UNIVERSITI PUTRA MALAYSIA

A RETROSPECTIVE STUDY (2006-2021) OF FINAL YEAR PROJECT INVOLVING TWO VETERINARY SCHOOLS (UPM and UMK) IN MALAYSIA FOCUSING IN LARGE RUMINANT LIVESTOCK

DHARSHINI A/P SUBRAMANIAM

A RETROSPECTIVE STUDY (2006-2021) OF FINAL YEAR PROJECT INVOLVING TWO VETERINARY SCHOOLS (UPM and UMK) IN MALAYSIA FOCUSING IN LARGE RUMINANT LIVESTOCK

DHARSHINI A/P SUBRAMANIAM

FACULTY OF VETERINARY MEDICINE
UNIVERSITI PUTRA MALAYSIA
SERDANG, SELANGOR
2022/2023

A RETROSPECTIVE STUDY (2006-2021) OF FINAL YEAR PROJECT INVOLVING TWO VETERINARY SCHOOLS (UPM and UMK) IN MALAYSIA FOCUSING IN LARGE RUMINANT LIVESTOCK

DHARSHINI A/P SUBRAMANIAM

A project paper submitted to the Faculty of Veterinary Medicine, Universiti Putra Malaysia
In partial fulfilment of the requirement for the
DEGREE OF DOCTOR OF VETERINARY MEDICINE
Universiti Putra Malaysia
Serdang, Selangor Darul Ehsan.

DECEMBER 2022

CERTIFICATION

It is hereby certified that I have read this project paper entitled "A Retrospective Study (2006-2021) Of Final Year Project Involving Two Veterinary Schools (UPM and UMK) In Malaysia Focusing In Large Ruminant Livestock", by Dharshini a/p Subramaniam, and in my opinion, it is satisfactory in terms of scope, quality, and presentation as partial fulfilment of the requirement for the course VPD 4999 – Final Year Project.

PROFESSOR DR. FAEZ FIRDAUS JESSE ABDULLAH
DVM (UPM), PHD (UPM),
Lecturer,
Faculty of Veterinary Medicine,
University Putra Malaysia
(Supervisor)

DEDICATION

This thesis is especially dedicated to:

My beloved parents (Subramaniam and Anbarasi)

My respected supervisor (Professor Dr. Faez Firdaus Jesse Abdullah)

My fellow DVM friends

ACKNOWLEDGMENT

I would like to extend my gratitude to the Almighty. It is the blessings from the Almighty that helped me obtain the guidance I needed throughout my Final Year Project.

Next, I would like to thank my supervisor, Prof Dr Faez Firdaus Jesse Abdullah who guided me throughout this project. His patients, guidance and encouragement were helpful for me.

I would also like to thank my fellow co – fyp mate, Alisya. I was able to complete my project work with her support and teamwork.

Not forgetting my family for being there for me and giving me moral support throughout this project.

I am also very grateful to my DVM friends who helped me in one way or another in completing my Final Year Project.

CONTENT

LIST OF FIGURES

LIST OF ABBREVIATIONS

UPM	Universiti Putra Malaysia
UMK	Universiti Malaysia Kelantan
FYP	Final Year Project
DVS	Department of Veterinary Services
OIE	World Organisation for Animal Health
HS	Hemorrhagic septecimea
FMD	Foot and Mouth Disease
CBPP	Contagious Bovine Pleuropneumonia
MCF	Malignant Catarrhal Fever
LSD	Lumpy Skin Disease
IBR	Infectious Bovine Rhinotracheitis

ABSTRAK

Abstrak daripada kertas projek yang dikemukakan kepada Fakulti Perubatan Veterinar untuk memenuhi sebahagian daripada keperluan kursus VPD 4999 – Projek Tahun Akhir.

Kajian Retrospektif (2006-2021) Projek Tahun Akhir melibatkan Ternakan Ruminan Besar daripada dua Fakulti Perubatan Veterinar (UPM dan UMK) di Malaysia.

oleh

Dharshini a/p Subramaniam

2022

Penyelia: Professor Dr Faez Firdaus Jesse Abdullah

Daripada manuskrip saintifik yang diterbitkan didapati terdapat laporan kes klinikal dan manuskrip saintifik daripada dapatan penyelidikan yang diterbitkan melibatkan ternakan ruminan besar di Malaysia. Sehingga pada hari ini, didapati mempunyai kekangan dan kekurangan dalam kajian melibatkan analisis berkaitan kajian penyelidikan projek tahun akhir dalam haiwan ruminan besar yang melibatkan dua buah Fakulti Perubatan Veterinar iaitu Universiti Putra Malaysia (UPM) dan Universiti Malaysia Kelantan (UMK) di Malaysia. Maka kajian ini dilaksanakan bagi mengenal pasti dan menganalisis tren kajian penyakit berjangkit dan tidak berjangkit yang melibatkan ternakan ruminan besar yang telah dijalankan bagi projek tahun akhir oleh graduan program Doktor Perubatan Veterinar (DPV) dan mengenalpasti bidang fokus kajian penyelidikan mengikut ketetapan lokasi geografi yang berbeza bagi kedua dua buah fakulti (UPM dan UMK). Bagi pengumpulan data untuk memenuhi objektif kajian ini, tesis projek tahun akhir daripada tahun 2006 sehingga tahun 2021 telah diperolehi daripada perpustakaan UPM dan UMK dan data daripada tesis ini telah direkodkan. Bilangan disertasi projek tahun akhir yang melibatkan kajian berkaitan penyakit ruminan besar di UPM adalah sebanyak 68 kajian manakala di UMK hanya 12 kajian sahaja. Daripada analisis kajian ini menunjukkan bahawa kajian di UPM dan UMK telah menunjukkan tren yang sama di mana sejumlah besar topik kajian mereka menumpu kepada punca penyakit berjangkit pada kadar 91.2% (62/68 kajian) dan 100% (12/12 kajian) masing-masing. Kedua-dua buah fakulti perubatan veterinar menunjukkan tren yang serupa bagi kajian yang melibatkan penyakit sistem pembiakan mana UPM dan UMK masing-masing merekodkan sebanyak 25/62 (40.3%) dan 6/12 (50%) kajian. Bagi faktor lokasi geografi kajian mana sebanyak 44/56 (78.6%) kajian daripada UPM dan 1/11 (9.1%) kajian daripada UMK telah dijalankan di kawasan bandar manakala sebanyak 12/56 (21.4%) kajian dan 10/11 (90.9%) kajian dilaksanakan di kawasan luar Bandar bagi UPM dan UMK masing-masing. Dapatan daripada analisis kajian ini i akan membantu para-penyelidik untuk menyusun strategi bagi topik dan bidang penyelidikan bagi projek tahun akhir untuk haiwan ruminan besar bagi masa akan datang kelak.

Kata kunci: Ruminan besar; Penyakit; Projek Tahun Akhir; Fakulti Perubatan Veterinar; UPM; UMK; Tren.;

ABSTRACT

An abstract of the project paper presented to the Faculty of Veterinary Medicine in partial fulfilment of the course VPD 4999 – Final Year Project.

A Retrospective Study (2006-2021) of Final Year Project involving Two Veterinary Faculties (UPM and UMK) in Malaysia Focusing on Large Ruminant Livestock

by

Dharshini a/p Subramaniam

2022

Supervisor: Professor Dr Faez Firdaus Jesse Abdullah

There are case reports and research manuscripts published involving large ruminant livestock in Malaysia. Till date, there is lack of analyses on the large ruminant studies that were embarked for the past 15 years involving Final Year Projects by Doctor of Veterinary Medicine graduates from 2 Veterinary Faculties, Universiti Putra Malaysia (UPM) and Universiti Malaysia Kelantan (UMK) in Malaysia. Therefore, this study aims to identify and analyse the trends of infectious and non-infectious caused disease studies involving large ruminant livestock that was carried out in DVM FYP projects and to determine the focal studies at different geographical settings (UPM and UMK). FYP thesis from the year 2006 till 2021 was obtained from the library of UPM and UMK to record the information needed. Total number of FYP studies involving large ruminant diseases in UPM was 68 studies while in UMK only 12 studies. UPM and UMK showed the same trend where the majority of their studies focused on the infectious causes with 91.2% (62/68 studies) and 100% (12/12 studies) respectively.

Both veterinary faculties showed similar trends where the majority FYP studies involve reproductive system where UPM and UMK recorded 25/62 (40.3%) and 6/12 (50%) studies respectively. For geographical settings, 44/56 (78.6%) studies in UPM and 1/11 (9.1%) studies in UMK were done in urban areas while 12/56 (21.4%) studies in UPM and 10/11 (90.9%) studies in UMK were done in rural areas. The outcomes from this study will aid the researcher to strategize the upcoming FYP research in ruminant disease subject matter in the future.

Keywords: Large ruminant; Diseases; FYP; Veterinary Faculties; UPM; UMK; Trends.

1.0 INTRODUCTION

Domesticated cattle and buffalo make up the majority of large ruminants. They are useful mammals for humans because they can obtain energy from plant-based feed and transform it into food (Zakaria et al., 2019). Ruminants still play a significant part in agricultural research. Large ruminant livestock may be affected by infectious or non-infectious diseases (Badruzzaman et al., 2014).

