KNOWLESI MALARIA

UNIVERSITY OF MALAYA

Inaugural Lecture

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FACULTY OF MEDICINE
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BIOGRAPHY

Professor Dr Lau Yee Ling is at present the Head of the Department of Parasitology, Faculty of Medicine at University of Malaya (UM). She started her academic career as a lecturer at Monash University Sunway Campus while waiting for her PhD viva in 2008. During her time as a lecturer in Monash University, she was awarded two Monash University Research Grants in which enabled her to continue her research in the field of molecular parasitology. She then returned to her alma mater, University of Malaya, as a Senior Lecturer in 2009. She was granted tenure in 2010 and promoted to Associate Professor in 2013, and Professor in 2019.

Professor Lau's scientific career has been dedicated to the study of protozoan parasites, including *Plasmodium knowlesi* and *Toxoplasma gondii*, the causative agents of malaria and toxoplasmosis, respectively. These parasitic diseases exact enormous social and economic burdens. Her research interest mainly focuses on using molecular methods for the detection and characterization of these parasites infecting humans and animals. She has collaborated with local and international researchers, leading to publication of more than 170 ISI journals, with total citations index of 1767 and H-index of 22. This research excellence has enabled her to acquire and be a part of many international and local research grants, i.e., Hubert Curien Partnership-Hibiscus (PHC-Hibiscus), ASEAN-India Collaborative R&D scheme, GCRF Global Impact Acceleration Account (GIAA) Impact Fund, High Impact Research Grant, University of Malaya Research Grant, FRGS, E-science, LRGS and others, with cumulative research funding amounting to at least RM5 million. These were followed by several intellectual property rights under her belt on rapid molecular diagnosis of dengue, malaria and COVID-19. Since 2009, 13 Masters and 17 PhDs have completed their studies with success under her guidance. Currently, they are 4 Masters and 8 PhDs under her supervision.

With her experience in grant management, she had held numerous administrative posts such as the Head of Grant Management Unit, of Health and Translational Medicine Cluster and Faculty of Medicine, besides being a committee member in evaluating applications for FRGS, LRGR and TRGS at the national and international levels. She established the Science Café in 2017, which continues to be the main channel of research communication between clinicians and scientists at the Faculty of Medicine. She was also a committee member of the University of Malaya Institutional Biosafety and Biosecurity Committee (IBBC), Animal Experimental Unit, Faculty of Medicine Risk and Quality Management and an internal auditor of Faculty of Medicine.

Currently, she is the editor-in-chief for the Journal of Health and Translational Medicine (JUMMEC) for University of Malaya, editor of Asia Pacific Journal of Molecular Biology & Biotechnology and associate editor of BMC Infectious Diseases. Through her contribution to the field of science, she is a regular reviewer for a few international journals such as Nature Scientific report, Lancet, PLOS One, Parasites & Vectors, Malaria Journal, International Journal of Tropical Disease & Health and others. With her extensive experience and reputation in the field of molecular parasitology, Professor Lau has been much sought after as speaker and consultant both locally and internationally.

Professor Lau has been an active member of the Malaysian Society of Parasitology and Tropical Medicine (MSPTM). She was a council member of the MSPTM in year 2018-2019. She is also active in the Malaysian Society for Biochemistry and Molecular Biology (MSBMB). She was the Honorary Secretary of the MSBMB in 2017-2019 and the current President.

Professor Lau's passion for research can only be matched with her passion for teaching and education. When conducting classes, besides ensuring her lectures are easy to follow, she makes all attempts to infuse interest and solicit students' participation by incorporating more recent articles and real life scenarios in order to illustrate the day-to-day relevance of the teaching subject matter. And because of her enthusiasm for education, she has volunteered to be the Problem-Based Learning (PBL) Phase II coordinator in 2011 then became the PBL main coordinator in 2018. Recently, she has been actively participating in organizing PBL training workshops for UMMP program.

Professor Lau has been awarded University of Malaya Excellent Service Award three times in 2011, 2013 and 2015. She was awarded MSPTM Nadchadtram Medal in 2014. She has also been awarded a few times for her innovation in research including the Grand Prize in National Exclusive Innovation Challenge Award 2018.

Synopsis

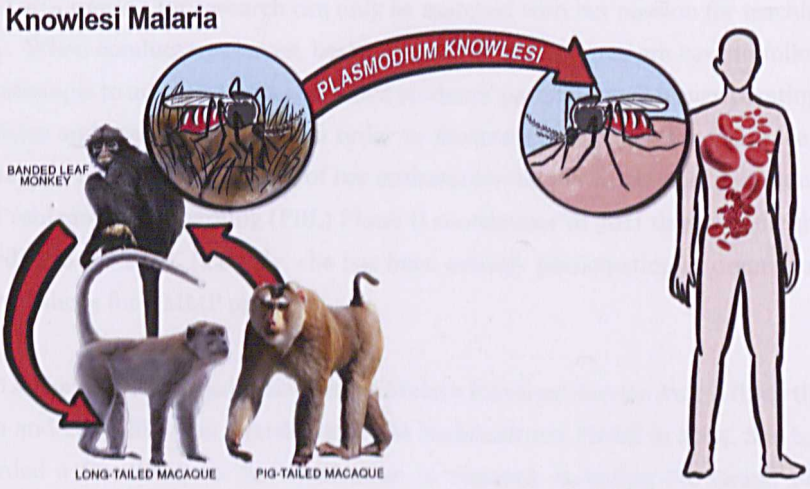
Originally a simian malaria, *Plasmodium knowlesi* is now known as the fifth human malaria species. Since the report of a large focus of human knowlesi cases in Sarawak in 2004, many more human cases have been reported in all of the countries in Southeast Asia and in travellers returning from these countries. The zoonotic nature of this infection hinders malaria elimination efforts. In order to grasp the current perspective of knowlesi malaria, this inaugural lecture explores the different aspects of the disease including risk factors, diagnosis, treatment, molecular and functional studies. Current studies do not provide sufficient data for an effective control programme. Therefore, future direction for knowlesi research is highlighted here with the final aim of controlling, if not eliminating the parasite.

Knowlesi malaria

Introduction

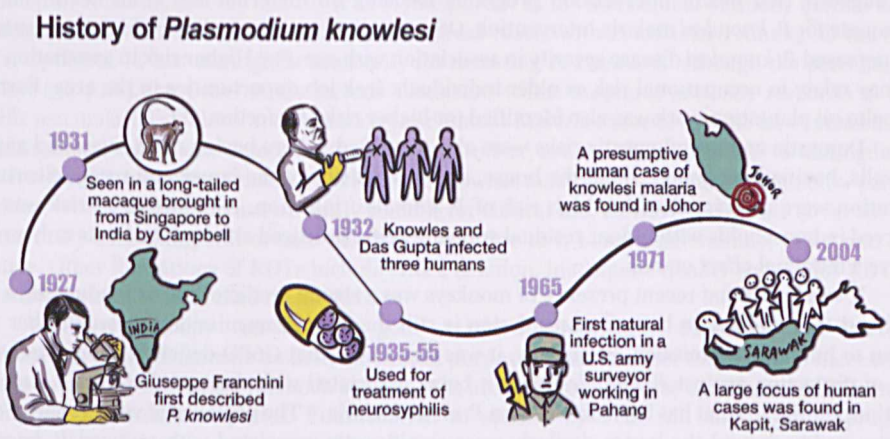
Plasmodium knowlesi, originally a simian malaria, is now recognized as the fifth human malaria parasite.[1] Human knowlesi infections have been reported in nearly all of the countries in Southeast Asia and in travellers returning from these countries.[2,3,4] The cumulative cases of knowlesi malaria in the Southeast Asia region from 2004-2015 is 3413 cases with 91.47% of these found in Malaysian Borneo.[5] From 2013-2017, Malaysia reported a total of 11380 human knowlesi malaria which contributed to 69% of the country's total malaria cases. Out of this, 9902 cases were from Malaysian Borneo.[6]

The parasite's natural reservoir hosts are the long-tailed macaque (*Macaca fascicularis*),[7] pig-tailed macaque (*Macaca nemestrina*)[8] and the banded-leaf monkey (*Presbytis melalophos*).[9] Thus far, several mosquito species belonging to the Leucosphyrus Group have been incriminated as vectors for knowlesi malaria, namely *Anopheles hackeri*,[10] *An. latens*,[11] *An. cracens*,[12] *An. balabacensis*,[13] *An. dirus*,[14] and *An. introlatus*.[15] It is not surprising that the geographical distribution of *P. knowlesi* is confined to Southeast Asia since it follows the limits of natural distribution of both its natural hosts and vectors.[16] To date, the pattern of knowlesi infection in humans does not indicate that they are transmitted via human-mosquito-human.[17-19]



There are several factors leading to the increase of reported *P. knowlesi* cases. These include better diagnostic capacity, decreasing human malaria cases which in turn reduces relative immunity, increased awareness to *P. knowlesi* and close proximity of humans with natural reservoir hosts or infected vectors due to changes in human land use.[5,19] Many studies have been done on *P. knowlesi* ever since it was first described in 1932 by Knowles and Gupta.[7] This has led to important findings in malarialogy which include the discovery of antigenic variation in malaria[20] and demonstration of an absolute requirement for the Duffy receptor for the invasion of red cell by the parasite.[21] Furthermore, since the report of the large focus of naturally acquired *P. knowlesi* infection in humans by Singh *et al*,[22] the disease and the parasite has been further characterized, both clinically and molecularly. In order to grasp the current perspective of knowlesi malaria, this literature review explores the different

aspects of the disease including risk factors, diagnosis, treatment, molecular and functional studies, mainly focusing on publications from the last five years.



Ecological and individual-level factors associated with infection

Risk factors associated with *P. knowlesi* infection has been an area of interest over the past few years as researchers begin to investigate links between environmental, occupational, sociodemographic and domestic factors that may contribute to an increased risk of infection. The understanding and identification of these risk factors would be invaluable in designing appropriate and effective public health interventions for knowlesi malaria.

With the advancement of technology; including the use of unmanned aircraft systems (UAV) or drones, the task of mapping spatial and geographic data to identify environmental factors has been greatly improved.[23] Fornace *et al* studied the association between *P. knowlesi* incidence and various environmental variables via satellite-based remote sensing data in Kudat and Kota Marudu, Sabah.[24] The study found that greater than 65% forest cover in a 2 km radius, higher historical forest loss and lower elevations were significantly associated with higher incidence of *P. knowlesi* infection. The authors postulated that the association may be a result of shifts in human settlement as well as changes in the macaque and mosquito habitat due to deforestation and agricultural activities.

With the current ever-changing economic landscape of Malaysia and its surrounding countries in Southeast Asia, economic pressures and needs have caused a dramatic increase in land use particularly in Borneo Malaysia. The deforestation and use of land may play an important role in influencing the distribution of *P. knowlesi* host and vector populations that may be unnoticed in comparison with other more well-known factors that drive knowlesi infections.[25] In a Malaysian context, large deforestation efforts for agricultural or resettlement purposes may have caused population migration of macaques to move closer to the fringes of the forest and consequently to semi-urban areas.[26] This also inadvertently causes a shift with the *Leucosphyrus* mosquito vector extending their range to farms, villages and logging areas on the fringes of the forest culminating in an area where the vector, monkey host and humans co-exist which increases the risk of *P. knowlesi* infections in these areas.[27]

Sociodemographic and individual-level factors may also carry increased risk for knowlesi malaria infection. A two-year case-control study was carried out by Grigg *et al* from 2012 to 2015 in Sabah, Malaysia.[24] From a demographic standpoint, participants with ages over 15 years were found

to have increased risk of *P. knowlesi* whereas other *Plasmodium* infections were found to be higher in individuals that were younger than 15 years or age. There was also a strong gender bias towards male participants indicating males over the age of 15 carried a higher risk of *P. knowlesi* infection. This suggests that health intervention programs focusing on maternal and child health may be inadequate for *P. knowlesi* malaria intervention. Other studies have also indicated higher parasitemia and increased *P. knowlesi* disease severity in association with age .[28-31] Higher risk in association with age may relate to occupational risk as older individuals seek job opportunities in the area. Farming and palm oil plantation work was also identified for higher risk of infection.

Domestic and peri-domestic risks were also identified; where having open eaves and gaps in the walls, having long grass around the house, sleeping outside of the house and recent clearing of vegetation were associated with a high risk of *P. knowlesi* infection. A reduction of risk was also observed in households with indoor residual spraying being practiced although bed nets only proved to have a marginal effect on risk.

It was noted that recent presence of monkeys was a strong predictor for risk indicating a high likelihood that monkey to human transmission is still the main transmission pathway rather than human to human transmission. Separately, it was also noted that G6PD deficiency conferred some form of protection against *P. knowlesi* with it being associated with decreased risk of *P. knowlesi* infection, similar to what has been observed in *P. vivax* malaria.[32] The presence of young sparse forest and rice paddy around the house similarly were significantly associated with reduced *P. knowlesi* risk.[24]

A study by Herdiana *et al* in 2016 also looked at malaria risk factor assessment using both active and passive surveillance in Indonesia.[33] Initial screening revealed a total of 19 *P. knowlesi* cases which was an unexpected discovery in the study. A comparison of *P. knowlesi* cases to non-cases indicated risk factor findings similar to the study by Grigg *et al*, with increased risk for *P. knowlesi* infection in the male gender, participants of adult age, and forest exposure or forest related work as well as spending time overnight in the forest. When comparing *P. knowlesi* cases with *P. falciparum* and *P. vivax* infections, it was noted that *P. knowlesi* cases were more likely linked to forest exposure and peri-domestic factors.

A study by De Silva *et al* compared the distribution of the different Duffy genotypes among *P. knowlesi* infected patients and healthy donors to determine if there was an association between Duffy genotypes and susceptibility to *P. knowlesi* infection.[34] The authors argue that due to the overwhelming homogeneity of the Duffy distribution in the region, assessment of susceptibility was not feasible. However, further studies into the Duffy distribution between *P. knowlesi* patients in Peninsular and Borneo Malaysia may allow for *P. knowlesi* susceptibility studies particularly if the Duffy distribution between both regions is markedly different.

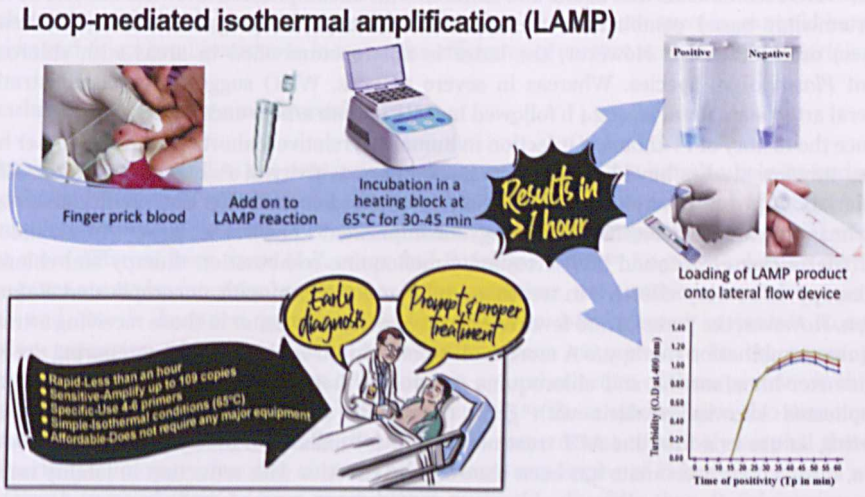
Diagnosis

Microscopy is the gold standard for malaria diagnosis but has its limitations as ring forms of *P. knowlesi* resemble *P. falciparum* and trophozoites and schizonts resemble those of *P. malariae*, and hence cannot be reliably differentiated.[2,35,36] Most *P. knowlesi* infections have been identified as more benign *P. malariae* which has been associated with failure to diagnose severe malaria and consequent delayed parenteral artesunate, with fatal outcomes.[37] In areas of significant *P. knowlesi* endemicity, parasites with the microscopic diagnosis of *P. malariae* should be reported and treated as *P. knowlesi* to reduce *P. knowlesi* case-fatality rates.[38] Limitation of miscroscopic diagnosis has been reported in Sabah, where 21% and 38% of blood films of *P. malariae/P. knowlesi* were diagnosed as *P. falciparum* and *P. vivax*, respectively by PCR.[39] Low parasitemia is fairly common in knowlesi malaria and can cause fever.[39] Knowlesi malaria with low parasitemia may not be detected by microscopy. Better methods for the diagnosis of knowlesi malaria such as molecular methods are needed.

