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Neglected, Tropical and Vector Borne Diseases: The Evolution of One Health from Challenges to Solutions

E-Abstract Book
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How A One Health Approach Mitigates Neglected Tropical Diseases

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Birth Control Technique – Repurposing for Aedes Control

Secondary Dengue Virus Infection in Communities with Pre-existing Multiple Heterotypic Dengue Virus Antibodies: A Longitudinal Study in Malaysia

Vectors and Parasites in the Simuliidae: Understanding, Predicting and Preventing Problems

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# 3rd ASIAN SIMULIIDAE SYMPOSIUM

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First Report on a Black Fly (Simuliidae) Attracted to Human in Peninsular Malaysia

Merthithid Parasitism of Black flies in Peninsular Malaysia

Temporal Variation in Diversity and Community Structure of Preimaginal Blackflies (Diptera: Simuliidae) in a Tropical Forest Reserve in Malaysia

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First Report on a Black Fly (Simuliidae) Attracted to Human in Peninsular Malaysia

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**KEYNOTE**

Abstract No: 12947

**How A One Health Approach Mitigates Neglected Tropical Diseases**

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**Abstract**

One billion people, or 1/6 of the world’s population, suffer from neglected tropical diseases (NTDs) in 149 countries. The World Health Organization lists 18 NTDs that include taeniosis and neurocysticercosis, dengue and rabies. The One Health approach recognizes the interconnectedness of human, animal and ecosystem health and encourages collaborations between diverse disciplines to address NTD challenges. Applying One Health brings skills together to define the intersection and integration of animals, humans and environment, builds effective teams and establishes trust with communities and stakeholders. The goal of applying this approach is to mitigate and effectively manage societal needs such as NTDs. Proposed steps for building a One Health Platform are outlined. Potential steps include identifying a societal need (e.g., an NTD); investing time and effort to engage with stakeholders to build trust; assembling interdisciplinary collaborative teams to recommend public health interventions to accelerate prevention, control, elimination and eradication of an NTD; establishing a platform roadmap, and building sustainable research, education and outreach programs to support mitigating this platform. Finally, it is critical to “measure well to manage well”.

**Keywords:**

Neglected tropical diseases; NTDs; One Health approach; interdisciplinary collaborative teams
PLenary

Abstract No: 12986

Birth Control Technique – Repurposing for Aedes Control

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Abstract

Both species of Aedes aegypti and Aedes albopictus are geographically widespread in Malaysia and are prolific breeders in artificial/natural containers. These two species are vectors of human arboviruses of dengue, Zika and chikungunya, with Ae. aegypti being the primary vector for dengue. Despite intensive and extensive control efforts by health agencies, these diseases continue to spread unabated. WHO has recommended the use of Sterile Insect Technique (SIT) as an innovative tool in the Global Vector Control Response 2017–2030 (GVCR), which provides a new strategy to strengthen vector control worldwide through increased capacity, improved surveillance, better coordination and integrated action across sectors and diseases. Hence, SIT has emerged as an potential control tool in managing Aedes vector population. SIT application against agricultural pest has been very successful for eradication as well as elimination of certain pests. SIT application in public health has been studied intensively for the past decades, however, implementation of SIT on Aedes mosquitoes, particularly Ae. aegypti is limited to date. SIT relies on the production and sustained release of sufficient sterile males to induce sterility in the wild females which, over time, causes the target population to crush. The use of SIT has no regulatory requirements in Malaysia. This study served as a preliminary investigation in exploring the possible application of SIT as one of the dengue control strategies. The study aimed at determining the optimum sterilizing dose rate from Caesium 137 (¹³⁷Cs) gamma irradiation and to observe the life stage parameters of gamma ray irradiated wild-type and laboratory Aedes aegypti male. This serves as a first attempt in comparing the differences between lab strain versus wild strain in terms of emergence rate, longevity and mating ability. Laboratory and wild strain pupae were exposed to six different dosages (5 Gy - 100 Gy) of ¹³⁷Cs gamma irradiation. The results indicated that the effective and optimum irradiation dose was 50 Gy and complete sterility was achieved, without adversely affecting the male mating competitiveness of Ae aegypti. Field evaluation of radiation-sterilized Ae aegypti in dengue hotspots is in progress.
Secondary Dengue Virus Infection in Communities with Pre-existing Multiple Heterotypic Dengue Virus Antibodies: A Longitudinal Study in Malaysia

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Abstract

Dengue is endemic in Malaysia. The principal dengue mosquito vectors of \textit{A.aegypti} and \textit{A. albopictus} exist and all the 4 DENV serotypes circulate in the population. The circulation of all the four DENV serotypes result in the presence of preexisting heterotypic immunity in the population. Varying pre-existing antibody titer against any one, two, three or all four DENV serotypes can result in protective or enhancement effects. Antibody-dependent enhancement places a high risk on the majority of the population to develop secondary dengue infection and a high incidence of the severe complications of the disease. A prospective longitudinal study of dengue viral infections in two cohorts of healthy adult communities was conducted in a high and low burden dengue sites of Shah Alam and Segamat in Malaysia for 12 and 6 months, respectively. Serum samples from participants were collected at a quarterly interval, i.e 4 times for Segamat and 2 times for Shah Alam. ELISA to detect low-titer IgG, high-titer IgG and IgM indicative of past, recent secondary and active infection respectively, and focus reduction neutralization test (FRNT) to demonstrate DENV serotype-specific neutralizing antibodies and titer, in relation to dengue manifestations were conducted in the two communities. Irrespective of a high, moderate or low preexisting neutralizing antibody level, upon secondary infection, adults with pre-existing multiple heterotypic DENV antibodies demonstrated inapparent dengue outcomes. Thus, broad neutralizing pre-existing multiple heterotypic antibodies seemed to have a protective role upon secondary infections in the communities. Despite these findings, dengue viral infection in the country is rising every year. The occurrence of dengue is multifactorial and still not fully understood.
Abstract No: 12923

Vectors and Parasites in the Simuliidae: Understanding, Predicting and Preventing Problems

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Abstract

More than 95% of the 2300 species of black flies (Simuliidae) in the world feed on vertebrate blood and, therefore, have the potential to damage economies, either directly through blood-feeding or through transmission of disease agents to humans, domesticated animals, and wildlife. Simulid-borne problems of parasitism and disease are, however, not uniformly distributed throughout the world. Many tropical areas suffer disproportionately. Yet, other tropical areas are apparently free of economically significant simulid problems. Simulid-borne parasite and disease problems also can appear suddenly in new geographic areas and under novel circumstances. This presentation explores the evolution and current status of simulid-borne parasite problems, such as human onchocerciasis, and seeks to explain the geographical patchwork of simulid-caused problems. The different pathways by which the Simuliidae reach economic and public health importance are highlighted. The ability to predict simulid problems and proactively prevent them is also discussed, as is the critical, and often challenging, need to identify vectors and parasites as the first step in control programs.
Abstract

Currently, dengue control relies largely on reactive vector control programs. Proactive vector-control using a rational, well-balanced Integrated Vector Management (IVM) approach may prove more successful for dengue control. As part of the development of a cluster randomized controlled epidemiological trial, a study was conducted in Johor Bahru, Malaysia. The study included one control site and two intervention sites to be treated with targeted outdoor residual spraying (ORS) and deployment of auto dissemination devices (ADD). The primary entomological measurement was ovitrap index (OI). The comparison between study sites on OI was analysed by One-way ANOVA. Relative to the control site, the ORS and ADD sites showed reduction in the *Aedes* ovitrapp index (51.00 ± 2.70 and 39.00 ± 3.30 respectively). Analysis by species showed that as compared to the control site, *Ae. aegypti* density was lower in ADD (7.64 ± 1.097) and TORS (12.45 ± 1.233). The present study provides insights on the methods to be used for the main trial. Further work is required to strengthen our understanding of how these interventions impact dengue vector populations and dengue transmission.

