



**UNIVERSITI PUTRA MALAYSIA**

***EPIDEMIOLOGY AND CHARACTERISATION OF MAJOR BOVINE  
MASTITIS PATHOGENS IN SELECTED DAIRY HERDS OF  
PENINSULAR MALAYSIA***

**BASHIR ALI**

**FPV 2021 5**



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PENINSULAR MALAYSIA**

By

**BASHIR ALI**

**Thesis Submitted to the School of Graduate Studies, Universiti Putra  
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Doctor of Philosophy**

**September 2020**

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

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**September 2020**

**Chairman : Professor Zunita Zakaria, PhD**  
**Faculty : Veterinary Medicine**

Bovine mastitis is a costly endemic disease in dairy cows. In recent times, there was need by Malaysian government to boost local dairy production in order to cater for local consumption. Mastitis research; involving the epidemiology and antimicrobial resistance profile studies as well as identification of vaccine candidate targets against major mastitis pathogens, is central in enhancing dairy production. This research was aimed at studying the epidemiology of bovine mastitis pathogens from selected states of Malaysia, molecular characterise the major pathogens implicated, and identify vaccine candidate target of selected mastitis pathogens. The objectives of the study were; to determine the bacterial pathogens associated with bovine intramammary infections from selected states of Malaysia and antimicrobial resistance pattern of most prevalent pathogens; to determine the prevalence of subclinical mastitis and its associated risk factors from selected states of Malaysia; to characterise *Staphylococcus aureus* isolates as the most prevalent implicated pathogens associated with mastitis in selected states of Malaysia; and to identify immunogenic targets for development of candidate vaccines against selected mastitis pathogens by reverse vaccinology approach. Total of 1945 quarter samples from 517 cows across 33 farms were collected using a cross-sectional study design. All samples were subjected for California mastitis test (CMT). Isolation and identification of mastitis pathogens was carried out based on standard bacteriological procedures for all CMT positive samples. Antimicrobial resistance profile of selected most prevalent pathogens associated with mastitis was conducted by disk diffusion

technique. Risk factors associated with subclinical mastitis were analysed. *Staphylococcus aureus* isolates implicated in mastitis were characterised by multi locus sequence typing (MLST). Immunogenic proteins as targets for candidate vaccine development against three mastitis isolates namely; *Staphylococcus aureus*, *Escherichia coli* and *Streptococcus agalactiae* were identified by reverse vaccinology approach. The overall culture proportion positive was recorded as 68.3% (n=503/736, CI= 64.9-71.6). The respective states' culture proportion positive was 68.3% (n=71/104, CI= 58.9-76.4), 60.5% (184/304, CI= 54.6-65.8), 58.4% (n=94/161, CI= 50-65.6), 100% (n=75/75, CI= 93.9-100), and 85.9% (n=79/92, CI= 73.8-89.8) for Pahang, Perak, Selangor, Negeri Sembilan and Johor respectively. Significant difference was observed between states' culture prevalence ( $\chi^2=63.8$ ,  $P<0.001$ ). Mastitis risk factors such as breed, age, parity, lactation stage, teat lesion score, were found to be statistically associated with occurrence of mastitis ( $P < 0.05$ ). The most prevalent isolates identified were non-aureus staphylococci (NAS) 39.5%, *S. aureus* 13.1%, *K. pneumoniae* 6.5%, *S. agalactiae* 4.8%, *S. uberis* 4.3% and *E. coli* 2.6%. Resistance profile of *K. pneumoniae* isolates against ampicillin and Penicillin G were 70.4% and 88.9% respectively while that of *Actinobacter* spp. against chloramphenicol and streptomycin were 71.4% and 35.7% respectively. For *S. uberis* isolates, 66.7% and 73.3% have shown resistance to tetracycline and streptomycin respectively. The multi-locus sequence and typing (MLST) identified six sequence types (STs) of *S. aureus* isolates. The ST97 was the most prevalent (40%) followed with ST1 (20%). The rest belong to ST1496 (10%), ST4427 (10%), ST221 (10%) and ST2125 (10%). A total of 18 immunogenic proteins comprising of surface exposed and secretory components were identified as targets for candidate vaccine against three major mastitis pathogens (*S. aureus*, *S. agalactiae* and *E. coli*). Their conserved and consensus epitopes for B-cells and T-cells were identified. These composed of six from *E. coli*, three from *S. aureus* and nine from *S. agalactiae*. In conclusion, the prevalence of mastitis, the distribution and composition of mastitis associated pathogens as well as the key predisposing factors have been established. The molecular characteristics of *S. aureus* as the most prevalent mastitis associated pathogen were uncovered, targets for potential vaccine candidates against major mastitis pathogens were determined. These outcomes would assist in formulating policies and designing of mastitis control and preventive programs with the view to curbing the losses and costs incurred due to mastitis. This would ultimately help in meeting up the target for dairy milk self-sufficiency and improve the economies of dairy farmers in Malaysia.

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

**EPIDEMIOLOGI DAN PENCIRIAN PATOGEN UTAMA MASTITIS  
PADA LEMBU TENUSU TERPILIH DI SEMENANJUNG MALAYSIA**

Oleh

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Mastitis lembu merupakan satu penyakit endemik pada lembu tenusu yang menelan kos yang tinggi. Di kebelakangan ini, terdapat keperluan bagi kerajaan Malaysia untuk meningkatkan pengeluaran tenusu tempatan bagi memenuhi keperluan negara. Penyelidikan mastitis, termasuk kajian epidemiologi dan profil kerintangan antimikrobial termasuk pengenalpastian calon vaksin terhadap patogen utama mastitis adalah penting dalam meningkatkan pengeluaran tenusu. Kajian ini bertujuan untuk mengkaji epidemiologi patogen mastitis lembu dari negeri-negeri terpilih di Malaysia, pencirian molekul patogen utama yang terlibat, dan mengenal pasti sasaran calon vaksin patogen mastitis yang dipilih. Objektif yang terlibat dalam kajian ini adalah; untuk menentukan kaitan patogen mastitis dengan infeksi intramamari dari negeri-negeri terpilih di Malaysia; mengkaji corak kerintangan antimikrobial patogen paling lazim yang terpilih; untuk menentukan kelaziman mastitis subklinikal dan faktor risiko yang berkaitan dari negeri terpilih di Malaysia; untuk menentukan jenis jujukan (ST) isolat *Staphylococcus aureus* yang menyebabkan mastitis dalam negeri-negeri terpilih di Malaysia; dan untuk mengenal pasti sasaran imunogenik untuk pembangunan vaksin terhadap patogen mastitis yang dipilih dengan pendekatan vaksinologi terbalik. Sejumlah 1945 sampel daripada 517 ekor lembu di 33 ladang telah dikumpulkan secara kajian keratan rentas. Kesemua sampel diuji menggunakan ujian mastitis California (CMT). Pengasingan dan pengenalpastian patogen mastitis dijalankan menurut prosedur bakteriologi piawai bagi sampel yang positif CMT. Profil kerintangan antimikrobial patogen prevalen yang terpilih dijalankan secara teknik difusi cakera. Faktor