To date, there are no immunochromatographic rapid diagnostic tests (RDTs) specifically designed for *P. knowlesi* detection. Currently available malaria RDTs have been mainly used for detection of *P. falciparum* and *P. vivax* infections. OptiMAL-IT, one of the first RDT that could detect *P. knowlesi*, could mistakenly identify it as *P. falciparum* as the monoclonal antibody used to detect *P. falciparum* histidine rich protein II (HRP-2) cross-reacts with *P. knowlesi*. Among all the other RDTs, OptiMAL-IT has the highest sensitivity for detecting *P. knowlesi,* although the percentage is still low (32-72%).[40-42] Other RDTs include BinaxNow which measures antibody response to non-specific pan malarial aldolase, and Paramax-3 and Entebe Malaria Cassette specific for *P. vivax* lactate dehydrogenase, which can detect *P. knowlesi* as *P. vivax*, are mostly still unable to distinguish *P. knowlesi* from *P. vivax*.[41,42] Sensitivity of RDTs to knowlesi malaria is poor, particularly at low parasite densities,[40,41,43] and they are not currently suitable for clinical use. However, RDTs are so far the only commercially available point-of-care diagnostic tool due to it being user-friendly, rapid and cost-effective. Other limitations of RDTs include HRP2 deletion, inadequate quality control for RDT and limited heat stability to be used on the field.[44]

While microscopy remains the gold standard for malaria diagnosis and RDTs as supplementary test, diagnostic method for clinical purposes must consider the potential inaccuracies of these two, thus, molecular methods such as PCR are needed to further confirm and differentiate the human *Plasmodium* species. Confirmation of species by PCR will also allow appropriate administration of primaquine to patients with *P. vivax* or *P. ovale* infection.[40]

Molecular methods such as PCR and real-time PCR are more accurate in detecting *P. knowlesi* and are valuable for species identification in cases of mixed malaria infection.[42] Nested and real-time PCR based on 18S rRNA gene can detect *P. knowlesi* in as low as 1 parasite/μL of blood.[46,47] However, due to lack of facilities and the lengthy procedure, PCR is not widely used in all endemic areas. Loop-mediated isothermal amplification (LAMP) is another promising molecular diagnostic technique that is applicable for bedside use as it is sensitive, specific, rapid (60-90 min) and easy to use. LAMP does not require costly machine and expertise.[48] The Eiken Loopamp™ MALARIA Pan Detection kit targeted at *Plasmodium* genus can detect all malaria species. It has been shown to be highly sensitive to *P. falci*parum, *P. vivax* [49-52] and *P. knowlesi*.[53] However, this method is unable to identify species of infecting *Plasmodium* and quantification of positive samples is also impossible. Species-specific LAMP assays for all five human malaria species have been developed and were highly sensitive and specific. [54] However, due to its high sensitivity nature of LAMP, cross-contamination can occur easily.[54]



To mitigate the requirements for facilities and professional personnel required by other nucleic acid-based tests, recombinase polymerase amplification (RPA) is another isothermal amplification technique that can be performed. RPA is potentially to develop as a point-of-care technique since it operates in a short timing (<20 min) and is capable of detecting extremely low concentrations of parasite. The end product can be loaded on a lateral flow cassette and result can be obtained within 2 min.[55] To circumvent the challenges in malaria diagnostics with technologies that address performance of sensitivity and specificity of diagnostic method, CRISPR-based methods are a new class of highly sensitive and specific assays that can be performed. SHERLOCK (Specific High Sensitivity Enzymatic Reporter UnLOCKing) is a combination assay of CRISPR and RPA. A SHERLOCK assay has been developed for the detection of *P. falciparum* with 94% sensitivity and 94% specificity in clinical samples as compared to real time PCR. This novel SHERLOCK assays have potential to promote as a new generation of molecular diagnostics for malaria.[56]

Point-of-care molecular tools for rapid malaria diagnosis have also been reported. A lab-on-chip PCR diagnostic platform for malaria, the Accutas system, can detect five species of human malaria with high sensitivity (97.4%) and specificity (93.8%) and it can be performed directly with unprocessed blood (time saving).[57] Truelab Uno, based on TaqMan chemistry has sensitivity and specificity of 100% compared to the nested PCR.[58] Other point-of-care molecular tools for malaria include Illumigene Malaria LAMP workflow, nanomal and nucleic acid lateral flow immunoassay DIAGMAL.[59] However, these molecular methods were not tested specifically for *P. knowlesi*.

Although molecular methods are the most efficacious in diagnosing *P. knowlesi* infection, most of these tests, especially nested PCR can produce a false-positive *P. knowlesi* result in *P. vivax* infections.[60] On top of that, it requires expensive equipment and clean facility. An ideal molecular diagnostic test for point-of-care diagnosis of all five human malaria species which is cost-effective and suitable for the resource-limited setting is yet to be developed.

Treatment and drug resistance

Due to its short asexual cycle of 24-h, infection with *P. knowlesi* can rapidly progress into severe malaria which can be fatal.[61] The treatment guidelines developed by the World Health Organization (WHO) for all human malaria including knowlesi malaria is based on the four core principles: early diagnosis and prompt effective treatment, rational use of antimalarial agents, combination therapy and appropriate weight-based dosing.[62] The proposed choice of treatment depends mainly on whether the patient presents with uncomplicated or severe infection. In 2015 guidelines for the treatment of malaria, WHO recommends that adults and children with uncomplicated knowlesi malaria be treated with artemisinin-based combination therapy (ACT) (except for pregnant women in their first trimester) or chloroquine. However, the latter is not recommended in areas with chloroquine-resistant *Plasmodium* species. Whereas in severe malaria, WHO suggests the administration of parenteral artesunate for at least 24 h followed by ACT in both adults and children.[62]

Since the history of *P. knowlesi* infection in humans is relatively short compared to other human malaria, only few studies have been done to assess the sensitivity of *P. knowlesi* towards different antimalarials. A prospective observational study in adults demonstrated that chloroquine together with primaquine were successful in treating uncomplicated knowlesi malaria.[63] In a randomized control trial, Grigg *et al* found both artesunate-mefloquine combination therapy and chloroquine monotherapy to be very effective in treating adults and children with uncomplicated *P. knowlesi* infection. However, the parasite and fever clearance were notably faster in those receiving artesunate-mefloquine combination therapy.[64] A more recent randomized controlled trial comparing the efficacy of arthemeter-lumefantrine and chloroquine concluded that the former was effective in treating uncomplicated knowlesi malaria with good tolerability and rapid therapeutic response; thus supporting its use as a first line ACT treatment policy for malaria in Malaysia.[27] In severe knowlesi malaria, intravenous artesunate has been shown to be effective with reduction in fatality rate.[29,65-66]

Additionaly, deaths from knowlesi malaria has been linked to the delay in administering intravenous artesunate.[67,68]

An *ex vivo* drug sensitivity assay using clinical *P. knowlesi* isolates revealed that they were sensitive to artemisinins and chloroquine but were less sensitive towards mefloquine.[69] Despite no evidence of mefloquine resistance from these studies and its monotherapy has been reported to successfully treat uncomplicated knowlesi malaria,[70,71] using mefloquine as monotherapy for knowlesi malaria is discouraged.[61] This is likely due to concerns arising from treatment failures reported in rhesus monkeys[72,73] and in a single human knowlesi case.[74]

In studying the drug resistance mutations, Tiyagi *et al* found that the orthologs for known *P. falciparum* drug resistance genes namely chloroquine resistance transporter (*Pkcrt*) and dihydrofolate reductase (*Pkdhfr*) of their *P. knowlesi* isolates were all wild type.[75] Grigg *et al* did a similar study and found moderately diversed *Pkdhfr* sequence amongst their *P. knowlesi* isolates. Nevertheless, there was no evidence of selective drug pressure in humans.[76] In addition to crt and dhfr, other orthologs of *P. falciparum* drug resistance genes including multidrug resistance-1 (mdr1), dihydropteroate synthase (dhps) and kelch K13 were also looked at, with no signs of positive selection.[77] Since only human hosts would be expected to have antimalarial drug exposure and as long as the transmission of *P. knowlesi* remains zoonotic, the absence of drug selection pressure will make it unlikely to develop antimalarial drug resistance.

Although current state of *P. knowlesi* treatment shows no resistance towards antimalarials, research on new therapeutic candidates should not be halted as multiple antimalarials resistant *Plasmodium* sp. strains are emerging in Southeast Asia countries particularly in Cambodia, Myanmar and Thailand.[78] To address this issue, *in vitro* susceptibility studies of *P. knowlesi* to a range of established antimalarial drugs and investigational antimalarial compounds have been done and compared to *P. falciparum*.[79,80] Although the two species showed equal susceptibility to most antimalarial compound, *P. knowlesi* was more susceptible to dihydrofolate reductase (DHFR) inhibitors (pyrimethamine, cycloguanil and trimethoprim) and three other antimalarial compounds (KAF156, halofantrine and MMV884705) compared to *P. falciparum*. However, *P. knowlesi* is less susceptible than *P. falciparum* to several inhibitors of the dihydroorotate dehydrogenase (DHODH) enzyme (DSM1, DSM265, DSM421), the sodium channel ATP4 (cipargamin, SJ733 and PA21A092), cladosporin, pentamidine and AN13762. When tested against combined antimalarials, dihydroartemisinin and quinine were shown to have additive effects for both *P. knowlesi* and *P. falciparum*.[80,81] Additional antimalarials susceptibility testing are important to confirm equipotency and to ensure that new combinations are likely to be effective. These therapeutic candidates could aid in resolving the antimalarials resistance problems in other *Plasmodium species*, or could be used as synergists and drugs combinations to increase the efficiency of current available antimalarials.

Molecular epidemiology and diversity

Genetic polymorphism studies not only guide malaria vaccine design[82] but also help us understand the population history and structure of a parasite, and thus its adaptive potential. Hitherto, proteins of *P. knowlesi* involved in invasion of erythrocytes are generally under purifying (negative) selection, in most cases different from those of *P. vivax* and *P. falciparum*.[82-92] Negative selection may imply that the genes are under functional constrains. At the same time, the mutations are deleterious to the parasite and the *P. knowlesi* population is screening for best-adapted variants.[75] Long-term population expansion of *P. knowlesi* in Malaysia has been suggested to be the cause of this selection.[82,88,92] There are however some differences in natural selection of these proteins in different geographical regions and different parts of the protein.[80,87,93] These studies have also demonstrated that most of these genes are genetically diverse and to some extent more polymorphic than their counterparts in *P. falciparum* and *P. vivax*. Whole genome sequencing of *P. knowlesi* clinical isolates from Sarawak revealed them to have much higher nucleotide diversity than *P. falciparum* and *P.*

vivax.[80] Furthermore, the gamma protein region II (γRII)[88] and circumsporozoite protein CSP[87] of different isolates from varying regions and isolation time exhibit different lengths.

Assuming that the above sequenced proteins from various sources (human and macaque) are representative of the gene pool in macaques, the high genetic diversity and the deviation of selection pressure on these proteins from those of *P. vivax* and *P. falciparum* demonstrate intrinsic differences in the immunological targets used by the respective host species (macaques and humans).[94] The *P. knowlesi* proteins' immunogenic roles have placed them under selection pressure to generate high polymorphism for immune evasion.[88] These polymorphisms are probably results of recombination and reproduction cycle of *P. knowlesi* in multiple hosts.[84] Indeed, the *Anopheles* vector may exact strong evolutionary pressure on vector-related genes of the parasite, thus evidence of adaptation of the parasite to the vector distribution or vectorial capacity.[95]

These genetic diversity studies also uncovered the existence of multiple *P. knowlesi* lineages. It began with the observation of consistent dimorphisms (two distinct groups) in many of the studied proteins originating from humans and macaques. This distinction is not only associated with two separate geographical regions ie Peninsular Malaysia/Thailand and Borneo [82,85,86,87,91,93,96-99], but also correlate with macaque host types ie with the long-tailed and pig-tailed macaque.[100] Further genome sequencing revealed three distinct clusters. The two major sympatric clusters are associated with the long-tailed or pig-tailed macaque, and one cluster consisting of isolates from Peninsular Malaysia.[80,95,100] This was also evident from the study on NBPXa protein, with the third cluster found only in Peninsular Malaysia. This led Ahmed *et al* to postulate that the negative selection on this gene could be the driving force in evolution and separation of the protein into three clusters.[83]

The data shows that genetic divergence of *P. knowlesi* resulted not only from long-term geographic isolation (between Peninsular and Bornean isolates), but also through extended, isolated transmission cycles within different macaque hosts but with evidence of recombination when coming in contact with each other.[95] These phenomena, clearly driven by evolution, are pertinent to understanding knowlesi infection in humans and macaques. The genomic diversity seen in *P. knowlesi* is likely caused by geography, as well as the myriad of hosts, vector distribution and ecological changes.

When studying the adaptation of *P. knowlesi in vitro* to different host erythrocytes, deletion of 13 genes in clones adapted to cynomolgus blood; and deletion of two and duplication of four genes in clones adapted to human blood were observed. *In vitro* adaptation from macaque erythrocyte to human erythrocyte shows that, there is a gradual increase in human erythrocyte invasion efficiency. Hence, *P. knowlesi* shows immense ability to adapt via improved ability to invade human erythrocytes, thereby increasing virulence and multiplication rates.[101]

Currently, we know very little of the differences in characteristics and pathogenesis of the three subpopulations of *P. knowlesi*.[100] There are some early evidences that they may exhibit differential pathogenesis.[96,97,102] Moreover, the dimorphisms seen in MDR2 and MRP1 (transporter genes related to antimalarial drug resistance)[98] should not be overlooked as their phenotypic characteristics and how they react to current antimalarials remain obscure to us. Isolation and investigation of these three subpopulations will be needed to shed more light on these. More importantly, we do not know if human-to-human transmission is naturally happening. The genetic diversity in MSP1 and AMA1 observed among isolates of humans than those from monkeys in Thailand and non-human isolates of Malaysia suggests that it is possible.[90,94] More recent data showed that pkmsp1-42, pk41, pkmsp8 and the 5′ and 3′ regions of msp7D clusters geographically according to Malaysian Borneo and Peninsular Malaysia/Thailand, while population expansion and purifying (negative) selection was continued to be observed.[103-105]

Furthermore, results also revealed that there is low level of polymorphism in both pk41 s48/45 domains[106]; while evidence of intragenic recombination at the central region of pkmsp7D along with absence of geographical clustering of this gene among parasite populations, indicate the potential for both antigens to be a vaccine target.[107]

Besides that, genetic differentiation in human *P. knowlesi* isolates was more significant than in long-tailed macaque isolates, with a very low fixation index. Humans are mostly afflicted by monoclonal infections of *P. knowlesi*, while polyclonal infections are more prevalent among the long-tailed macaques, indicating a higher rate of transmission among the reservoir hosts. This higher transmission rate also contributes to the higher genetic diversity observed in highly endemic areas as compared to lower-endemicity areas.[108]

Moreover, on the 3 clusters of *P. knowlesi*, recent studies have now shown that the *P. knowlesi* cluster 1 (associated with the long-tailed macaque) was the most common subpopulation infecting humans in Malaysian Borneo, followed by cluster 2 (associated with the pig-tailed macaque), whereas only 2% of the infections were positive for both clusters.[109] On the other hand, samples from Peninsular Malaysia belonged to cluster 3 and is highly divergent from both cluster 1 and 2. Most interestingly, the cluster 3 clinical samples constituted 3 distinct subpopulations, with no apparent geographic separation, and can be found in sympatry in Peninsular Malaysia.[110]

These recent studies further highlight the complexity in dissecting *P. knowlesi* transmissions among the hosts. Many questions remained unanswered. More studies are needed to determine whether any difference in clinical outcomes exist between the different subpopulations. Such investigations require analysing detailed clinical and laboratory data on *P. knowlesi* patients infected with the 3 different subpopulation clusters[109] Insights are also needed to determine the impact of such population genetic structures on transmission and epidemiology among the three hosts.[110]

Functional studies in *P. knowlesi*

In 2013, *P. knowlesi* was reported to be successfully adapted to continuous culture in human erythrocytes by Moon *et al*[111] and Lim *et al*[112] This breakthrough serves as an important model for *P. knowlesi* studies especially in validation of vaccine and drug targets. Several *P. knowlesi* vaccine/therapeutic candidates with their recent findings are discussed in this review.

An important parasite adhesin, the reticulocyte binding-like (RBL) family, is found to be involved in host cell erythrocyte receptor binding to facilitate merozoite invasion. NBPXa is one of the members in *P. knowlesi* RBL family and is expressed within the microneme organelles.[113] With the human erythrocytes-adapted *P. knowlesi* strain, Moon *et al* (2016) further identified NBPXa as a key mediator for knowlesi infection in human, as this protein is crucial for invasion of human erythrocytes but not cynomolgus erythrocytes.[101] By disrupting the *NBPXa* gene, *in vitro* multiplicative growth of parasites in human erythrocytes is prevented through impaired merozoite invasion, which support the potential of NBPXa in vaccine development.

Erythrocyte binding-like (EBL) family is another group that mediates interaction with host cell erythrocyte receptors.[114] One of the important members in *P. knowlesi* EBL family, Duffy binding protein α (PkDBPα), interacts with the Duffy antigen receptor for chemokines (DARC) to invade human erythrocytes.[115,116] Genetic polymorphisms in PkDBPα has been postulated to lead to improved parasite binding ability to erythrocytes thus enhancing the disease severity. This postulation was supported by Lim *et al* (2017), in which their recent finding showed that two genetically distinct PkDBPα haplotypes from different geographical area demonstrated a different binding activity level to human erythrocytes by using erythrocyte rosetting assay.[102]

Tryptophan-rich antigens (TRAgs) are involved in rosetting formation and merozoite invasion, hence contributing to disease severity.[117-119] *Plasmodium knowlesi* TRAgs are mostly expressed in its blood stage.[120] By using erythrocyte binding assay and parasite growth inhibition assay, Tyagi *et al* (2015) identified three TRAgs in *P. knowlesi* which were able to bind to human erythrocytes.[121] Two of them compete with *P. vivax* TRAgs for receptors on human erythrocytes. Besides, all of these PKTRAgs were found to inhibit the *P. falciparum* growth *in vitro*, further demonstrating the biological significance of this TRAgs-receptor interaction in heterologous parasites by sharing host receptors.

Apical membrane antigen 1 (AMA1) and its interaction with rhoptry neck protein 2 (RON2) is essential for merozoite invasion. *Plasmodium knowlesi* AMA1 (PkAMA1) has been tested in vaccine trials and results revealed that immunized macaques were protected against infection with controlled parasitemia.[122] In 2015, crystal structure of ectoplasmic region of PkAMA1 and its invasion-inhibitory monoclonal antibody R31C2 was developed.[123] R31C2 binds to the hydrophobic groove and interferes with the exposition of complete binding site on AMA1. This monoclonal antibody is found to be cross-strain reactive as it targets on a non-polymorphic epitope. Besides, no polymorphism near RON2-binding site of AMA1 was detected. The lack of polymorphism suggests that *P. knowlesi* has not developed a mechanism to evade the host's humoral response. Muh *et al* (2018) demonstrated that rabbit-raised anti-PkAMA1 antibodies have strong inhibitory effect on the *in vitro* parasite growth in concentration-dependent manner. On the other hand, additive effect was observed when anti-PkAMA1 antibodies were used in combination with anti-PkDBPα antibodies, paving the way for development of effective vaccine with combination of antibodies with functional difference.[124]

Proteins which demonstrated different mechanisms in parasite metabolic pathways from those found in human host are also of interest. Garg et al (2015) have carried out a study on P. knowlesi enzyme phosphoethanolamine methyltransferases (PkPMTs), which regulates the synthesis of phosphatidylcholine. Structural, biochemical properties and inhibition profile of PkPMTs were evaluated using X-ray crystallography, enzyme kinetics and mutant gene expression studies. PkPMTs enzyme activity could be inhibited by amodiaquine, chloroquine, and NCI compound NSC158011; whereas the yeast carrying mutant PkPMT genes are unable to carry out phosphatidylcholine biosynthesis from phosphoethanolamine.125 Disruption of phosphatidylcholine synthesis in Plasmodium would lead to failure of intact Plasmodium membrane formation and thus inhibit parasite proliferation. These finding suggest that PkPMTs are suitable targets for chemotherapy, and the data from this study could further contribute to a better design of more selective antimalarial drugs against P. knowlesi.