Keywords: Malaysia; Aedes; vector control; integrated vector management; dengue
3RD ASIAN SIMULIIDAE SYMPOSIUM

Abstract No: 13024

An Overview of Blackfly Research in Malaysia

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Abstract

Blackflies (Diptera: Simuliidae) are arthropods of medical and veterinary importance. The females of certain species, when they bite and draw blood, not only cause severe skin diseases to humans and animals, but also serve as vectors of various pathogens. Malaysia is home to the type localities of many blackfly species in the Oriental region, yet most of their biology and medico-veterinary implications remain unexplored. Accordingly, the blackfly studies conducted in Malaysia are summarized from the perspectives of taxonomy, systematics, ecology, and genetics. Knowledge gaps which required attention are also discussed.

Keywords: Simuliidae; taxonomy; ecology; genetics; Malaysia
First Report on a Black Fly (Simuliidae) Attracted to Human in Peninsular Malaysia

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Abstract

The adult females of some black fly (Diptera: Simuliidae) species are hematophagous insects that feed on avian and mammals blood including humans. In Peninsular Malaysia, a total of 63 species of black flies have been recorded yet there is no record of human attracted species. In September 2017, two individuals of adult females were attracted to a human during a biodiversity survey conducted at Tasik Kenyir, Terengganu, Peninsular Malaysia. Their blood-feeding activity, however, could not be confirmed because the samples were captured quickly after landing on the forehead of a volunteer. The DNA barcoding COI gene showed that the sample has 96% similarity with Simulium (Gomphostilbia) maleewongae of the Gombakense species-group. This is the first report on human attracted black fly in Peninsular Malaysia. Further morphological analysis is warranted to determine if this is an undescribed species.

Keywords:
Black fly; human attracted; Peninsular Malaysia; Simuliidae
Abstract No: 13026

**Mermithid Parasitism of Black flies in Peninsular Malaysia**

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**Abstract**

Mermithid parasitism in black flies (Simuliidae) has been recorded extensively and is often associated with gynandromorphism in black fly adults. The discovery of mermithid parasites in the black fly population at Mount Pulai, Johor marks the first recorded instance of this phenomenon in Peninsular Malaysia. In the initial sampling, only one species, *S. trangense* was infected with mermithids while the other three species present, *S. angulistyllum*, *S. bishopi* and *S. cheongi* were uninfected. Twelve gynandromorphs of *S. trangense* were also described for the first time in Malaysia. However, recent sampling suggests that all four species present at the study site are susceptible to infection through microscopic examination of black fly larvae. Further work will be carried out to characterize the prevalence of mermithid infection in this black fly population and to identify if temporal variation in abiotic factors may affect this prevalence.

**Keywords:**
Black fly; Simuliidae; mermithids; parasitology; Malaysia
Abstract No: 13000

Temporal Variation in Diversity and Community Structure of Preimaginal Blackflies (Diptera: Simuliidae) in a Tropical Forest Reserve in Malaysia

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Abstract

Blackflies (Diptera: Simuliidae) are ecologically and medically important insects but they have been understudied in Malaysia. Accordingly, a study on the temporal variation in diversity and community structure of preimaginal blackflies was conducted for the first time in Malaysia. A total of 865 preimaginal blackflies were collected in 120 samplings from five streams across three monsoon seasons from February 2018 until January 2019. Ten species were recorded and most frequently collected species were *Simulium cheongi*, *Simulium vanluni* and *Simulium jeffreyi*. Relatively common species were *Simulium roslihashimi*, *Simulium tani* complex and *Simulium trangense*. No significant changes of rainfall was observed between three monsoon seasons as well as the seasons with species and physiochemical parameters except acidity (pH) (P<0.01). Species relative abundance was varied between seasons, as high value of Shannon index (H) was found in northeast monsoon and lowest in the southwest monsoon. Principal Component Analysis (PCA) of all stream variables revealed two PCs that accounted for 61.4% of the total variance of physicochemical characteristics. Regression analysis revealed that species richness was positively and significantly associated with wider, deeper, faster, low conductivity and larger streambed particle with less canopy cover. Forward logistic regression analysis on three frequently collected species (>20%) indicated that *S. vanluni* and *S. jeffreyi* were commonly associated with wider, deeper and fast-flowing streams with low conductivity and larger streambed particle. In contrast, *S. cheongi* was associated with smaller, slower and small streambed particle. This first extensive bimonthly study has uncovered the species community structure as well as the changes of stream physicochemical parameters over time although they were not greatly and significantly influenced by the monsoon seasons. Species distribution, richness and abundance, however, were highly determined by the stream width, depth and velocity, therefore, were vital in shaping diversity and community structure of preimaginal blackflies.

Keywords:
Blackflies; *Simulium*, vector; temporal variation; diversity; community structure.
Abstract

Plasmodium knowlesi is the main cause of human malaria in Malaysia, with wild macaques as the important reservoir hosts. As elimination is a public health challenge, it is essential to understand whether there has been recent adaptation and ongoing evolution that may affect the epidemiology of malaria. Previous extensive population genetics and genomic studies revealed two divergent P. knowlesi populations in Malaysian Borneo (termed Cluster 1 and 2) associated with long-tailed macaques and pig-tailed macaques, respectively. These studies also showed an exclusive population in peninsular Malaysia (Cluster 3) but with limited archived samples. Here, we analyzed P. knowlesi genome sequences from 28 new clinical infections from peninsular Malaysia in order to understand the parasite population structure and test for evidence of recent adaptation. These parasites all belong to a major genetic population of Cluster 3 with high genome-wide divergence from Cluster 1 and Cluster 2 populations of Malaysian Borneo. Unexpected local genetic subdivision was also revealed; most parasites belonging to two sub-populations sharing a high level of diversity except at particular genomic regions, with the largest being a region of chromosome 12 showing evidence of recent directional selection. Surprisingly, a third sub-population comprised of P. knowlesi infections that are almost identical to each other throughout most of the genome, indicating separately maintained transmission and recent genetic isolation. Each sub-population could evolve to present a broader health challenge in Asia.

