



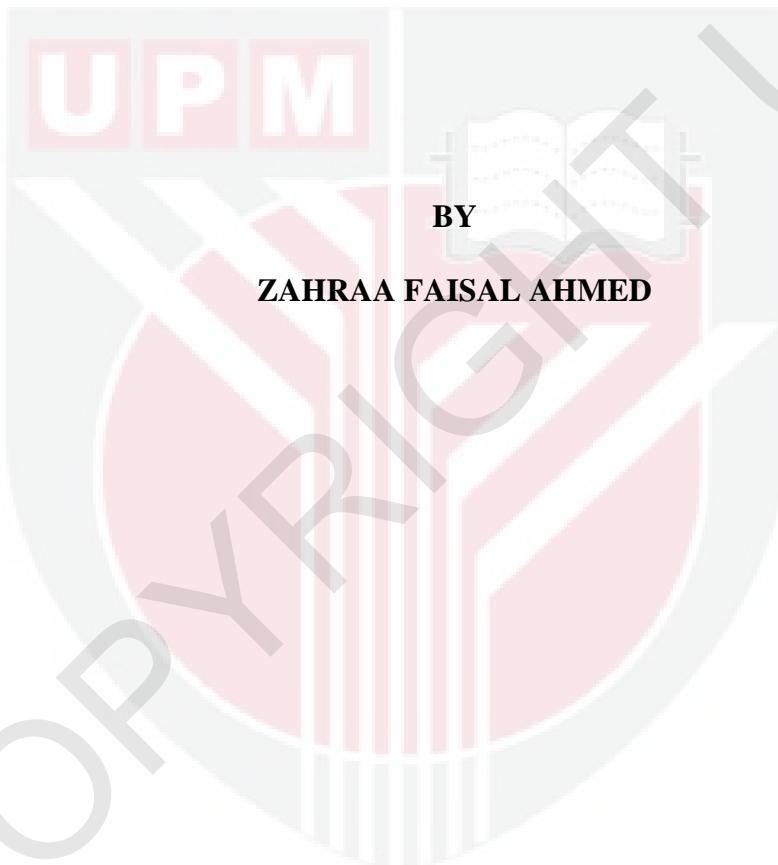
UNIVERSITI PUTRA MALAYSIA

***PREVALENCE AND MOLECULAR PATHOGENIC MARKERS OF
MYCOPLASMA GALLISEPTICUM INFECTION IN COMMERCIAL
CHICKENS AND PROGENIES***

ZAHRAA FAISAL AHMED

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**PREVALENCE AND MOLECULAR PATHOGENIC MARKERS OF
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CHICKENS AND PROGENIES**



ZAHRAA FAISAL AHMED



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

September 2011

**This thesis is dedicated to my father, mother, and
sisters for their patience, support and
encouragements in completion**



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

**PREVALENCE AND MOLECULAR PATHOGENIC MARKERS OF
MYCOPLASMA GALLISEPTICUM INFECTION IN COMMERCIAL
CHICKENS AND PROGENIES**

BY

ZAHRAA FAISAL AHMED

September 2011

Chairman: **Professor Datin Paduka Aini Ideris, PhD**

Faculty: **Faculty of Veterinary Medicine**

Mycoplasma gallisepticum (MG) causes chronic respiratory disease and the infection is very costly to the poultry industry. There are few published data on avian mycoplasmosis and there is no report on molecular pathogenicity of MG infection in Malaysia. Therefore, this study was carried out to determine the prevalence of MG, and the molecular pathogenic markers of MG infection in the commercial chickens and their progenies (pipped embryos, normal chicks and poor quality chicks), in order to understand the molecular level of pathogenicity. The prevalence of MG infection in chickens was determined in selected commercial farms (breeder, broiler and layer) and the progenies [pipped embryos (PE), day old poor quality chicks (PQC) and normal chicks (NC)]. All samples were obtained from farms in Peninsular Malaysia. A total of 3056 swab samples were collected of which 1243 are from pipped embryos, 248 from day-old poor quality chicks, 340 from day-old normal chicks and 1225 from adult commercial chickens. Conventional polymerase chain

reaction (PCR) test was performed using specific gene target sequence and encoding the surface protein for detection of MG directly from the clinical samples without prior isolation of the target MG. The primer used was designed to bind to the Adherence protein A gene (*gapA*) and amplify a 505 bp DNA fragment.