In infected erythrocytes, *P. falciparum* skeleton-binding protein 1 (PfSBP1) is required to transport the erythrocyte surface ligand, erythrocyte membrane protein 1 (EMP1) to the surface of erythrocyte for mediating the surface ligands exposition.[126] Its ortholog in *P. knowlesi*, PkSBP1 has been recently localized to the 'Sinton and Mulligan' stipplings in the cytoplasm of infected erythrocytes.[127] By using immunofluorescence assay and immunoelectron microscopy, transgenic *P. knowlesi* expressing the tagged recombinant PkSBP1 demonstrated an analogous trafficking pattern as in *P. falciparum*, supporting the hypothesis that *Plasmodium* has evolutionarily conserved protein export pathways. These pathway-related proteins could be used as malaria intervention targets as the disruption of the protein export structures would then interfere with the exposition of virulent ligands at the surface of infected erythrocytes.

Wickramarachchi *et al* (2008) has identified an apical asparagine (Asn)-rich protein in *P. falciparum* (PfAARP).[128] This protein is carrying a N-terminal signal sequence and a C-terminal transmembrane region, and localized in the epical ends of the merozoite rhoptries that contain essential proteins needed for directional attachment and merozoite invasion (Iyer et al., 2007).[129] Antibodies raised against this protein exhibited the ability to inhibit parasite invasion *in vitro*, thus suggesting PfAARP could be a putative vaccine/drug target candidate. Its ortholog in *P. knowlesi*, PkAARP, contains a signal peptide at the N-terminus and Asn- and proline (Pro)-rich regions towards the C-terminus. The mouse- and rabbit-raised anti-PkAARP N-terminus antibodies were able to inhibit the *P. knowlesi in vitro* merozoite invasion in a concentration-dependent manner (Muh et al., 2018).[130] Interestingly, the antibodies raised against *P. vivax* AARP (PvAARP) N-terminus also demonstrated the inhibitory effects towards *P. knowlesi in vitro* culture. This cross-species reactivity could be due to the high homology between N-terminus of PvAARP and PkAARP, hence this region could be a suitable target to induce cross-species protective immunity between *P. vivax* and *P. knowlesi*.

Hitherto, *P. knowlesi* vaccine target antigens have not been evaluated in human trial, while the use of non-human primate models involves serious ethical concerns. Despite higher physiological similarity between human and primate compared to other animal models, vaccine studies of *P.*

knowlesi in primate models are unable to completely represent the efficacy and safety of the targets in human due to the differences in host immunity regulations and pathogenic responses towards malaria. Taking into account that majority of *P. falciparum* single antigen was unable to raise specific antibodies up to protective level in human vaccine trials,[131-133] the importance of multi-antigens combination and incorporation of immune-stimulants should be considered in *P. knowlesi* vaccine development.

Future directions and conclusion

There remains a clear risk of continuous *P. knowlesi* infections, especially when land-use change and human behavior may have driven behavior change in the reservoir and vector, enabling closer contact and higher chances of spillover to the human population.[134] The current literature on risk factors associated with *P. knowlesi* has identified significant key risks that will prove helpful for the development of effective intervention programs and highlights the important environmental factors that intermingle with individual risk factors to *P. knowlesi* transmission. Further research into the way these risk factors associate with each other and further spatial mapping and geographic monitoring of *P. knowlesi* hotspots will prove to be an essential part of *P. knowlesi* research as a whole going forward.

WHO (2019) recommends to perform parasite-specific diagnosis in malaria-suspected patients before treatment to prevent unnecessary drug wastage and to halt anti-malarial drug resistance.[114] Therefore, efforts should be invested to develop a point-of-care tool which will be able to detect and differentiate all human *Plasmodium* species to be used in limited-resources environment.

In-depth population genetic studies for both human and primate isolates are needed to shed light on possible human-to-human transmission of *P. knowlesi* and more importantly for us to understand the disease epidemiology and to guide knowlesi infection control. Knowlesi malaria cases have been showing an upward trend in Malaysian Borneo for the past decade and is also forecasted to increase.[38,136,137] Experimental transmission of *P. knowlesi* from monkey-to-man, from man to man, and from man back to monkey have been shown by Chin *et al.*[138] Besides, gametocytes can be found in infected patients[139,140] and most vectors of *P. knowlesi* (e.g. *An. dirus*, *An. balabacensis*, *An. cracens*) are also vectors of human malarias .[141] Thus, though there is yet any direct evidence of natural human-to-human transmission of *P. knowlesi*, the likelihood of it occurring cannot be ignored until proven otherwise. Experimental studies on the vectors that transmit this parasite and knowing the distribution of vectors harboring this parasite will also lend credence to solving this issue.

Rapid development in genome editing tools such as zinc finger nucleases (ZFNs)[142,143] and clustered regularly interspaced short palindromic repeats with CRISPR-associated protein 9 (CRISPR-Cas9) highly increase the efficiency to engineer the *Plasmodium* genome.[144,145] Transfections for labelling, knockout/knockdown and gene editing can be carried out in *in vitro P. knowlesi* parasites to understand its pathogenesis, drug susceptibility and gene functions.[111] These *in vitro* culture-transfection systems coupled with suitable animal models could overcome the bottleneck that is hampering the translational malaria research. Besides, the breakthrough of *P. knowlesi* long term *in vitro* culture and genome editing tools also provide new opportunities to study other closely related *Plasmodium* species especially *P. vivax* which lack of long-term *in vitro* culture system. Mohring *et al* (2019) has established CRISPR-Cas9 genome editing in *P. knowlesi* by replacing PkDBPα gene with its orthologous gene PvDBP.[146] A transgenic *P. knowlesi* line reliant on the PvDBP protein was created successfully to study the functions of PvDBP during erythrocyte invasion. Besides, the structure of a complex of antibody bound to PvDBP indicating the molecular basis for inhibition was also determined by using this transgenic *P. knowlesi* line,[147] thus provide invaluable insights to support *P. vivax* vaccine development.

The WHO Global Malaria Programme has appropriate interventions focused on falciparum and vivax malaria, which cause major global morbidity and mortality. However, effort for malaria control and elimination in certain Southeast Asia countries such as Malaysia are greatly impeded by the uncontrollable passage of *P. knowlesi* in macaque populations, which could lead to human malaria outbreak via zoonotic transmission. In conclusion, different strategies and interventions are needed to prevent *P. knowlesi* transmission from macaques to human. Effective vaccines are in need to control, if not eliminate the parasite.

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93. Putaporntip C, Kuamsab N, Jongwutiwes S. Sequence diversity and positive selection at the Duffy-binding protein genes of *Plasmodium knowlesi* and *P. cynomolgi*: Analysis of the complete coding sequences of Thai isolates. *Infect Genet Evol*. 2016;44(Supplement C):367-375.
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145. Ghorbal M, Gorman M, Macpherson CR, Martins RM, Scherf A, Lopez-Rubio JJ. Genome editing in the human malaria parasite *Plasmodium falciparum* using the CRISPR-Cas9 system. *Nat Biotechnol*. 2014;32(8):819-821.
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ACADEMIC QUALIFICATION

PhD (Parasitology), University of Malaya, 2004-2008 (4 August 2008)
Master of Medical Science, University of Malaya, 1999-2002 (2 September 2002)
Bachelor of Science (Major: Biochemistry), First Class Honours, University of Malaya, 1996-1999

AREAS OF EXPERTISE

Molecular Parasitology
Molecular Cloning and Expression
Molecular Diagnosis

PROFESSIONAL AFFILIATION/MEMBERSHIP

Malaysian Biosafety and Biosecurity Association, May 2015-May 2018
Malaysian Society for Molecular Biology and Biotechnology (MSMBB), Life Member
Malaysian Society of Parasitology and Tropical Medicine, Member, 2010-2020
American Society for Cell Biology, Member, 2008-2013

CAREER HISTORY

Professor, University of Malaya, 21/06/2019-current
Associate Professor, University of Malaya, 21/06/2013- 21/06/2019
Tenure, 26/06/2010
Senior Lecturer, University of Malaya, 03/02/2009-21/06/2013
Lecturer, Monash University Malaysia 15/08/2007-16/01/2009
Research Assistant, National University of Singapore, 23/02/2001-23/08/2004

PATENT

1. Method for Detection of SARS-CoV-2, PI2020002230
2. Recombinant antigen of *Toxoplasma gondii* and use thereof, PI20093771
3. LAMP Primers for *P. knowlesi* detection, PTA6.26
4. LAMP Primers for *P. falciparum* detection, PTA6.28
5. LAMP Primers for *P. vivax* detection, PTA6.27
6. A Method of Detecting Dengue Virus, PTA8.98

MEDIA

1. Knowlesi Malaria, Docquity, 19th May 2020
2. Translation of special terms for COVID-19, China Press, 16 March 2020
3. Developing rapid molecular method for the detection of *Plasmodium knowlesi*, University of Malaya, 13 March 2018
4. Asia Research News 2018: Developing rapid molecular method for the detection of *Plasmodium knowlesi*. Article Released 12 March 2018. Asia Research News 2017: Turning a *Toxoplasma* protein into a tool against infection, (International), 1 January 2017
5. HIR Breaking News (2016): PNAS and Scientific Reports Publication Resulting from *Plasmodium knowlesi* Study, (University), 15 June 2016
6. Astro Awani Interview: Malaria kembali? Expert Advisor, December 20, 2016, Astro Awani
7. Milestone@UM: The multiplex reverse transcription loop-mediated isothermal amplification (RT-Lamp) method, University of Malaya, 29 June 2016
8. UM HIR Breaking News: Publication in Blood, 28 March 2014
9. BFM interview: Genetics in Malaria Research, 26th October 2013
10. The Star, Delving into deadly DNA, Sunday, 9 December 2012

ADMINISTRATIVE DUTIES

1. President, Malaysian Society for Molecular Biology and Biotechnology Executive Council 2019-2021
2. Pengerusi Jawatankuasa PBL, Fakulti Perubatan, University Malaya, 3 April 2019 - 30 June 2021
3. Head of Department, Parasitology, Faculty of Medicine, University Malaya 6 March 2019 - 5 March 2021
4. Council member, Malaysian Society of Parasitology and Tropical Medicine (MSPTM), 2018-2019
5. Honorary Secretary of the Malaysian Society for Biochemistry and Molecular Biology (MSBMB) 2017-2019
6. Jawatankuasa Induk Audit Makmal Fakulti Perubatan, 20 September - 20 October 2018
7. Ahli Jawatankuasa Editor Journal Universiti Malaya, 3 October 2018 - 3 October 2020
8. PBL Coordinator, Faculty of Medicine, 8 August 2018 - 8 August 2020
9. Committee member of Faculty of Medicine Risk and Quality Management, 2018-2020
10. Editor, Asia Pacific Journal of Molecular Biology and Biotechnology (APJMBB), 2018-current
11. Chief Editor of the Journal of Health and Translational Medicine (JUMMEC), 1 February 2018-2022.
12. Acting Head of Department, Department of Parasitology, Faculty of Medicine
13. The University of Malaya Institutional Biosafety and Biosecurity Committee (IBBC), Head of Arthropods, 2015-2019
14. Himpunan Bakat University of Malaya (Talent Pool), University Malaya, 8 May 2017-2018
15. Ahli Jawatankuasa Kurikulum Fakulti (JKKF) Program Ijazah Tinggi, Faculty of Medicine, 2016-2019
16. Science Café coordinator, Faculty of Medicine, 2016-2019
17. Committee member of Faculty of Medicine Risk and Quality Management, 2016-2018
18. Jawatankuasa Induk Audit Makmal Fakulti Perubatan, Faculty of Medicine, 10 February 2017-2018
19. Committee member of Animal Experimental Unit, Faculty of Medicine, 2012 to 2019
20. Department Committee Member of Postgraduate Study (JKITJ), Department of Parasitology, Faculty of Medicine, 2016-2019
21. Head of Satellite Animal Facility, Department of Parasitology, 2013-2019
22. Programme Coordinator, Methodologi Penyelidikan, Department of Parasitology, Faculty of Medicine, 2017-2019
23. UMMP PBL Committee member, Faculty of Medicine, 2016-2018
24. Committee member of University of Malaya PPP Grant Evaluation Panel, 2015-2018
25. Deputy Chief Editor of the Journal of Health and Translational Medicine (JUMMEC), 2015-2018
26. Academic Editor of JUMMEC, 2013-2015
27. Associate Editor of Editorial Board of BMC Infectious Diseases, 2016-current

28. Committee member of University of Malaya IPPP Grant Evaluation Panel, 2015-2016
29. Sub-editor of Frontiers-Microbiology Research Topics, 2015-2016
30. MBBS Phase II PBL Coordinator, Faculty of Medicine, 2011 to 2015
31. Head of Research Management Unit, Faculty of Medicine, University of Malaya, 2014-2015
32. Head of Research Management Unit, Health and Translational Medicine Cluster, University of Malaya, 2013- 2014
33. Coordinator of E-learning, Department of Parasitology, 2010-2012
34. Health and Translational Medicine Cluster website coordinator, HTMC, 2011 to 2012
35. Coordinator of Pharmaceutical Microbiology (Parasitology), 2009-2011

CONSULTATION/EVALUATION ACTIVITIES

1. Evaluation Panel member of TRGS (National), 2020
2. Evaluation Panel member of (National), 2020
3. Member of the International Scientific Committee (ISC) of the 11th World Congress of World Society for Pediatric Infectious Diseases (WSPID), International, 7-9 November 2019
4. Poster Judge of the 3rd International Conference on Molecular Biology & Biotechnology 2019, National, 24-25 April 2019
5. Evaluation Panel member of LRGS (University), 2019
6. Evaluation Panel member of FRGS (Faculty and University), 2019
7. Ahli Panel Forum Sifar Malaria Bermula Dengan Kita, Ministry of Health, 2019-2019
8. Panel Juri Pertandingan University Malaya 3-minute Thesis 2018 bagi Fakulti Perubatan.
9. Committee Member for The Colloquium on Biorisk Management in Malaysia: Implementation & Challenges, 2018
10. Poster Judge, International Conference on Biochemistry, Molecular Biology and Biotechnology 2018 (ICBMBB 2018), 15-16 August 2018
11. Project Management Consultant, Canvio Sdn Bhd, 1 January 2017-current
12. Project consultant, Bioquip Sdn Bhd, 1 February 2018-current
13. External Examiner for the Bachelor of Medical Sciences Degree of IMU intake 1/2018
14. Evaluation Panel of FRGS, Phase 1/2018 at University level
15. Scientific consultant, Canvio Sdn Bhd, 12 Feb 2018-current
16. Project consultant, SD Biosensor, Inc., Korea, 1 February 2018-current
17. Advisor, Bionova Research Sdn. Bhd., January 2018-current
18. Panel Reviewer of Czech Science Foundation, Czech Republic, 7 June 2017-current
19. Panel Reviewer of Deanship of Scientific Research, Jazan, Kingdom of Saudi Arabia, 7 June 2017-current
20. Validation and development of ELISA for malaria diagnostics. Euroimmun Ag, Germany, 2017-2018
21. Project Management Consultant, Canvio Sdn Bhd, 1 January 2017-31 December 2017
22. Expert Consultant on International Grant application, United Scientific Co Ltd, Vietnam, 2017-2019
23. WHO Expert Consultation on *Plasmodium knowlesi* Malaria to Guide Malaria Elimination Strategies, 1 & 2 March 2017, Le Meridian Hotel, Kota Kinabalu, Expert Advisor, 2017-2017, World Health Organization
24. Advisor for Good Laboratory Practice Committee, Faculty of Medicine, 2016-current
25. Panel Reviewer of Taylor's University Research Grant application, Expert Advisor, 2016-2016, Taylor's University
26. Chairperson Session 12: General Topics II, 51st Annual Scientific Conference of MSPTM, 3-4 March 2015
27. Usage of Gel Documentation System, Consultant, Chemoscience Sdn Bhd, 15 March 2010 to 2014
28. Panel Reviewer of University of Malaya Fundamental Research Grant (FRGS), 2014-2017
29. Panel Reviewer of University of Malaya University of Malaya Research Grant, 2014
30. Panel Reviewer of University of Malaya E-Sciencefund, 2014
31. Technical Trainer of interns from Ministry of Health, Consultant, 2012
32. Project Consultant, United Scientific Co Ltd, Vietnam, 2011

33. Invited lecturer of Basic Medical Parasitology (Kursus Pos Basik Parasiologi Perubatan), College of Laboratory Medical Technology, Ministry of Health, 2011

INTERNATIONAL COLLABORATORS

1. Prof Georges Snounou, Directeur de Recherche 2ème Classe (DR2) CNRS. Senior Scientist Université Pierre et Marie Curie (Paris VI), France
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RESEARCH FUNDING

Principal Investigator of HIR projects, UMRG, FRGS, E-Science, Monash Research Fund and PPP with cumulative research funding of ~RM5 million. Sub-project leader of two HIR projects and two LRGS with total research funding of ~RM3 million.

1. Hubert Curien Partnership – Hibiscus (PHC-Hibiscus), Preserving the Biodiversity of the Non-Human Malaria Parasites of Malaysia, Oct 2019-Oct 2021.
2. RU Grant – UMCIC, Rapid Point of Care (poc) Molecular Test for the Detection of Malaria, Sep 2019-Sep 2020.
3. International Funding, Mypair Hibiscus, Epidemiology and Biodiversity of the Non-human Malaria Parasites of Malaysia – A Proposal for Preservation, Dissemination and Scientific Exploitation, May 2019-April 2021.
4. Long Term Research Grant Scheme (LRGS), A Multi-pronged Approach in Combating knowlesi Malaria, Rapid Point-of-Care (PoC) Tests for the Detection of Malaria, Jan 2019-Dec 2022.
5. Fundamental Research Grant Scheme (FRGS), Would Genetic Polymorphism in *Plasmodium knowlesi* Duffy Binding Protein Alpha (PkDBPalpha) Lead to Differences in Regulation of Immune Responses in Host? Jan 2019-Dec 2020. (Co-PI)
6. ASEAN-India Collaborative R&D scheme, Comparative Analysis of VIR Gene in Complicated and Uncomplicated Vivax Malaria, Nov 2018- 2020.
7. GCRF Global Impact Acceleration Account (GIAA) Impact Fund, Affordable Diagnostics for the Third World Underdeveloped Rural Areas in Malaysia, Mar 2019-Sep 2019.
8. Global Health Equity Scholars Program, Infectious Diseases among Migrants and Refugees in Malaysia, Sep 2017-2018. (Mentor)
9. Bantuan Khas Penyelidikan (BKP Special), The Anopheles Immune Signaling Pathway in the Defense against Malaria Infection, Apr 2017-Mar 2018.