risiko yang berkaitan dengan mastitis subklinikal dianalisis. Isolat *S. aureus* yang terlibat dalam mastitis dicirikan oleh teknik tip jujukan pelbagai lokus (MLST). Protin imunogenik sebagai sasaran untuk pembangunan vaksin terhadap tiga isolat mastitis iaitu; *Staphylococcus aureus*, *Escherichia coli* dan *Streptococcus agalactiae* telah dikenal pasti oleh pendekatan vaksinologi terbalik. Kelaziman isolat-isolat keseluruhannya dicatatkan sebagai 68.3% (n=503/736, CI= 64.9-71.6). Kelaziman isolat dari negeri-negeri yang terpilih adalah masing-masing 68.3% (n=71/104, CI= 58.9-76.4), 60.5% (184/304, CI= 54.6-65.8), 58.4% (n=94/161, CI= 50-65.6), 100% (n=75/75, CI= 93.9-100), and 85.9% (n=79/92, CI= 73.8-89.8) untuk Pahang, Perak, Selangor, Negeri Sembilan dan Johor. Perbezaan ketara lazim diperhatikan dalam kalangan kultur daripada negeri-negeri yang terpilih ( $\chi^2=63.8$ ,  $P<0.001$ ). Faktor risiko mastitis seperti baka, umur, pariti, peringkat laktasi, skor lesi puting, didapati secara statistik dikaitkan dengan terjadinya mastitis ( $P < 0.05$ ). Pengasingan yang paling lazim dikenal pasti adalah staphylococci non-aureus (NAS) 39.5%, *S. aureus* 13.1%, *K. pneumoniae* 6.5%, *S. agalactiae* 4.8%, *S. uberis* 4.3% dan *E. coli* 2.6%. Profil rintangan isolat *K. pneumoniae* terhadap ampicilin dan Penicillin G masing-masing adalah 70.4% dan 88.9% manakala *Actinobacter* spp. terhadap chloramphenicol dan streptomycin masing-masing adalah 71.4% dan 35.7%. Bagi isolat *S. uberis*, 66.7% dan 73.3% menunjukkan rintangan terhadap tetracycline dan streptomycin. Penaipan urutan pelbagai lokus (MLST) mengenal pasti enam tip urutan (ST) isolat *S. aureus*. ST97 adalah yang paling lazim (40%) diikuti dengan ST1 (20%). Selebihnya adalah ST1496 (10%), ST4427 (10%), ST221 (10%) dan ST2125 (10%). Sejumlah 18 protin imunogenik yang terdiri daripada komponen terdedah dan penyingkiran permukaan dikenalpasti sebagai sasaran untuk calon vaksin terhadap tiga patogen mastitis utama (*S. aureus*, *S. agalactiae* dan *E. coli*). Mereka terpelihara dan konsensus epitop untuk sel B dan sel T telah dikenalpasti. Ini terdiri daripada enam daripada *E. coli*, tiga daripada *S. aureus* dan sembilan daripada *S. agalactiae*. Sebagai kesimpulan, kelaziman mastitis, distribusi dan komposisi patogen yang berkaitan dengan mastitis serta faktor-faktor predisposisi utama telah dikenalpasti. Ciri-ciri molekul *S. aureus* sebagai patogen yang paling lazim berkaitan dengan mastitis telah ditemui, sasaran untuk calon vaksin yang berpotensi terhadap patogen mastitis utama telah ditentukan. Penemuan ini akan membantu dalam merangka dasar dan reka bentuk kawalan mastitis dan program pencegahan dengan tujuan untuk membendung kerugian dan kos yang timbul akibat mastitis. Ini akhirnya akan membantu dalam memenuhi sasaran kemandirian susu tenusu dan memperbaiki ekonomi petani tenusu di Malaysia.

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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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## Declaration by Members of Supervisory Committee

This is to certify that:

- the research was conducted and writing of this thesis was under our supervision;
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## LIST OF ABBREVIATIONS

μL	Microliter
μM	Micro Molar
AA	Amino acid
AMIR	Antibody-Mediated Immune Response
AMR	Antimicrobial Resistance
API	Analytical Profile Index
APPs	Acute Phase Proteins
BHI	Brain Heart Infusion
BLAST	Basic Local Alignment Search Tool
BOLA	Bovine Leukocyte Antigen
bp	Base pair
CC	Clonal Complex
CI	Confidence Interval
CM	Clinical Mastitis
CMT	California mastitis test
CNS	Coagulase-negative Staphylococci
Da	Daltons
DANMAP	Occurrence of Antimicrobial Resistance in Zoonotic, Indicator, and Pathogenic Bacteria from Animals, Food, and Humans in Denmark
DEG	Database of Essential Genes
DLV	Double Locus Variant
DNA	Deoxyribonucleic Acid
dNTPs	Deoxyribonucleotide triphosphates
DVS	Department of veterinary services
EC	Electrical Conductivity