Viral, bacterial, parasitic, and fungal infections can all be categorised as infectious caused large ruminant diseases that affect cattle and buffalo. Foot-and-mouth disease (FMD), rinderpest, vesicular stomatitis, Contagious Bovine Pleuropneumonia, Lumpy Skin Disease (LSD), Rift Valley fever, anthrax, bluetongue, leptospirosis, rabies, paratuberculosis, bovine anaplasmosis, babesiosis, brucellosis, genital campylobacteriosis, tuberculosis, cysticercosis, dermatophilosis, and enzootic bovine leucosis, haemorrhagic septicaemia, , infectious pustular vulvovaginitis, infected bovine rhinotracheitis (IBR), trypanosomiasis, trichomoniasis, theileriosis, bovine spongiform encephalopathy and malignant catarrhal fever (MCF) are the some of the examples infectious causes of large ruminant diseases. . The non-infectious causes of large ruminant disease are mineral and nutritional causes such as selenium-related illness, copper deficiency, iodine deficiency, phosphorus deficiency, poisoning, the dietary causes such as feed overload, intolerance and allergy, dietary indiscretion, foreign body ingestion, gastro-intestinal obstruction, mucosal injuries such as gastric ulcers, inflammatory bowel disease and neoplasia, intestinal dysbiosis, enzyme deficiencies and miscellaneous or congenital defects causes such as cancer and lameness (Gallagher A., 2020).

A study conducted in Peninsular Malaysia, by Saharee and Fatimah (1993) stated that Pasteurella spp. infections are the most common small and large ruminant disease Other ruminant diseases studied in Malaysia are brucellosis, pasteurellosis, hemorrhagic septicaemia, mannheimiosis, caseous lymphadenitis, mastitis, and parasitic gastroenteritis (Anka et al., 2014; Othman et al., 2014; Zamri-Saad and Annas, 2016; Fitri et al., 2017; Sadiq et al., 2019).

Till date, only 1 study was recorded to analyse ruminant disease in Malaysia where this study conducted by Zakaria et al. (2019) studied common health problems in ruminants involving Malaysia where this study analysed gross pathology cases involving ruminants between year 2006 till 2017.

1.1 Justification

Till date, there is lack of analyses on the large ruminant studies that were embarked for the past 15 years involving Final Year Projects by Doctor of Veterinary Medicine graduates from 2 Veterinary Faculties (UPM & UMK) in Malaysia. The outcome from this study will aid the researcher to strategize the upcoming research in this field and the data from this research will be used in teaching and learning for ruminant disease subject and clinical ruminant rotation.

1.2 Research Objectives

The objectives of this study are:

1. To identify and analyse the trends of infectious and non-infectious caused disease studies involving large ruminant livestock that was carried out in DVM FYP projects (UPM & UMK) over the time 2006-2021 (15 years).
2. To determine the focal studies involving large ruminant livestock at different geographical settings of the 2 veterinary faculties in Malaysia (UPM & UMK).

2.0 LITERATURE REVIEW

There are a few listed diseases that are reportable under World Organisation for Animal Health (OIE) and the Department of Veterinary Services (DVS).

(a) Anthrax

All mammals, including humans, and certain bird species are susceptible, anthrax is largely a disease of herbivorous animals. Mortality rates can be quite high, particularly in herbivores. Bacillus anthracis, Gram-positive rod-shaped bacteria, is the etiological agent (OIE, 2018).

In some places, gnawing insects may be linked to disease transmission. Years may occur between outbreaks because *B. anthracis* spores in the soil turn inactive and persist for a long time. Higher soil types, calcium concentrations, rising temperatures and humidity, a pH that is slightly alkaline, higher levels of decomposing organic waste, as well as the organism's ability to survive in a hostile environment are all natural factors that contribute to the spread of the disease. The spore is also resistant to heat, sunlight, drying, and a variety of disinfectants (Sushma et al., 2021).

The clinical signs of acute anthrax in cattle, sheep, and goats are fever, staggering, excitation/somnolence, recumbency, spasms, trembling, and dyspnea, and the infected animal dies within 48-72 hours. Acute symptoms include a high fever of 42°C, excitement, a congested and haemorrhagic mucosa, tachycardia, laboured breathing with terminal convulsions, and death. In dairy cattle, abortion, reduced milk production, and discoloured milk (blood-tinged or deep yellow) have all been reported. The characteristic clinical sign of chronic anthrax is swelling and oedema in the subcutaneous area, which is usually seen in the brisket, shoulder, thorax, perineum, and flank. Diarrhoea and dysentery are common symptoms of gastrointestinal tract involvement. There is localized tongue oedema as well as oedematous lesions in the throat, sternum, perineum, and flanks (Alam, 2022).

Anthrax can be confirmed by detecting *B.anthracis* in an animal carcass through examination of a stained blood smear, culture, or polymerase chain reaction (PCR). Culture and (or) PCR are thought to be superior to microscopy, but they necessitate infrastructure and consumables that few laboratories in developing countries have (Aminu et al., 2020).

(b) Brucella

Brucella disease in the herd is usually caused by biovars (bv.) of *Brucella abortus*. In few nations, specifically in south Europe, Africa, and Western Asia, where herds are retained in confined space accompanying sheep or goats, *B.melitensis* contamination can happen (Verger, 1985). *B. suis* can periodically cause contaminations in cattle. Although the affliction is extensive, many nations are considered innocent two together *B. abortus* and *B. melitensis* (OIE, 2022). Natural transmission happens through the ingestion of structures that are plentiful in aborted foetuses, foetal membranes, and uterine discharges. Cattle can consume infected feed and water or lick the genitals of different mammals. Venereal transmission of the bacterium from contaminated bulls to naive cows performs to be exceptional. Brucella has existed cured from foetuses and manure that has existed stocked in a cool atmosphere for as well two months. Direct sunlight kills the animals in a matter of hours (Nicoletti, 2016). The most accepted dispassionate manifestation in significant female bovine and confusion is failure. Abortion occurrence is affected by a type of variables, to a degree the stage of gestation, the load of pathogens present and animal opposition. As an alternative to failure, calves may be untimely, stillborn, or feeble. Metritis and placental memory are usually present in subsequent failure, and two together environments can cause infertility that is to say either lasting or temporary (Megid ., 2014). Brucella contamination can be rooted by observing the microorganisms in smears tainted with a tiny stain. Smears may be tested with Ziehl-Neelsen (MZN) stains and can be obtained from vaginal discharges, placenta, colostrum, fetal stomach fluid, aborting herd lochia, or aborted fetus abomasum. Smears of foetal stomach fluid, cotyledons, or lochia can again be groomed and contaminated with the enhanced Ziehl-Neelsen stain or stamp stain. Brucella animals act out cardinal intracellular coccobacilli or rod shapes in MZN-tainted smears, when in fact different microorganisms stain blue (Tulu, 2022). According to another study, DNA by PCR is the only arrangement that admits the fact of disease. Biotyping provides valuable epidemiological facts that admit contaminations traced back to their inceptions in nations where diversified biotypes co-exist (Godfroid et al., 2010).

(c) Foot and mouth disease

Foot and mouth disease (FMD) is ultimately contagious sickness, and susceptible animals with cloven hooves might undergo severe economic losses. Seven serotypes of the FMD virus (FMDV) exist namely, O, A, C, SAT 1, SAT 2, SAT 3, and Asia 1. One serotype's immunity does not provide immunity to another. Clinically, FMD and other vesicular illnesses such swine vesicular disease, vesicular stomatitis, and vesicular exanthema are identical. Thus, it is crucial to confirm any suspected FMD condition with laboratory testing (OIE, 2009).

Cattle are greatly susceptible to FMDV infection through the respiratory route, and particular regions of the nasopharyngeal epithelium harbouring MALT have been identified as the location of early viral replication (Arzt et al., 2018).

The viral strain, exposure dosage, animal age and breed, host species, and level of host immunity all affect how severe the clinical indications are. Mild, hardly noticeable, and severe symptoms are all possible. Morbidity might be close to 100%. Adult animals generally have lower mortality rates (1–5%), whereas young calves, lambs, and piglets have higher rates (20% or more). Recovery typically takes two weeks in simple circumstances. In cattle, vesicles on the buccal and nasal mucous membranes, and/or among the claws and coronary band, can cause pyrexia, anorexia, shivering, decline in milk production for 2-3 days, then smacking of the lips, grinding of the teeth, salivating, lameness, stamping or kicking of the extremities. After 24 hours, the vesicles rupture, leaving erosion Recovery usually takes 8 to 15 days. Some issues incorporate hoof deformities, tongue erosions, superinfecting of lesions, super infection of lesions alongside permanent milk production deterioration, myocarditis, abortion, irreversible weight deficit, and lack of heat regulation (OIE, 2013). The current methods for diagnosing FMD include virus isolation (VI), sandwich-ELISA (S-ELISA), liquid-phase blocking ELISA (LPBE), multiplex PCR (m-PCR), and indirect ELISA (DIVA), and real-time PCR can be used to find antibodies against non-structural proteins (Longjam et al., 2011).