10. Fundamental Research Grant Scheme (FRGS), Does Genetic Polymorphism in The *Plasmodium Knowlesi* Duffy Binding Protein (Pkdbp) Contribute to Increased Erythrocyte Invasion of This Malaria Parasite? 2016-2018. (Co-PI)
11. Postgraduate Research Grant (PPP), Analysis of *Sarcocystis spp.* Immunogenic Protein for Development of Human Sarcocystosis Serological Test, 2016-2018.
12. Postgraduate Research Grant (PPP), The Jak-Stat Pathway of *Anopheles dirus* Mosquito in Response towards Plasmodium Infection, 2016-2018.
13. Postgraduate Research Grant (PPP), Genetic Diversity Study, Expression and Immunocharacterization of *Plasmodium knowlesi* Merozoite Surface Protein 3-Beta in *Escherichia coli* and *Pichia pastoris*, 2016-2017.
14. Postgraduate Research Grant (PPP), Identification of Receptors for Surface Proteins of *Toxoplasma gondii* in Humans, 2016-2017.
15. Postgraduate Research Grant (PPP), Recombinant Expression of TES-32 and TESs-120 of *Toxocara canis* by *Escherichia Coli* for Diagnostic Use in Adult Asthmatic Patients, 2014-2017.
16. Postgraduate Research Grant (PPP), Binding Affinity of Duffy Binding Protein (PKDBPαII) of *Plasmodium knowlesi* Clinical Isolates from Peninsular Malaysia and Malaysia Borneo, 2014-2017.
17. HIR-MOHE, Expression Analysis of *Anopheles cracens*: Responses to *Plasmodium knowlesi* Infection, 2013–Jun 2016.
18. HIR MOHE 2, Identification and Genotyping of Medically Important Parasites and Mosquitoes, 2012-Jun 2016
19. UMRG PROGRAM, Sarcocystosis: An Emerging Parasitic Infection, 2012-Jun 2016.
20. E-Science Fund, Recombinant Expression of TES-26 and TES-30 of *Toxocara canis* by the yeast *Pichia pastoris* for diagnostic use, 2012-2014. (Co-PI)
21. HIR MOHE, Characterization of Epitopes on the Merozoite Surface Antigens of Zoonotic Simian Malaria, 2011-Jun 2016.
22. HIR UM-MOHE, Genomics and Molecular Characterization of Tropical Infectious Disease Agents, 2011-Jun 2016.
23. HIR MOHE. Beijing Genome Institute (Genomics and Bioinformatics Services). (RM 3256460.00). Sub-project Leader, 2011-Jun 2016.
24. Long Term Research Grant Scheme (LRGS), A Study to Investigate the Disease Mechanisms of Severe Dengue, 2011-2014.
25. E-Science, Specific, Sensitive and Rapid Detection of *Plasmodium knowlesi* Infection in Malaria Patients by Loop-mediated Isothermal Amplification (LAMP) Method, 2011-2013
26. EU. European Union, Innovative Tools and Strategies for Surveillance and Control of Dengue, 2011-2013. (Co-PI)
27. Fundamental Research Grant Scheme (FRGS), Molecular Diagnostic Method for Speedy and Accurate Identification of Malaria Parasite Species, 2011-2013. (collaborator)
28. Fundamental Research Grant Scheme (FRGS), Use of RNA Interference to Investigate Gene Function in *Toxoplasma gondii*, 2010-2012.
29. University Malaya Research Grant (UMRG), Molecular Differentiation of *Entamoeba histolytica*, *Entamoeba dispar* and *Entamoeba moshkovskii* in Human Stool Samples, 2010-2012. (Co-PI)
30. University Malaya Research Grant (UMRG), Characterization of Recombinant Surface Protein Containing an Altered Thrombospondin Repeat Domain (SPATR) of *Plasmodium knowlesi* produced in yeast *Pichia pastoris*. 2010-2012. (Co-PI)
31. University Malaya Research Grant (UMRG). Molecular Studies of Zoonotic Simian Malaria Parasite *Plasmodium knowlesi*, 2009-2010. (Co-PI)
32. Recombinant Expression of Chimeric Surface Antigen SAG1/2 of *Toxoplasma gondii* by the Yeast Pichia pastoris for Diagnostic Use (E-Science), 2008-2009.
33. University Malaya Research Grant (UMRG), Development of DNA and Recombinant Vaccines against *Toxoplasma gondii* infection, 2009-2011.
34. Immunological Characterization of *Toxoplasma Gondii* Surface Antigen SAG2 and its Subfragments Produced in the Methylotrophic Yeast Pichia pastoris (PJP), 2006-2007.
35. Cloning of *Toxocara canis* TES120 Gene into *Escherichia coli* and *Pichia pastoris*, 2003-2004.
36. Monash University Research Grant, Recombinant Expression of Chimeric Surface Antigen SAG1/2 of *Toxoplasma gondii* by the Yeast Methylotrophic Yeast, *Pichia* pastoris, 2007-2008.

37. Monash University Research Grant, Identification and Characterization of Lysophosphatidylcholine Acyltransferase from Peanut Microsomal Membranes, 2008-2009. (Co-Investigator)

PUBLICATIONS

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1. Amir, A., Shahari, S., Wee Kent Liew, J.W.K., de Silva, J.R., Khan, M.B., Lai, M.Y., Snounou, G., Abdullah, M.L., Gani, M., Rovie-Ryan, J.L. and Lau, Y.L. (2020). Natural Plasmodium infection in wild macaques of three states in peninsular Malaysia. Acta Tropica 211. (Tier 2, IF:2.555)
2. Muh, F., Kim, N., Nyunt, M.H., Firdaus, E.R., Han, J.H., Hoque, M.R., Lee, S.K., Park, J.H., Moon, R.W., Lau, Y.L., Kaneko, O. and Han, E.T. (2020). Cross-species reactivity of antibodies against *Plasmodium vivax* blood-stage antigens to *Plasmodium knowlesi*. PLOS Neglected Tropical Diseases 14(6): e0008323. (Tier 1, IF: 4.400)
3. Abdullahi, M.D., Chessed, G., Qadeer, M.A. and Lau, Y.L. (2020) Phytochemical screening, gas chromatography mass spectroscopy (GC-MS) and in-vitro antiplasmodial analysis of *Senna siamea* leaves as antimalarial, Yobe State, Nigeria. Nigerian Journal of Parasitology 41(1): 60-6.
4. Lau, Y.L., Ismail, I., Mustapa, N.I., Lai, M.Y., Tuan Soh, T.S., Hassan, A., Peariasamy, K.M., Lee, Y.L., Chong, Y.M., Sam, I.C. and Goh, P.P. (2020). Real-time reverse transcription loop-mediated isothermal amplification for rapid detection of SARS-CoV2. PeerJ. (accepted). (Tier 2, IF: 2.379)
5. De Silve, J.R., Ching, X.T. and Lau, Y.L. (2020). Investigative study on the role of the Toxo 5699 gene in the *Toxoplasma gondii* lytic cycle using the CRISPR/CAS9 system. Tropical Biomedicine 37(3). (Tier 4, IF:0.509)
6. Mahendran, P., Liew, J.W.K., Amir, A., Ching, X.T. and Lau, Y.L. (2020). Droplet digital polymerase chain raction (ddPCR) for the detection of *Plasmodium knowlesi* and *Plasmodium vivax*. Malaria Journal. (accepted). (Tier 1, IF: 2.798)
7. Noordin, N., Lee, P.Y.Z., Bukhari, M.F., Fong, M.Y., Abdul Hamid, M., Jelip, J., Mudin, R. and Lau, Y.L. (2020) Prevalence of asymptomatic and/or low-density malaria infection among high-risk groups in Peninsular Malaysia. The American Journal of Tropical Medicine and Hygiene. (accepted). (Tier 2, IF:2.126)
8. Lai, M.Y., Ooi, C.H., Jaimin, J.J. and Lau, Y.L. (2020). Evaluation of WarmStart colorimetric loop-mediated isothermal amplification assay for diagnosis of malaria. The American Journal of Tropical Medicine and Hygiene 102(6): 1370-1372. (Tier 2, IF:2.126)
9. Nadzirah, T.T.I., Fong, M.Y. and Lau, Y.L. (2020). Seroprevalence of *Sarcocystis falcatula* in two islands of Malaysia using recombinant surface antigen 4. The Korean Journal of Parasitology 58(1): 1-5. (Tier 3, IF:1.311)
10. Mokhtar, A.S., Lau, Y.L., Wilson, J. and Abdul-Aziz, N.M. (2020). Genetic diversity of *Pediculus humanus capitis* (Phthiraptera: Pediculidae) in Peninsular Malaysia and molecular detection of its potential associated pathogens. Journal of Medical Entomology 57(3): 915-926. (Tier 1, IF:1.925)
11. Rouhani-Rankouhi, S.Z., Kow, K.S., Liam, C.K. and Lau, Y.L. (2020). Seropositivity and risk factors of *Toxocara canis* infection in adult asthmatic patients. Tropical Biomedicine 37(3). (Tier 4, IF:0.509)
12. Liew, C.C., Lau, Y.L., Fong, M. Y. and Cheong, F.W. (2020). Two genetically distinct *Plasmodium knowlesi* duffy binding protein alpha region II (PkDBPαII) haplotypes demonstrate higher binding level to fy(a+b+) erythrocytes than fy(a+b-) erythrocytes. The American Journal of Tropical Medicine and Hygiene 102(5):1068-1071. (Tier 2, IF:2.126)
13. Cheong, F.W., Dzul, S., Fong, M.Y. and Lau, Y.L. (2020). *Plasmodium vivax* drug resistance markers: Genetic polymorphisms and mutation patterns in isolates from Malaysia. Acta Tropica 206. (Tier 2, IF:2.555)
14. Lee, W.C., Russell, B., Sobota, R.M., Ghaffar, K., Howland, S.W., Wong, Z.X., Maier, A.G., Dorin-Semblat, D., Biswas, S., Gamain, B., Lau, Y.L., Malleret, B., Chu, C., Nosten, F., and Rénia, L. (2020). Plasmodium-infected erythrocytes induce secretion of IGFBP7 to form type 3 II rosettes and escape phagocytosis. eLife 9: e51546. (Tier 1, IF:7.080)
15. Lai, M.Y. and Lau, Y.L. (2020). Detection of *Plasmodium knowlesi* using recombinase polymerase amplification (RPA) combined with SYBR Green I. Acta Tropica 208: 1-3. (Tier 2, IF:2.555)
16. Tan, W., Liew, J.W.K., Selvarajoo, S., Lim, X. Y., Foo, C. J., Refai, W. F., Robson, N., Othman, S., Abdul Hadi, H., Mohd Mydin, F. H., Abdul Malik, T. F., Lau, Y. L. and Vythilingam, I. (2020).

Inapparent dengue in a community living among dengue-positive mosquitoes and in a hospital in Klang Valley, Malaysia. Acta Tropica 204: 1-8. (Tier 2, IF:2.555)

17.Liew, J.W.K., Ooi, C.H., Snounou, G., and Lau, Y.L. (2019). Case Report: Two Cases of Recurring Ovale Malaria in Sarawak, Malaysia, after Successful Treatment of Imported *Plasmodium falciparum* Infection. Am J Trop Med Hyg 101(6):1402-1404. doi: 10.4269/ajtmh.19-0305. (Tier 2, IF:2.315)

18.Tengku-Idris I.N., Fong M.Y., and Lau, Y.L. (2019). Sarcocystosis seroprevalence in two islands of Malaysia using recombinant *Sarcocystis falcatula* surface antigen 4 (rSfSAG4). Korean Journal of Parasitology. (Tier 4, IF: 1.167)

19.Muh, F., Ahmed, M.A., Han, J.H., Nyunt, M.H., Lee, S.K., Lau, Y.L., Kaneko, O. and Han, E.T. (2019). The *Plasmodium falciparum* apical asparagine (Asn)-rich proteinCross-species analysis of apical asparagine-rich protein of *Plasmodium vivax* and *Plasmodium knowlesi*. Scientific Reports 8: 5781 | DOI:10.1038/s41598-018-23728-1 4. (Tier 1, IF: 4.011)

20.Abdullahi, M.D., Chessed, G., Muhammad, A.Q. and Lau, Y.L. (2019). Effect of *Senna occidentalis* (Fabaceae) leaves extract on the formation of β-hematin and evaluation of in vitro antimalarial activity. International Journal of Herbal Medicine 7(3): 46-51. (Non-ISI)

21.Mokhtar, A.S., Wilson, J., Lau, Y.L., Abdul-Aziz, N.M. (2019). Genetic diversity and molecular detection of potential associated pathogens in *Pediculus humanus capitis* in Peninsular Malaysia. J Med Entomol. doi: 10.1093/jme/tjz234. [Epub ahead of print] (Tier 1, IF: 1.902)

22.De Silva J.R., Amir A., Lau, Y.L., Ooi, C.H. and Fong, M.Y. (2019). Distribution of the Duffy genotypes in Malaysian Borneo and its relation to *Plasmodium knowlesi* malaria susceptibility. PLoS ONE 14(9): e0222681 (Tier 1, IF: 2.776)

23.Lai, M. Y., Majid, N. A. and Lau, Y. L. (2019). Identification of host proteins interacting with *Toxoplasma gondii* SAG1 by yeast two-hybrid assay. Acta Parasitologica 64(3):575-581. doi: 10.2478/s11686-019-00066-4 (Tier 4, IF: 0.968)

24.Clark, T., Benavente, E. D., Gomes, A., De Silva, J. R., Grigg, M. J., Walker, H., Barber, B., William, T., Yeo, T. W., De Sessions, P. F., Ramaprasad, A., Ibrahim, A., Charleston, J., Hibberd, M., Pain, A., Moon, R., Auburn, S. Lau, Y. L., Anstey, N., and Campino, S. (2019). Whole genome sequencing of amplified *Plasmodium knowlesi* DNA from unprocessed blood reveals genomic exchange events between Malaysian Peninsular and Borneo subpopulations. Scientific Reports. 9, 9873. https://doi.org/10.1038/s41598-019-46398-z (Tier 1, IF: 4.011)

25.Leong, S.C., Vythilingam,I., Liew. J.W.K., Wong, M.L., Wan-Yusoff, W.S. and Lau, Y.L. (2019). Enzymatic and molecular characterization of insecticide resistance mechanisms in field populations of *Aedes aegypti* from Selangor, Malaysia. Parasites & Vectors, 12:236, 1-17 (Tier 1, IF: 3.031)

26.Fong, M.Y., Lau, Y.L., Jelip, J., Ooi, C.H., Cheong, F.W. (2019). Genetic characterisation of the erythrocyte binding protein (PkβII) of *Plasmodium knowlesi* isolates from Malaysia. Journal of Genetics 98, 64. (Tier 4, IF: 0.825)

27.van Schalkwyk, D. A., Blasco, B., Nuñez, R. D., Liew, J. W. K., Amir, A., Lau, Y. L., Leroy, D., Moon, R.W. and Sutherland, C. J. (2019). *Plasmodium knowlesi* exhibits distinct in vitro drug susceptibility profiles from those of *Plasmodium falciparum*. International Journal for Parasitology: Drugs and Drug Resistance. 9:93-99. doi: 10.1016/j.ijpddr.2019.02.004. (Tier 2, IF: 2.951)

28.Fadil, M.F.H., Tengku Idris, T.I.N., Fong, M.Y., Shahari, S., Lau, Y.L. (2019). Molecular evidence of Sarcocystis species infecting reptiles in Peninsular Malaysia. Iranian Journal of Parasitology. DOI: 10.18502/ijpa.v14i4.2105. (Tier 4, IF: 0.735)

29.Tay, S.T., Kho, K. L., Vythilingam, I., Ooi, C.H. and Lau, Y.L. (2019). Investigation of possible rickettsial infection in patients with malaria. Tropical Biomedicine 36(1): 257–262. (Tier 4, IF:0.418)

30.Liew, J.W.K., Mahpot, R.B., Dzul, S., Abdul Razak, H.A.B., Ahmad Shah Azizi, N. A. B., Kamarudin, M. B., Russell, B., Lim, K.L., De Silva, J.R., Lim, B.S., Jelip, J., Mudin, R.N.B. and Lau, Y. L. (2018). Importance of proactive malaria case surveillance and management in Malaysia. Am J Trop Med Hyg 98(6): 1709-1713. doi:10.4269/ajtmh.17-1010 (Tier 2, IF:2.315)

31.Tengku Idris, Fong, M.Y., Lau, Y.L. (2018). Seroprevalence of sarcocystosis in the local communities of Pangkor and Tioman Islands using recombinant surface antigens 3 (rSAG3) of Sarcocystis falcatula. Tropical Medicine & International Health 23(12):1374-1383. doi: 10.1111/tmi.13160. (Tier 2, IF: 2.423)

32.Fong, M.Y., Cheong, F.W., Lau, Y.L. (2018). Erythrocyte-binding assays reveal higher binding of *Plasmodium knowlesi* Duffy binding protein to human Fya+/b+ erythrocytes than to Fya+/b- erythrocytes. Parasites & Vectors. 26;11(1):527. doi: 10.1186/s13071-018-3118-8. (Tier 1, IF: 3.031)

33.Amir, A., Cheong, F.W., de Silva, J.R., Liew, J.W.K., Lau, Y.L. (2018). *Plasmodium knowlesi* malaria: current research perspectives. Infection and Drug Resistance. 11:1145-1155. doi: 10.2147/IDR.S148664. (Tier 3, IF: 3.0)

34.Ahmed,A., Lau, Y.L., Quan, F. (2018). Diversity and natural selection on the thrombospondin-related adhesive protein (TRAP) gene of *Plasmodium knowlesi* in Malaysia. Malaria Journal, 17(1):274. doi: 10.1186/s12936-018-2423-1. (Tier 1, IF: 2.798)

35.Liew, J.W.K., Mahpot, R.B., Dzul, S., Abdul Razak, H.A.B., Ahmad Shah Azizi, N.A.B., Kamarudin, M.B., Russell, B., Lim, K.L., de Silva, J.R., Lim, B.S., Jelip, J., Mudin, R.N.B., Lau, Y.L. (2018). Importance of Proactive Malaria Case Surveillance and Management in Malaysia. Am J Trop Med Hyg 98(6):1709-1713. doi: 10.4269/ajtmh.17-1010. (Tier 2, IF:2.315)

36.Leong, C.S., Vythilingam, I., Wong, M.L., Wan Sulaiman, W.Y., Lau, Y.L. (2018). *Aedes aegypti*(Linnaeus) larvae from dengue outbreak areas in Selangor showing resistance to pyrethroids but susceptible to organophosphates. Acta Trop. 185:115-126. doi: 10.1016/j.actatropica.2018.05.008 (Tier 1, IF: 2.629)

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38.Barber, B.E., Russell, B., Grigg, M.J., Zhang, R., William, T., Amir, A., Lau, Y.L., Chatfield, M.D., Dondorp, A.M., Anstey, N.M., Yeo, T.W. (2018). Reduced red blood cell deformability in *Plasmodium knowlesi* malaria. Blood Adv. 2(4):433-443. doi: 10.1182/bloodadvances.2017013730.