EDCD	Epidemiology Disease Control Division
EMA	European Medicines Agency
ESBL	Extended-spectrum beta-lactamases
ESVAC	European Surveillance of Veterinary Antimicrobial Consumption
F	Forward Primer
FAO	Food and Agriculture Organization
GC	Guanine-Cytosine
GERMAP	Consumption of Antibiotics and the Spread of Antibiotic Resistance in Human and Veterinary Medicine in Germany
Hp	Haptoglobin
HPCIAAs	Highest Priority Critically Important Antimicrobials
IBM	International Business Machine
IgG	Immunoglobulin G
IL	Interleukin
IMIs	Intramammary Infections
Kb	kilobyte
LDH	Lactate Dehydrogenase
LFQ	Left Front Quarter
LHQ	Left Hind Quarter
MARAN	Monitoring of Antimicrobial Resistance and Antibiotic usage in Animals in the Netherlands
Mb	Megabyte
MHC	Major Histocompatibility Complex
ml	Milliliter
MLEE	Multi-Locus Enzyme Electrophoresis
MLST	Multi-locus sequence typing
MRSA	Methicillin Resistant <i>Staphylococcus aureus</i>

MSA	Multiple Sequence Alignment
MSCC	Microscopic Somatic Cell Count
MSSA	Methicillin Susceptible <i>Staphylococcus aureus</i>
NAGase	N-acetyl-b-D-glucosaminidase
NAS	Non-aureus Staphylococci
NGS	Next Generation Sequencing
NMC	National Mastitis Council
NORM-VET	Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway
OECD-FAO	Organisation for Economic Co-operation and Development and the Food and Agriculture Organization of the United Nations
PCR	Polymerase Chain Reaction
PFGE	Pulsed-Field Gel Electrophoresis
PG	Prostaglandin
PMNs	Polymorphonuclear Neutrophils
PPIs	Protein-Protein Interactions
QTL	Quantitative Trait Loci
R	Reverse Primer
RFQ	Right Front Quarter
RHQ	Right Hind Quarter
RNA	Ribonucleic Acid
RV	Reverse vaccinology
SAA	Serum Amyloid A
SCC	Somatic Cell Count
SFMT	Surf Field Mastitis Test
SLST	Sodium Laurylsulphate Test
SLV	Single Locus Variant

SM	Subclinical Mastitis
SPSS	Statistical Package for Social Science
STs	Sequence types
SVARM	Swedish Veterinary Antimicrobial Resistance Monitoring
TNF-a	Tumor Necrosis Factor-a
TSST- 1	Toxic Shock Syndrome Toxin-One
UK	United Kingdom
UPM	Universiti Putra Malaysia
USD	United State Dollar
VFdb	Virulence Factors Database
WHO	World Health Organization
WST	Whiteside Test

# CHAPTER 1

## INTRODUCTION

### 1.1 General overview

Historically, evidences suggested that dairy cows are known to produce milk since 3100 BC (Nemet-Nejat, 1998) and it is therefore likely that bovine mastitis has been in existence since that period. For thousands of years, the closely study needed by hand milking helped in easy detection of abnormal signs in milk and the mammary gland, but there was little or no knowledge of the causes or how to handle mastitis. A greater understanding of mastitis was not feasible until the advancement in microscopes that helped in detection of microorganisms which form the major mastitis aetiological agents (Ruegg, 2017).

Tremendous advancements in the area of animal breeding, animal nutrition, and animal husbandry practices have helped in boosting the milk quantity around the world from the last forty years. This helped in meeting the increasing need for milk and its products (Shook, 2006). As a result of better understanding of host responses to intramammary infections (IMIs) and treatment protocols resulting from adoption of a number of controls and preventive measures (Oviedo-Boyso et al., 2007; Atalla et al., 2010), continuous changes have been observed on the predominance of mastitis etiology (Zadoks and Fitzpatrick, 2009). The detrimental economic effects of bovine mastitis has largely remained unchanged over the last decades (Hogeveen et al., 2011; Detilleux et al., 2015).

Bovine mastitis is the infection of the mammary gland in cows (Mushtaq et al., 2018b). It is among one of the most prevalent health disorders of lactating cows in the world, caused by infectious and non-infectious agents. The infectious form is caused by invasion, colonization and inflammation of the mammary gland by disease causing microorganisms such as bacteria, fungi, or algae. The non-infectious mastitis is a result of injury, chilling, bruising or poor milking procedures (Kumar et al. 2011).

The most commonly isolated bacteria from bovine mastitis are the staphylococci (Leitner et al., 2011) and *S. aureus* is the most common cause of bovine mastitis (Oliveira et al., 2007). However, non-aureus staphylococci (NAS) have become the most prevalent isolates from bovine mastitis in many countries and are considered predominant over *S. aureus* in most countries, and could therefore be regarded as emerging mastitis pathogens (Tremblay et



al., 2013). In addition to staphylococci, coliforms, enterococci, and streptococci are also frequently isolated from intramammary infections (IMIs) (Bradley et al., 2007).

*Staphylococcus aureus*, although mostly considered as human pathogen, has been isolated from a number of vertebrate species, showing the ability to thrive in numerous host environments (Kloos, 1980). Some decades ago, phenotypic variations between human and animal strains of *S. aureus* were identified, signifying that *S. aureus* strains associated with different animal habitat had acquired distinctive phenotypic features unique for their hosts (Fitzgerald, 2012).

The aptitude to correctly differentiate between strains of disease-causing agents is important for effective epidemiological and surveillance studies, determining the microbial population structure and dynamics, and at the end, developing better ways for tackling the spread of diseases in a community. To achieve these objectives, different molecular techniques for identifying and characterizing bacterial isolates from global or local disease outbreaks have been proposed (Foley et al., 2009). However, multi-locus sequence typing (MLST) is a standard technique for molecular typing (Ibarz Pavón and Maiden, 2009).

Traditional vaccines are typically deactivated or attenuated vaccines resulting from inactivating the virulence of the pathogen through physical or chemical means (Skwarczynski and Toth, 2012; Karch and Burkhard, 2016). As a result of the incessant development in immunology and molecular biology, subunit vaccines have been studied based on small and specific pathogen fragments. This is to solve the problem associated with traditional vaccines, such as reversion, virulence, inability to culture pathogens, and problems resulted from allergies and autoimmunity induced by the traditional vaccines (Nezafat et al., 2016; Karch and Burkhard, 2016).

