolar
	mm	Millimeter
	MW	Molecular Weight
	MOI	Multiplicity of Infection
	mRNA	Messenger Ribonucleic Acid
	NaCl	Sodium Cloride
	NCBI	National Center for Biotechnology Information
	NCEM	Negative Contrast Electron Microscope
	ng	Nanogram
	nm	Nanometer
	nt	Nucleotide
	NTC	No Template Control
	OD	Optical Density
	ORF	Open Reading Frame
	PBS	Phosphate Buffer Saline
	PCR	Polymerase Chain Reaction
	PFU	Plaque Forming Unit
	pH	Hydrogen-ion Concentration
	PI	Post Infection
	POL	Polymerase
	РТА	Phosphotungstic Acid
	RNA	Ribonucleic Acid
	RNAase	Ribonuclease
	rpm	Revolution Per Minute
	RT	Reverse Transcriptase
	RT-PCR	Reverse Transcriptase-Polymerase Chain Reaction
	S	Spike
	sec	Second
	SNT	Serum Neutralization Test
	SPF	Specific Pathogen Free
	TAE	Tris-Acetate EDTA
	TC	Tissue Culture

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TCID	Tione Culture Infostivity Dees at Fifty Demont
$1CID_{50}$	Tissue Culture infectivity Dose at Fifty Percent
TE	Tris-EDTA
TEM	Transmission Electron Microscope
TGEV	Transmissible Gastroenteritis Virus
TEN	Tris-EDTA-NaCl
UK	United Kingdom
UPM	Universiti Putra Maslysia
USA	United States of America
UTR	Untranslated Region
UV	Ultraviolet
UVH	Universiti Veterinary Hospital
V	Voltage
VN	Virus Neutralisation
v/v	Volume/Volume
w/v	Weight/Volume
w/w	Weight/Weight –
Vero	Cell Line Derived From Green African Monkey Kidney
μg	Microgram
μ1	Micorliter
μm	Micrometer
μΜ	Micromolar

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## **CHAPTER I**

## **INTRODUCTION**

Feline coronavirus (FCoV) was first recognized in 1950s as a specific disease of cats (Holzworth, 1963) which came a disease named, feline infectious peritonitis (FIP). Wolfe and Griesemer (1966) was the first to show that the disease is caused by a virus. Ward (1970) recognized the close similarities of the FIP virus (FIPV) to members of the family *Coronaviridae*. Cases of FCoV infection have been reported world wild and in all known cat population known (Rottier, 1999).

FCoV is known to be prevalent and common b y cause infection in cat populations, with particularly high prevalence in catteries and multiple-cat households (Addie and Jarrett, 1992; Simons *et al.*, 2005). The generic name FCoV has been loosely applied to all biotype and serotype of feline coronavirus.

Circulating antibodies against FCoV are found in 90-100% of cats in catteries or multiple-cat households and 50% in pet cats (Addie and Jarrett, 1992; Herrewegh *et al.*, 1997; Arshad *et al.*, 2004).

There are two biological types of coronavirus in cats: feline enteric coronavirus (FECV) which causes from asymptomatic infection to severe enteritis and the other is a systemic pathogen known to cause feline infectious peritonitis (FIPV) (Pedersen, 1995).

These FCoVs can infect domesticated cats and other members of the family *Felidae* (Vennema *et al.*, 1998). FECV is the common form of FCoV, which is virtually non-pathogenic that can be transmitted in nature between cat populations. It causes subclinical or mild enteric infections due to lesions located in the apical columnar

epithelium of the intestinal villi, from the caudal part of the duodenum to the cecum, and can cause mild to severe diarrhea in young kittens (Pedersen et al., 1981a; Addie and Jarrett, 1992). Unlike FECV infection, the FIP is an immune-mediated disease characterized by peritonitis and/or pleuritis with occasional central nervous system and ocular involvement. The inflammatory infiltrate consist of lymphocytes, plasma cell, and macrophages resulting in either nonsuppurative or granulomatous inflammation (Horzinek and Pedersen, 1982; Horzinek and Osterhaus, 1979). It is the most important cause of death of infectious origin in cats worldwide, and was originally thought to be an uncommon and fatal disease manifestation of single ubiquitous coronavirus affecting both domestic and wild *felids* (Holzworth, 1963; Pedersen *et al.*, 1981; Cave *et al.*, 2002).

FIPV was found to be morphologically and antigenically indistinguishable from FECV and were therefore called biotypes of feline coronaviruses. These two viruses differ only biologically (Pedersen, 1983; Corapi *et al.*, 1992; Vennema, 1999) where they are divided into serotypes I and II on the basis of cross-reactivity with canine coronavirus (CCV) in virus neutralization assays. Type I viruses show hardly any or no neutralization with anti CCV sera and grow poorly in cell culture and cause a slowly developing cytopathic effect (CPE) in many cell lines. Whereas type II FCoVs are relatively easy to culture (Hohdatsu *et al.*, 1992; Motokawa *et al.*, 1996; Vennema, 1999) in many different cell lines including *felis catus* whole foetus (Fcwf-4) and Crandell feline kidney (Crfk) cells (Pedersen et al., 1984a). Based on the virus neutralisation activity and genomic analyses, serotype II FCoV strains show close antigenic and genetic relationship to CCV and transmissible gastroenteritis virus (TGEV), respectively. They seem to have been arisen by double recombination between FCoV serotype I and CCV (Herrewegh *et al.*, 1998).

The close genetic relationship between FIP and common FECV infections was first reported by Pedersen et al. (1981b). Molecular studies showed that mutations in the FECV genome induce the virulent FIPV variants in infected cats and the presence of these variants coupled with an inadequate immune response lead to the development of a fatal immune-mediated clinical disease of FIP (Vennema *et al.*, 1998).