39.Mallepaddi, P., Lai, M. Y., Podha, S., Ooi, C. H., Liew, J., Rathnagiri, P., Lau, Y. L. (2018). Development of LAMP-based lateral flow device (LAMP-LFD) method for the detection of malaria. Am J Trop Med Hyg. doi: 10.4269/ajtmh.18-0177 (Tier 2, IF:2.315)

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41.Amirah A., Cheong, F.W., De Silva, J.R., Lau, Y.L. (2018). Diagnostic Tools in Childhood Malaria. Parasites & Vectors. 23;11(1):53. doi: 10.1186/s13071-018-2617-y (Tier 1, IF: 3.031)

42.Lai, M.Y., Lau, Y.L.* (2017). Measurement of binding strength between prey proteins interacting with *Toxoplasma gondii* SAG1 and SAG2 using isothermal titration calorimetry (ITC). Acta Parasitologica, 2018, 63(1). (Tier 4, IF: 0.968)

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57.De Silva, J.R., Lau, Y L., Fong, M.Y. (2016). Genetic clustering and polymorphism of the merozoite surface protein-3 of *Plasmodium knowlesi* clinical isolates from Peninsular Malaysia. Parasites & Vectors, 10:2, DOI: 10.1186/s13071-016-1935-1. (Tier 1, IF: 3.031)
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135. Anthony, C., Mahmud, R., Lau Y.L.*, Syedomar, S. F., & Sri La Sri Ponnampalavanar, S. (2013). Comparison of two nested PCR methods for the detection of human malaria. Tropical Biomedicine, 30(3), 459-466. (Tier 3, IF:0.418)
136. Lau Y.L.*, Anthony, C., Fakhrurrazi, S. A., Ibrahim, J., Ithoi, I., & Mahmud, R. (2013). Real-time PCR assay in differentiating *Entamoeba histolytica*, *Entamoeba dispar*, and *Entamoeba moshkovskii* infections in Orang Asli settlements in Malaysia. Parasites & Vectors, 6(1), 250. doi: 10.1186/1756-3305-6-250 (Tier 1, IF: 3.031)
137. Ching, X. T., Lau Y.L.*, Fong, M. Y., & Nissapatorn, V. (2013). Evaluation of *Toxoplasma gondii*-recombinant dense granular protein (GRA2) for serodiagnosis by western blot. Parasitol Res, 112(3), 1229-1236. doi: 10.1007/s00436-012-3255-5 (Tier 2)
138. Parthasarathy, S., Fong, M. Y., Ramaswamy, K., & Lau Y.L.* (2013). Protective Immune Response in BALB/c Mice Induced by DNA Vaccine of the ROP8 gene of *Toxoplasma gondii*. The American journal of tropical medicine and hygiene, 88(5), 883-887 (Tier 1)
139. Lee, W. C., Chin, P. W., Lau Y.L.*, Chin, L. C., Fong, M. Y., Yap, C. J., . . . Mahmud, R. (2013). Hyperparasitaemic human *Plasmodium knowlesi* infection with atypical morphology in peninsular Malaysia. Malar J, 12. doi: Artn 88 (Tier 1)
140. Lee, W. C., Russell, B., Lau Y.L., Fong, M. Y., Chu, C., Sriprawat, K., . . . Renia, L. (2013). Giemsa-stained wet mount-based method for reticulocyte quantification: a viable alternative in resource limited or malaria endemic settings. Plos One, 8(4), e60303. doi: 10.1371/journal.pone.0060303 (Tier 1, IF: 2.776)
141. Cheong, W. C., Fong, M.Y., Mahmud, R., Lau Y.L.*(2013). Expression, purification, and evaluation of bacterial-expressed recombinant *plasmodium knowlesi* merozoites surface protien-133 (msp-133). American Journal of Tropical Medicine and Hygiene. 88(5), pp. 835-840 (Tier 1)
142. Amir, A., Sum, J. S., Lau Y.L.*, Vythilingam, I., & Fong, M. Y. (2013). Colonization of *Anopheles cracens*: a malaria vector of emerging importance. Parasites & Vectors, 6, 81. doi: 10.1186/1756-3305-6-81 (Tier 1, IF: 3.031)
143. Russell, B., Malleret, B., Suwanarusk, R., Anthony, C., Kanlaya, S., Lau Y.L., . . . Renia, L. (2013). Field-based flow cytometry for ex vivo characterization of *Plasmodium vivax* and *P. falciparum* antimalarial sensitivity. Antimicrob Agents Chemother, 57(10), 5170-5174. doi: 10.1128/AAC.00682-13 (Tier 1)
144. Palaeya, V., Lau Y.L.*, Mahmud, R., Chen, Y., & Fong, M. Y. (2013). Cloning, expression, and immunocharacterization of surface protein containing an altered thrombospondin repeat domain (SPATR) from *Plasmodium knowlesi*. Malar J, 12, 182. doi: 10.1186/1475-2875-12-182 (Tier 1)
145. Lau Y.L.*, Fong, M. Y., Idris, M. M., & Ching, X. T. (2012). Cloning and expression of *Toxoplasma gondii* dense granule antigen 2 (GRA2) gene by Pichia pastoris. Southeast Asian J Trop Med Public Health, 43(1), 10-16. (Tier 4, IF: 0.287)
146. Ngui, R., Angal, L., Fakhrurrazi, S. A., Lian, Y. L. A., Lau Y.L., Ibrahim, J., & Mahmud, R. (2012). Differentiating *Entamoeba histolytica*, *Entamoeba dispar* and *Entamoeba moshkovskii* using nested polymerase chain reaction (PCR) in rural communities in Malaysia. Parasites & Vectors, 5. doi: Artn 187. Doi 10.1186/1756-3305-5-187 (Tier 1, IF: 3.031)
147. Shafiyyah, C. O. S., Jamaiah, I., Rohela, M., Lau, Y. L., & Aminah, F. S. (2012). Prevalence of intestinal and blood parasites among wild rats in Kuala Lumpur, Malaysia. Tropical Biomedicine, 29(4), 544-550. organization. Genetics and Molecular Research, 13(3), 5803-5814. doi: Doi 10.4238/2014.July.29.8 (Tier 3, IF:0.418)
148. Ithoi, I., Ahmad, A. F., Mak, J. W., Nissapatorn, V., Lau, Y. L., & Mahmud, R. (2011). Morphological Characteristics of Developmental Stages of Acanthamoeba and Naegleria Species before and after Staining by Various Techniques. Southeast Asian Journal of Tropical Medicine and Public Health, 42(6), 1327-1338 (Tier 4)
149. Fong, M. Y., Noordin, R., Lau Y.L., Cheong, F. W., Yunus, M. H., & Idris, Z. M. D. (2013). Comparative analysis of ITS1 nucleotide sequence reveals distinct genetic difference between *Brugia malayi* from Northeast Borneo and Thailand. Parasitology, 140(1), 39-45. doi: Doi 10.1017/S0031182012001242 (Tier 1)
150. Lau Y.L.*, Thiruvengadam, G., Lee, W. W., & Fong, M. Y. (2011). Immunogenic characterization of the chimeric surface antigen 1 and 2 (SAG1/2) of *Toxoplasma gondii* expressed in the yeast *Pichia pastoris*. [Research Support, Non-U.S. Gov't]. Parasitol Res, 109(3), 871-878. doi: 10.1007/s00436-011-2315-6. Doi 10.1186/1475-2875-12-88 (Tier 2)

151. Lau Y.L.*, Tan, L. H., Chin, L. C., Fong, M. Y., Noraishah, M. A. A., & Rohela, M. (2011). *Plasmodium knowlesi* reinfection in human. Emerging infectious diseases, 17(7), 1314 (Tier 1, IF: 7.187)

152. Nissapatorn, V., Suwanrath, C., Sawangjaroen, N., Lau Y.L., & Chandeying, V. (2011). Toxoplasmosis-Serological Evidence and Associated Risk Factors among Pregnant Women in Southern Thailand. American Journal of Tropical Medicine and Hygiene, 85(2), 243-247. doi: DOI 10.4269/ajtmh.2011.10-0633 (Tier 1)

153. Jothy, S. L., Zakaria, Z., Chen, Y., Lau Y.L., Latha, L. Y., & Sasidharan, S. (2011). Acute oral toxicity of methanolic seed extract of *Cassia fistula* in mice. Molecules, 16(6), 5268-5282 (Tier 2)

154. Thiruvengadam, G., Init, I., Fong, M. Y., & Lau Y.L.* (2011). Optimization of the expression of surface antigen SAG1/2 of *Toxoplasma gondii* in the yeast *Pichia pastoris*. Tropical Biomedicine, 28(3), 506-513 (Tier 3, IF:0.418)

155. Lau Y.L.*, Fong, M. Y., Mahmud, R., Chang, P. Y., Palaeya, V., Cheong, F. W., . . . Chen, Y (2011). Specific, sensitive and rapid detection of human *plasmodium knowlesi* infection by loop-mediated isothermal amplification (LAMP) in blood samples. Malar J, 10, 197. doi: 10.1186/1475-2875-10-197 (Tier 1)

156. Chang, P. Y., Fong, M. Y., Nissapatorn, V., & Lau Y.L.* (2011). Evaluation of *Pichia pastoris*–Expressed Recombinant Rhoptry Protein 2 of *Toxoplasma gondii* for Its Application in Diagnosis of Toxoplasmosis. The American Journal of Tropical Medicine and Hygiene, 85(3), 485-489. (Tier 1)

157. Jothy, S. L., Zakaria, Z., Chen, Y., Lau Y.L., Latha, L. Y., Shin, L. N., & Sasidharan, S. (2011). Bioassay-directed isolation of active compounds with anti-yeast activity from a *Cassia fistula* seed extract. Molecules, 16(9), 7583-7592 (Tier 1)

158. Ithoi, I., Ahmad, A. F., Nissapatorn, V., Lau Y.L., Mahmud, R., & Mak, J. W. (2011). Detection of Naegleria Species in Environmental Samples from Peninsular Malaysia. Plos One, 6(9). doi: ARTN e24327. DOI 10.1371/journal.pone.0024327 (Tier 1, IF: 2.776)

159. Fong, M. Y., Lau Y.L., Chin, L. C., & Al-Mekhlafi, A. M. (2011). Sequence analysis on the mitochondrial COXI gene of recent clinical isolates of *Plasmodium knowlesi* in Klang Valley, peninsular Malaysia. [Research Support, Non-U.S. Gov't]. Tropical Biomedicine, 28(2), 457-463 (Tier 3, IF:0.418)

160. Tan, L. H., Fong, M. Y., Mahmud, R., Muslim, A., Lau Y.L., & Kamarulzaman, A. (2011). Zoonotic *Brugia pahangi* filariasis in a suburbia of Kuala Lumpur City, Malaysia. Parasitol Int, 60(1), 111-113. doi: 10.1016/j.parint.2010.09.010 (Tier 2)

161. Lau, Y. L.*, Meganathan, P., Sonaimuthu, P., Thiruvengadam, G., Nissapatorn, V., & Chen, Y. (2010). Specific, sensitive, and rapid diagnosis of active toxoplasmosis by a loop-mediated isothermal amplification method using blood samples from patients. Journal of clinical microbiology, 48(10), 3698-3702 (Tier 1)

162. Lau Y.L.*, Hasan, M. T., Thiruvengadam, G., Idris, M. M., & Init, I. (2010). Cloning and expression of *Toxoplasma gondii* dense granular protein 4 (GRA4) in Pichia pastoris. Tropical Biomedicine, 27(3), 525-533 (Tier 3, IF:0.418)

163. Syahmi, A. R. M., Vijayarathna, S., Sasidharan, S., Latha, L. Y., Kwan, Y. P., Lau Y.L., ... & Chen, Y. (2010). Acute oral toxicity and brine shrimp lethality of Elaeis guineensis jacq.,(oil palm leaf) methanol extract. Molecules, 15(11), 8111-8121 (Tier 2)

164. Fong, M. Y., Wong, K. T., Rohela, M., Tan, L. H., Adeeba, K., Lee, Y. Y., & Lau Y.L. (2010). Unusual manifestation of cutaneous toxoplasmosis in a HIV-positive patient. [Case Reports]. Tropical Biomedicine, 27(3), 447-450 (Tier 3, IF:0.418)

165. Init, I., Lau Y.L., Arin Fadzlun, A., Foead, A. I., Neilson, R. S., & Nissapatorn, V. (2010). Detection of free-living amoebae, Acanthamoeba and Naegleria, in swimming pools, Malaysia. [Research Support, Non-U.S. Gov't]. Tropical Biomedicine, 27(3), 566-577 (Tier 3, IF:0.418)

166. Meganathan, P., Singh, S., Lau Y.L., Singh, J., Subrayan, V., & Nissapatorn, V. (2010). Detection of *Toxoplasma gondii* DNA by PCR following microwave treatment of serum and whole blood. Southeast Asian J Trop Med Public Health, 41(2), 265-273 (Tier 4, IF: 0.287)

167. Lau Y.L.*, Ithoi, I., & Fong, M. Y. (2010). Optimization for High-Level Expression in *Pichia Pastoris* and Purification of Truncated and Full Length Recombinant Sag2 of *Toxoplasma Gondii* for Diagnostic Use. Southeast Asian Journal of Tropical Medicine and Public Health, 41(3), 507-513 (Tier 4)

168. Lau Y.L.*, & Yik Fong, M. (2008). *Toxoplasma gondii*: Serological characterization and immunogenicity of recombinant surface antigen 2 (SAG2) expressed in the yeast *Pichia pastoris*. Experimental parasitology, 119(3), 373-378 (Tier 3)
169. Fong, M. Y., Lau Y.L., & Zulqarnain, M. (2008). Characterization of secreted recombinant *Toxoplasma gondii* surface antigen 2 (SAG2) heterologously expressed by the yeast *Pichia pastoris*. Biotechnology Letters, 30(4), 611-618. doi: DOI 10.1007/s10529-007-9609-x (Tier 3)
170. Fong, M. Y., Thanabalan, A., Muslim, A., Lau Y.L., Sivanandam, S., & Mahmud, R. (2008). Inferring the phylogenetic position of *Brugia pahangi* using 18S ribosomal RNA (18S rRNA) gene sequence. Tropical Biomedicine, 25(1), 87-92 (Tier 3, IF:0.418)
171. Lau Y.L., Fong, M. Y., Shamilah, R. H. R., & Zulqarnain, M. (2007). Recombinant expression of a truncated *Toxoplasma gondii* SAG2 surface antigen by the yeast *Pichia pastoris*. Journal of Tropical Medicine and Public Health, 38(1), 6-14 (Non-ISI)
172. Lau Y.L., Shamilah, H., & Fong, M. Y. (2006). Characterisation of a truncated *Toxoplasma gondii* surface antigen 2 (SAG2) secreted by the methylotrophic yeast *Pichia pastoris*. Tropical Biomedicine, 23(2), 186-193 (Tier 3, IF:0.418)
173. Yu, H. B., Zhang, Lau Y.L., Y. L., Yao, F., Vilches, S., Merino, S., . . . Leung, K. Y. (2005). Identification and characterization of putative virulence genes and gene clusters in *Aeromonas hydrophila* PPD134/91. Appl Environ Microbiol, 71(8), 4469-4477. doi: 10.1128/AEM.71.8.4469-4477.2005 (Tier 1, IF: 4.077)
174. Fong, M. Y., & Lau Y.L. (2004). Recombinant expression of the larval excretory-secretory antigen TES-120 of *Toxocara canis* in the methylotrophic yeast *Pichia pastoris*. Parasitol Res, 92(2), 173-176. doi: 10.1007/s00436-003-1020-5 (Tier 2, IF: 2.067)
175. Fong, M. Y., Lau Y.L., Init, I., Jamaiah, I., Anuar, A. K., & Rahmah, N. (2003). Recombinant expression of *Toxocara canis* excretory-secretory antigen TES-120 in *Escherichia coli*. [Evaluation Studies. Southeast Asian J Trop Med Public Health, 34(4), 723-726 (Tier 4, IF: 0.287)
176. Zhang, Y. L., Lau Y.L., Arakawa, E., & Leung, K. Y. (2003). Detection and genetic analysis of group II capsules in *Aeromonas hydrophila*. Microbiology, 149(Pt 4), 1051-1060 (Tier 1, IF: 1.027)

BOOK

1. Parasites and vectors: with special focus on Southeast Asia, 20132.
2. Nissapatorn, V., Lau, Y.L., Yazar, S., and Pelloux, H. (2017). Parasites in the Tropic-A New Paradigm Shift, Frontiers in Microbiology, E-book, 2017