The combination of immuno-proteomics with bioinformatics tools, such as reverse vaccinology (RV) and other in silico approaches, were used to analyze the surface exposed proteome of *S. aureus* with the view to identify vaccine antigenic targets (Misra et al., 2018). This method have been employed to identify conserved targets for candidate vaccines against many bacterial pathogens like *Pseudomonas aeruginosa* (Rashid et al., 2017), *Helicobacter pylori* (Naz et al., 2015), *Brucella melitensis* (Vishnu et al., 2017), and *Vibrio cholerae* (Nezafat et al., 2016).

## 1.2 Problem statement and significance of the study

Dairy farming is an important universal agricultural production. It forms an essential part of global food system and serve critical role in the sustainability of people in the rural areas in particular. The Malaysian dairy sector which consists of about 32,826 heads of cattle, 826 dairy farms cannot produce the dairy milk needed for local consumption (DVS, 2018) and as such Malaysia depends heavily on imports with a value added chain of RM 1.2 billion (Sim and Suntharalingam, 2015).

In order to boost local dairy production, the Malaysian dairy sector has received more government attention in recent years than in the past, part of which mastitis research was identified as a means of boosting production, and addressing the challenges of huge losses faced by local dairy farmers due to subclinical mastitis. The research areas identified includes but not limited to studying the epidemiology of mastitis pathogens, investigating antibiotic resistance profiles of mastitis pathogens and identifying candidate vaccines against most common mastitis pathogens in Peninsular Malaysia.

In addition, mastitis poses potential danger to human health because of possible zoonotic infection and food poisoning (Fernandes et al., 2011). There is serious concern in veterinary medicine on the rise of antimicrobial resistance among infectious agents that affects animal health. This trend of increasing resistance in animals have continued to pose serious threat to humans through possible zoonotic infection by those resistant pathogens. Mastitis is considered one of the largest cause of antibiotic use in dairy farms (Moon et al., 2007). Treatment of mastitis is associated with some setbacks mainly caused as a result of antibiotic misuse before *in-vitro* testing against the causal agents. This tradition contributes not only to the increase of the treatment failures in association with commonly used antimicrobials, but also to the economic losses (Owens et al., 1997). To ensure best treatment, isolation of bacterial pathogen and antibiotic sensitivity testing is important (Kaliwal et al., 2011).

Large scale data on the pervasiveness and microbial etiology of mastitis pathogens associated with subclinical mastitis as well as their antimicrobial resistance profiles are scanty. Knowledge on the molecular epidemiology and population structure of *S. aureus* as probable most prevalent mastitis pathogen is lacking. Identification of conserved immunogenic targets for candidate vaccines against major mastitis pathogens in Malaysia have never been attempted.

### 1.3 Research hypothesis

Studying the epidemiology of bovine mastitis and identifying vaccine targets against most common mastitis pathogens in Peninsular Malaysia would help in enhancing local dairy milk production and boost economy.

### 1.4 Aim and specific objectives

The aim of this study is to determine the epidemiology and characterise major bovine mastitis pathogens in selected dairy herds of Peninsular Malaysia

The specific objectives of the study were:

1. to determine the bacterial pathogens associated with bovine IMIs in selected dairy herds of Peninsular Malaysia and antimicrobial resistance profile of selected prevalent pathogens;
2. to determine the prevalence and risk factors of subclinical mastitis in selected dairy herds of Peninsular Malaysia;
3. to characterise *S. aureus* isolates from bovine mastitis cases in Malaysia; and
4. to identify immunogenic targets for the development of candidate vaccines against selected mastitis pathogens of Malaysian origin by reverse vaccinology approach.

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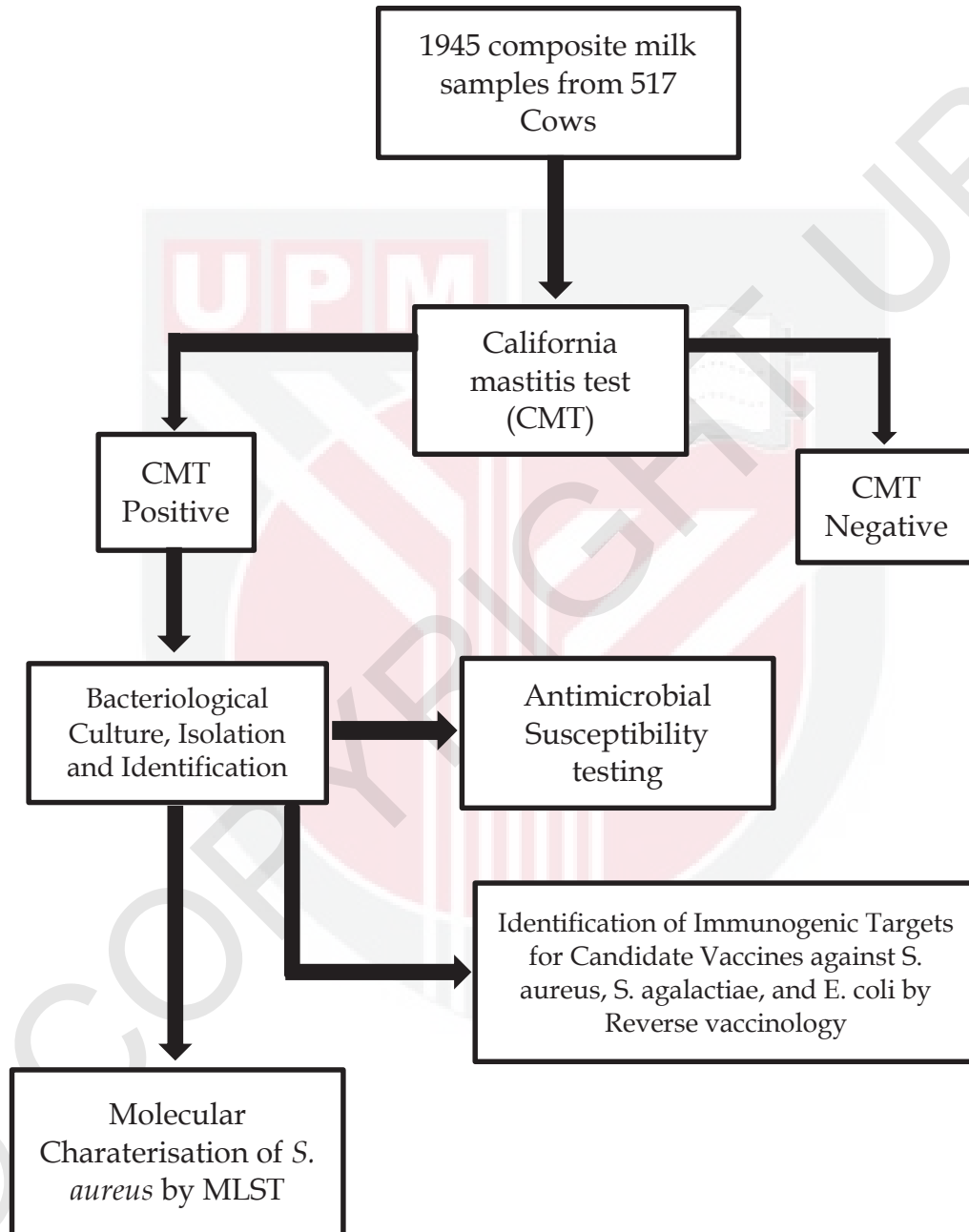
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## APPENDICIES