In this study, 571 positive samples of MG out of 3056 samples with overall prevalence of 18.68% were detected from different progenies and adult commercial chickens. The total prevalence rates were 13.7 % in the pipped embryos, 16.9 % in the poor quality chicks, 12.6% in the normal chicks, and 25.8% in the adult commercial chickens. This study shows the high prevalence of MG infection through vertical and horizontal transmission from many geographically distinct areas of the country, although these farms have vaccination and treatment history. The present study demonstrated that the control of MG was not successful, despite the use of live and /or killed MG vaccines, an extensive medication program and strict biosecurity.

These positive MG samples were used for molecular characterization by amplification of selected gene target specific sequences to MG, hemagglutinin protein A gene (*pMGA*) and Phase-variable putative adhesin protein A gene(*pvpA*), using conventional PCR of published sequence specific primers. These two genes, *pMGA* and *pvpA* genes have gene size polymorphism on specific target sequence. The PCR results demonstrated, a total of 281 MG positive field samples out of 571 MG samples were detected with the primer targeted *pMGA* gene and a total of 188 MG positive field samples out of 571 MG samples were detected with the primer targeted *pvpA* gene. Similar and identical banding patterns were observed among MG positive samples obtained from progenies, however there was a variable on the

banding pattern among MG positive samples obtained from adult commercial chickens using the agarose gel electrophoresis. The sequencing and phylogenetic analysis results of MG based on selected genes targeted specific sequences were obtained using Bioinformatics software (Bioedit and MEGA 4. software).

The characteristics of the positive MG field positive samples were determined. The genetic diversity of the *pMGA* and *pvpA* genes of MG positive samples originated from adult commercial chickens and progenies were investigated. In the present study, we evaluated the genetic variability of 77 field positive samples of MG using the *pMGA* gene and 49 field positive samples of MG using the *pvpA* gene, detected in progenies and adult commercial chickens and compared them to the reference and vaccine strains of MG obtained in this study. Genetic variation patterns were evaluated by partial nucleotide sequencing of the *pMGA* and *pvpA* genes, which encode putative cytadhesion proteins. The gene size variation patterns of the *pMGA* and *pvpA* genes among MG field positive samples shared identical gene size variation patterns with the pathogenic reference and vaccine strains, that is, an insertion bp fragments by using the *pMGA* gene primer set and a deletion bp fragments by using the *pvpA* gene primer set. Therefore, it showed that there was identical genes size variation patterns of the MG positive samples with the pathogenic reference and vaccine strains which are pathogenic by nature and can be transmitted vertically. However, the gene size variation patterns are quite different from the variation pattern of the less pathogenic vaccine strain that cannot be transmitted vertically.

This study concluded the identification of two amplification based genetic markers that highly correlate with the existing pathogenicity studies of MG infection. It also proved the importance of these two primer sets and showed that the primer of *pMGA* gene might be considered as a vertical genetic marker, and the gene size polymorphism patterns by both of selected primer sets of the *pMGA* and *pvpA* genes might be considered as potential pathogenic molecular markers. The present study proved the ability of both selected primer sets of the *pMGA* and *pvpA* genes in differentiating avirulent ts11 strain and virulent reference strains. Therefore both these selected primer sets are good pathogenic markers of MG that can be used to differentiate whether the MG field strains are pathogenic or less pathogenic.