CONFERENCE/SEMINAR/PRESENTATION

1. Poster, 5th SINGMALNET Singapore Malaria Network Meeting, 5th SINGMALNET Singapore Malaria Network Meeting 2020, NUS Yong Loo Lin School of Medicine, International, 21-23 October 2020
2. Council member for The 56th Annual Scientific Conference of the Malaysian Society of Parasitology And Tropical Medicine (MSPTM), National, 15 March 2019 - 14 March 2020
3. Role of simian malaria in malaria elimination, The 20th International Congress for Tropical Medicine and Malaria, Faculty of Tropical Medicine, Mahidol University, International, 20-24 September 2020
4. Neglected Tropical Diseases, 19th International Congress on Infectious Disease, International Society for Infectious Diseases, International, 23 May 2020
5. Conference, Post-era MDA: An Update on Intestinal Parasitic Infections (IPI) among Selected Urban Poor Communities in West Coast of Peninsular Malaysia, NTDASIA2019, Khon Kaen University, International, 6-8 August 2019
6. PBL Case Design Workshop for UMMP, University Malaya, 18-20 June 2019
7. Poster, Comparison of the Binding Level of Different Human Erythrocyte Duffy (Fy) Antigens to *Plasmodium Knowlesi* Duffy Binding Protein Alpha Region II (PkDBP II), 10th Malaysian Symposium of Biomedical Science, Universiti Sains Malaysia (USM), National, 26-28 April 2019
8. Poster, Investigative study on the role of the Toxo 5699 gene in the *Toxoplasma gondii* lytic cycle using the CRISPR/Cas9 System, 3rd International Conference on Molecular Biology and Biotechnology 2019 (ICMBB2019), Malaysian Society for Molecular Biology and Biotechnology (MSMBB) and UCSI University, International, 24-25 April 2019

9. Presenter, 3rd International Conference on Molecular Biology & Biotechnology 2019, 3rd International Conference on Molecular Biology & Biotechnology 2019, Malaysian Society for Molecular Biology and Biotechnology (MSMBB) and UCSI University, National, 24-25 April 2019
10. Poster, Development of LAMP-Based Lateral Flow Device (LAMP-LFD) Method for the Detection of Malaria, 3rd International Conference on Molecular Biology and Biotechnology, MSMBB and UCSI University, International, 24-25 April 2019
11. PBL tutor training workshop for UMMP, University Malaya, 11-12 April 2019
12. Invited speaker, Scientific Writing Seminar, Faculty of Medicine, University of Malaya, 3 April 2019
13. Invited speaker, Asia-Pacific Network on Drug and Diagnosis Innovation on Neglected Tropical Diseases, Shanghai, China, 21-22 March 2019
14. Discovery of *Plasmodium knowlesi* in Malaysia, 2019 Queenstown Molecular Biology (QMB) Meetings, National Institute of Parasitic Diseases, China CDC, International, 21-22 March 2019
15. Presenter, Scaling Up Efforts in Tropical Disease and Vector Control through Evidence-Based Research, 55th Annual Scientific Conference of the Malaysian Society of Parasitology and Tropical Medicine (MSPTM), Malaysian Society of Parasitology and Tropical Medicine (MSPTM), National, 13 March - 14 May 2019
16. Organising committee, 1st international health and sciences conferences, Taylor's University, March 2019.
17. Workshop on Biorisk Assessment for Laboratory: Principle and Methodology, Wisma RnD University of Malaya, 21 December 2018
18. Invited Participant, *Plasmodium cynomolgi* Culture Workshop Scientific Meeting, Dunedin, Otago, New Zealand, 13-14 September 2018
19. PBL tutor training workshop for UMMP, Faculty of Medicine, University of Malaya, 9-10 September 2018
20. Invited speaker, The 8th Asean Conference of Tropical Medicine and Parasitology (ACTMP) 2018, Nha Trang, Vietnam, 26-29 July 2018
21. Plenary speaker, The 9th Malaysian Symposium of Biomedical Science, Department of Biomedical Science, Faculty of Medicine, University of Malaya, 12-13 May 2018
22. Immune Sandiego Leadership Committee, 2018
23. Poster, Human muscular sarcocystosis due to *Sarcocystis nesbitii* causing a persistent inflammatory myopathy with overexpression of major histocompatibility complex class I (MHC-I) on muscle tissue. ASID Annual Scientific Meeting 2018. Marriott Hotel Surfers Paradise, Gold Coast, QLD, 10-12 May 2018
24. Oral presentation. MSPTM 2018 Annual Scientific Conference, Connexion Conference & Event Centre @ Nexus, Bangsar South City, Kuala Lumpur, Malaysia, 14 – 15 March 2018
25. 54th Annual Scientific Conference of the Malaysian Society of Parasitology and Tropical Medicine, MSPTM 2018, Organising Committee, Connexion Conference & Event Centre, Bangsar South City, 14 – 15 March 2018
26. Symposium on Malaysian Scholarly Communication, Kementerian Pendidikan Tinggi, Putrajaya, 6 February 2018
27. Bengkel Editor's Day Bersama Clarivate Analytics, Kementerian Pendidikan Tinggi, Putrajaya, 5 February 2018
28. International Conference on Biochemistry, Molecular Biology and Biotechnology 2018 (ICBMBB 2018). A joint conference of the Malaysian Society for Biochemistry & Molecular Biology (MSBMB) and the Malaysian Society for Molecular Biology & Biotechnology (MSMBB) in conjunction with the 43rd Annual Conference of MSBMB and the 25th Scientific Meeting of MSMBB
29. Scientific Writing Seminar, Facilitator, University of Malaya, 15 January 2018
30. Invited speaker, WAAVP 2017 Conference, Rapid detection of *Plasmodium knowlesi* by isothermal recombinase polymerase amplification assay (RPA), Kuala Lumpur Convention Centre, Malaysia, 4-9 July 2017
31. Invited speaker, A One Health Approach to Parasite Control in South East Asia, Bangkok, Thailand. International, 19-21 June 2017
32. Invited participant Tech Plan Demo Day in Malaysia 2017, IPPP, University of Malaya, 13 May 2017
33. Seminar for Reviewers and Editors of Biomedical Journal, Park Royal Hotel, Kuala Lumpur, APAME and MMA, International, 25 April 2017

34. Introduction to Mathematic Modeling of Infectious Diseases, Ho Chi Minh, Pasteur Institute, International, 30 Oct - 4 Nov 2016
35. Taylor's University Scientific Seminar: Research Grants Application, Scientific Seminar: Research Grants Application, Taylor's University, Malaysia, 2 Jun 2016
36. Invited Guest, APMEN VII: APMEN's seventh annual meeting, Vietnam, 25-27 March 2015
37. Bengkel Editors Day Bersama Thomson Reuters, Jemputan ke Bengkel Editor's Day Bersama Thomson Reuters, Kementerian Pendidikan Tinggi, National, 23 March 2016
38. Student oral, Courage Fund Conference on Infectious Diseases, High Genetic Polymorphism Observed in the Negative Selected Gene of Rhoptry Associated Protein I (RAP-1) of *Plasmodium knowlesi* in Malaysian Clinical Isolates, Singapore, 11-13 March 2015
39. Invited speaker, International Conference on Molecular Biology and Biotechnology (ICMBB) & 23rd Scientific Meeting of MSMBB 2016. Colorimetric detection of dengue by single tube reverse-transcription-loop-mediated isothermal amplification, 9-11 March 2016
40. Towards Impactful Collaborations in Parasitology and Tropical Medicine, 52 Annual Scientific Conference of Malaysian Society of Parasitology and Tropical Medicine, Malaysian Society of Parasitology and Tropical Medicine, 2-3 March 2016
41.Enhancing student's participation in PBL process, Bengkel Problem Based Learning Kolej Sains Kesihatan UMMC, UMMC, University, 18 December 2014
42. Oral, International Postgraduate Research Awards Seminar, 2014, Molecular Characterizations of *Sarcocystis Spp.* In Cattle and Goat Sampled In Abattoir Shah Alam, KL, 10-11 December 2014
43. Poster, Beating Malaria London, 2014, Epitope mapping of *Plasmodium knowlesi* merozoite surface protein-142 (msp-142) using synthetic peptide library and phage display library, UK, 1-3 July 2014
44. Invited, Beating Malaria London, 2014, Immunogenicity of bacterial-expressed recombinant *Plasmodium knowlesi* merozoite surface protein-142 (MSP-142), UK, 1-3 July 2014
45. Oral, International Postgraduate Research Awards Seminar, 2014, Genotyping of the Duffy blood group among *Plasmodium knowlesi*-infected patients in Malaysia, KL
46. Loop-Mediated Isothermal Amplification Assay for Dengue, LRGS Dengue Colloquium 2013, TIDREC, National, 11-12 Jun 2013
47. Loop-mediated isothermal amplification (LAMP): a rapid and cost-effective diagnostic method for infectious diseases, 24th National Scientific Conference, 3-5 September 2013
48. Poster, Seminar Bioteknologi Kebangsaan 2013, Recombinant expression of TES-26 and TES-30 of *Toxocara canis* by the yeast *Pichia pastoris* for diagnostic use, Penang, Malaysia 6-8 June 2013
49. Poster, Seminar Bioteknologi Kebangsaan 2013, Specific, sensitive and rapid detection of human *Plasmodium knowlesi* infection by loop-mediated isothermal amplification (LAMP) in blood samples, Penang, Malaysia, 6-7 June 2013
50. Poster, 9th Annual BioMalPar I EVIMalaR Conference, cloning and expression of *Plasmodium Knowlesi* MSP-119 in *Escherichia coli* and *Pichia pastoris*, EMBL Heidelberg, Germany, 13-15 May 2013
51.Poster, International Malaria Symposium 2013, Molecular Polymorphisms of *Plasmodium vivax* Transporters and Sensitivity to Chloroquine and Artesunate, Sabah, Malaysia, 16-17 April 2013
52. Oral, International Malaria Symposium 2013, Rosetting phenomenon in vivax malaria isolates from Thai-Myanmar border, Sabah, Malaysia, 16-17 April 2013.
53. Poster, International Malaria Symposium, 2013, Cloning, Expression, and Immunocharacterization of Surface Protein Containing an Altered Thrombospondin Repeat Domain (SPATR) Gene of *Plasmodium knowlesi*, Sabah, Malaysia, 16-17 April 13
54. Oral, The 5th ASEAN Congress of Tropical Medicine and Parasitology (ACTMP), Cloning, expression and purification of *Toxoplasma gondii* dense granular protein2 and 5 (GRA2 and GRA5) in *Escherichia coli*, Phillipines, 15-17 May 2012
55. Poster, Singapore Malaria Network meeting 2012, Cloning, Expression and Purification of recombinant MSP-133 of *Plasmodium knowlesi* in bacterial system, Singapore, 16-17 February 2012
56. Poster, 16th Biological Science Graduate Congress (BSGC), Molecular Differentiation of *Entamoeba histolytica*, *Entamoba dispar* and *Entamoeba moshkovskii* in human stool, Singapore, 12-14 December 2011
57.Oral, Joint International Tropical Medicine Meeting 2011(JITMM), DNA vaccination against *Toxoplasma gondii* using Rhoptry gene 8 in mice model system, Bangkok, Thailand, 1-2 December 2011

58. Poster, Joint International Tropical Medicine Meeting 2011(JITMM), Evaluation of *toxoplasma gondii* recombinant dense granular protein (GRA2) for serodiagnosis by western blot, Bangkok, Thailand, 1-2 December 2011
59. Poster, The 11th International Congress on Toxoplasmosis, Expression of Surface Antigen SAG1/2 of *Toxoplasma gondii* in the yeast *Pichia Pastoris*, Ottawa, Canada, 25-29 June 2011
60. Poster, 47th Malaysian Society of Parasitology and Tropical Medicine (MSPTM) 3-4 March, 2011- International Medical University (IMU), Genotyping of *Toxoplasma gondii* strains associated with human toxoplasmosis: a current status. Kuala Lumpur, Malaysia, 3-4 March 2011
61. Invited Speaker, Parasitology Symposium 13th ACCLS, Current molecular techniques in diagnostic parasitology, Royal Chulan Hotel, Kuala Lumpur, 26 September 2010
62. Poster, The XIIth International Congress of Parasitology (ICOPA), Cloning, expression and characterization of *Toxoplasma gondii* dense granular protein 4 (GRA4) in *Pichia pastoris*, Melbourne, Australia 16-20 August 2010
63. Poster, The XIIth International Congress of Parasitology (ICOPA), Vaccination of mice with TgSAG1/2 induces Th1 type immune response and confer a high level of protection against mice challenged with *Toxoplasma gondii* tachyzoites, Melbourne, Australia, 16-20 August 2010
64. Poster, The XIIth International Congress of Parasitology (ICOPA), Specific, Sensitive and Rapid Detection of Active Toxoplasmosis in Patients by Loop-mediated Isothermal Amplification (LAMP) Method in Blood Samples. Melbourne, Australia, 15-20 August 2010
65. Student Oral Presentation, 46th Annual Scientific Conference of MSPTM, Genotypic determination of *Toxoplasma gondii* strains by PCR-RFLP from clinical samples in Malaysia, 24-25 March 2010
66. 46th Annual Scientific Conference of MSPTM, Cloning and expression of *Plasmodium knowlesi* Merozoite Surface Protein (MSP-119) in yeast *Pichia pastoris*. Grand Season Hotel, Kuala Lumpur, 24-25 March 2010
67. Poster, 46th Annual Scientific Conference of MSPTM, *Toxoplasma gondii*: Molecular cloning and expression of full length rhoptry protein 2 (ROP2) gene in *Pichia pastoris*. Grand Season Hotel, Kuala Lumpur, 24-25 March 2010
68. Poster, 46th Annual Scientific Conference of Malaysian Society of Parasitology and Tropical Medicine, Vaccination against toxoplasmosis by *Toxoplasma gondii* recombinant dense granular DNAs and proteins, Grand Season Hotel, Kuala Lumpur, 24-25 March 2010
69. Poster, 46th Annual Conference of Malaysian Society of Parasitology and Tropical Medicine, Expression of *Toxoplasma gondii* dense granule antigen (GRA2) in the yeast *Pichia pastoris* for the use in serodiagnosis of toxoplasmosis, Grand Season Hotel, Kuala Lumpur, 24-25 March 2010
70. Poster, 49th Annual Meeting of The American Society for Cell Biology, Heterologous expression of the chimeric SAG1/2 of *Toxoplasma gondii* in the yeast *Pichia pastoris*. San Diego, CA, USA, 5-9 December 2009
71. Poster, Joint International Tropical Medicine Meeting 2009, Cloning, Expression and Functional Characterization of Rhoptry Protein Gene (Rop8) Of *Toxoplasma Gondii* In Yeast *Pichia Pastoris*. Bangkok, Thailand, 2-4 December 2009
72. Poster, 83rd Annual Meeting of the American Society of Parasitologist, Lau YL and Fong MY (2008). Recombinant Expression of *Toxoplasma gondii* Surface Antigen SAG2 in the Methylotrophic Yeast *Pichia pastoris*. Texas, USA, 27-20 June 2008
73. Poster, 44th Annual Scientific Seminar of the Malaysian Society of Parasitology and Tropical Medicine, Phylogenetic study of *Brugia pahangi* using 18S rRNA and cytochrome oxidase I (COXI) gene sequences. Kuala Lumpur, Malaysia, 01 February 2008
74. Poster, 2nd ASEAN Congress of Tropical Medicine and Parasitology, Recombinant expression of the *Toxoplasma gondii* surface antigen SAG2 in the yeast *Pichia pastoris*. Bandung Indonesia, 1 February 2006
75. Poster, 43rd Annual Scientific Seminar of the Malaysian Society of Parasitology and Tropical Medicine & Centenary Celebration of the RSTMH (London), Heterologous expression of the surface antigen SAG2 of *Toxoplasma gondii* in the methylotrophic yeast *Pichia pastoris*. Kuala Lumpur, Malaysia, 1 February 2007
76. Poster, 43rd Annual Scientific Seminar of the Malaysian Society of Parasitology and Tropical Medicine & Centenary Celebration of the RSTMH (London), Cutaneous toxoplasmosis in an HIV-positive patient. Kuala Lumpur, Malaysia, 1 February 2007

77.Poster, 42nd Annual Scientific Seminar of the Malaysian Society of Parasitology and Tropical Medicine, Yeast-derived recombinant antigens for use in immunodiagnosis of parasitic infections. Ipoh, Malaysia, 1 February 2006
Poster, 5th Seminar on Food- and Water-borne Parasitic Zoonoses, Recombinant expression of a truncated *Toxoplasma gondii* SAG2 surface antigen by the yeast *Pichia pastoris*. Bangkok Thailand, 1 February 2006