### Appendix A

General methodology flow chart



## Appendix B

### QUESTIONNAIRE ON BOVINE MASTITIS IN PENINSULAR MALAYSIA ADMINISTERED TO DAIRY FARMERS

#### SOAL SELIDIK MASTITIS PADA LEMBU DI SEMENANJUNG MALAYSIA YANG DIBERIKAN KEPADA PENTERNAK TENUSU

**NB:** All information obtained from this questionnaire will be used for the purpose of research only and nothing else and will be treated with utmost confidentiality.

**Nota:** Semua maklumat yang diperolehi dari soal selidik ini akan digunakan untuk tujuan penyelidikan sahaja. Semua maklumat adalah dirahsiakan.

**FARM LOCATION (LADANG):**.....

1. What is your farm size (Apakah saiz ladang anda)?
  - a) >50 cows (> 50 lembu)
  - b) 50 - 150 cows (50 - 100 ekor lembu)
  - c) >150 cows (> 150 ekor lembu)
  
2. What system of management do you practice in the farm (Apakah sistem pengurusan yang anda amalkan di ladang)?
  - a) Intensive (Intensif)
  - b) Semi intensive (Semi intensif)
  - c) Extensive (Ekstensif)
  
3. How often do you vaccinate your animals in the farm (Berapa kerap anda memvaksinasi haiwan di ladang)?
  - a) Never vaccinate (tidak pernah)
  - b) Rarely vaccinate (jarang)
  - c) Occasionally vaccinate (kadang-kadang)
  - d) Regularly vaccinate (sentiasa memvaksinasi)
  - e) Usually vaccinate (biasa memvaksinasi)
  
4. How often do you deworm your animals in the farm (Berapa kerap anda nyahcacing haiwan di ladang)?
  - a) Never deworm (tidak pernah)
  - b) Rarely deworm (jarang)
  - c) Occasionally deworm (kadang-kadang)



## Appendix C

### ANIMAL DATA FORM (DATA HAIWAN BORANG)

Farm Location (*Farm lokasi*) .....

1. Tag No (Tag No.) .....

2. Sample No. (No. sampel) .....

3. Age (Umur) .....

4. Breed (baka) .....

5. Parity

a) Primiparous

b) Multiparous

6. Stage of lactation (Peringkat laktasi)

a) Early lactation (laktasi awal)

b) Mid lactation (Mid laktasi)

c) Late lactation (Laktasi lewat)

d) Dry and calving period (Tempoh kering dan melahirkan)

7. Milking interval (Selang pemerah susu)

a) Once daily (sekali setiap hari)

b) Twice daily (dua kali setiap hari)

8. Milk yield per head/ day (hasil susu seekor/hari)

.....

9. Type of mastitis (jenis mastitis)

a) Clinical (klinikal)

b) Subclinical (subklinikal)

10. Udder quarter(s) affected (suku raba(s) terjejas)

a) Front Right (depan kanan)

b) Hind Right (belakang kanan)

c) Front Left (depan kiri)

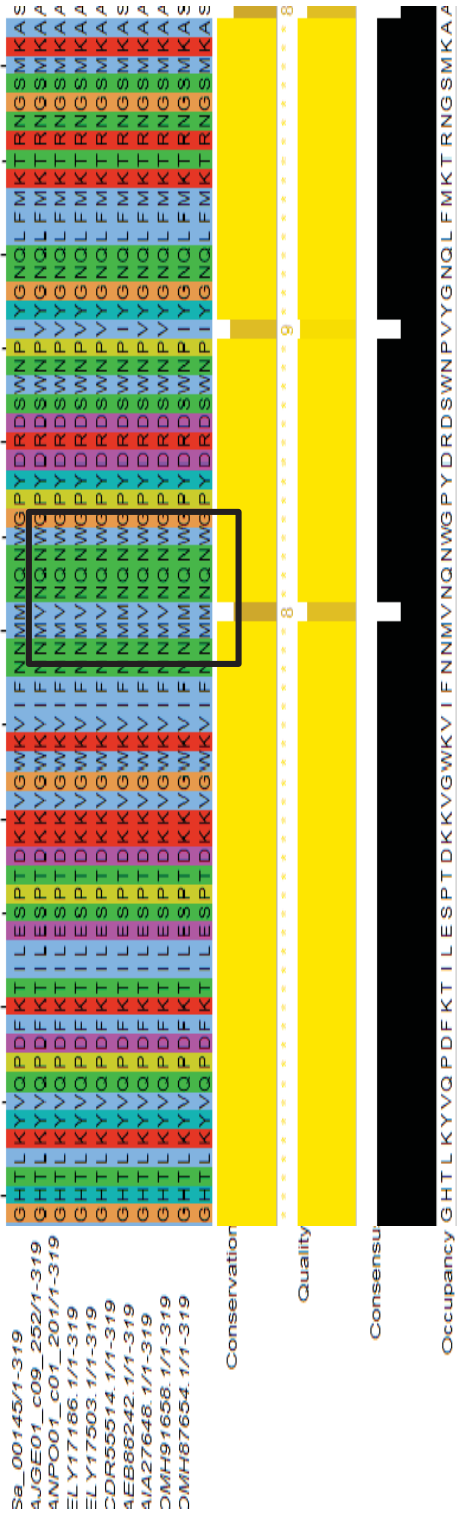
d) Hind Left (belakang kiri)