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

**PREVALENS DAN PETANDA MOLEKUL PATOGEN BAGI INFENSI
MYCOPLASMA GALLISEPTICUM PADA AYAM KOMERSIAL DAN
PROGENI**

Oleh

ZAHRAA FAISAL AHMED

September 2011

Pengerusi: **Profesor Datin Paduka Aini Ideris, PhD**

Fakulti: **Fakulti Perubatan Veterinar**

Mycoplasma gallisepticum (MG) menyebabkan penyakit pernafasan kronik dan jangkitan ini melibatkan kos yang tinggi kepada industri poltri. Hanya ada beberapa data yang diterbitkan pagi “mycoplasmosis” unggas dan tidak ada laporan mengenai patogenisiti molekul jangkitan MG di Malaysia. Oleh kerana itu, kajian ini dilakukan untuk menentukan prevalens MG, dan petanda molekul patogen bagi jangkitan MG pada ayam komersial dan progeni mereka (embrio “pipped”, anak ayam normal dan anak ayam yang rendah kualitinya), untuk memahami patogenisiti pada tahap molekul. Prevalens jangkitan MG pada ayam ditentukan, di ladang komersial yang dipilih (ayam pembiakbaka, ayam pedaging dan petelur) dan progeni [embrio “pipped” (PE), anak ayam berumur satu hari yang rendah kualitinya (PQC) dan anak ayam normal (NC)]. Semua sampel diperolehi dari ladang di Semenanjung Malaysia. Sejumlah 3056 swab sampel telah dikumpulkan dimana 1243 daripada nya ialah embrio “pipped”, 248 daripada anak-anak ayam berumor satu hari dan mempunyai

kualiti rendah, 340 dari anak-anak ayam normal dan 1225 daripada ayam dewasa komersial. Ujian rantaian reaksi polimerase konvensional (PCR) dilakukan dengan menggunakan gen urutan target khusus dan mengekod protein permukaan untuk mengesan MG secara langsung dari sampel klinikal, tanpa mengisolat sasaran MG terlebih dahulu. Primer yang digunakan direka bentuk untuk mengikat protein “Adherence” A (*gapA*) dan mengembangkan 505 bp fragmen DNA.

Dalam kajian ini, 571 sampel positif MG daripada 3056 sampel dengan prevalens keseluruhan 18.68% dikesan dari progeni berbeza dan ayam dewasa komersial. Kadar prevalens adalah 13.7% dalam embrio “pipped”, 16.9% pada anak ayam berkualiti rendah, 12.6% pada anak ayam normal, dan 25.8% dalam ayam dewasa komersial. Kajian ini menunjukkan prevalens jangkitan MG yang tinggi melalui sebaran menegak dan mendatar, dari banyak kawasan geografi yang berbeza di negara ini, walaupun ladang-ladang ini mempunyai sejarah vaksinasi dan rawatan. Kajian ini menunjukkan bahawa kawalan MG tidak berjaya, walaupun penggunaan vaksin MG hidup dan / atau mati, program ubatan yang ekstensif dan biosekuriti yang ketat.

Sampel MG yang positif digunakan bagi pencirian molekul dengan cara amplifikasi sekuen khusus target gen yang dipilih untuk MG, gen protein A hemagglutinin (*pMGA*) dan “phase variable putative adhesion gen protein A” (*pvpA*), melalui PCR konvensional dengan menggunakan primer urutan spesifik yang telah diterbitkan. Kedua-dua gen, *pMGA* dan *pvpA*, mempunyai saiz polimorfisme pada urutan target khusus. Keputusan PCR menunjukkan, jumlah keseluruhan 281 MG sampel lapangan positif dari 571 sampel MG yang dikesan dengan menggunakan target gen

primer *pMGA* dan jumlah 188 MG sampel lapangan positif dari 571 sampel MG yang dikesan dengan target gen primer *pvpA*. Paten band yang serupa dan identikal dilihat antara MG sampel positif yang diperolehi daripada progeni, namun ada pembolehubah pada paten band antara MG sampel positif yang diperolehi dari ayam dewasa komersial dengan menggunakan elektroforesis gel agaros. Urutan dan hasil analisis filogenik MG berdasarkan gen pilihan sasaran urutan khusus telah diperolehi dengan menggunakan perisian bioinformatik (Perisian Bioedit dan MEGA 4.).