(d) Bovine anaplasmosis

Anaplasma marginale infection causes outbreaks of bovine anaplasmosis. Although *Anaplasma centrale* can cause mild anemia, clinical outbreaks in the field are intensely infrequent. *Anaplasma phagocytophilum* and *A. bovis* (Dumler et al., 2001), the two of which have a fundamental reservoir in rodents, have been found to contaminate cattle but do not cause clinical disease (Hofmann-Lehmann et al., 2004; Dreher et al., 2005; &OIE, 2018).

Studies have proved that few animals display manifestations as early as a 10% loss of RBCs (Wanduragala and Ristic, 1999), while others display manifestations 65% before clinical indications manifest, accompanying a mean between 35% and 50% (Susan, 1999; Zaugg et al., 1999). As the anaemia increases, the acutely afflicted animals swiftly deteriorate. Icterus, weight loss, dehydration, constipation with greenish-hard, dry faeces, dark yellow urine, and developing respiratory syndromes might occur. Additionally, aggressive behaviour, animal abortion, and hypoxia-related mortality are again potential results (Ramanoon, 2003).

A. marginale can be seen in Giemsa-stained blood smears from clinically infected animals during the acute phase of the illness, aiding in the diagnosis of bovine anaplasmosis. It cannot be used to find carriers or animals exhibiting early symptoms. In these situations, the infection is often identified by the serologic display of antibodies, which is followed by confirmation through molecular detection techniques. Numerous enzyme-linked immunosorbent assays (ELISA) such as cELISA, indirect ELISA, and dot ELISA, as well as the complement fixation (CF) test, capillary agglutination assay, card agglutination test (CAT), indirect fluorescent antibody (IFA) test, and other serological tests such as the complement fixation (CF) test, have been frequently used in epidemiological studies. (Aubry., 2010). The two serological tests now used to determine infected animals are the cELISA and the CAT (OIE, 2008). In order to identify the presence of low-level infection in carrier cattle and tick vectors, nucleic acid-based Polymerase Chain Reaction (PCR) assays have also been developed. The gold standard for confirming *A. marginale*-free blood is sub inoculation of blood from the suspicious animal into a splenectomised calf that is very vulnerable to infection. (Coetzee et al., 2006).

(e) Babesiosis

Babesiosis is a tick-borne infection caused by various species of Babesia protozoa. Babesiosis in bovine animals is caused by the pathogens *Babesia bigemina* and *Babesia bovis*. Other species of bovine babesiosis consist of *Babesia divergens*, *Babesia major*, *Babesia jakimovi*, *Babesia ovata*, and *Babesia occultans*. The primary vector is an Ixodidae tick accompanying a single host. The coarse vector for *B.bigemina* is *Boophilus annulatus*, while the vector for *B. bovis* is *Boophilus microplus* (Rahman W.A. et al., 2010).

The basic vectors *of B.bigemina* and *B.bovis* are 1-host Rhipicephalus (Boophilus) spp ticks, which are established during the whole of the tropics and subtropics. Transovarial transmission happens. Although these Babesia spp. possibly easily transmitted by blood inoculation in the laboratory, mechanical transmission by insects or during surgical procedures is of no practical importance. Intrauterine contamination has been reported, but it is exceptional (Carter et al., 2022). Water buffaloes contaminated with *B.bovis* displayed milder (less severe) clinical signs of infection when compared to cattle contaminated with *B. bovis*. These clinical signs included a significant increase in body temperature (40-41.5 °C), anemic conjunctival and vaginal mucous membranes, and a loss of body condition (Mahmood, 2013). The affected buffaloes did not have icterus, hemoglobinuria, or nervous manifestations (Alvarez et al., 2019).

(f) Bovine spongiform encephalopathy

Bovine spongiform encephalopathy (BSE) is a fatal neurodegenerative condition that affects bovines and is classified as a transmissible spongiform encephalopathy (TSE) (Kumagai et al., 2019).

Classic BSE is caused by ingesting infected animal-source proteins (meat and bone meal) that are fed to cattle. The source of new BSE contagions isn't primarily via horizontal transmission. Compared to calves born to uninfected cows, calves born to infected cows are more likely to develop BSE. Nonetheless, this medium of transmission is less significant than diseases acquired through contaminated feed sources. Aerosols or touch don't horizontally transmit BSE. No coitus or breed predilection exists (Seuberlich, 2016).

The condition is distinguished by changes in behaviour, perception, and locomotion, as well as gradual weight loss and decreased milk production. The most common behavioural differences are apprehension and an abnormal temperament. Extreme muzzle licking, kicking during milking, and hypersensitivity to tactile, auditory, and visual stimuli are the most common differences in sensitivity. Some of the most serious locomotive issues are ataxia, falling down, and difficulty getting back up (Braun University, 2002).

The typical laboratory diagnosis of BSE includes an examination of the brain's histopathology and the detection of the mutant prion protein, PrP (BSE), in brain tissue. These tests have the disadvantage of being laborious and time-consuming, so the results will not be available for several days. ID-Lelystad has recently been developed as the new post-mortem test that allows for the rapid screening of larger numbers of brain samples for PrP. This BSE test is only for slaughterhouse surveillance. In comparison to the gold standard of diagnosis in histology, an early validation study discovered that both sensitivity and specificity were 100 percent (van Keulen et al., 2000).

(g) Haemorrhagic septicaemia

A rapid, severely lethal septicaemia with significant morbidity and mortality is the feature of haemorrhagic septicaemia (HS), a serious condition that affects cattle and buffaloes. It is brought on by specific *Pasteurella multocida* serotypes that are only found in particular regions of Asia, Africa, the Middle East, and southern Europe. Animals' nasopharynx are home to the Gramnegative coccobacillus *Pasteurella multocida*, which lives there mostly as a commensal (OIE, 2021).

The two primary routes of infection are ingestion of contaminated feed or water and contact with infected oral or nasal secretions from either healthy carrier animals or animals displaying clinical illness. The infection begins in the tonsil and nearby nasopharyngeal tissues. Bacteraemia then causes tissue damage, a host cytokine response, the production of lipopolysaccharides, and the fast progression of endotoxaemia as a result of the dissemination and rapid development of bacteria in numerous locations. After infection, clinical signs might appear one to three days later, and death can occur between eight and twenty-four hours afterwards. (Mosier, 2022).

The initial signs of HS in cattle and buffalo are fever, lethargy, and a reluctance to move (OIE, 2021). Later, oedematous swellings in the pharyngeal area become evident before extending to the ventral cervical region and brisket. Salivation and a serous nasal discharge also occur. Generally speaking, buffaloes are more prone to HS than cattle and display more severe forms of the illness with significant clinical symptoms. Acute disease is characterised by a temperature of 104°-106°F (40°-41.1°C), lethargy or restlessness and a reluctance to move, hyper salivation, lacrimation, and nasal discharge that starts off serous and proceeds to mucopurulent. Acute disease can last up to 3 days and, less frequently, up to 5 days. Along with growing respiratory distress, cyanosis, terminal recumbences, and subcutaneous oedema in the pharyngeal area that spreads to the ventral neck and brisket (and occasionally the forelimbs), there may also be stomach discomfort coupled with diarrhoea. (Mosier, 2022).

The slide agglutination test (Namioka and Murata, 1961), the indirect haemagglutination test for capsular typing (Carter, 1955), and the agar gel immunodiffusion test are among the serological procedures used to identify the HS (Heddleston et al., 1972). A sensitive and precise test was ELISA (El-Jakee et al., 2016).

(i) Contagious Bovine PleuroPneumonia

Contagious Bovine PleuroPneumonia (CBPP) is a severe OIE notifiable respiratory disease of cattle caused by *Mycoplasma mycoides subsp. mycoides*, characterized by severe fibrinous bronchopneumonia and pleural effusion during the acute to sub acute stages and by pulmonary sequestrate in chronic cases. CBPP can cause important productivity losses for the bovine industry due to the high mortality and morbidity rates (Teodoro et al., 2020). Many diagnostic methods for CBPP are based on serological reactions like those in enzyme-linked immunosorbent assays (ELISA), complement fixation tests, immunohistochemical tests, and protein immunoblotting methods which can be time-consuming and some of which are not sufficiently specific or sensitive (Dedieu, 1996). PCR has the advantage of being a fast, specific, and very sensitive technique. Most of the diagnostic PCR systems which are used today (Hotzel H., 1996) are designed to target the CAP-21 gene, whose gene product has an unknown function. Alternative diagnostic PCR systems based on other parts of the genome can be useful. The 16S rRNA genes provide well-examined sequences with segments of different evolutionary variability, which are ideal target regions for primers in group-specific or species-specific amplification. Mycoplasmas belonging to the *M. mycoides* cluster have two rRNA operons (Pettersson, 1994). Species identification based on PCR of the 16S rRNA genes and restriction in positions where unique differences (polymorphisms) occur between the two operons has been demonstrated previously for *M. capricolum subsp.capripneumoniae* (Bascuñana, 1994).

(j) Theileria

Numerous species of protozoan parasites that infect domestic and wild ruminants in tropical and subtropical areas of the world belong to the genus Theileria (Uilenberg, 1981; Morrison, 2015). *Theileria parva* and *Theileria annulata*, two of the most significant species impacting cattle, result in high rates of illness and death in sensitive animals (Uilenberg, 1981; Irvin and Morrison, 1987).