Keywords:
Malaria; zoonosis; genomics; population genetics; selection
Abstract No: 13022

Dengue Surveillance and Evolution of the Control Program in Indonesia

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Abstract

According to WHO the dengue epidemic worldwide has increased by 30 times since WW II. The first Dengue outbreak in Indonesia happened in 1968 in 2 cities with 58 cases, CFR was 41%. Since then every 5-10 years occurred a large dengue outbreak. The MOH set up the unit in charge of National Dengue Control Program and its control program with emphasize in Community engagement. Review the evolution of Dengue Control program and correlation with dengue data surveillance. Qualitative research using literature policy review of dengue policy documents and data collected from 1968 to 2018. In 1968 the activities were training the medical doctors in hospital and outbreak control by fogging. Five years later in 1973, Indonesia facing another big outbreak with 10.000 cases as well as increasing the district affected (69 districts). Began develop National Dengue Control Program, focused to outbreak control with little of community involvement. In 1978 delivered the National Campaign and messages on Source reduction (PSN–Pemberantasan Sarang Nyamuk) and Regular Larvae Checking every 3 month. The Dengue Prevention and Control Program continued to evolution up to 2016 with delivered the program called the movement of 1 House 1 Cadre (Gerakan 1Rumah 1Jumantik). On contrary the Dengue Cases showed increasing in number (incidence rate) and in the geographical areas, it is spread to rural area. There are some obstacle and disruption on the evolution of Dengue Control Program. The Effort to control Dengue infection is by making an adjustment to Dengue Prevention and control program, yet it was not giving good result, dengue cases kept going up and outbreak still occurred in various districts in Indonesia. It is influenced by a multi factors such as increase number of cities/districts, changing lifestyle, population density, community participation in cleaning the breeding sites. The solition is need commitment and support of the local government to implement the community-based dengue control activities.

Keywords:
Dengue; prevention & control, surveillance
Land Use Modification is Linked with Human Infections with Two *Plasmodium knowlesi* Subpopulations in Kapit Division, Sarawak

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Abstract

Humans acquire *Plasmodium knowlesi* through mosquitoes from forest-dwelling macaques, creating a new threat to public health and to the national efforts to eliminate malaria. In the Kapit division, two divergent *P. knowlesi* sub-populations (termed Cluster 1 and Cluster 2) infect humans and are associated with long-tailed macaque and pig-tailed macaque reservoir hosts, respectively. It was suggested that man-made activities and environmental modifications trigger the increasing numbers of knowlesi malaria cases. Since there is a steady increase of *P. knowlesi* infections over the past decade in Sarawak, particularly in the Kapit division, we aimed to identify hotspots of knowlesi malaria cases and their association with forest activities at a geographical scale using the Geographic Information System (GIS) tool. We studied a total of 1064 *P. knowlesi* infections (identified by nested PCR assays) from 2014 – 2019 in the Kapit and Song districts of Kapit Division, Sarawak. The demographic data showed that the most frequently infected were males (64%), with a median age of 41 years, and 35% of all infected persons were involved in farming activities. Average Nearest Neighbour (ANN) analysis showed that humans infected with both *P. knowlesi* subpopulations exhibited a clustering distribution pattern of infection. The Kernel Density Analysis (KDA) indicated that areas surrounding Kapit and Song towns were classified as high-risk for knowlesi malaria transmission. Furthermore, most sites associated with land-use were linked to malaria hotspots. Progressive insight showed that the changes in land use associated with knowlesi subpopulations varied inversely. Each year from 2014 to 2019, as infections with Cluster 1 subpopulation increased, there was a decrease in the prevalence of patients infected with Cluster 2 subpopulations. Malaria hotspot analysis provides useful information for the Vector-Borne Disease Control Programme in their efforts to control and prevent malaria.

Keywords: Long-tailed macaques; pig-tailed macaques; Geographical Information System (GIS); malaria hotspots; land use
Persistent Microfilaria in Post MDA in Kotawaringin Barat, Central Kalimantan

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Abstract

Kotawaringin District is located in Central Kalimantan, an endemic district for brugian lymphatic filariasis where five years rounds of mass drug administration (MDA) were completed in 2011 (2007 to 2011). The objectives of this study were to evaluate the Lymphatic Filariasis elimination program in Kotawaringin Barat. Conventional PCR (C-PCR) for detecting filarial parasites in animal reservoir hosts and mosquito vector. Mosquitoes were collected using modified human landing in bed net in Sungai Bakau and Dawak village of Kotawaringin Barat. Microfilariae (Mf) were detected using blood smears collected from inhabitants. A total of 620 individuals were participated finger blood prick examination in this study. Five Mf carriers were detected yielding an overall prevalence of 0.8% The mean mf density was 14.4 mf/60 μl. Animal reservoir host blood samples from 79 feline, 17 canine and 5 cynomolgus monkeys were also investigated and found that 3 of the domestic cats, 1 (one) cynomolgus monkeys (Macaca fascicularis) and 1 (one) Canis familaris were also infected with B. malayi. Likewise, the C-PCR profile amplified having size of 322 bp product of Hha1 gene Brugia malayi demonstrated that 6 felines, 1 canine and 1 cynomolgus monkeys contained DNA of B. malayi. Result indicated that domestic cat plays, Canis familaris and Macaca fascicularis an important role as the animal reservoirs for B. malayi in Kotawaringin Barat. For mosquitoes the predominant species are Mansonia spp., Culex spp., Aedes spp. and PCR of DNA extracts from pooled mosquitoes result showed no DNA B. malayi detected. Our results show that reappearance of infection of lymphatic filariasis in Sungai Bakau and Dawak village after MDA, and thus, further intervention is required in that area for possible resurgence of lymphatic filariasis. However, monitoring should be continued as part of post MDA activities until the endpoint of complete elimination is achieved.

Keywords:
Persistent; lymphatic filariasis; Brugia malayi; Kotawaringin Barat
Detection of Insecticide Resistance among Malaysian Aedes albopictus Larvae Using Updated Diagnostic Concentrations of Larvicides

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Abstract

The resistance occurrence among Malaysian Aedes albopictus larvae trapped from residential localities against larvicides of four insecticide classes were detected using the updated diagnostic concentrations resulting from the doubling of LC99 values of the reference strain. After 24-hour recovery time of WHO larval bioassay, incipient to high resistance were displayed among Ae. albopictus larvae from dengue prone residential areas against dichlorodiphenyltrichloroethane (DDT) (97.33% mortality), fenitrothion (88.67% mortality), fenthion (83.33% mortality), temephos (84.00% mortality), chlorpyrifos (63.00% mortality), propoxur (79.67% mortality), bendiocarb (65.67% mortality) and permethrin (91.00% mortality). Alternatively, Ae. albopictus larvae from fogging-free residential areas were either moderately or highly resistant to fenthion (94.00% mortality), temephos (89.33% mortality), chlorpyrifos (83.33% mortality), propoxur (92.33% mortality) and bendiocarb (83.00 mortality). The susceptibility bioassays using revised diagnostic concentrations established from the local reference strain could minimize the chance of undervaluing or overvaluing the insecticide resistance development among field strain populations.