Ciri-ciri sampel lapangan yang positif MG telah ditentukan. Kepelbagaian genetik gen *pMGA* dan *pvpA* lapangan MG sampel positif yang berasal dari ayam dewasa komersial dan progeni dikaji. Dalam kajian ini, kami menilai kepelbagaian genetik 77 sampel lapangan positif MG menggunakan gen *pMGA* dan 49 sampel lapangan positif MG menggunakan gen *pvpA*, dikesan dari progeni dan ayam dewasa komersial, dibandingkan dengan strain rujukan serta strain vaksin MG yang diperolehi dalam kajian ini. Pola variasi genetik dinilai oleh urutan nukleotida separa dari gen *pMGA* dan *pvpA*, yang mengekod protein *cytadhesion* putatif. Pola gen variasi saiz *pMGA* dan gen *pvpA* antara MG sampel positif bersama pola saiz gen variasi identikal dengan strain rujukan patogenik dan strain vaksin, iaitu, “insertion” sebuah fragmen pb dengan menggunakan gen asas set *pMGA* dan “deletion” fragmen bp dengan menggunakan set primer gen *pvpA*. Oleh kerana itu, ianya menunjukkan bahawa ada pola variasi gen saiz identical bagi sampel positif MG dengan strain rujukan patogenik dan strain vaksin yang patogenik semula jadi dan boleh disebarluaskan secara menegak. Namun, pola variasi gen saiz sangat berbeza dari pola variasi strain vaksin kurang patogenik yang tidak dapat menular secara menegak.

Kajian ini mengesahkan pengenalan berdasarkan amplifikasi dua penanda genetik yang sangat berkaitan dengan kajian patogenisiti sedia ada jangkitan MG. Ianya juga membuktikan pentingnya dua set primer ini dan menunjukkan bahawa asas gen *pMGA* mungkin dianggap sebagai penanda genetik menegak, dan pola polimorfisme gen saiz kedua-dua set pilihan primer bagi gen *pMGA* dan *pvpA* mungkin dianggap sebagai potensi penanda molekul patogen. Kajian ini membuktikan kemampuan kedua-dua set primer pilihan daripada gen *pMGA* dan gen *pvpA* dalam membezakan strain tidak virulen ts11 dan strain rujukan virulen. Oleh itu, kedua-dua set primer pilihan ini adalah penanda yang baik bagi MG patogenik dan boleh digunakan untuk membezakan sama ada strain MG lapangan bersifat patogenik atau kurang patogenik.