11. Previous treatment history for mastitis (sejarah rawatan mastitis)

a) Treated (dirawat)

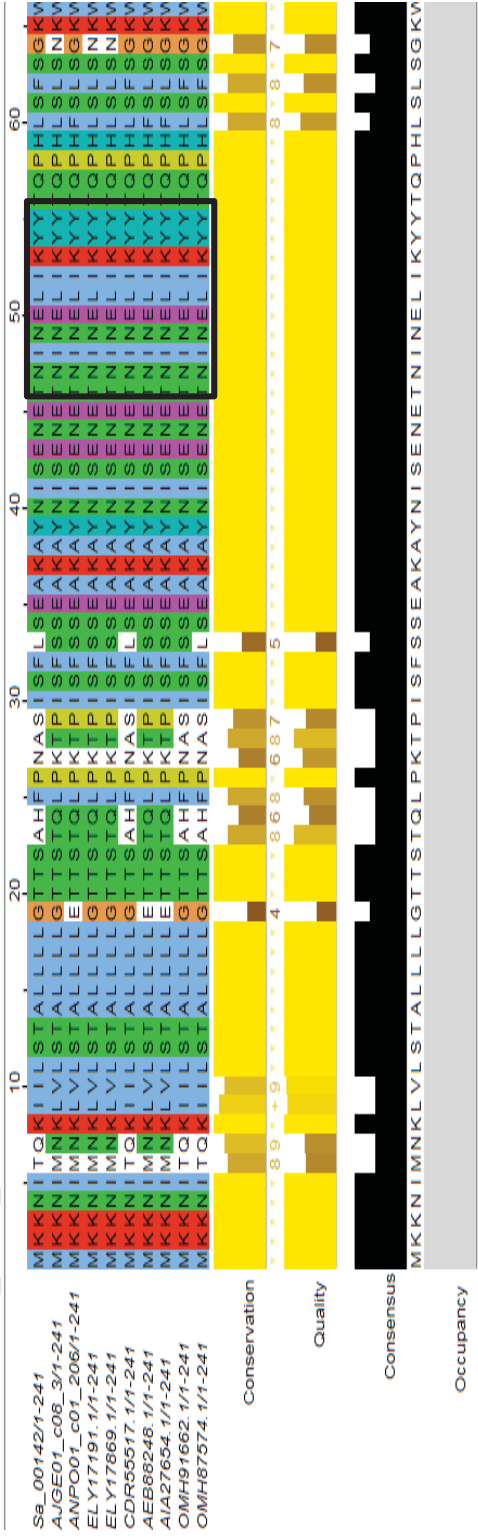
b) Never treated (tidak dirawat)