While *Theileria parva*, which is primarily spread by *Rhipicephalus appendiculatus*, is present throughout a large portion of eastern and southern Africa, *Theileria annulata*, which is transmitted by a number of species of Hyalomma ticks, is found in a large subtropical zone extending from southern Europe and North Africa through the Middle East into Asia (Pipano, 1989). (Irvin and Morrison, 1987; Lawrence et al., 1994). The Asian and African varieties of buffalo are also affected by these parasites (*Bubalis bubalis* and *Syncerus caffer*, respectively). African buffalo are infected with *T. parva* across the tick vector's range, but unlike cattle, the illness does not appear to affect the buffalo. However, they represent a reservoir of infection for transmission of the parasite to cattle and hence are an important consideration in the application of disease control measures (Morrison et al., 2019).

Anorexia, emaciation, reduced rumination, lacrimation, corneal opacity, nasal discharge, diarrhoea, terminal dyspnea, and frothy nasal discharge are some of the clinical indications of theileriosis infection in cattle (Fukasawa, 2003).

The development of molecular diagnostic technologies such as polymerase chain reaction (PCR) has made diagnosis more effective than with earlier methods (Collins et al. 2002). Studies on a variety of parasites have led researchers to the conclusion that PCR is more sensitive than traditional methods (Bishop et al., 1992; Tahar et al., 1997). For the identification of *T. annulata*, four diagnostic techniques, including blood and lymph node biopsy smear analysis and PCR of blood and lymph node biopsy material, were established. Among these, it was discovered that the PCR assay was more accurate and sensitive than the microscopic inspection. (Dehkordi et al., 2012).

(n) Lumpy skin disease

A severe viral illness in cattle known as lumpy skin disease (LSD) is thought to be mechanically spread by blood-feeding arthropods (Magori-Cohen et al., 2012). The LSD virus (LSDV), a member of the *Poxviridae* family's *Capripoxvirus* genus, is the culprit behind the illness (Babiuk et al., 2008). It is widespread in several African nations (Tuppurainen et al., 2011). LSD is a serious danger to the rest of Asia and Europe and is still readily available in the Middle East (Abutarbush et al., 2013; Tageldin et al., 2014).

Arthropod-vectored transmission is thought to be the primary method. Although no particular vector has been found so far, the virus may be transmitted by mosquitoes, biting flies, and male ticks. The function of direct touch in the virus's transmission is thought to be minimal, if any at all (OIE, 2017).

Large variability can be seen in the clinical presentation of LSDV infection, which can range from subclinical illness to mortality (Carn & Kitching, 1995). These include fever, the development of skin nodules on the neck, back, tail, hind legs, and sexual organs, the growth of the superficial lymph nodes, and, in a small number of animals, swelling of the limbs and brisket along with lameness. Emaciation, decreased or stopped milk supply, low weight increase, miscarriage, myiasis, and permanent damage to hides that lowers their market value all result in significant economic losses (Abutarbush et al., 2013; Al-Salihi, 2014; Abera et al., 2015). Dependent on insect activity, sensitivity, and cow immunological condition, morbidity and death might vary substantially. Morbidity has been measured in the range of 2% to 85% and even higher. Though it is rare (1%–5%), mortality can occasionally reach 40% (Davies, 1991).

(o) Q fever

Except for New Zealand, the world is generally endemic with Q fever (or coxiellosis). Almost all animal kingdoms, including arthropods, have the disease's causative agent, *Coxiella burnetii*, but people, cattle, sheep, and goats are the primary hosts (Lang, 1990). Domestic ruminants are thought to be the principal *C. burnetii* reservoirs, however cats, dogs, rabbits, birds, etc. have also reportedly been linked to human illness or infection.

The virus is mostly spread by the inhalation of dried aerosol particles and through contact with infected animals, their reproductive tissues, or other animal products, such as wool, according to epidemiological and experimental data (ECDC, 2010). Although ingesting has frequently been theorised, notably through the intake of dairy products made from tainted raw milk, there is currently little convincing evidence of major food-borne disease transmission to people. Even while exposure during delivery, through sexual transmission, or through blood transfusion is conceivable, Q fever appears to be extremely seldom contagious from person to person. Although their significance is unknown, sexual and vertical transmission in animals may occur. Finally, the spread of Q fever may be aided by arthropods, particularly ticks (OIE, 2018).

Ruminant coxiellosis infection is mostly asymptomatic; however it can cause anorexia and late abortion. Compared to animals that have experienced an abortion, sub clinically infected animals shed substantially lower bacterial loads of the organism in foetal fluids and vaginal secretions. Infertility, sporadic abortions, and necrotizing placentitis in ruminants have all been linked to *C burnetii* in reports. However, further research is needed to confirm *C.burnetii* as the causal agent. New data has linked *C. burnetii* to subclinical mastitis in dairy cows. Experimental infection results in several-day-long anorexia, malaise, and short-lived fever in cats (Plummer, 2022).

Microscopy on clinical samples and positive serological findings has historically been used to diagnose Q fever in ruminants, including distinguishing it from other causes of miscarriage (Lang, 1990). The techniques of choice for clinical diagnosis should be direct detection and quantification by PCR and serological ELISA (enzyme-linked immunosorbent assay), as there is currently no gold standard methodology available (Sidi-Boumedine et al., 2010; Niemczuk et al., 2014).

2.2 Department of Veterinary Services

Some published reports and data by Department of Veterinary Services (DVS) via Veterinary Research Institute (VRI) stated that the presence of important infectious disease among ruminants in Malaysia such as trypanosomiasis, caused by Trypanosoma evansi, FMD infections in cattle, buffaloes, and pigs, Johne's disease in ruminants, and bovine babesiosis.

2.3 Studies in Malaysia

Till date, no study was recorded or published in Malaysia in the analyses of the large ruminant studies that were embarked for the past 15 years involving Final Year Projects by Doctor of Veterinary Medicine graduates from 2 Veterinary Faculties (UPM & UMK) in Malaysia. The outcome from this study will aid the researcher to strategize the upcoming research in this field and the data from this research will be used in teaching and learning for ruminant disease subject and clinical ruminant rotation.

3.0 MATERIALS AND METHODS

3.1 Search strategy

This study is designed to collate detailed information on trends of infectious and non-infectious caused disease studies and focal studies involving large ruminant livestock that was carried out in DVM FYP projects over the time 2006-2021 (15 years) of the 2 veterinary faculties in Malaysia (UPM & UMK) from the thesis stored at Library of UPM and UMK. E-library UPM was used to access the thesis from the library. Keywords used were large ruminant, diseases, FYP, veterinary schools, UPM, UMK, trends & 2006-2021. In UMK, the thesis was found manually.

3.2 Screening of thesis

Only those cases involving disease and diseases causing agents were included in this study. Thesis that does not involve diseases and are related to sexual status, management and behaviour were excluded.

3.3 Data extraction

Information of each case, including infectious or non-infectious disease, agent studied, system involved, type of study and place of study were analysed. Infectious diseases were categorized based on the affected body systems; the circulatory, respiratory, GIT, ocular, neurology, limb/hoof, lymph node, reproductive and integumentary systems. The data extracted from the abstract were infectious/non-infectious disease, disease, system, area and type of study.

3.4 Data analysis

All these data that are collected will be analysed and will be presented as bar charts and pie charts. The data will also be analysed to answer the objectives and hypotheses of this study.

In this study comparison is made for the data studied in this study for the two veterinary faculties and this study was designed to obtain data studied that have been conducted previously according to the content of table stated above. The data will be presented as percentage (descriptive data). The data will be used to compare the trend of infectious and non-infectious cause of disease that has been studied by both veterinary faculties in UPM and UMK.

4.0 RESULTS

A total of 80 theses were selected and analysed, consisting of 68 from UPM (2006-2021) and 12 from UMK (2015-2021). The most frequently affected body systems for cattle and buffalo in both the veterinary faculties were the same, which is the reproductive system. In UPM, out of 68 theses studied, only 6 studies have been done on non-infectious disease while for UMK none was done.

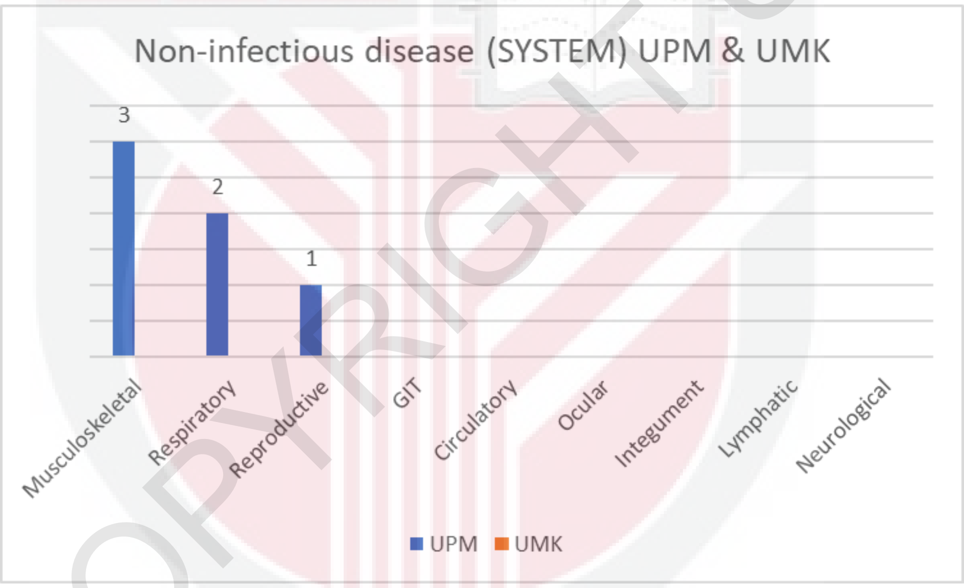

Figure 4.1 Non-infectious disease (SYSTEM) in large ruminant in UPM and UMK from 2006-2021

For non-infectious diseases categorized by system, musculoskeletal system was most studied with 3/6 (50%) followed by respiratory system 2/6 (33%) and finally reproductive system 1/6 (17%).