Keywords:
Insecticide resistance; Aedes albopictus; larvae; Malaysia
Mosquito Detoxification Enzymes: Their Response Towards Acute Toxicology Challenges

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Abstract

Detoxification enzymes play a central role in defense systems against insecticides in insects including mosquitoes. They act in the cellular metabolism of xenobiotic substances and endogenous compounds which results in cellular and tissue damage, such as compounds derived from the oxidative stress. In this study, enzymatic involvement of glutathione s-transferase (GST), esterase (Est), cytochrome P450 (Cyt P450) and acetylcholinesterase (AChE) enzymes in *Aedes albopictus* under xenobiotic challenge were investigated. Profiling of *Ae. albopictus* enzymatic activities towards time-dependent acute treatment was conducted by using the pre-established LC50 of malathion (0.099mg/L) and permethrin (0.023mg/L) separately for different durations which were 6, 12 and 24 hours. For acute permethrin treatment, the specific activity of GST increased gradually and the highest activity was observed at 24 hours (2.635±0.08 μmol/min/mg). There was a similarity in the specific activity of ESTs and P450 whereby the activity increased at the 6 hours of exposure (82.58±0.34 nmol of 1-NA/min/mg, 74.27±0.42 nmol of 2-NA/min/mg and 9.61±0.05 nmol/min/mg respectively) and then decreased gradually up to 24 hours of exposure. Upon acute treatment with malathion, the specific activity of GST and P450 increased with the highest activity was observed at 24 hours of exposure (2.502±0.050 μmol/min/mg and 7.78±0.06 μmole/min/mg respectively). The specific activity of α-est gradually decreased upon acute treatment with malathion and reached the lowest level at 24 hours of exposure (46.68±0.39 nmol of 1-NA/min/mg). However, the specific activity of β-est increased upon 6 hours (75.68±0.64 nmol of 2-NA/min/mg) of exposure and then consistently decreased up to 24 hour of exposure. Knowledge of the detoxification enzymes profile allows for a better understanding on chemical resistance mechanisms in mosquito, and to better select insecticides that will be effective when applied.

Keywords:
*Aedes albopictus; detoxification enzymes; toxicology challenge; enzymatic profiling*
Abstract No: 12991

The Occurrence of Inapparent dengue in the Community and Hospital Settings in a Hyperendemic Area of Klang Valley, Malaysia

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Abstract

While dengue is hyperendemic in tropical areas, the public health burden of the disease is most likely under-reported, especially since current dengue control measures have only considered the transmission of symptomatic dengue. Hence, there remains a paucity of information on the epidemiology of inapparent dengue. Between October 2018 and March 2019, surveys were performed and blood samples collected from (i) 108 baseline individuals residing at Damansara Damai, Malaysia; (ii) 174 individuals living near sites with dengue-positive Aedes mosquitoes at Damansara Damai; and (iii) 38 relatives of suspected/confirmed dengue patients at a tertiary medical center in Kuala Lumpur, Malaysia. These bloods were then subjected to dengue NS1/IgM/IgG rapid tests, fluorescence immunoassays, and polymerase chain reactions (real-time and nested reverse transcription), and the positivity rates for each test determined. Despite having no past history of dengue infection, almost 10% and 70% of the individuals from Damansara Damai (a dengue hotspot) were positive for IgM and IgG respectively. Where dengue-positive mosquitoes were detected in the hotspot, 11 (6.3%) individuals were viremic, of whom 10 were asymptomatic. Likewise, 21 (55.2%) of the 38 relatives were asymptomatic, but 5 (23.8%) of the 21 were positive for recent dengue as per the NS1 and IgM results. Apparently, individuals who resided with acutely infected people were more likely to be viremic vis-à-vis those who lived near sites with dengue-positive Aedes mosquitoes (14.3% vs 5.8%). Many people in dengue-prevalent areas have unknowingly been infected by the disease. Upon detection of a dengue-infected mosquito, disease transmission is already widespread. In clinical settings, people residing with dengue patients are likely to have been exposed to dengue, symptomatic or otherwise. Collectively, these results indicate that early dengue detection systems and public education are needed in place of passive surveillance. Since the occurrence, diagnostic methods, and control of inapparent dengue are still poorly understood, future studies should duly focus on these areas.

Keywords: inapparent dengue; asymptomatic dengue, Aedes, epidemiology, prevalence
Abstract No: 13046

**Monitoring Insecticide Resistance at Papua Province, Indonesia**

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**Abstract**

The use of insecticides has been very long, especially in high malaria cases in Papua province. This study aims to determine the intensity of malaria vector resistance to insecticides in Papua Province. Anopheles samples taken in four districts of high malaria cases were Mimika, Yapen, Keerom and Jaya pura, in June-July 2019. Resistance testing was performed with susceptibility WHO test and CDC Bottle test. Statement of vector susceptible if mortality > 98%, possible resistance mortality 80% -98% and resistance mortality < 80%. Malaria vectors in the Mimika District susceptible for Deltamethrin 0.05%, Alpha-Cypermethrin 0.75% and malathion 5%. Possible resistance for Bendiocarb 0.1% and Permethrin 0.75%. In the Yapen District susceptible for Deltamethrin 0.05% and Bendiocarb 0.1%. In the Keerom District susceptible for Deltamethrin 0.05%, Permethrin 0.75% and Bendiocarb 0.1%. In the Jaya Pura Possible resistance for Deltamethrin is 0.05% and resistance for Bendiocarb 0.1%. The existence of resistance and possible resistance malaria vectors needs to be carried out research into the use of PBO in insecticide LLINs.