**b. Cytolysin**

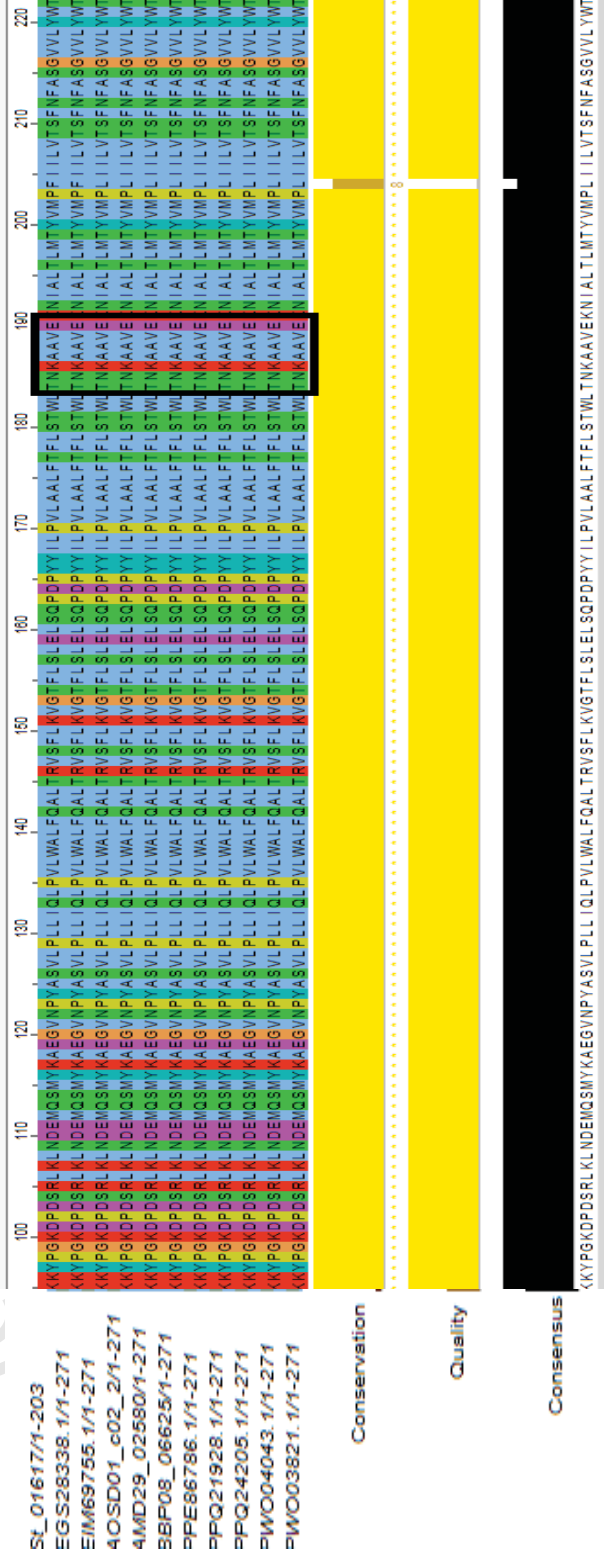




c. Super antigen-like protein SSL14







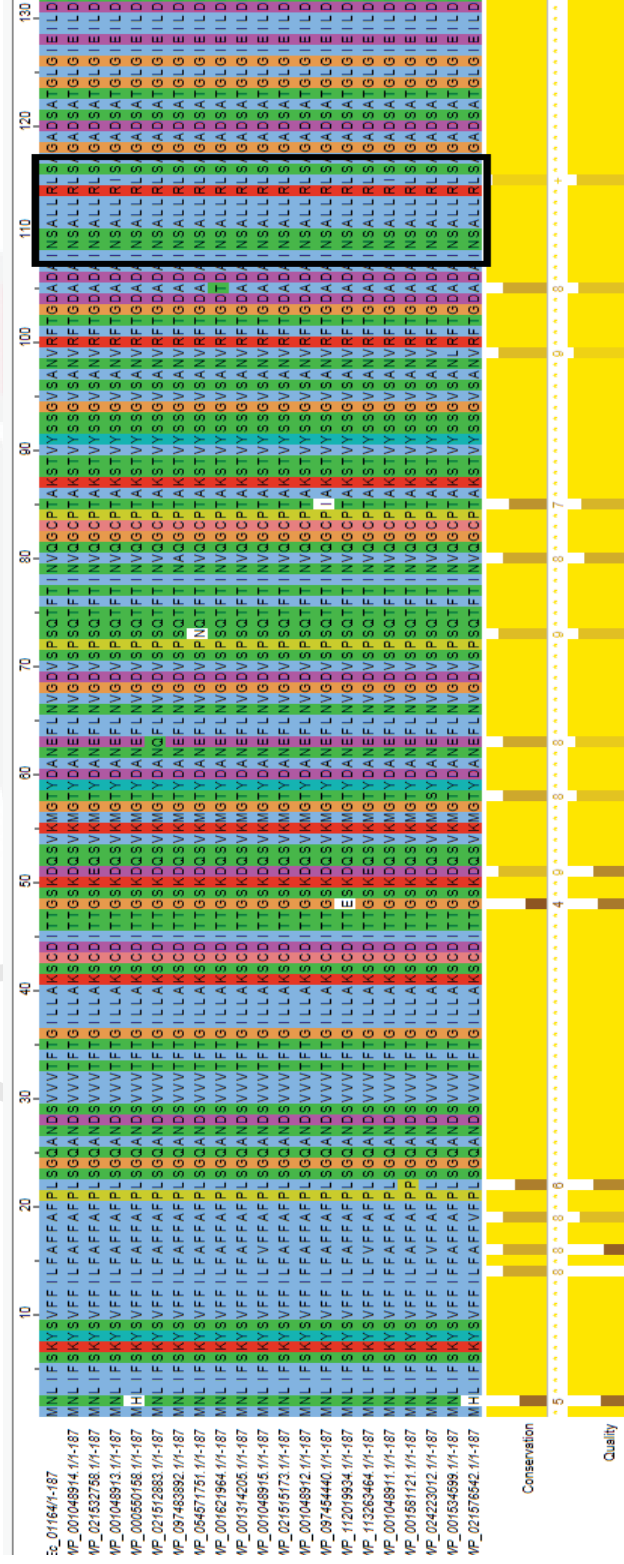
b. Stage III sporulation protein





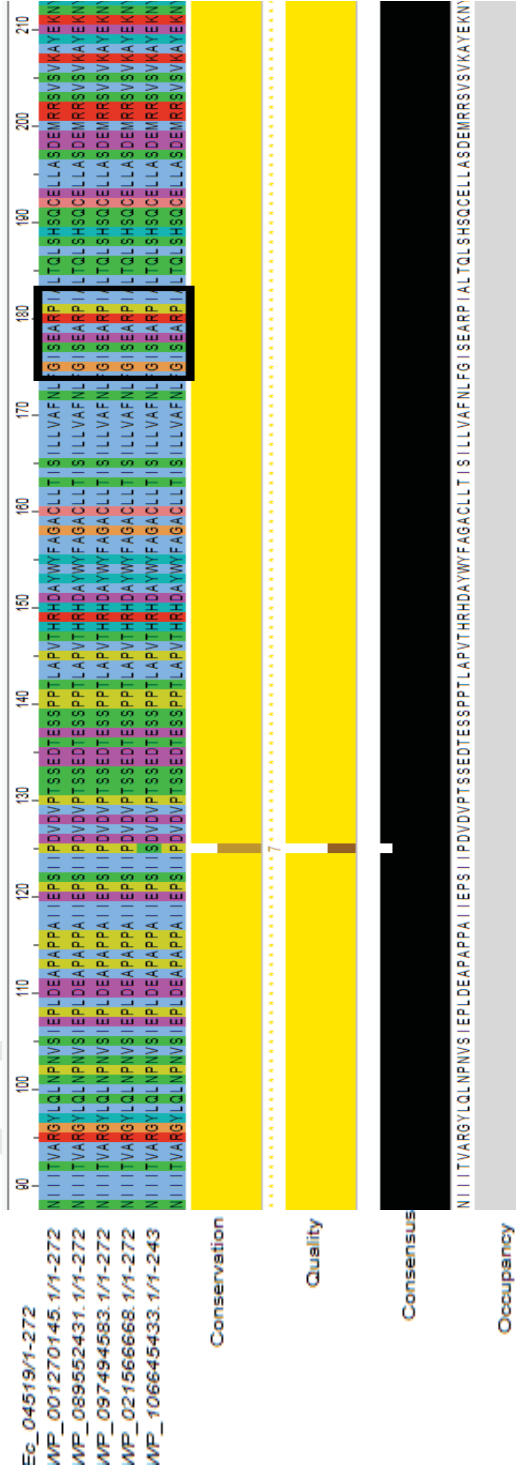
## Appendix F

Aligned regions showing conserved epitopes among various strains of *E. coli* for some of the prioritized proteins.