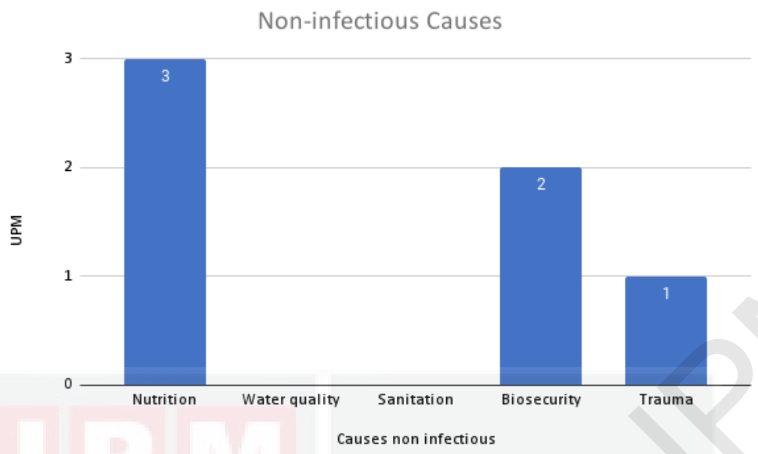

Figure 4.2 Non-infectious causes in large ruminants in UPM and UMK from 2006-2021

Nutrition [2/6(33%)], biosecurity [3/6(50%)] and trauma [1/6(17%)] were covered by UPM involving non-infectious causes from 2006-2021.

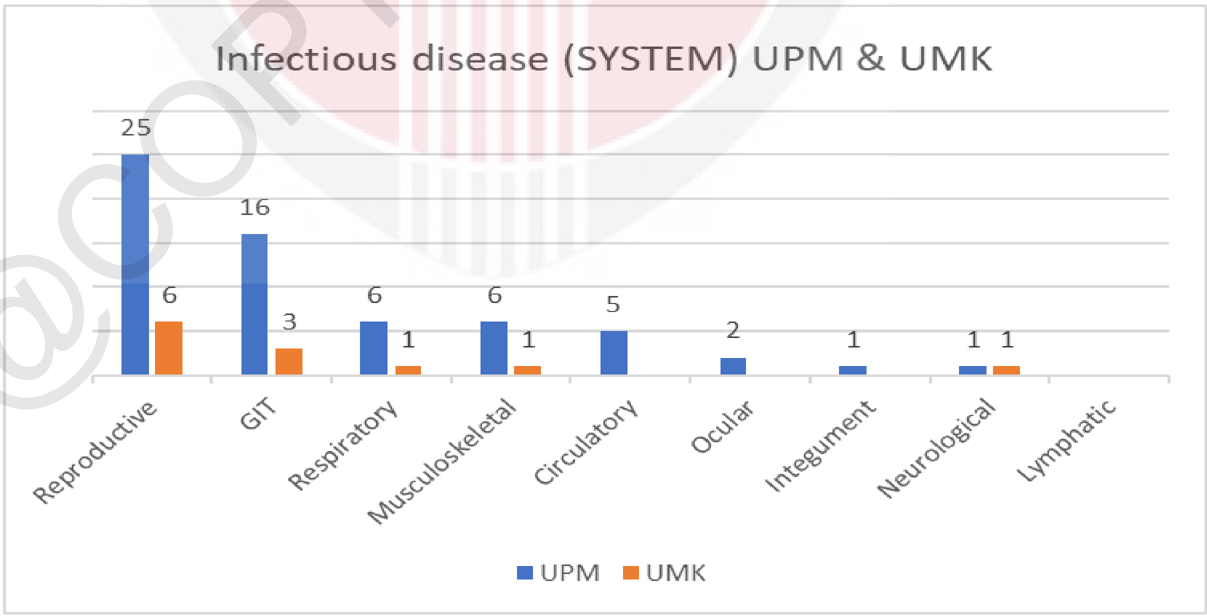

Figure 4.3 Infectious disease (SYSTEM) in Large Ruminant in UPM & UMK from 2006-2021

Total of 62 thesis studies in UPM and all 12 in UMK covers infectious disease. The trend of study done in UPM and UMK are almost the same because the system studied the most by both veterinary faculties is the reproductive system followed by GIT. UPM has covered 25 studies on reproductive which is 40.3% of the total study done by the particular veterinary faculties whereas UMK has 6 studies which is 50% of studies covered by them. The GIT system is the second most covered with 16/62(25.8%) and for UMK, 3/12 (25%). Both the veterinary faculties have only 1 study done on the neurological system, UPM 1/62 (1.6%) and UMK 1/12(8.3%). UPM has done study on ocular system 2/62 (3.2%), integumentary system 1/62 (1.6%) and circulatory system 5/62(8.1%) but UMK has yet to do so. Musculoskeletal studies have 6/62 (9.7%) studies covered in UPM while only 1/12 (8.3%) in UMK. Respiratory system has 6/62 (9.7%) studies covered in UPM but only 1/12 (8.3%) in UMK. There have been no studies done on the immune system in both veterinary faculties.

There are 62 infectious agents studied by UPM involving various agents that affect various systems from the 68 theses obtained while in UMK only 12 infectious causes were studied.

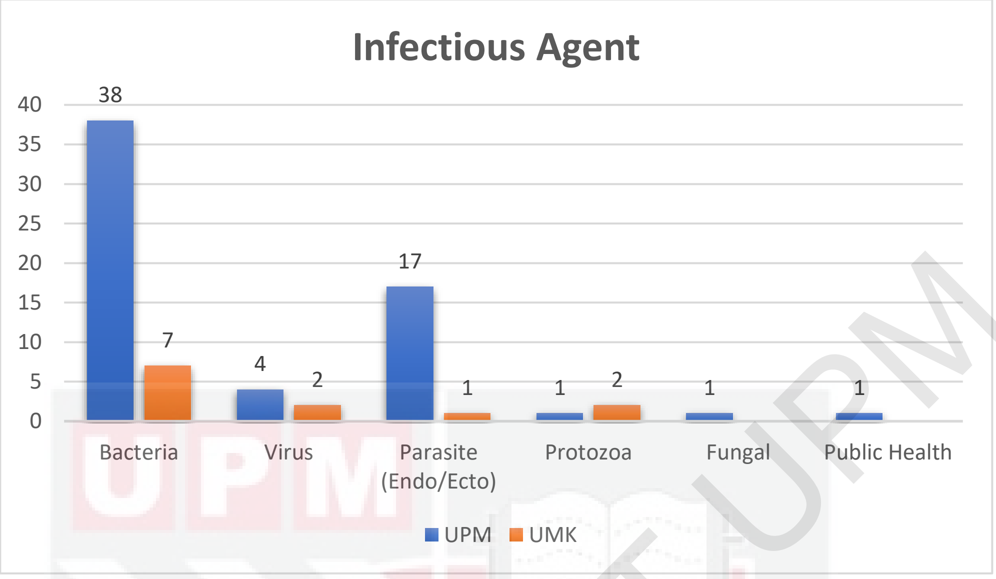

Figure 4.4 Infectious agents in large ruminants in UPM and UMK from 2006-2021

There were a few infectious causes that were studied such as bacteria, virus, parasite, protozoa, fungal and public health. Bacteria were the most studied agent in both UPM and UMK. [39/62(62.9%)] in UPM and [7/12(58.3%)] studies were done respectively. In UPM [4/62 (6.5%)] studies were done involving viruses and in UMK [2/12(16.7%)] studies were done. Followed by parasites, where in UPM and UMK there were [17/62(27.4%)] and [1/12(8.3%)] studies done respectively. Protozoa was studied in both the veterinary faculties with [1/62(1.6%)] study in UPM and [2/12(16. 7%)] studies in UMK. There was no study on fungal and public health done in UMK but [1/62(1.6%)] study on fungal and [4/62(6.5%)] study on public health done in UPM.