**Keywords:**

Insecticide resistance and malaria vectors
Abstract No: 13038

Prevalence and Detection of Rickettsiae and Bartonella from Ticks and Mites (Acarina) from Small mammals in Mangrove Forests

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Abstract

Small mammals are host to various ectoparasites, which attach on them for blood meal, but their infestation and their role as vector-pathogen in mangrove ecosystem is seldom investigated. Therefore, we want to determine the prevalence of ectoparasites and detect the presence of pathogenic bacteria in a diversity of small mammal in this habitat. Three mangroves sites located in Peninsular Malaysia were chosen and 100 cage traps were deployed randomly along the river. Capture-release method was applied, and ectoparasites were extracted from each captured individual before released. Morphological identification was performed on each ectoparasites, and molecular verification was made using 16S rDNA genes. Next PCR detection of Bartonella and Rickettsiae were performed on each of the ectoparasites. A total of 94 individuals of small mammals were captured throughout one month sampling in each site, with Rattus tiomanicus encompassed the most dominant species (n=74). From these number, 15 individuals (15% prevalence) were infested by ticks, 22 individuals (23%) were infested by mites, whereas 4 individuals (4%) were infested by both ticks and mites. Amblyomma cordiferum was the most dominant tick found (26 individuals), followed by Dermacentor atrosignatus (5 individuals), Dermacentor auratus (4 individuals), Ixodes granulatus (2 individuals) and Haemaphysalis hystricis (1 individual). The small mammals only host to one mite species (Echinolaelaps echidninus), which was most prevalent in Rattus tiomanicus. Two ticks species (5.26%) from R. tiomanicus were positive for Bartonella, whereby 29/38 (76.3%) tick and 20/23 (87%) mites from various host species were positive for Rickettsiae. This study reveals that the high diversity of small mammals in the mangrove ecosystem were heavily infested with ectoparasites, and these ectoparasites are highly prevalent with pathogenic bacteria which calls for serious precaution measures for visitor to this habitat. Future study could determine the seroprevalence of these bacteria among local residents and workers that frequent the area.

Keywords:
Ectoparasite; Rattus tiomanicus; pathogenic bacteria; riparian zone.
ORAL PRESENTATION: VECTORS & VECTOR BORNE DISEASES

Abstract No: 12994

Screening of Small Mammals and Chiggers from an Orang Asli Village and the Surrounding Agricultural Land for Orientia

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Abstract

Previous seroprevalence studies showed that 2.6% to 48.4% of the Orang Asli (OA) population tested were exposed to infections with Orientia tsutsugamushi (Ot), the agent for scrub typhus. The vectors of Ot, trombiculid chigger mites, are commonly found on small mammals. The present study aims to determine the diversity of small mammals found in an OA village and the surrounding agricultural land, and the infection rate of Ot in these animals and the associated chiggers. The study sites were an OA village and the surrounding oil palm plantation and paddy fields in Perak. Sampling was conducted from Dec 2018 to July 2019. Small mammals were captured using cage traps and humanely euthanized for tissue and chigger collection. DNA extraction from tissues and chigger pools was performed using commercial kits. Animal species was confirmed by PCR amplification and sequencing of the mtCOI gene. Presence of Ot was screened by PCR amplification of the TSA47 gene. Out of 177 small mammals captured, molecularly confirmed species included Rattus R3 phylogenetic group species (R3, n = 104), Rattus argentiventer (Ar, n = 32), Rattus exulans (Ex, n = 18), Rattus tiomanicus (Ti, n = 13), Tupaia glis (Tg, n = 8), Rattus tanezumi (Ta, n = 1) and Callosciurius notatus (Ca, n = 1). R3 and Ex were commonly found across all three habitats. Ar were primarily found in the paddy fields. Ti were mainly found in the plantation. Out of 70 animals tested, 11 were PCR-positive for the Ot TSA47 gene. PCR-positive animal species included R3 (n = 6), Ar (n = 3) and Ex (n = 1). None of the chigger pools tested were PCR-positive for TSA47. Ot screening from more animal tissues and chigger pools, and the ecological analyses of the small mammal diversity are currently underway. These baseline data will help determine the role of these mammals and chiggers in the transmission cycle of Ot.

Keywords:
Scrub typhus; Orientia; vector-borne disease; Orang Asli; tropical infectious diseases
Abstract No: 13008

The Tick Cell Biobank – Arthropod Cell Lines and the TCB Asia Outpost

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Abstract

Continuous cell lines derived from ticks and other arthropods are essential tools for laboratory-based research on vector-borne viruses, bacteria, protozoa and helminths of importance in human and veterinary medicine. The Tick Cell Biobank (TCB), the world’s only dedicated culture collection for cell lines derived from ticks and other arthropods, underpins this research through provision of existing cell lines and training in their maintenance to scientists worldwide, and generation and characterization of novel tick cell lines. As well as housing the world’s largest collection of tick cell lines, the TCB is working to generate new cell lines from biting midges, sand flies, tsetse flies, mosquitoes, triatomid bugs, bees and mites. The burden of vector-borne disease falls disproportionately on lower- and middle-income countries (LMIC) in the Tropics, and the TCB’s emphasis on tropical arthropod vectors reflects this. To facilitate dissemination and uptake of arthropod cell line technologies by LMIC scientists, the TCB is establishing Outposts in Asia, Africa and South America. The TCB Asia Outpost, located at the Universiti Malaya’s Tropical Infectious Diseases Research and Education Centre (TIDREC) in Kuala Lumpur, will supply popular and regionally-relevant tick cell lines and training in their maintenance, thereby supporting and enhancing research on ticks and tick-borne pathogens such as arboviruses and intracellular bacteria of the order Rickettsiales in Malaysia and other South-East Asian countries.

Keywords:
Tick; vector; cell line; training; pathogen
Abstract No: 13032

**A Study of Mites in Pet Hedgehog (Atelerix albiventris) in Klang Valley, Malaysia**

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**Abstract**

Mite infestation is one of the common health problems in pet hedgehog (Atelerix albiventris). The objective of this study is to identify species of mite that infests the pet hedgehog. It is important to create awareness among the pet hedgehog owners and encourage the pets to be routinely examined by veterinarian. This study was conducted at Faculty of Pharmacy, Universiti Teknologi MARA, Selangor (UiTM) and the samples were taken from Veterinary Exotic Animal Clinic, Taman Melawati, Kuala Lumpur. Direct microscopic examination was done on both samples of body and ear of the affected hedgehog. The samples were fixed and identified using light microscope under 10× and 40× magnification. The species of mite were identified based on their morphology. Results obtained shows that all samples contain Caparinia tripilis. There was no presence of other mites like Otodectes cynotis and Sarcoptes scabiei. Findings show that Caparinia tripilis is the highly species of mite that infests the hedgehog. Symptoms of mite infestation in hedgehog include loss of hair and quills associated with dry, scaly and flaking of the skin. The positive cases were treated with topical 1% ivermectin which is given based on their body weight. It is important to eradicate the mites to avoid zoonotic problem among the owners.