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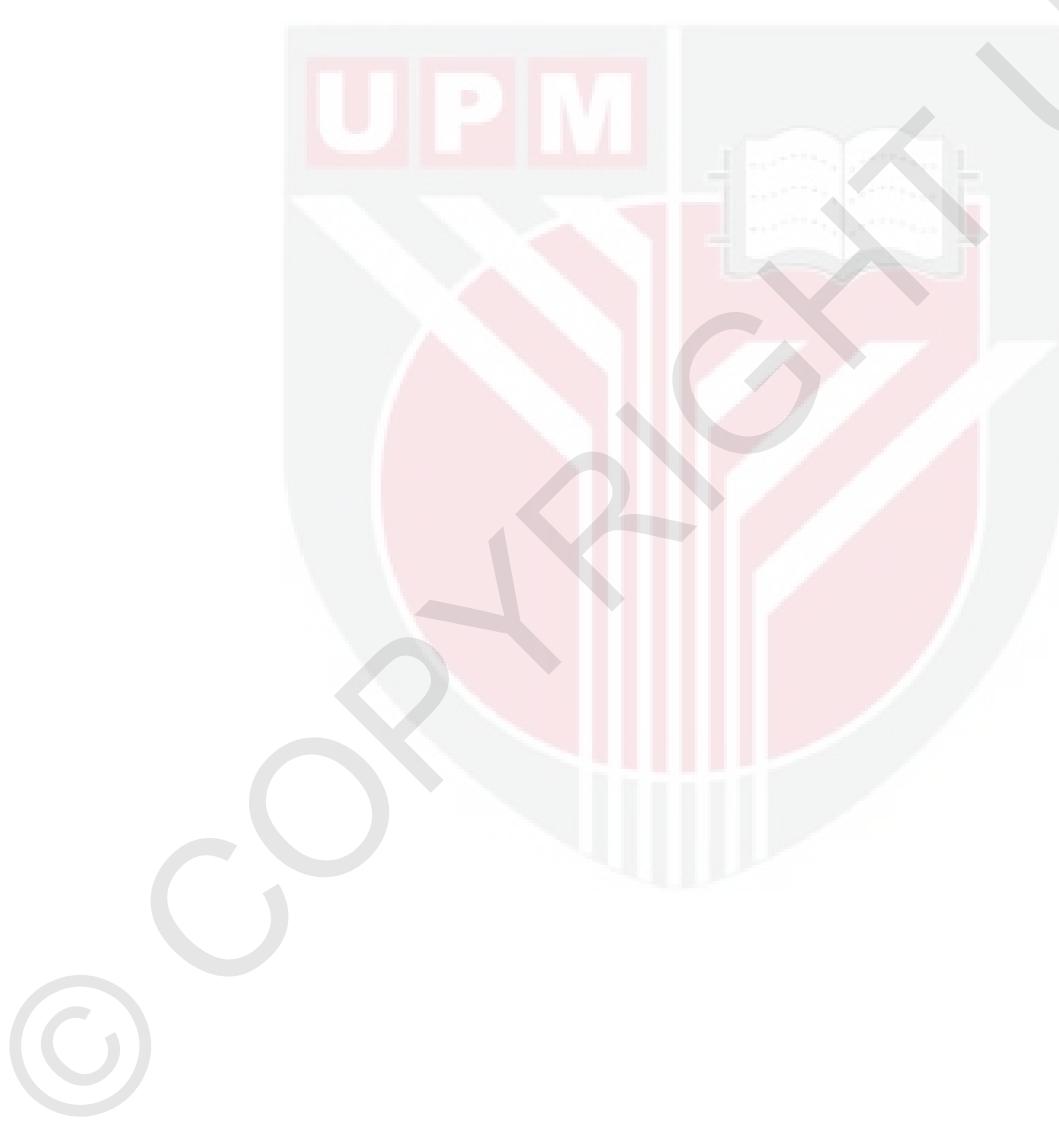
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I certify that a Thesis Examination Committee has met on 26 September 2011 to conduct the final examination of Zahraa F. A. AL-Barghash on her thesis entitled "Prevalence and Molecular Pathogenic Markers of *Mycoplasma gallisepticum* Infection in Commercial Chickens and Progenies" in accordance with the Universities and University College 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 Master of Science.

Members of the Thesis Examination Committee were as follows:

Saleha binti Abdul Aziz, PhD

Professor

Faculty of Veterinary Medicine

Universiti Putra Malaysia

(Chairman)

Jalila binti Abu, PhD

Senior Lecturer

Faculty of Veterinary Medicine

Universiti Putra Malaysia

(Internal Examiner)

Abdul Rahim bin Abdul Mutualib, PhD

Associate Professor

Faculty of Veterinary Medicine

Universiti Putra Malaysia

(Internal Examiner)

Zaini Mohd Zain, PhD

Associate Professor

Faculty of Medicine

Universiti Teknologi MARA

(External Examiner)

SEOW HENG FONG, PhD

Professor and Deputy Dean

School of Graduate Studies

Universiti Putra Malaysia

Date: 22 November 2011

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:

Aini Ideris, PhD

Professor

Faculty of Veterinary Medicine

Universiti Putra Malaysia

(Chairman)

Abdul Rahman bin Omar, PhD

Professor

Faculty of Veterinary Medicine

Universiti Putra Malaysia

(Member)

Mohd. Hair Bejo, 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:

DECLARATION

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 at any other institutions.