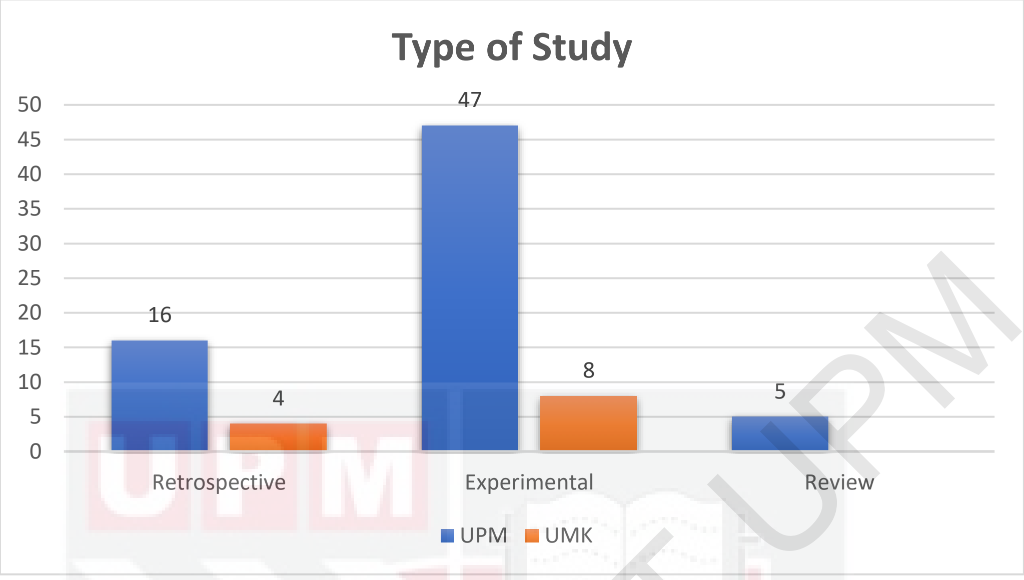

Figure 4.5 Type of study in large ruminants in UPM and UMK from 2006-2021

Experimental study is the most preferred choice by the both veterinary faculties. 47 out of 68 (69.1%) studies were experimental studies in UPM and 8 out of 12 (66.7%) were studies involving experiment in UMK. Experimental studies which include field sampling and laboratory testing. Second preferred choice of study by both veterinary faculties are the retrospective study where 16/68 (23.5%) was done in UPM and 4/12 (33.3%) in UMK. Review type of study was only conducted in UPM and with involvement of 5/68 studies (7.4%).

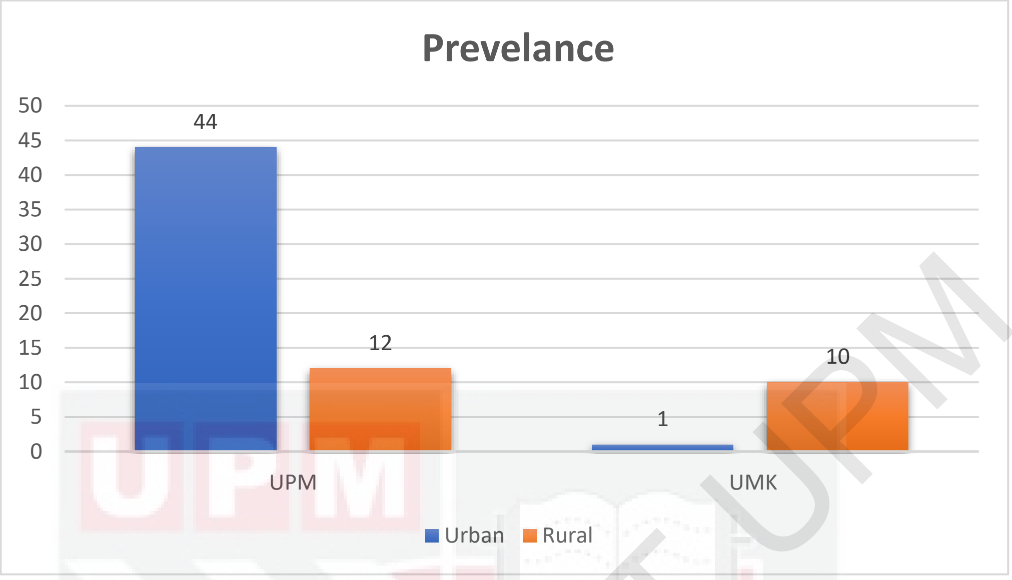

Figure 4.6 Prevalence of study in large ruminants in UPM and UMK from 2006-2021

For prevalence, 12/56 (21.4%) of study done by UPM and 10/11(90.9%) study done by UMK is in the rural setting. 44/56(78.6%) study in UPM was done in urban areas and 1/11(9.1%) study in UMK took place in urban areas.

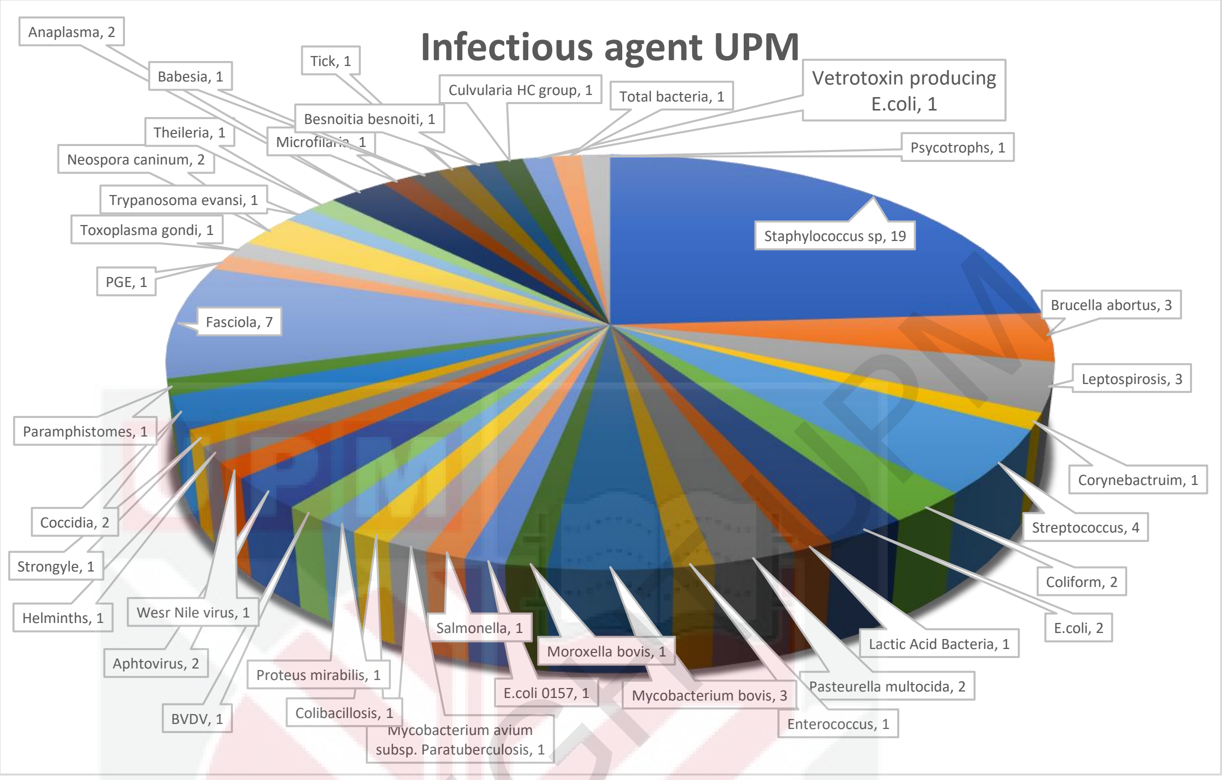

Figure 4.7 Infectious agent in large ruminant in UPM from 2006-2021

Out of the 68 theses studied, there were 79 infectious agents studied by the students from UPM for the past 15 years. *Staphylococcus sp*. (19), *Brucella abortus* (3), *Leptospirosis sp.* (3), *Corynebacterium* (1), *Streptococcus sp.* (4), Coliform (2), *E.coli* (2), Lactic acid bacteria (1), *Pasteurella multocida* (2), *Enterococcus* (1), *Mycobacterium bovis* (3), *Moroxella bovis* (1), *E.coli 0157* (1), Salmonella (1), *Mycobacterium avium subsp. Paratuberculosis* (1), Colibacillosis (1), *Proteus mirabilis* (1), Bovine Viral Diarrhea Virus (1), *Aphtovirus* (2), West Nile Virus (1), Helminths (1), Strongyle (1), Coccidia (2), Paramphistomes (1), Fasciola (7), PGE (1), *Toxoplasma gondi* (1), *Trypanosoma evansi* (1), *Neospora caninum* (2), Theileria (1), Anapalsma (2), Babesia (1), Microfilaria (1), Besnoitia besnoiti (1), Tick (1), Culvularia HC group (1), Verotoxin producing *E.coli* (1) and Psycotrophs (1) was covered.