**Keywords:**
Hedgehog; pet; mites; zoonotic; Caparinia tripilis
Prevention and Control of Schistosomiasis: A Community Empowerment Approach in Poso District

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Abstract

Schistosoma japonicum is endemic in Indonesia. The distribution of schistosomiasis in Poso lies in Napu and Bada Valley. The control effort of schistosomiasis program has been carried prior in parasitology, malacology, rats survey, molluscidal activity, and Mass drug administration (MDA). However, the infection level in human, rat and snail is tend to fluctuate and recurrent infection in humans. Malacology survey determined that snails are still found in around community house and their workplace e.g. paddy field, cocoa plantation. The appropriate strategies called Gema Beraksi has been initiated as a part of implementation strategy in Poso district to get the goal of elimination. This intervention aiming to reduce infection level in human and number of snails habitat and increases the community compliance to participate in stool survey. This intervention was conducted descriptively through Gema Beraksi in Bada Valley. This approach activity through socialization, training, formation of community groups in the village. The group committed and eliminated the existing snail focus and situations related to the environment, landfill and land management which is carried out routinely and continuously every 2 weeks. The stool survey with kato katz technique was implemented before and after the intervention. The infection rate of schistosomiasis in human is 0.84% and dramatically drop to 0%. The number of snail habitat is only 2 foci. Community compliance in participation stools from 44.69% in 2016, now increase to 81.74%. Gema Beraksi in schistosomiasis control program is effective to reduce the number of snail habitat and infection in human in Poso district. This model is recommended to implement in endemic area. Community empowerment which integrate with schistosomiasis control program activities, targeting the life cycle, is the only approach that will lead to sustainability and future elimination.

Keywords:
Schistosomiasis; community empowerment; Gema Beraksi; Poso
Abstract No: 13053

**Daboia siamensis** Bites in Lomden (Lembata Island East Nusa Tenggara Indonesia)  
First Case Survival  

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**Abstract**

Indonesia, like many other developing countries, faces a heavy burden in snakebites. This is exacerbated by the unavailability of reliable data on snake bites, although recent localized studies (Maharani etc, 2017) highlights that numbers may be much higher than nationally reported figures, and that even a comprehensive record of formal healthcare system cases of snake bites may significantly underestimate real incidence. Further, there is still low awareness and skill both in healthcare providers and the general community on the prevention, control and handling of snakebites. This is made worse with the scarcity of antivenom, and the incomplete nature of existing home-manufactured antivenom, that does not yet cover several key venomous species in Indonesia.

Cases detail: A child 12 male bitten daboia siamensis with respiratory failure, spontan bleeding, acute kidney injury with highest creatinine 7,4, trombositopeni and low HGB, prolonged APTT, PTT, Inr, hematuria and epistaxis. The GCS 111 Discussion: Lomden is little island near ende and komodo, they are exclusive island with wallacea line, weber line, and lydekker line and the species snake variation. Daboia siamensis species snake no antivenom in Indonesia and 74 years many people death about it. This case first survival and management with guideline WHO 2016. The doctors give antivenom monovalent daboia ruselli siamensis 4 vial and all abnormalitas decrease. Bleeding stop, GCS increase and respiratory failure stop, acut kidney injury decrease. Limitation this cases daboai bites is antivenom in Indonesia but collaboration lembata hospital and Indonesia toxicology can give this antivenom from Bangkok Thailand from QSMI and make the patient life and survival only 4 vial monovalent daboia russeli siamensis antivenoom.

**Keywords:**  
Daboia siamensis; antivenom; lomden
Abstract

Worldwide, colorectal cancer (CRC) incidences and deaths are on the rising trend. In Malaysia, CRC is the second most common cancer and its incidence rate is expected to rise in next few years if preventive measures or early detection is not recommended. Numerous studies have evidenced that apart from genetic inheritance, gut pathogens including intestinal bacteria do contribute to the pathophysiology of CRC. *K. pneumonia* is a gram negative bacterium that often habitat in the lower GIT track. Numerous studies have reported on the association of this bacterium with irritable bowel disease and irritable bowel syndrome which are the contributing conditions of CRC. However, studies on its role as causative agents or promoting agent of CRC is very limited. Here we aimed to investigate the interlink between *K. pneumonia* and CRC in in vitro model using cell lines derived from various stages of CRC. The exacerbation factor was investigated by accessing the ability of the bacterial antigen to proliferate and cause oxidative damage towards cancer cells that were exposed to antigen. Electric Cell-substrate Impedance Sensing (ECIS) was used to study the pattern of CRC cell proliferation at point of *K. pneumoniae* antigen introduction (Day 3 & Day 6). The results revealed an increase in cell proliferation rate compared to untreated CRC cells. However, the increase was more significant at Day 6 introduction compared to Day 3. This finding suggests that CRC cells' proliferative rate could be increased upon prolonged exposure to bacterial antigens like in the case of chronic bacterial infection. In addition, the oxidative damage levels were also assessed results of all experiments carried out thus far will be discussed further.

Keywords:
Colorectal cancer; gut pathogens; *Klebsiella pneumoniae*
Abstract No: 13025

Non-typhoid Salmonella Lung Abscess in a Diabetic Patient: A Case Report

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Abstract

Non-typhoidal salmonella is a very rare cause of lung abscess. Literature review (Medline search) revealed only four reported cases of nontyphoid lung abscess so far. The case of a 45 year old Malay gentleman from interior district of Pekan, Pahang with background of modestly controlled Type 2 Diabetes Mellitus (HbA1C of 7.6%) is reported. Diagnosis was established with a positive blood culture of nontyphoid salmonella with chest radiograph and Contrast-Enhanced CT Thorax of multiple lung abscess alongside echocardiography and ultrasound abdomen to rule out other sources of abscess. Treatment with Intravenous Ceftriaxone for two weeks followed by Oral Amoxycillin-clavulinc acid for 6/52 (total duration of eight weeks) resulted both in clinical and radiographic resolution without surgical drainage. Type 2 Diabetes Mellitus, an immune-compromised state seems to play an important role, but the exact pathophysiological mechanism and why only the lungs are involved remains unknown.

Keywords:
Salmonella; lung; abscess; diabetes
Prevalence of *Platynosomum* sp. in Stray Cats in Kuala Lumpur and Selangor, Malaysia

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Abstract

Platynosomosis or commonly known as lizard poisoning is a hepatic disease in cats caused by *Platynosomum* sp. Cats get infected through consumption or accidental ingestion of lizard or cockroaches which is the intermediate host of *Platynosomum* sp. The aim of this study is to determine the prevalence of *Platynosomum* sp. infection among stray cats in Kuala Lumpur and Selangor and their correlation with the gender of animals. Liver and bile samples from 42 euthanized cats obtained from city councils were collected via necropsy. Bile samples were examined under microscope for ova detection followed by liver necropsies to detect adult flukes. The adult flukes were collected and their DNA was extracted using QIAGEN DNEasy Blood and Tissue kit. The extracted DNA were subjected for Polymerase Chain Reaction (PCR) and sequencing. The sequences were BLAST to GenBank for species identification. The results of this study show a prevalence of 21.43% (CI 0.12 – 0.37) cat liver fluke and showed no significant association with the gender of the cats (p>0.05) using Chi-Square Test. The result of sequencing from adult flukes detected showed seven out of nine are *Platynosomum illiciens* (96.96% - 99.89%) and the other two were identified as *Platynosomum fastosum* (99.12% - 99.78%). In conclusion, the prevalence of *Platynosomum* sp. in shelter cats from Selangor and Kuala Lumpur is significant with no gender association and are molecularly identified as *Platynosomum illiciens* and *Platynosomum fastosum* where both species were confirmed to be identical from previous work.