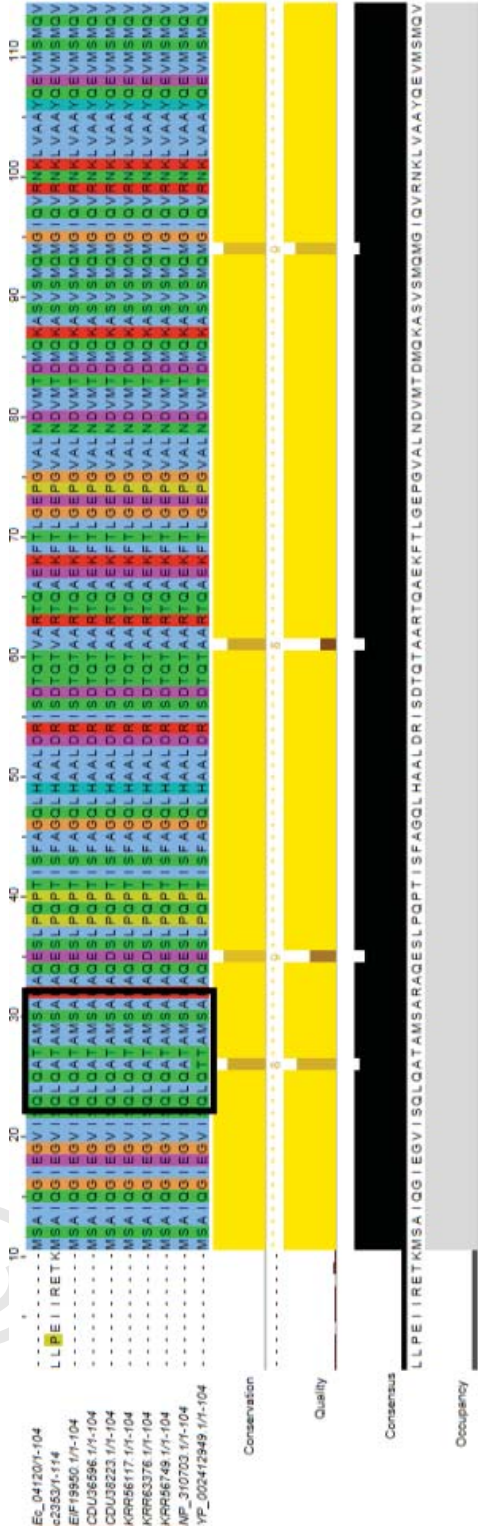


a. Type 1 fimbrial protein





b. Winged helix family transcriptional



c. Flagella hook body complex



## BIODATA OF STUDENT

Bashir Ali was born in Sabon Garin Ya'ya' Town of Taura Local Government on 20<sup>th</sup> January 1984, to the family of Alhaji Ali Yaro and Mallama Rafi'atu Muhammad. He attended Sabon Garin Ya'ya' Primary School from the year 1989 to 1995. In the year 1995 he went to Government Secondary School Roni, Jigawa State for his Junior Secondary School education. When he was in JS two, he was chosen to write Science and Technical School's Entrance Examination in the year 1997. He proceeded with his Secondary School education at Science Secondary School Kafin-Hausa from 1997 to 2000. In the year 2001 Bashir Ali was enrolled into the Interim Joint Matriculation Board (IJMB) programme at then Hussaini Adamu Polytechnic, College of Engineering and Technology, now Federal Polytechnic, Kazaure. In the year 2004, Bashir Ali started his undergraduate studies at Department of Biological Sciences, Bayero University, Kano, where he obtained his first degree in Microbiology (B.Sc.) in the year 2008. In August 2008, He went for National Youth Service Corps, where he served at Ibn Fartuwa Islamic Science Secondary School, Monguno in Borno State. During his service year, he held a position of Vice Principal Academics and President of Peer Education Trainers (PETs), a group shouldered with the responsibility of campaigns and awareness on HIV/AIDS and reproductive health. In the year 2009, Bashir Ali started his working career as Education Officer II under the Ministry of Education Jigawa State, where taught in Government Secondary School Harbo in Jahun Local Government, Jigawa State until the year 2011. In the year 2011, Bashir Ali moved to Joint Admissions and Matriculation Board (JAMB) where he served as Administrative Officer II until 2014. In the year 2014, because of his readiness to accept academic challenges, Bashir Ali moved to the then newly established Jigawa State University, now Sule Lamido University as Graduate Assistant. He obtained his master's degree in Medical Microbiology in the 2015 from Bayero University Kano. In the year 2017 he started his PhD studies in Faculty of Veterinary Medicine, Universiti Putra Malaysia where he is enrolled to study PhD Bacteriology. Bashir Ali is happily married and blessed with three children.

## LIST OF PUBLICATIONS

- Bashir, A., Zunita, Z., Jesse, F. F. A., Ramanoon, S. Z., & Mohd-Azmi, M. L. (2019b). Whole-Genome Shotgun Sequence of *Streptococcus agalactiae* Sequence Type 176 Strain 3966RFQB from a Dairy Herd in Selangor, Malaysia. <https://doi.org/10.1128/MRA.01618-18>.
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- Bashir, A., Zunita, Z., Jesse, F. F. A., Ramanoon, S. Z., & Mohd-Azmi, M. L. (2019). Emergence of *staphylococcus argenteus* as Bovine Mastitis Pathogen in Malaysia. *14<sup>th</sup> Proceedings of Seminar on Veterinary Sciences, Veterinary Association of Malaysia Congress*.pp.68.
- Bashir, A., Zunita, Z., Jesse, F. F. A., Ramanoon, S. Z., & Mohd-Azmi, M. L. (2019a). Interrogating the Whole-Genome Shotgun Sequence of *Escherichia coli* Sequence Type 127 Strain 1538RHQ, Which Harbors Virulent Antigenic Factors, Isolated from a Mastitic Cow. *Microbiology Resource Announcements*, 8(48). <https://doi.org/10.1128/MRA.01057-19>.
- Short Communication: Genomic Based Antimicrobial Resistance and Virulence Genes of *Staphylococcus argenteus* ST2250 Associated with Bovine Mastitis in Malaysia. (Submitted)
- Prevalence of Subclinical mastitis and its associated risk factors in Malaysian Dairy herds. (Submitted).
- Prevalence of Pathogens Associated with Intramammary Infections and Antimicrobial Resistance Profiles from Dairy herds in Malaysia. (Submitted).
- Multilocus sequence typing of *S. aureus* isolates from subclinical mastitis in Malaysia. (Drafted Manuscript).
- Identification of Candidate Vaccine Targets against Mastitis Pathogens in Malaysia: A Reverse Vaccinology Approach. (Drafted Manuscript).



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