SEMINAR/CONFERENCE ORGANIZER

1. Chair, 2nd International Conference on Molecular Biology and Biotechnology (ICMBB) & 24th Scientific Meeting of MSMBB, PAUM, University of Malaya, 1-2 November 2017
2. Clinical Manifestation from Thelcticopsis malayensis bite envenoming. Carrion Ecology and Forensic Entomology: Current Research and Its Future, Clinical Manifestation from Thelcticopsis malayensis bite envenoming. Carrion Ecology and Forensic Entomology: Current Research and Its Future, Department of Parasitology, University, 26 February 2020
3. Stress Response, Proteasomes, & Artemisinin Resistance, Stress Response, Proteasomes, & Artemisinin Resistance, Department of Parasitology, University, 18 February 2020
4. When Data Science Meets Biology, When Data Science Meets Biology, Department of Parasitology, University, 8 January 2020
5. Exploring Nerve Cells: One Step at a Time, Exploring Nerve Cells: One Step at a Time, Department of Parasitology, University, 27 November 2019
6. A Multi-pronged Approach in Combating Knowlesi Malaria, Taklimat Kajian "A Multi-pronged Approach in Combating Knowlesi Malaria", Unit Vektor, Jabatan Kesihatan Negeri Kelantan, National, 16 October 2019
7. A Multi-pronged Approach in Combating Knowlesi Malaria, Taklimat Kajian "A Multi-pronged Approach in Combating Knowlesi Malaria", Unit Kawalan Jangkitan Bawaan Vektor, Jabatan Kesihatan Negeri Perak, National, 3 October 2019
8. Rethinking Biology: Synthetic Biology and the IGEM Competition, Rethinking Biology: Synthetic Biology and the IGEM Competition, Department of Parasitology, University, 2 October 2019
9. Building Your Academic Brand on Social Media, Journal Club, Department of Parasitology, University, 11 September 2019
10. Passive Cooling Technology for a Nuclear Power Plant, Journal Club, Department of Parasitology, University, 29 August 2019
11. 3rd Intervarsity Parasitology Quiz and Oratorical Competition 2019, 3rd Intervarsity Parasitology Quiz and Oratorical Competition 2019, Department of Parasitology, National, 27 August 2019
12.The Impending Victory of Neglected Tropical Diseases, The Impending Victory of Neglected Tropical Diseases, Department of Parasitology, University, 7 August 2019
13.Malaria Treatment & Prophylaxis, Malaria Treatment & Prophylaxis, Department of Parasitology, University, 6 August 2019
14.Basic Concept & Troubleshooting Guide on qPCR, qPCR Consultation On-Demand, Department of Parasitology & Canvio Sdn. Bhd., University, 25 July 2019
15.Emerging Arboviruses, Emerging Arboviruses, Department of Parasitology, University, 24 July 2019
16.SporeSat: Lab-on-Chip for Study of Single Cell in Space, SporeSat: Lab-on-Chip for Study of Single Cell in Space, Department of Parasitology, University, 24 July 2019
17.Malaria Microscopy Workshop, Malaria Microscopy Workshop, Department of Parasitology, University, 10 July 2019
18.Conference Organising committee, the 4th international conference on molecular biology and biotechnology (ICMBB2020) in conjunction with the 27TH MSMBB Scientific Meeting, National Science Center, Malaysia, 3-4 June 2019
19.Organising committee, The 3rd International Conference on Molecular Biology & Biotechnology, co-organized by MSMBB and UCSI University, 24-25 April 2019
20. Organising committee, The 55th Annual Scientific Conference of the Malaysian Society of Parasitology and Tropical Medicine (MSPTM) 2019, InterContinental Hotel Kuala Lumpur, Malaysia, 13-14 March 2019
21.Organizing committee (Social) of The 26th World Association for the Advancement of Veterinary Parasitology conference, The 26th World Association for the Advancement of Veterinary Parasitology

conference, The World Association for the Advancement of Veterinary Parasitology and MSPTM, International, 28 January 2016 - 8 September 2017
22. Basic and Clinical Immunology Course, Faculty of Medicine, University of Malaya, 5-9 July 2017
23. Organising committee of The 55th Annual Scientific Conference of the Malaysian Society Of Parasitology And Tropical Medicine (MSPTM) 2018
24. Organising committee, the 3rd International Conference on Molecular Biology & Biotechnology, co-organized by MSMBB and UCSI University, 24-25 April 2019.
25. Organising committee of The 29th Annual General Meeting in Conjunction with the MSMBB Seminar Series, 18 May 2018, Faculty of Biotechnology and Biomolecular Sciences (BIOTECH) Universiti Putra Malaysia
26. Organising committee of The 54th Annual Scientific Conference of the Malaysian Society Of Parasitology And Tropical Medicine (MSPTM) 2018
27. Organising committee of International Conference on Biochemistry, Molecular Biology and Biotechnology 2018 (ICBMBB 2018), 15-16 August 2018
28. Event Organiser, 19th MSMBB (Malaysian Society for Molecular Biology & Biotechnology) Scientific Meeting, Member of the Organizing Committee, UM, 30 October - 01 November 2012
29. Event Organiser, PBL Tutor Training Workshop, UM, 27 November - 3 December 2012
30. Event Organiser, Editing Your Manuscript for Publication: Workshop for Postgraduate Students, UM, 12-14 September 2012
31. Real-time PCR workshop, Organizer, Chemoscience Sdn Bhd, 15-16 April 2009

SUPERVISION

First Degree/Diploma/Pre-Degree

1. Internship, Lavisma Nathan, UCSI University, May- August 2020, 2020/2021, 3
2. Internship, Luqman Arif Yusri and Ng Wei Quan, UCSI, 13 May- 13 July 2020, 2020/2021, 2
3. Internship, Maackara Michael John B, University of Malaya, 17 February-22 May 2020, 2020/2021, 1
4. Internship, Tai Jie Yi, Tunku Abdul Rahman University College, 17 February- 26 April 2020, 2020/2021, 1
5. Internship, Liew Zhen Wei, Wong Kuan Yee, Liem Shyang Jye, Tan Jia Sen, Pang Juan Fei, UCSI University Kuala Lumpur, 1 March- 30 April 2019, 2019/2020, 4
6. Internship, Law Ruo Xie, Newcastle University Malaysia, 16 July-30 August 2019, 2019/2020, 1
7. Internship, Nisha Krishnan, Nadia Bee Hooi San, Jackson Felgenhauer Wiriya, Hans Christian Halim, Hishmietaa a/p Krishna Moorthy, Kong Jing Ying, UCSI University, September-November 2019, 2019/2020, 6
8. The Genetic Diversity of *Plasmodium Knowlesi* Normocyte Binding Protein Xa Region II (NBPXaII) Corresponding to High and Low Parasitaemia, 2019/2020, 1
9. Genetic Diversity of *Plasmodium Cynomolgi* Duffy Binding Protein 1 (II) Gene, 2019/2020, 1
10. Internship, Ng Xue Wei, Chen Jzit Weii and Wong Kar Yee, UCSI Kuala Lumpur, September-November 2019, 2020/2021, 3
11. Establishment of In Vitro Production of *Plasmodium Knowlesi* Gametocytes, 2018/2019, 1
12. Comparison of The Binding Level of Different Human Erythrocyte Duffy (Fy) Antigens to *Plasmodium Knowlesi* Duffy Binding Protein Alpha Region II (PkDBP II), 2018/2019, 1
13. Internship, Jia Yi Gan and Jia Min Choo, Tunku Abdul Rahman College, 18 February-27 April 2019, 2018/2019, 2
14. Establishment of in vitro culture of *Plasmodium knowlesi* gametocytes, 2018/2019, 1
15. Internship, Kong Zhi Wei, UCSI University, 16 October- 17 December 2018, 2018/2019, 1
16. Elucidating the link between polymorphism of *Plasmodium knowlesi* normocyte-binding protein and enhanced erythrocyte invasion by the parasite, 2018/2019, 1
17. Internship, Jeevetha A/P Muruthi and Raameswary A/P Kanan, Lincoln University College, 17 September- 9 November 2018
18. Internship, Aizzat Hanafi, Muhammad Afiq Bin Lokman, Management & Science University, 30 July- 14 December 2018
19. Internship, Ng Yee Ling, Tunku Abdul Rahman University College, February 19- May 15, 2018
20. Internship, Ng kai song-aaron, Tunku Abdul Rahman University College, February 19- May 15, 2018

21. Internship-Atiqah Azam, Fong Jung Yin, Shobha Elizabeth and Eric Low Kat Jun (UCSI), 6 Nov-29 Dec 2017
22. Internship, Lim Ee Jing, Taylor's University, Malaysia, 7 August 2017- 19 January 2019
23. Internship, Muhammad Asyraaf B Iskandar and Habibah Zahari, Universiti Teknologi Mara (UiTM), 24 July-15 September 2017
24. Internship, Lim Bing Sheng and Qryztal Lim, Tunku Abdul Rahman University College, 2 January-22 April 2017
25. Sequence diversity and natural selection of *Plasmodium knowlesi* Duffy binding protein α, β, γ region II in monkey isolates from Malaysia, 2016/17, Ong Cheng Yee, University of Malaya
26. Polymorphism in the DARC gene in humans and macaques with naturally acquired *Plasmodium knowlesi* infections in Malaysia, 2015/16, Nadia Tandai Anak Davis @ David, University of Malaya
27. Prevalence of *sarcocystis spp* in Malaysian captive snakes and lizards, 2015/16, Nahdatul Fatihah Mohd Fadil (MEB120019), University of Malaya
28. The prevalence of hookworm in stray dogs & PCR identification, 2013/14, Nur Syaqila Osman
29. Genotyping of *anopheles* group mosquitoes using cytochrome c oxidase subunit ii (mt-coii), 2013/14, Chui Yuet Yee, University of Malaya
30. Genetic polymorphism of circumsporozoite protein (CSP) gene in *Plasmodium knowlesi* in Malaysia, 2013/14, Syadaitul Atira Bt. Othman (MEB100038), University of Malaya
31. Phylogenetic analysis of *Plasmodium knowlesi* infection, 19 August- 23 December 2013, Internship, Siripakorn Prakobkeaw, Faculty of Medical Science, Naresuan University, Phitsanulok, Thailand.
32. Molecular Differentiation of Entamoeba histolytica and Entamoeba dispar in human stool samples. 2011/12, 2, completed, Azaratul Haizum binti Salamon, University of Malaya
33. Molecular Characterisation of Filarial Worms in Animals. 2011/12, completed, NG FUI CHEE
34. Cloning and Expression of GRA5 of *Toxoplasma gondii* in *Escherichia coli*, 2011/12, completed, Lim Yit Zie@Lim Edie, University of Malaya
35. Cloning and Expression of MSP-119 of *Plasmodium knowlesi* in *Escherichia coli*, 2011/12, completed, Gan Ming Jack (MEB090006), University of Malaya
36. Recombinant cloning and expression of dense granule protein 4 of *Toxoplasma gondii*, 2008/2009, 1, Monash University undergraduate
37. Cloning of SAG1/2 in Pichia pastoris, 2007/2008, completed, Felicia Tay, Monash University undergraduate
38. Cloning and expression of GRA2 in *Pichia pastoris*, 2007/2008, completed, Stacey Lim, Monash University undergraduate

Master Degree

1. Master Degree, Ng Yee Ling, Genetic diversity and immunogenicity profiling of *Plasmodium knowlesi* apical membrane antigen 1 (PkAMA-1) from Peninsular Malaysia and Malaysian Borneo 2019-2020, Date of register: 20/02/2020
2. Master Degree, Ummi Kalthum bt Azlan, The effect of genetic polymorphism of *Plasmodium knowlesi* duffy binding protein alpha II (PkDBPαII) gene in the regulation of host immune response 2019-2020, Date of register: 25/09/2019
3. Master Degree, Lee Phone Youth @ Zen Lee, Development of a simplified Loop mediated isothermal amplification-Lateral flow (LAMP-LF) method for field detection of Plasmodium species. Date of register: 31/03/2019
4. Master Degree, Fatma Diyana Binti Mohd Bukhari, Binding Activity of Plasmodium knowlesi Duffy Binding Protein Alpha Region II (PkDBPαII) Corresponding to High and Low Parasitaemia Isolates, 2018/2019, Date of register: 22/03/201
5. Master Degree, Lim Khai Lone, Binding Affinity of Duffy Binding Protein (PKDBPαII) Of *Plasmodium Knowlesi* Clinical Isolates from Peninsular Malaysia and Malaysia Borneo / Parasitology. Date of register: 31/03/2016 Completed 2018
6. Master Degree, Wong Yien Ping, Development of Molecular Diagnostic for Malaysian Human Rhinovirus C, Date of register: 03/05/2016 Completed 2019
7. Master Degree, Mohammad Behram Khan, Identification of Immune factors in *Anopheles cracens* during *Plasmodium knowlesi* infection, Date of register: 01/01/2015, Completed

8. Master Degree, Mira Syahfriena Amir Rawa, Analysis of the Effect of Natural Selection on Low Polymorphic Gene Encoding Rhoptry- Associated Protein 1 (RAP-1) in *Plasmodium*, Date of register: 01/01/2015, Completed

9. Master Degree, Ruhani binti Yusof Phylogenetic analysis of Plasmodium knowlesi in Malaysia, Date of register: 09/03/2013, CGPA: 3.51, Completed

10. Master Degree, Ng Yit Han, Characterization of Sarcocystis spp. from cattle in Shah Alam, Selangor Darul Ehsan, 2013/14, Date of register: 02/09/2013, cGPA: 3.39, Completed

11. Master Degree, Sum Jia Siang, Molecular identification and phylogeny of malaria vectors in Malaysia, 2012/2013, Date of register:16/10/2012, cGPA: 3.14, Completed

12. Master Degree, Vanitha Palaeya, Cloning and expression of Surface Protein Containing an Altered Thrombospondin Repeat Domain (SPATR) gene of Plasmodium knowlesi in Escherichia coli and yeast Pichia pastoris, 2010/2011, Date of register: 28/09/2011. cGPA: 3.5, Completed

13. Master Degree, Claudia Nisha Anthony, Drug Resistance of Plasmodium vivax, 2010/2011, Date of register: 06/10/2011, cGPA: 3.68, Completed

14. Master Degree, Hemah A/P Andiappan, Genotyping of Toxoplasma gondii strains from pregnant women and their newborns, 2010/2011, Registration Date: 03/12/2010, CGPA: 3.21, Completed

15. Master Degree, Chin Lit Chein, Cloning and expression of Merozoite Surface Protein (MSP) of Plasmodium knowlesi in yeast Pichia pastoris. 2009/2010, Date of register: 26/09/2009. cGPA: 3.11, Completed

16. Master Degree, Chang Phooi Yee, Expression and characterization of Toxoplasma gondii rhoptry protein 2 (ROP2) produced by yeast Pichia pastoris, 2009/2010, Date of register: 25/09/2009. cGPA: 3.58, Completed

17. Master Degree, Mona A. Al-Areeqi, molecular epidemiology of *Entamoeba histolytica*, *E. dispar* and *E. moshkovskii* infections in Yemen: different species-specific associated risk factors, Yemen, 2012/13, Date of register: 13/09/2001, Completed

Doctoral Degree (PhD)

1. Doctoral Degree (PhD), Shahhaziq Shahari, The prevalence and genetic diversity of *Plasmodium knowlesi* in macaques from Peninsular Malaysia and the establishment of a *P. knowlesi* in vitro culture, 2019/2020

2. Doctoral Degree (PhD), Phang Wei Kit, Genetic diversity of *Plasmodium knowlesi* and modelling of its transmission in Peninsular Malaysia, 2019-2020, Date of register: 24/02/2020

3. Doctoral Degree (PhD), Ummi Wahidah bt Azlan, Genetic diversity and immunogenicity profilling of *Plasmodium knowlesi* surface protein thrombospondin repeated domain (PkSPATR) and rhoptry associated protein-1 (PkRAP1), 2019-2020, Date of register: 18/02/2020

4. Doctoral Degree (PhD), Aimi Diyana Gapor, Investigation on the multiplicity and diversity of *Plasmodium knowlesi* infections in Malaysia based on the merozoite surface protein-1, 2019-2020, Date of register: 1/10/2019

5. Doctoral Degree (PhD), Tan Jia Hui, Development and optimization for immunochromatographic test (ICT) for rapid diagnosis of human malaria and its field evaluation, 2019-2020, Date of register: 11/09/2019

6. Doctoral Degree (PhD), Naqib Rafieqin Noordin, Genetic and Phenotypic Characterisation of *Plasmodium knowlesi* Normocyte Binding Protein Xa II (PKNBPXaII) Corresponding to High and Low Parasitemia Level, 2019-2020, Date of register: 15/03/2019

7. Doctoral Degree (PhD), Manal Ali Saleh Al-ashwal, Epidemiological and Genetic Studies on Zoonotic Parasitic Infections in Yemen: Implications for Effective Control Programmes, 2019/2020

8. Doctoral Degree (PhD), Izzah Ruzana Binti Mohd Hanapi, Assessment of health status and parasitic infections amongst the refugees in Klang Valley, Malaysia, 2019/2020

9. Non-graduating research program, Fathima Wardha Refai, PhD, Fatimah Jinnah Medical College, University of Punjab, Pakistan, 27 Jan 2018-27 Jan 2019, Completed

10. Non-graduating research program, Abdullahi Muhammad Daskum, PhD, Modibbo Adama University of Technology, Yola, Nigeria, 5 March 2018-5 March 2019, Completed

11. Doctoral Degree (PhD), Aida Syafinaz Binti Mokhtar, DNA Barcoding of Medically-Important Arthropods Including Molecular Detection of Associated Potential Pathogens in Head Lice, 2012/14, Date of register: 25/09/2014, Completed

12. Doctoral Degree (PhD), Wahib Mohammed Mohsen Atroosh, In Vivo and Molecular Evaluation of Artesunate-Sulfadoxine-Pyrimethamine Efficacy for Uncomplicated Falciparum Malaria in Tehama Region, Yemen, Date of register: 25/09/2014, Completed with Distinction.
13. Doctoral Degree (PhD), Jonathan Liew, The JAK-STAT immune signalling pathway of Anopheline mosquito in response towards malaria parasite infection, Date of register: 0/10/2014, Completed 2017
14. Doctoral Degree (PhD), Tengku Idzzan Nadzirah, Analysis of Sarcocystis spp. Immunogenic Protein for Development of Human Sarcocystosis Serological Test Kit, Date of register: 01/10/2014, Completed 2018
15. Doctoral Degree (PhD), Leong Cherng Shii, Detection of resistance status of Aedes aegypti (Linnaeus) collected from 9 districts in Selangor using biochemical and molecular tools and comparison of dengue virus susceptibility between resistant strain and susceptible strain of Aedes aegypti, Date of register: 01/12/2014, Completed 2019
16. Doctoral Degree (PhD), Jeremy Ryan de Silva, Genetic diversity study, expression and immunocharacterization of Plasmodium knowlesi Merozoite Surface Protein 3-Beta in Escherichia coli and Pichia pastoris. Date of register: 22/02/2013, Completed 2017
17. Doctoral Degree (PhD), Lai Meng Yee, Receptor of SAG 1 and SAG2 of Toxoplasma gondii, 2012/13, Date of register: 12/10/2012, CGPA 3.08, Completed 2018
18. Doctoral Degree (PhD), Amirah Amir, Genome Expression Analysis of *Anopheles cracens* and Anopheles latens Responses to *Plasmodium knowlesi* Infection, 2012/13, Date of register: 13/09/2011, MBBS, Completed
19. Doctoral Degree (PhD), Lee Wenn Chyau, Association of rosette formation and pathogenesis of Plasmodium vivax malaria, 2011/2012, Date of register: 09/10/2011, cGPA: 3.75, Completed with Distinction.
20. Doctoral Degree (PhD), Cheong Fei Wen, Identification and characterization of epitopes on the merozoite surface protein of Plasmodium knowlesi, 2010/2011, Date of register: 29/12/2010. cGPA: 3.96, Completed with Distinction.
21. Doctoral Degree (PhD), Abdulsalam Mohammed Qasem Al-Mekhlafi, Epidemiology of Malaria and Molecular Genotyping of Malaria Parasites in Yemen (1/09/09-31/01/10, Acting Supervisor), Completed
22. Doctoral Degree (PhD), Parthasarathy Sonaimuthu, Vaccination of mice by Rhoptry proteins of Toxoplasma gondii produced by yeast Pichia pastoris, 2008/2009, Date of register: 09/07/2009. cGPA: 61% (First class In India), Completed
23. Doctoral Degree (PhD), Ching Xiao Teng, Development of DNA and recombinant vaccines against Toxoplasma gondii infection, 2008/2009, Date of register: 25/09/2009. cGPA: 3.81, Completed
24. Doctoral Degree (PhD), Girija Thiruvengadam, Molecular cloning, *characterization and function* analysis of the chimeric *gene* encoding *Toxoplasma gondii* surface antigen 1 and 2, 2007/2008, Date of register: 1/06/2008. cGPA: 66.6% (First class In India), Completed
25. Doctoral Degree (PhD), Lina M. Q. Alareqi, Malaria burden and the distribution of genetic markers associated with drug resistance in Mawza district, Taiz governorate, Yemen, 2012/13, Date of register: 13/09/2001, Completed