Keywords:
*Platynosomum sp.; lizard poisoning; stray cats; Malaysia*
Abstract No: 13005

**Interaction between *Haemonchus contortus* and *Trichostrongylus colubriformis* During A Co-infection in Boer goats**

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**Abstract**

Natural infection by mixed gastrointestinal nematodes is common among small ruminants. Thus, it is important to explore the potential interactions between nematode species and the significant consequences that may occur during a co-infection within a nematode community. Thirty Boer goats were deliberately infected with mixed L3 nematodes namely *H. contortus*, *Trichostrongylus* spp. and *Oesophagostomum* spp. Fecal and blood samples were collected twice a week for eight weeks at three-four-three day intervals. The fecal samples were subjected to modified McMaster method to determine fecal egg counts (FEC). The blood samples were used to measure IgA by ELISA assay, PCV and peripheral eosinophil counts. The goats were slaughtered 52 days post-infection to collect the gastrointestinal tracts for total worm counts, identification, sexing and measurement of length. Correlations between the means of variables at necropsy (nematode number, length, index) and the means of phenotypic variables (FEC, IgA, peripheral eosinophil counts, PCV) were generated using Pearson correlation. Multiple linear regression models were conducted to examine the relationship between observations at necropsy and phenotypic variables. FEC was positively associated with Log *T. colubriformis* number ($r=0.62$, $p<0.05$) while IgA had a positive correlation with peripheral eosinophil counts ($r=0.65$, $p<0.05$). *T. colubriformis* length also had a negative correlation with Log *H. contortus* number ($r=-0.56$, $p<0.05$). Log *T. colubriformis* index had positive correlations with *H. contortus* length ($r=0.69$, $p<0.01$) and Log *H. contortus* index ($r=0.52$, $p<0.05$). The regression models show that the mucosal browser *T. colubriformis* appeared to contribute significantly to the variation in FEC than *H. contortus* while the blood feeder species was unable to affect PCV levels in the goats. Additionally, co-infection induced an IgA response which was only effective against *T. colubriformis* but not protective against *H. contortus* infection. In conclusion, interactions occurred between *H. contortus* and *T. colubriformis* during a co-infection in Boer goats.

**Keywords:**  
*Haemonchus; Trichostrongylus; co-infection; interaction; goats*
Abstract No: 13028

Anisakiasis - Zoonotic Disease in Tropical Countries

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Abstract

Anisakiasis is a zoonotic parasitic disease which is caused by consuming raw or undercooked fish infected by Anisakis spp. Its symptoms include acute and abdominal pain, urticaria and anaphylaxis. Besides that, allergic reaction such as IgE-mediated hypersensitivity can be caused by consuming infected fish. Ani s 1 and Ani s 4 are the major allergen with heat-stable properties found from Anisakis spp. which cause allergic reaction to human even in well cooked fish. From recent studies, only two species of Anisakis species are found to have the ability to migrate to muscle of fish which is Anisakis simplex and Anisakis pegreffii. Apparently, there are lower presence of Anisakis nematode present in muscle via intra-vitam migration. However, post-mortem migration of Anisakis occur within 4 hour after host death. This action may increase the appearance of Anisakis spp. in muscle. Ungutting and deep freezing at -80°C or -40°C for a specific time period after catch were suggested to prevent post-mortem migration. Prevalence of Anisakis spp. in Japanese Threadfin Bream, Nemipterus japonicas and Shortfin Scad, Decapterus macrosoma were determined in this study. A total 50 samples for each fish species were examined for parasites. Prevalence and mean intensity of Anisakis nematode were analyzed. D. macrosoma were found having higher prevalence and mean intensity of Anisakis spp. compared with N. japonicas. Besides that, appearance of Anisakis spp. were found correlated to weight and length of both fish species. Comparing in specific site, Anisakis spp. in D. macrosoma were highly specific to reproductive organ, while N. japonicas were at the stomach. Both of the specific site were showing similar properties: fatty organ. This study showed the prevalence of Anisakis spp. are affected by host habitat, food chain and host size. Pelagic fish are having higher probability to infect by Anisakis spp. compared with demersal fish. Other than that, Anisakis spp. having higher appearance at fatty organ. Species identification of parasite and allergen protein determination will be conducted for further study.

Keywords:
Anisakiasis; allergen; migration; Nemipterus japonicas; Decapterus macrosoma; South China Sea
RAPID ORAL PRESENTATION

Abstract No: 12962

Detection of Acanthamoeba sp. from Contact Lens Cleaning Solutions and Household Tap Water Source of Contact Lens Users

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Abstract

Acanthamoeba keratitis (AK) is one of the diseases that cause corneal infections due to the contamination of contact lenses and water by an organism called Acanthamoeba. This study aimed to determine the transmission potential of Acanthamoeba sp. from contact lens cleaning solutions and household water sources of contact lens users. It was a cross-sectional study. Samples of contact lenses, cleaning solutions and household water was collected from 53 medical students who used contact lenses between January and May 2019. An examination of Acanthamoeba was carried out in the Parasitology Laboratory, Faculty of Medicine, University of Indonesia using page-salt agar culture media. From 53 contact lens samples, there were two positive samples of Acanthamoeba sp. and three samples, positive free-living ameba (5.6%). From household water samples, five cultures were positive of Acanthamoeba sp. (9.4%) and 34 positive cultures other free-living amoeba (64.1%). Contact lens users have more women than men. PAM water in the West Jakarta area has been contaminated with Acanthamoeba sp. with the discovery of Acanthamoeba sp. in PAM tap water samples in the region. There is a risk of transmission of Acanthamoeba sp. from household water and contact lens cleaners.

Keywords:
Acanthamoeba sp.; Acanthamoeba keratitis; contact lens; household water
Abstract No: 12996

**Infinity War against Antifungal Resistance: Potential of Lactoferrin as New Antifungal Substance**

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**Abstract**

With the continued demand for new, effective, potential and safe antifungal drugs due to antifungal resistance, the aim of this study was assessment of efficiency and fluconazole synergistic activity of the lactoferrin isolated from bovine, goat, and human milk against fluconazole resistant-Candida albicans. Lactoferrin was extracted from bovine, goat and human milk by alkalizing the milk, contacting the alkalized milk with air, and precipitating lactoferrin using an organic solvent. Extracted lactoferrin was identified using sodium dodecyl sulfate-polyacrylamide gel (SDS-PAGE). Antifungal effectiveness and the fluconazole synergistic activity of the lactoferrin against fluconazole resistant-C. albicans (ATCC 10231) was determined using disk diffusion and microdilution method. The inhibition zones and minimum inhibitory concentration (MIC) induced by lactoferrin were compared to fluconazole. The inhibition zone of fluconazole was 23 mm and lactoferrin was 20 to 25 mm against C. albicans. The MIC of lactoferrin was 3.125% to 1.5625%. But in combination of fluconazole with each bovine, goat, and human lactoferrin, this inhibition zone was from 31 to 36 mm, and the fractional inhibitory concentration was from 0.07 to 0.14 indicating that this combination exerted a marked synergistic effect against C. albicans. Highest inhibition was shown by bovine lactoferrin. These results showed that lactoferrin isolated from bovine, goat, and human milk could be a new potential antifungal drug. The lactoferrin isolated from bovine, goat, and human milk showed potential antifungal activity and have synergistic effect with current antifungal. These lactoferrins could become a useful natural bioactive agents that have antifungal activity against fluconazole resistant-C. albicans and could be used as a new potential antifungal drug.