There are two forms of FIP that occur in nature. The classical effusive or wet form of the disease is the most common and easiest to diagnose, seen in approximately 75% of FIP cases. The disease is characterized by accumulation of fluid in the chest or abdomen. The proteinaceous fluid often contains fibrin clots and variable amount of cells, mostly non-degenerated neutrophils, macrophages and lymphocytes (Pedersen, 1995; Paltrinieri *et al.*, 1999; Hartmann, 2005). Dry form or noneffusive FIP result when a cell-mediated immune response dominates and form granulomas in various organs. The granulomatous lesions are usually found in the eyes, central nervous system (CNS), and parenchymatous abdominal organs, (Pedersen *et al.*, 1981; Hartmann, 2005).

Many attempts have been made to develop dependable clinical method or laboratory test to isolate the virus and to diagnose FIP (Pedersen, 1987a; Sparkes *et al.*, 1991). The diagnosis of FIP is difficult because the rare consequence of the infection where only 1-5% of seropositive cats eventually came down with FIP. The FIP occurred mainly in kittens, but sometimes also in old cats (Evermann *et al.*, 1991; Addie and Jarrett, 1992; Rottier, 1999).

The pathogenesis, viral morphology, and morphogenesis of FIPV are studied in tissues of naturally and experimentally infected cats, as well as in tissue cultures. Following *in vitro* infection in cell culture, myriad viral particles were observed both extracellularly and intracellularly (Hoshino and Scott, 1980; Pedersen and Boyle, 1980; Beesley and Hitchcock, 1982; Klumperman *et al.*, 1994; Ng *et al.*, 2003). Virus replication occurred in the cytoplasm of infected cells with no apparent nuclear involvement. Viral particles were found most frequently singularly or in groups in the cisternae of the dilated smooth and rough endoplasmic reticulum. They were observed to be present in vacuoles of various size and shapes or present freely in the cytoplasm (Hoshino and Scott, 1980; Klumperman, 1994; Lai and Cavanagh, 1997).

A definitive diagnosis of FCoV can be achieved by direct immunohistochemical examination of cells in the ascites fluid of cat suspected of FIP (Paltrinieri *et al.*, 1999). Indirect immunofluorescence test is several times more sensitive than immunoperoxidase for detection of viral antigens in natural infection with FCoV or infected cell culture (Pedersen, 2009). Although these immunohistochemical diagnostic assays are a helpful tool for FIP diagnosis, result can only be interpreted in correlation with clinical symptoms (Sparkes *et al.*, 1991), because the clinical or pathological manifestation of the infection are nonspecific and confused by those of many other diseases of cats (August, 1984).

Nowadays in all laboratories, polymerase chain reaction (PCR) assay has been used as a rapid and sensitive test to diagnose viral diseases. Compared with serological tests, PCR provides obvious advantage of direct detection of FCoV genome rather than

documenting a previous immunological activity encountered with a coronavirus (Hartmann, 2005).

FCoV disease had also been diagnosed by reverse transcriptase polymerase chain reaction (RT-PCR) assays by using primers targeted to highly conserved regions of the viral genome at the 3' untranslated region (3' UTR) (Herrewegh *et al.*, 1995b; Fehr *et al.*, 1997), or S-protein gene (Li and Scott, 1994; Gamble *et al.*, 1997). These genomic regions are common to all FCoV strains and served as a valuable tool for detection of the virus in blood, peritoneal fluid, feces and tissue samples of infected cats.

Moreover, the N-terminal domain of the S-protein gene of the spike regions allows the differentiation between type I and type II FCoVs (Posch *et al.*, 1999). Many countries have reported the occurrence of type I and type II FCoVs amongst the cats population in respective geographical region. Surveyed on the FCoV prevalence in cats have been documented in USA (Vennema, 1999), UK (Addie *et al.*, 2003), Japan (Hohdatsu *et al.*, 1992; Shiba *et al.*, 2007), Austria (Benetka *et al.*, 2004), Switzerland (Kummrow *et al.*, 2005) and Taiwan (Lin *et al.*, 2009).

The current information on the geographical distribution of FCoV indicates a high incidence of type I in many countries.

The first FIP case in Malaysia was reported in 1981 (Wong *et al.*, 1983). The preliminary study on FCoV antibody titer showed that FCoV is highly prevalent in Malaysia where 100% of cats in catteries were seropositive (Arshad *et al.*, 2004).

However, recent studies in cats kept in catteries using RT-PCR assay showed that 84% of the cats were positive (Sharif *et al.*, 2010). Based on the reported serological test and RT-PCR assay, we believed the virus is present in the local cats. Therefore, it is imperative to isolate the virus and examined their biological properties and compared with reference viruses.

The main aim of this study is to isolate the virus in sensitive feline cell cultures. Isolated cell culture adaptable virus will be further identified by examining their physical properties, morphogenesis, and locating their replication site in the cell. In addition to that, information on the serotypes and genotypes that are circulating in the region are ascertained.

Therefore, the objectives of this study were

1. to isolate FCoVs from ante and post-mortem cases from naturally infected cats and cats suspected of being infected with FCoV.

2. to examine the biological characteristic of local isolates of FCoV in cell cultures.

3. to clone purified selected local virus isolates of FCoV by limiting dilution technique.

4. to detect local FCoV isolates by indirect immunofluorescent (IIF) and immunoperoxidase (IIP) techniques.

5. to observe the histopathology of FCoV infected cell culture by H&E staining.

6. to study of morphogenesis of clone purified FCoV UPM11C/08 isolate in Fcwf-4 cell.

7. to detect and differentiate FCoV type I and type II among local isolate of FCoV by RT-PCR assay.

8. to sequence the S region and examine the relatedness of Malaysian FCoV and reference strain by phylogenetic analysis.



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