ZAHRAA FAISAL AHMED

Date: 26 September 2011



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LIST OF ABBREVIATIONS

%	Percentage
AFLP	Amplified fragment length polymorphism
bp	Base pair
°C	Degree in Celsius
CO ₂	Carbon dioxide
CRD	Chronic respiratory disease
CCRD	Complicated chronic respiratory disease
DNA	Deoxyribonucleic acid
dNTPs	Deoxynucleotide triphosphate
<i>E. coli</i>	<i>Escherichia coli</i>
EDTA	Ethylene diamine tetra acetic acid
ELISA	Enzyme linked immunosorbent assay
gapA	Adherence protein A
GTS	Gene-targeted sequencing
HI	Hemagglutination inhibition
IBV	Infectious bronchitis virus
IFA	Immunofluorescence antibody
IGSR	16S-23S rRNA intergenic spacer region sequencing
Kbp	kilobase pairs
KDa	kilo Daltons
LP	Surface lipoprotein
MI	<i>Mycoplasma iowae</i>
MG	<i>Mycoplasma gallisepticum</i>
mg	Milligram
mgc2	Cytadhesion membrane protein
ml	milliliter
MM	<i>Mycoplasma meleagridis</i>
mm	Millimeter
mM	Milli molar
MS	<i>Mycoplasma synoviae</i>
NC	Normal chick
NDV	Newcastle disease virus

ng	Nanogram
nm	Nanometer
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
PCR-RFLP	PCR based restriction fragment length polymorphism
PE	Pipped embryo
pMGA	Hemagglutinin protein
pmole	Picomole
PPLO	Pleuropneumonia like organism
PQC	Poor quality chick
pvpA	Phase-variable putative adhesin protein
RAPD	Random amplified polymorphic DNA
REA	Restriction endonuclease analysis
RFLP	Restriction fragment length polymorphism
RNA	Ribonucleic acid
rpm	Radius per minute
rRNA	Ribosomal ribonucleic acid
SDS	Sodium dodecyl sulphate
SPA	Serum plate agglutination
TAE	Tris-acetate EDTA
USA	United States of America
UV	Ultraviolet
μg	Microgram
μl	Microlitre
μm	Micro-meter
VTP	Vertical transmission progeny

CHAPTER I

INTRODUCTION

Mycoplasma gallisepticum (MG) is one of the important pathogens and the infection has a high prevalence causing major economic losses to the poultry industry. Therefore MG is considered as one of the costly diseases for the poultry industry worldwide. *Mycoplasma gallisepticum* caused complicated chronic respiratory disease (CCRD) of chickens when there are multiple infections with *E. coli* and respiratory viral infections such as Newcastle disease virus and infectious bronchitis virus (Ley and Yoder, 1997; Ley, 2003; 2008).

The horizontal transmission of MG infection occurs in poultry flocks and consequently the breeder progeny flocks become infected by the vertical transmission (Bradbury, 2005). The vaccination program was practiced in some countries for controlling the spread of the infection but it has proven to be ineffective at clearing MG infection from the breeder flocks (Ley, 2003). MG control program should be based on the elimination of the organism from the primary breeder flocks and on the maintenance of Mycoplasma free conditions in the breeders and breeder progeny flocks using premises biosecurity (Kleven, 2008).

The detection by culture for isolation and identification are complicated because MG is identified as a fastidious bacteria (Ley, 2003). Usually the serological methods are used for the MG infection diagnosis, however the non specific reactions limit these methods effectiveness (Avakian *et al.*, 1988; Levisohn and Kleven, 2000; Hess *et al.*, 2007). Additionally the antigenic variation (Bencina *et al.*, 1988a, b; Garcia *et al.*,

1994; Ferraz and Danelli, 2003) and the interspecies cross reactivity (Yogev *et al.*, 1989) may cause the delay in MG diagnosis.