TEACHING

1. Recombinant DNA Technology
2. Biochemistry
3. MBBS Phase II PBL
4. MJEB2401-Basic Course in Diagnostic Parasitology
5. MJEB3401-Advanced Course in Diagnostic Parasitology
6. DMLT2822-Diagnostic Parasitology
7. MWEF2111-Pharmaceutical Microbiology
8. MBBS-Parasitology
9. DMLT2092-Parasitology
10. MLT (IMR)-Basik Modul Parasitologi Perubatan
11. MJEB3402-Advance course in diagnostic Parasitology
12. MBEB1109-Basic Parasitology
13. Postgraduate Research Methodology

AWARD

1. Gold medal, 6th Korea Creative Invention Contest CiC 2020, Korea, 2020
2. Gold medal, 4th Korea Creative Invention Contest CiC 2018, Korea, 2018
3. Biorisk Management certification, 11th July 2018
4. Grand Prize Award, National Exclusive Innovation Challenge Award 2018
5. Second Prize Award, National Exclusive Innovation Challenge Award 2018
6. Best Lecturer for Parasitology Session 2015/2016, Faculty of Medicine, University of Malaya, 26 April 2017
7. Gold medal, 4th Korea Creative Invention Contest CiC 2017, Korea, 2017
8. Outstanding reviewer award, International Journal for Parasitology, 2017
9. Cambridge Certificate for Outstanding Medical Achievement, 2016
10. Anugerah Perkhidmatan Cemerlang (Excellent Service Award) University of Malaya, 2016
11. Neuroscience Best Publication Award, 2015
12. Minister of Health Innovation & Research Award (PhAMA Awards), 2015
13. Nadchadtram Medal, Malaysian Society of Parasitology and Tropical Medicine, 2014
14. Anugerah Cemerlang (Excellent Award for Young Scientist) University of Malaya, 2013
15. Anugerah Perkhidmatan Cemerlang (Excellent Service Award) University of Malaya, 2011
16. Sijil Perkhidmatan Cemerlang (Excellent Service Certificate) University of Malaya, 2012

SOCIAL CONTRIBUTION

1. Myanmar Refugee Community Learning Centre, 8th April 2021
2. Donation to Lost Food Project, 25th May 2020
3. Donation to Persatuan Care Selangor, 25th May 2020
4. Adopt an Animal: Malayan Elephant (*Elephas maximus hirsutus*), Zoo Negara, 2020
5. Edustem Workshop in collaboration with USIM FAST LAB, sponsored by MSMBB, 8 April, 2020
6. Stop Child Exploitation Virtual Run, 8th Oct 2019 - 8th Jan 2020
7. Girl Scout volunteer, 1st Oct 2018 – 30th Sept 2019
8. Setia Foundation Volunteer, 6th March 2018
9. UNHCR Malaysia, UN Refugee Agency, Volunteer, Sep-March 2018
10. Child Sponsorship World Vision 29th Jan 2018-current
11. Facilitator of Let's go to mummies lab, 23rd Feb 2018
12. Adopt a Community Park: The Winged-Fruit Trees Campaign, 22nd Feb 2018
13. Charity runs, 2016-2017
14. Parent Volunteer at Tenby International School, International day, 14th July 2017
15. World Vision Child Sponsorship, 2008-current
16. Committee of 5th Animal Awareness Day, 25th March 2015
17. Committee of 3rd Animal Awareness Day, 18th March 2014
18. Committee of 2nd Animal Awareness Day, 17th Oct 2013
19. Committee of 1st Animal Awareness Day, 17th Jan 2013
20. Orphanage Lice Removal Outreach
21. Scientific advisor of Secondary School Science Program co-organizes with Mianto Sdn Bhd
22. Member of Donation drive, Taiwan Buddhist Tzu Chi Foundation Malaysia.

Acknowledgement

HIR GRANT (2010-2017)

Jeremy, Partha, Girija, Xiao Teng, Fei Wen, Amirah, Meng Yee, Wenn Chyau, Claudia, Yit Han, Sum, Jonathan, Leong, Behram, Khai Lone, Mira, Idzzan, Zahra, Vanitha, Lit Chein, Pooi Yee, Mona, Hemah, Aida

LRGS (2019-2022)

Shah, Wai Kit, Wahidah, Kalthum, Fatma, Aimi, Jia Hui, Zen, Naqib, Elaine, Manal

Most of our works were/are supported by two major grants, High Impact Research (HIR) Grant and Long Term Research Grant Scheme (LRGS) from Ministry of Higher Education, Malaysia. I sincerely appreciate all the resources and funding opportunities provided by Prof Tan Sri Dr Ghauth Jasmon, Emeritus Professor Dato' Dr Lam Sai Kit, Prof Noorsaadah Abdul Rahman and Prof Dr Rais Bin Mustafa, to support our vision to produce globally significant research with local relevance and to make a positive contribution to society as a whole. Over the past 10 years there have been a large number of postgraduate students, undergraduate students, and research assistants who have been part of the Molecular Laboratory (MolLab). You have worked long hours and devoted much effort to our research and I am deeply grateful to each and every one of you. I don't think it would have been possible to achieve the goal without your efforts!

THANK YOU

COLLABORATORS (UM & NATIONAL)

IT IS AN HONOR TO WORK WITH YOU.

I would also like to extend my deepest gratitude to our collaborators. Thank you for believing in us and for providing the time, talents, and treasures that are crucial to our students and projects' success. I am truly delighted in working with you and getting to know you better through this teamwork! Each of you is an incredible collaborator!

THANK YOU

INTERNATIONAL COLLABORATORS

WE COULDN'T DO IT WITHOUT YOU

Bruce Russell, University of Otago; Georges Snounou, IDMIT; Laurent Rénia, Singapore Immonolgy network; Dr Rathnagiri Polavarapu, Genomix, India; Tony Holder and Robert Moon, London School of Hygiene & Tropical Medicine; Caroline Ng, University of Nebraska Medical Center; Prof Eun-Taek Han, Kangwon National University College of Medicine; Dr Myat Htut Nyunt, Department of Medical Research, Yangon, Myanmar and many more.

Dean of Faculty of Medicine

DATO' PROF. DR. ADEEBA BINTI KAMARULZAMAN



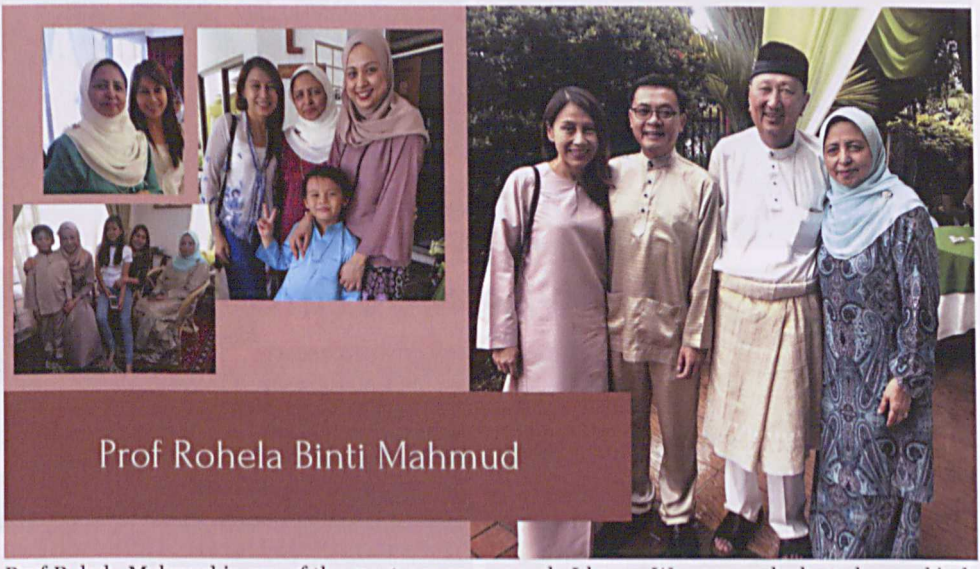



I want to offer my deep appreciation to Dato' Prof Dr Adeeba Kamarulzaman, for her remarkable stewardship of this great faculty, who is a constant source of inspiration. Thank you for your support, confidence, and belief in me and my work.


PROF FONG MUN YIK

A SUPERVISOR, COLLEAGUE AND FRIEND

I am deeply indebted to my Master and PhD supervisor, Prof Fong Mun Yik for his fundamental role in my postgraduate studies and my career. When I was a student, he gave me the freedom to do whatever I wanted, at the same time continuing to contribute valuable feedback, advice, and encouragement that I will remember for years to come. In addition to our academic collaboration, I greatly value the close personal rapport that Prof Fong and I have forged over the years.



Prof Rohela Binti Mahmud

Prof Rohela Mahmud is one of the most generous people I know. We were so lucky to have a kind-hearted boss like you, who cares for us so much up until today after you have retired. While I still have the opportunity, let me thank you for all that you have done not only for me but for the whole Department. You are the most supportive boss we ever had.

To me, one of the most enjoyable roles as an academician is teaching. I have so much fun with all our undergraduate students. Whenever I chat with them, I come away feeling optimistic because I believe we are in good hands. The future of our society depends on your passion and commitment. I would have been happy to spend the rest of my career as a teacher, but somehow, I stumbled into administration.

Prof. Dr. Debra Sim & PBL Team & MERDU (2011-current)

I volunteered to be the PBL stage II coordinator in 2011 when I had just joined the faculty in less than 2 years. Prof Debra trusted me and put in extra effort and time in training me. I was appointed as the PBL overall coordinator in 2018 when she retired. I'm thankful to MERDU and PBL committee members for sharing your knowledge and experience with me in almost a decade.

PROF MOHD RAIS BIN MUSTAFA & TEAM

Research Management Unit, HTMC & Faculty of Medicine

2013-2015

I joined Research Management Unit of Health and Translational Medicine Cluster and Faculty of Medicine in 2013 and 2014, respectively, under the leadership of Prof Rais Bin Mustafa. Thank you for giving me the chance to fulfill my potential here. To be honest, everyone in RMC respect and love you! I wish you all the best in the new ventures because you deserve it.

THE ANIMAL EXPERIMENTAL UNIT

A/P DR. WONG POOI FONG
(2012-2019)

I was also blessed to be part of Animal Experimental Unit (AEU) of Faculty of Medicine from 2012 to 2019. Working with A/P Dr Wong and the rest of the colleagues to get the accreditation for AEU was challenging but fulfilling!

INSTITUTIONAL BIOSAFETY AND BIOSECURITY COMMITTEE (IBBC)

PROF SAZALY ABU BAKAR
(2015-2019)

Prof Sazaly Abu Bakar invited me to be part of The University of Malaya Institutional Biosafety and Biosecurity Committee in 2015. Prof Sazaly has a winner's attitude. You won't have survived working with him if you're not up to par. Thank you for sharing your vision, dedication and humour.

Faculty of Medicine
Risk and Quality Management

DATIN PROF. DR. HAMIMAH BINTI HAJI HASSAN (2016-2019)

I joined FOM Risk and Quality Management team under the leadership of Prof Hamimah in 2016. Being an auditor was a tough job that none of us would do quite as well without Prof Hamimah's support and guidance!

JUMMEC

PROF.DR.TUNKU KAMARUL ZAMAN

JUMMEC.UM.EDU.MY

Prof Tunku Kamarul Zaman revived JUMMEC when he was the Editor-in-Chief in 2013 by recruiting a few new editors including me. He handed over his role to me in 2018. Managing a journal is not an easy task. I wish to acknowledge the contributions made by the dedicated and professional members of our Editorial Board and the hard working, admin staff, Fatin. I am indebted to the Dr Cheong and Dr Amirah, for their tremendous support in managing the journal. Special note of appreciate to Prof Kamarul, the interest that you show in my success and development is something for which I feel very grateful. I could not have gotten through it without you. Thank you for being the perfect role model for the next generation!

MALAYSIAN SOCIETY FOR MOLECULAR BIOLOGY AND BIOTECHNOLOGY (MSMBB) HTTPS://WWW.MSMBB.MY/

I was the Honorary Secretary of Malaysian Society for Biochemistry and Molecular Biology (MSBMB) in 2017-2019 and the current President. I want to acknowledge everyone's extra efforts in organizing conferences, seminars and community activities for the society and managing the journal APJMBB.

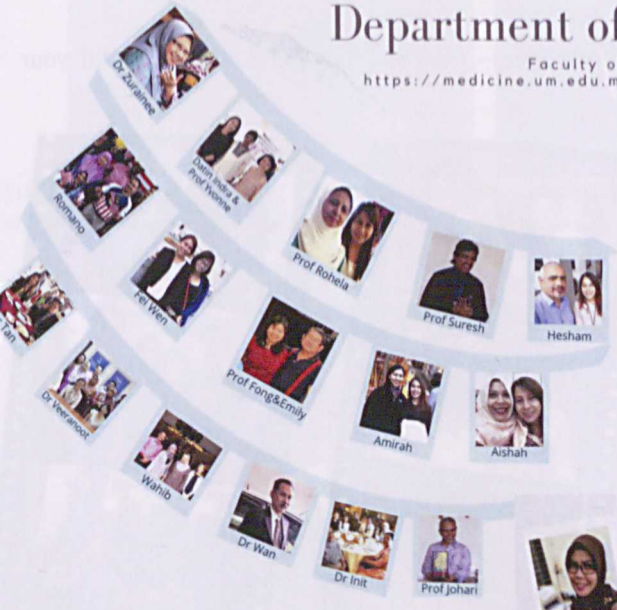
MALAYSIAN SOCIETY OF PARASITOLOGY AND TROPICAL MEDICINE (MSPTM) HTTP://MSPTM.ORG/

It really felt good to operate with a team that was so self-reliant and motivated. I was the council member of MSPTM in year 2018-2019. The amount of effort that the team put into the society was tremendous. The energy levels and the sincerity which was displayed was exemplary. I couldn't have asked for better teammates! You guys made the work feel a lot easier.

I love teaching, especially kids, and am good at it. I fulfilled part of my community service with my passion in mine. Thank you so very much to 'my' kids at Myanmar Refugee Community Learning Centre, for making this dream come true, and for making it come true in such a wonderful and lovingly way! I will be back!

Department of Parasitology

Faculty of Medicine
https://medicine.um.edu.my/parasitology-department

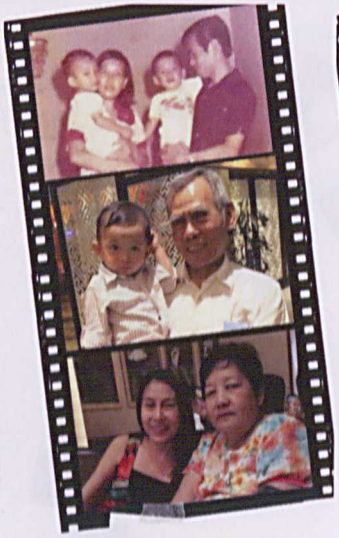


I am deeply grateful for the wonderful students, colleagues, staff, and alumni who make up the Department of Parasitology. I'm so proud to be part of the family. In fact, we should be awarded the happiest department in the whole UM.

Thank you to my colleagues and friends, you make Department of Parasitology beautiful from the inside out. To the support staff, thank you for your hard work and dedication for keeping our department so organized!

Many thanks to all my friends and colleagues– from so many parts of my life– for your encouragement and guidance.

The Vu Family



Parents

The Lau Family

To my parents, parents in laws who are far away in USA, siblings, aunties and uncles, I can't thank you enough for all that you have done for me. Words cannot express the feelings I have for my parents for their constant unconditional support both in my study and my career. I would not be here without you. Family and friends are treasures.

MIA

Antonio

To Mia and Antonio, thank you for your great love of a working mom. You, being my children, are the greatest gifts I could have received or will ever receive.

TONY

And most of all, to my husband, Tony, who knows me more than I know myself. Thank you for believing in me and supporting me, all of which have helped me grow into the woman I am today. Above all, thank you for providing me a safe, happy and loving home.

Last but not least, to my country, Malaysia. Even though I have roamed the world, it is still my home I long to see. You will always be a part of me. Malaysia, tanah tumpahnya darahku. I would like to conclude this lecture by reciting the pledge of Rukun Negara.

MAKA KAMI, rakyat Malaysia, berikrar akan menumpukan seluruh tenaga dan usaha kami untuk mencapai cita-cita tersebut berdasarkan prinsip-prinsip yang berikut:

NOW THEREFORE, we, the people of Malaysia, pledge to concentrate our energy and efforts to achieve these ambitions based on the following principles:

- Kepercayaan Kepada Tuhan- Belief in God
- Kesetiaan Kepada Raja dan Negara- Loyalty to the King and Country
- Keluhuran Perlembagaan- Supremacy of the Constitution
- Kedaulatan Undang-undang- Rules of Law
- Kesopanan dan Kesusilaan- Courtesy and Morality