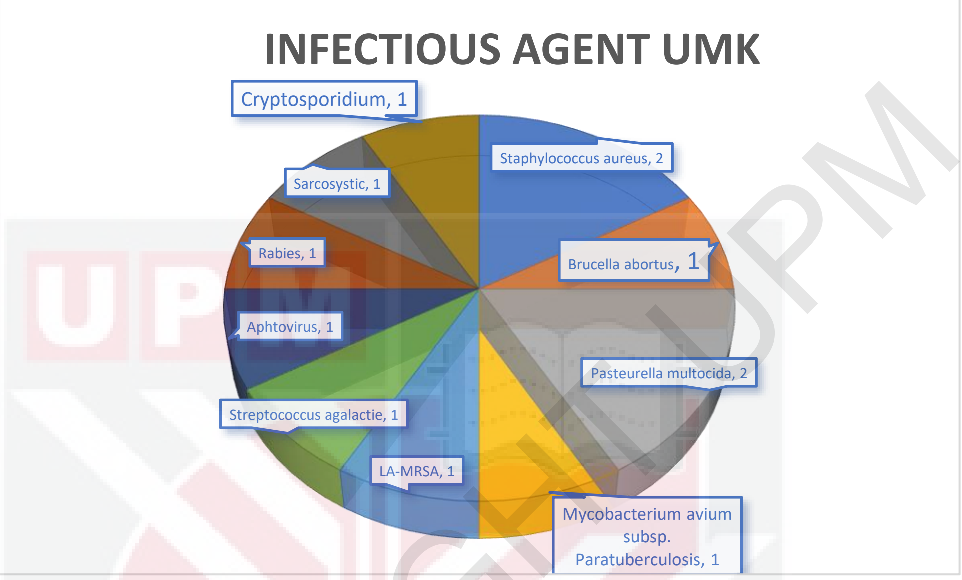

Figure 4.8 Infectious agent in large ruminant in UMK from 2006-2021

Out of 12 theses studied, 12 infectious agents were covered by UMK which are *Staphylococcus aureus* (2), *Brucella abortus* (1), *Pasteurella multocida* (2), *Mycobacterium avium subsp. Paratuberculosis* (1), LA-MRSA (1), *Streptococcus agalactiae* (1), Aphtovirus (1), Rabies (1), Sarcorcystic (1) and cryptosporidium (1).

5.0 DISCUSSION

As we can observe in this study that out of 68 theses only 6 studies covered non-infectious disease while in UMK no study was recorded. This shows that the trend of infectious disease study is the highest among both the veterinary faculties Where else the non-infectious causes are studied the least.

It is very important to know that the non-infectious disease is the major contributor to production loss and economy in ruminant industry. This is in agreement with a study stated that maintaining cattle in good health is not only important for animal well-being, but also has implications on animal productivity which directly affects the economy (Michelle, 2019). For instance, non-infectious causes may lead to infertility. Major non-infectious causes of infertility in dairy cattle includes congenital abnormalities, acquired lesions, nutritional, seasonal and environmental causes which may be overlooked in most cases (Tsige et al., 2019). Biosecurity and husbandry may also lead to various diseases in large ruminants such as respiratory problems, lameness, and many more. A study by Underwood (2015)stated that when ruminants are confinement housed, proper ventilation is critical. Ammonia build-up and other waste gases may induce respiratory problems. Most of the time non-infectious diseases are caused by poor management factors and studies on this aspect should be increased to bring awareness and to identify the wrong and right management in order to increase production.

Diseases involving reproductive system due to infectious cause was studied extensively by the both veterinary faculties in this study. The economic and environmental sustainability of dairy, meat, and working farmers are impacted both directly and indirectly by improvements in reproductive efficiency, according to Vecchio et al. (2021). Another possible reason why this system has received the most attention in this study is may due to clear-cut of the clinical symptoms that are present in diseases involving this system where examples of the symptoms such as abortion, placenta retention, endometritis, and others. In both veterinary faculties, the neurological system is the least studied and this might be the result of a neurological illness being challenging to diagnose based solely on clinical signs. This can be because of the size of the population as well as concerns over the security of the students and supervisors. An article stated that claims that failure to diagnose neurological cases in large ruminants is due to the animal's large size or nature, which negatively impacts the quality of the neurological examination, lends weight to this assertion (Constable, 2017). For instance, in a case an ataxic belligerent beef cow that is still able to walk, there are high possibilities that it may attack the tester may make it exceedingly challenging to conduct an adequate neurologic examination. The immune system also has not been studied by both the veterinary faculties in Malaysia. This particular system needs more research as large ruminants often challenged by disease outbreak due to bacteria, viruses, parasites, and toxins emitted by feed, air, water, wildlife, other cattle, and even humans. (Cooke, 2010).

In UPM and UMK, there wasonly one study recorded for fungi study. Fungal research is crucial since it causes a variety of harmful diseases, including mycosis. All large ruminant animals are susceptible to mycosis, which is caused by various agricultural fungus. The illness results in financial loss due to morbidity and mortality (Ahmad, 2016). Fungi can also improve animal health and provide excellent contributions to animal feed. There are medicinal and edible fungi in addition to brewing fungi. (Chuang et al., 2020).

6.0 CONCLUSION AND RECOMMENDATION

In conclusion, this retrospective study reveals that the trend of infectious study is higher than non-infectious study. Not only that, the geographical setting of the veterinary faculties seems to play a role in the prevalence of study that has taken place. Thus, it is recommended that in future more studies on non-infectious disease should be conducted. The veterinary faculties in Malaysia should also expand the research ground to a more diverse geographical setting.

7.0 REFERENCES:

Ahmad, R.Z. and Gholib, D. (2016): Important mycotic diseases in animal livestock caused by some agriculture fungi in Indonesia. Int. J. Trop. Vet. Biomed. Res. 1(1): 38–44.

Alam, M. E., Kamal, M. M., Rahman, M., Kabir, A., Islam, M. S., and Hassan, J. (2022): Review of anthrax: A disease of farm animals. J. Adv. Vet. An. Res., 9(2): 323–334.

Alvarez, J. A., Rojas, C., and Figueroa, J. V. (2019): Diagnostic Tools for the Identification of Babesia sp. in Persistently Infected Cattle. Pathogens., 8(3): 143.

Aminu, O. R., Lembo, T., Zadoks, R. N., Biek, R., Lewis, S., Kiwelu, I., Mmbaga, B. T., Mshanga, D., Shirima, G., Denwood, M., and Forde, T. L. (2020). Practical and effective diagnosis of animal anthrax in endemic low-resource settings. PLoS Neglected Tropical Diseases., 14(9): 1–17.

Arzt, J., Belsham, G. J., Lohse, L., Bøtner, A., and Stenfeldt, C. (2018): Transmission of Foot-and-Mouth Disease from Persistently Infected Carrier Cattle to Naive Cattle via Transfer of Oropharyngeal Fluid. MSphere, 3(5): 00365-18.

Aubry, P., and Geale, D. W. (2011). A review of Bovine anaplasmosis. In Transboundary and Emerging Diseases., 58(1): 1–30.

Badruzzaman, A.T.M., Siddiqui, S.I., Faruk, M.O., et al. (2015): Prevalence of infectious and non-infectious diseases in cattle population in Chittagong district of Bangladesh. Int. J. Biol. Res., 3(1):1-4.

Bascuñana, C. R., Mattsson, J. G., Bölske, G., and Johansson, K. E. (1994): Characterization of the 16S rRNA genes from Mycoplasma sp. strain F38 and development of an identification system based on PCR. J. Bacteriol., 176(9): 2577–2586.

Braun, U. (2002): Klinische Symptome und Diagnose von BSE [Clinical signs and diagnosis of BSE]. Schweizer Archiv fur Tierheilkunde., 144(12): 645–652.

Chuang, W. Y., Hsieh, Y. C., & Lee, T. T. (2020). The effects of fungal feed additives in animals: A review. In Animals., 10 (5): 1-15.

Constable, P. D., Hinchcliff, K. W., Done, S. H. Grunberg, W. (2017): Diseases of the Nervous System. Vet. Med. pp. 1155–1370.

Daud, A., Fuzi, N. M. H. M., Arshad, M. M., Kamarudin, S., Mohammad, W. M. Z. W., Amran, F., & Ismail, N. (2018). Leptospirosis seropositivity and its serovars among cattle in Northeastern Malaysia. Veterinary world., 11(6): 840–844.

Dedieu, L., Bréard, A., Le Goff, C., and Lefèvre, P. C. (1996): Diagnosis of contagious bovine pleuropneumonia: problems and recent developments. International Office of Epizootics., 15(4): 1331–1353.

Derks, M., Werven, T.V., Hogeveen, H., and Kremer, W.D.J. (2013): Veterinary herd health management programs on dairy farms in the Netherlands: Use, execution, and relations to farmer characteristics. J. Dairy. Sci., 96(3):1623-1637.

di Teodoro, G., Marruchella, G., di Provvido, A., D'Angelo, A. R., Orsini, G., di Giuseppe, P., Sacchini, F., and Scacchia, M. (2020): Contagious Bovine Pleuropneumonia: A Comprehensive Overview. In Veterinary Pathology., 57(4): 476–489.

El-Jakee, J. K., Ali, S. S., El-Shafii, S. A., Hessain, A. M., Al-Arfaj, A. A., and Mohamed, M. I. (2016): Comparative studies for serodiagnosis of haemorrhagic septicaemia in cattle sera. Saudi. J. Biol. Sci., 23(1): 48–53.

Fagiolo, A., Roncoroni, C., Lai, O., and Borghese, A. (2005): Buffalo pathologies. Buffalo Production and Research. pp. 249-296.