The rapid and appropriate differentiation of MG strains are essential for the epidemiological study of the MG occurrence, to find the origin sources of the MG infection, and to design effective control measures (Ley *et al.*, 1997a). Many techniques have been used for MG strain differentiation, which include profile analysis (Khan *et al.*, 1987; John *et al.*, 2006), restriction fragment length polymorphism (RFLP) (Kleven *et al.*, 1988a; Hong *et al.*, 2005), PCR with strain specific primers (Nascimento *et al.*, 1993; Feberwee *et al.*, 2006, Fan *et al.*, 1995b), gene-targeted sequencing (GTS) (Ferguson *et al.*, 2005) and random amplification of polymorphic DNA (RAPD) (Geary *et al.*, 1994; Fan *et al.*, 1995a; Rawadi, 1998; Charlton *et al.*, 1999a, b). Also the RAPD method has been used effectively for the identification of MG vaccine strains in field and experimental conditions (Ley *et al.*, 1997a; Kleven *et al.*, 1998; Turner and Kleven, 1998; Kleven *et al.*, 2004), as well as for tracking epidemiologically related isolates in the field (Charlton *et al.*, 1999 a, b; Levisohn and Kleven, 2000; Ferguson *et al.*, 2005). However, there was difficulty in standardizing protocols among the laboratories. Therefore, the RAPD test was not permitted for long term epidemiological investigations or inter laboratory comparisons.

Most of the investigations have switched to the molecular techniques as the basis of MG identification. Sequencing methods have been developed as an approach for molecular biology of MG and the complete genome sequence availability has driven the idea to estimate the gene target sequencing as a typing tool for differentiating

MG strains (Raviv *et al.*, 2007). With reference to Papazisi *et al.* (2003), the authors completed sequencing of the genome of MG. It was also mentioned that some of the genes are conserved while others are not. Such information provides an added advantage during differentiation, particularly when the PCR assay is being investigated.

Significant attempt has been made to recognize MG antigens, especially the cytadhesion properties antigens, which may play key roles in the pathogenesis and immune response to infection. Two of MG gene families, *pMGA* and *pvpA* genes, have been described and these genes encode major surface proteins with pathogenic, antigenic and immune evasion properties (Boguslavsky *et al.*, 2000; Evans *et al.*, 2005). The expression of *pMGA* and *pvpA* genes and the antigenic variation, major immunogenic surface proteins, were correlated with the response of antibody *in vivo* studies, suggesting that modulation of the immune system may have important role in producing the surface diversity (Levisohn *et al.*, 1995; Bencina, 2002; Papazisi *et al.*, 2003; Razin, 2006).

Avian mycoplasma serotypes were found to differ in their potential for producing embryo mortality, with most strains of MG being pathogenic for chicken embryos (Levisohn *et al.*, 1985). Pathogenic MG strains cause high embryo mortality, but it may be possible that the *in ova* virulence was enhanced by egg adaptation (Levisohn *et al.*, 1986). Studies showed that MG strains varied in their *in ovo* pathogenicity and there was no correlation between *in ovo* pathogenicity and *in vivo* or *in vitro* methods for pathogenicity evaluation.

The concern in many poultry farms in Malaysia is that most of the farms practice protective measures including vaccination and treatment, to control the epidemic MG infection. The investigation on the diagnosis of MG infection is inadequate, thus reliable tests for MG detection and strain differentiation might help in understanding the occurrence and spread of the infection since they produce the essential information to recognize and identify new MG outbreaks. Due to lack of studies and understanding of the molecular pathogenicity of MG infection, it is therefore crucial to determine their molecular level of pathogenicity using commercial birds and progenies. Therefore, the correlation of the molecular finding towards existing pathogenicity study of the MG strains may be carried out to detect and identify the potential pathogenic molecular marker. The combination of the gene size polymorphism in *pvpA* and *pMGA* genes act as potential pathogenic molecular marker of MG infection.

The hypothesis of this study was that MG positive samples from commercial chickens under different conditions in different farms in Malaysia, have high degree of gene size polymorphism of certain genes, suggesting that some of the MG positive samples are highly pathogenic and others are less pathogenic. Therefore, the objectives of this study were to determine:

- 1) the prevalence of MG infection, in selected commercial farms (breeder, broiler and layer), progeny-pipped embryos (PE), day old poor quality chicks (PQC) and normal chicks (NC) obtained from Peninsular Malaysia.

- 2) the molecular characteristics of the local MG positive samples based on selected target genes specific sequences encode for a putative surface cytadhesion protein.
- 3) the phylogenetic tree of MG positive samples based on targeted specific sequences of specific selected genes.
- 4) the pathogenic marker that can facilitate the specific molecular detection, characterization and differentiation between the highly and the less pathogenic MG strains.



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