Gallagher, A. (2022): Noninfectious diseases of the GI tract in animals – digestive system, MSD Veterinary Manual. MSD Veterinary Manual.

Godfroid, J., Nielsen, K., and Saegerman, C. (2010): Diagnosis of brucellosis in livestock and wildlife. Int. Croat. Med. J., 51(4): 296-305.

Gu, X., and Kirkland, P. D. (2008): Infectious Bovine Rhinotracheitis Part 1. Diagnostic Overview. pp. 1-18.

Haran, K. P., Godden, S. M., Boxrud, D., Jawahir, S., Bender, J. B., and Sreevatsan, S. (2012): Prevalence and Characterization of Staphylococcus aureus, Including Methicillin-Resistant Staphylococcus aureus, Isolated from Bulk Tank Milk from Minnesota Dairy Farms. J.Clin. Microbiol., 50(3): 688-695.

Hegde, R., Gomes, A. R., Giridhar, P., Kowalli, S., Shivashankar, B. P., Sudharshana, K. J., Nagaraj, K., Sesharao, R., Mallinath, K. C., Shankar, B. P., Nagaraj, D., Seema, C. M., Khan, T. A., Nagaraj, G. V., Srikala, K., Dharanesh, N. K., Venkatesha, M. D., and Renukaprasad, C. (2014): Epidemiology of foot and mouth disease in Karnataka state, India: a retrospective study. Virus disease., 25(4): 504–509.

Khodakaram-Tafti, A., and Farjanikish, G. H. (2017): Persistent bovine viral diarrhea
virus (BVDV) infection in cattle herds. Iran. J. Vet. Res., 18(3): 154–163.

Kumagai, S., Daikai, T., and Onodera, T. (2019): Bovine Spongiform Encephalopathy – A Review from the Perspective of Food Safety. Food Safety., 7(2): 21–47.

Kundave, V. R., Patel, A. K., Patel, P. v., Hasnani, J. J., and Joshi, C. G. (2015): Detection of theileriosis in cattle and buffaloes by polymerase chain reaction. J. Parasitic. Dis., 39(3): 508–513.

Longjam, N., Deb, R., Sarmah, A. K., Tayo, T., Awachat, V. B., and Saxena, V. K. (2011): A brief review on diagnosis of foot-and-mouth disease of livestock: Conventional to molecular tools. Vet. Med. Int., 2011: 17.

Mahmmod, Y. (2013): Natural Babesia bovis Infection in Water Buffaloes (Bubalus bubalis) and Crossbred Cattle under Field Conditions in Egypt: a Preliminary Study. J. Arthropod. Dis., 8(1): 1–9.

Megid, J., Antonio Mathias, L., and A. Robles, C. (2014): Clinical Manifestations of Brucellosis in Domestic Animals and Humans. The Open Veterinary Science Journal., 4(1): 119–126.

Mohamad, A., and Shaari, N. F. (2022): Foot and Mouth Disease on Cattle in Peninsula Malaysia: Towards A Sustainable Livestock. J. Sus. Sci. Manage., 17(5): 149–156.

Monecke, S., Kuhnert, P., Hotzel, H., Slickers, P., and Ehricht, R. (2007): Microarray based study on virulence-associated genes and resistance determinants of Staphylococcus aureus isolates from cattle. Veterinary Microbiology., 125(1-2): 128–140.

Morrison, W. I., Hemmink, J. D., and Toye, P. G. (2020): Theileria parva: a parasite of African buffalo, which has adapted to infect and undergo transmission in cattle. Int. J. Parasitol., 50(5): 403–412.

Mosier, D.A. (2022): Hemorrhagic septicemia in water buffalo and cattle – generalized conditions, MSD Veterinary Manual. MSD Veterinary Manual.

Nurulaini, R., Premaalatha, B., Zaini, C.M., Adnan, M., Chandrawathani, P., Fazly, A.Z.A., Enie, A. A. and Ramlan, M. (2013): Trypanosomiasis Outbreak in Deer, Cattle, Buffaloes and Pigs In Perak. Malaysian J. Vet. Res., 4(1): 55-58.

Persson, A., Pettersson, B., Bölske, G., and Johansson, K. E. (1999): Diagnosis of contagious bovine pleuropneumonia by PCR-laser- induced fluorescence and PCR-restriction endonuclease analysis based on the 16S rRNA genes of Mycoplasma mycoides subsp. mycoides SC. J. Clin. Microbiol., 37(12): 3815–3821.

Peter, D. C., Kenneth, W., Hinchcliff, Stanley, H., Done, and Walter, G., (2017). Diseases of the Nervous System. Veterinary Medicine (Ed.) 11th. ed., W.B. Saunders Co. pp. 1155–1370.

Plummer, P.J. (2022): Coxiellosis in animals - generalized conditions, MSD Veterinary Manual. MSD Veterinary Manual.

Premaalatha, B., Tan, W. W., Jamnah, O., Zaini, C. M., Erwanas, A., Reuben, S. K. S., Chandrawathani, P., Ramlan, M. (2016): Biting Flies and Tryponosomiasia in Sahom Livestock Farm: The Missing Link. Malaysian J. Vet. Res., 7(2): 1–8.

Rahman, W. A., Lye, Y. P., and Chandrawathani, P. (2010): The seroprevalence of bovine babesiosis in Malaysia. Tropical biomedicine.,c 27(2): 301–307.

Reinaldo, F. C. (2010): Overview of the cattle immune system - college of agricultural sciences. Oregon State University – Beef Cattle Library. pp. 1-5.

Roseliza, R., Khoo, E., Mohammad, F. S., Normah, M. A., Saifu, N. R., Siti, N. R., Norazariyah, M. N., and Faizah, H. M. S. (2019): Diagnosis of Paratuberculosis By Microbiological Culture In Veterinary Research Institute From 2001 to 2018. Malaysian J. Vet. Res., 10(1). pp. 15-21.

Saravanajayam, M., Kumanan, K., and Balasubramaniam, A. (2015): Seroepidemiology of infectious bovine rhinotracheitis infection in unvaccinated cattle. Veterinary World., 8(12): 1416–1419.

Seegers, H., Fourichon, C., and Beaudeau, F. (2003): Production effects related to mastitis and mastitis economics in dairy cattle herds. Veterinary research., 34(5): 475–491.

Seuberlich, T. (2022) Overview of bovine spongiform encephalopathy – nervous system, MSD Veterinary Manual. MSD Veterinary Manual.

Sinclair, M., Fryer, C., and Phillips, C. J. C. (2019): The Benefits of Improving Animal Welfare from the Perspective of Livestock Stakeholders across Asia. Animals: an open access journal from MDPI., 9(4). 123.

Sushma, B., Shedole, S., Suresh, K. P., Leena, G., Patil, S. S., and Srikantha, G. (2021): An estimate of global anthrax prevalence in livestock: A meta-analysis. Veterinary World., 14(5): 1263–1271.

Thomas, H.S. (2009): The Cattle Health Handbook: Preventative Care, Disease

Treatments & Emergency Procedures. North Adams, MA: Storey, Pub.

Tizard, I. R. (2021): Chapter 16 - Bovine vaccines, Editor(s): Ian R. Tizard, Vaccines for Veterinarians. Elsevier. pp. 193-214.

Tsige, T. Z., and Ahmed, W. (n.d.). Non-Infectious Causes of Infertility in Dairy Cows:

A Review. J. Repro. Inf., 10 (3): 51-57.

Tulu, D. (2022): Bovine Brucellosis: Epidemiology, Public Health Implications, and Status of Brucellosis in Ethiopia. Veterinary Medicine: Research and Reports., 13: 21–30.

Underwood, W. J., Blauwiekel, R., Delano, M. L., Gillesby, R., Mischler, S. A., and Schoell, A. (2015): Biology and Diseases of Ruminants (Sheep, Goats, and Cattle). Laboratory Animal Medicine. pp. 623–694.

V, R. (2022): Spatial Risk Factors Influencing on the Occurrence of Foot and Mouth Disease Outbreaks in Karnataka. Int. J. lnf. Dis., 116: 63–S64.

van Keulen, L. J. M., Langeveld, J. P. M., Garssen, G. J., Jacobs, J. G., Schreuder, B. E. C., and Smits, M. A. (2000): Diagnosis of bovine spongiform encephalopathy: A review. Veterinary Quarterly., 22(4): 197–200.

World Organisation of Animal Health (OIE) (2009). Foot and Mouth Disease.

World Organisation of Animal Health (OIE) (2013). Foot and Mouth Disease.

World Organisation of Animal Health (OIE) (2018). Anthrax.

World Organisation of Animal Health (OIE) (2018). Bovine Anaplasmosis.

World Organisation of Animal Health (OIE) (2018). Identification of the agent Anthrax.

World Organisation of Animal Health (OIE) (2018). Infectious Bovine Rhinotracheitis.

World Organisation of Animal Health (OIE) (2018). Q Fever.

World Organisation of Animal Health (OIE) (2018). Trichomoniasis.

World Organisation of Animal Health (OIE) (2021). Haemorrhagic Septicemia.

World Organisation of Animal Health (OIE) (2022). Brucellosis (Infection with B. Abortus, B. Melitensis and B. Suis).