**Keywords:** lactoferrin; antifungal; resistance; synergistic; Candida albicans
Abstract No: 12960

Effects of Maja Leaf (*Aegle marmelos*) Extracts on the Morphological of *Aedes aegypti* Larvae

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Abstract

The use of synthetic insecticides continuously can cause adverse affects in the form of environmental pollution, such as death of living things, insects become more resistant with pesticide, even gene mutations can occur in insects. Therefore we need insecticide from plants that more safer to use. One of them is a plant from the Rutaceae family known as Maja or Bael (*Aegle marmelos*) which is used for controlling vector-borne diseases. Maja leaves have the potential as an insecticide because they contain several chemical compounds such as alkaloids, terpenoids, saponin, and tannin. The purpose of the study was to look at the morphological changes of *Aedes aegypti* larvae due to administration of maja leaves extract with acetone solvent. This experimental study used a completely randomized design with negative control in the form of aquadest, positive control in the form of temephos 1% and maja leaves extract treatment with acetone solvent concentration of 0.1 g/mL, 0.2 g/mL, 0.4 g/mL, 0.6 g/mL, 0.8 g/mL and 1.6 g/mL. *Ae. aegypti* larvae mortality was assessed for 24 hours and the morphological changes were immediately seen using a light microscope. Within one hour, mortality of *Ae. aegypti* larvae appeared at concentrations of 1.6 g/mL. The negative control group did not show morphological changes. While the positive control group using temephos showed a change in the color of the head to blackish brown, damage to the abdomen and pecten and the rear abdomen changed to a more blackish brown color. Maja leaves extract with acetone concentration of 1.6 g/mL causes color changes in the head of *Ae. aegypti* larvae and damage to the abdomen. Abdomen larvae of the *Ae. aegypti* appear to shrank. The effective dose of maja leaves extract needed to kill *Ae. aegypti* larvae is 1.6 g/mL with damage especially to the abdomen.

Keywords:
*Aegle marmelos*; *Aedes*; *Insecticide*
Abstract

Fly control plays an important role in poultry farm management due to its possible economic losses from morbidity and mortality of poultry. House flies and other non-biting flies may become a vector in spreading various types of diseases. The aim of this study is to determine the fly’s population in both closed and open house systems of poultry farms across five districts in Perak using *Perangkap Kain Biru*. In this study, the fly trap or *Perangkap Kain Biru* was placed for two hours in seven poultry farms in Perak between March 2019 until July 2019. The entrapped flies were transported in collection canisters at 4°C prior to macroscopic species identification at Parasitology Laboratory, Veterinary Research Institute (VRI), Ipoh, Perak. A total of 10,701 flies including *Musca* spp. and *Chrysomya* spp. with 99.55% \((n_1=10,653)\) and 0.45% \((n_2=48)\) were entrapped, respectively. Results indicated that, *Perangkap Kain Biru* successfully captured higher percentage of flies with 96.63% \((10,294 \text{ of } 10,653)\) *Musca* spp. and 100.00% \((48 \text{ of } 48)\) *Chrysomya* spp. in open house systems compared to close house systems with 3.37% \((359 \text{ of } 10,653)\) and 0.00% \((0 \text{ of } 48)\) of *Musca* spp. and *Chrysomya* spp., respectively. Based on this study, the use of this physical trap is not only efficient in capturing flies, but also ecofriendly as it does not need chemicals or fly bait to entrap the flies. Therefore, reducing the harmful risks to the environment as well as other living organisms.

*Keywords:* Fly trap; *Perangkap Kain Biru*; *Musca* spp.; *Chrysomya* spp.
Abstract No: 13018

**A Knowledge Transfer Workshop on Vector-Borne Diseases for School-Aged Children from Oil Palm Plantation Communities**

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**Abstract**

Vector-borne diseases are commonly affecting the rural communities in Malaysia. Effective community engagement is important in improving the awareness within the communities of these diseases and the prevention strategies that can be taken. On 20 June 2019, we conducted a knowledge transfer workshop for school-aged children from the SK FELCRA Sungai Ara, Jemaluang, a school located among oil palm plantation communities. Past studies have shown that these communities are at risk of exposure to mosquito- and other arthropod-borne diseases, such as scrub typhus and spotted fever. In this workshop, approximately 50 children between the ages of 9 and 12 years old were invited to attend. The workshop was conducted at the UM Plantations Sdn. Bhd. Research Estate. Contents of the workshop include classroom lectures on topics based on mosquito-borne infections, other arthropod-borne infections carried by ticks, fleas and chiggers, and the blackfly-transmitted onchocerciasis. Activities and games were also incorporated to reinforce the messages of the lectures. These included jigsaw puzzles and a “tick check” competition. Finally, a proper hand washing technique demonstration was also conducted to emphasize the importance of maintaining personal hygiene. Quizzes before and after the lectures and activities suggested that there was improvement in the understanding of the workshop topics. The school children were also invited to participate in a “lab in the field” in which they were allowed to observe researchers collecting samples from wild rodents from a safe distance using wireless camera and projector. It is our hope that these outreach activities will inspire the younger generation of these rural communities to have greater interest in science education and research, especially in the field of tropical infectious diseases.

**Keywords:**
Community engagement; knowledge transfer; vector-borne disease; tropical infectious disease; school children
Abstract No: 12995

Gastrointestinal Helminthiasis in Small Ruminants in Perak in 2019

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Abstract

Gastrointestinal helminthiasis is an important disease that causes high morbidity and in severe cases can cause high mortality in small ruminants such as goats and sheep. The aim of this study is to determine the status of helminthiasis in goats and sheep in Perak based on samples that were submitted to Veterinary Research Institute (VRI), Ipoh, Perak in 2019. A total of 494 samples from goats (n₁ = 410) and sheep (n₂ = 84) consisting of 490 fecal samples and four intestines were received. Fecal samples were processed by simple floatation method and McMaster technique while intestinal scraping was performed on intestine samples. Microscopic examination revealed that 81.17% (401 out of 494) of the samples were detected positive with at least one type of helminth egg. Goats had a higher percentage with 82.20% (337 out of 410), while sheep were at 76.19% (64 out of 84). Findings also revealed, 81.17% (335 out of 410) and 72.62% (61 out of 84) were positive for round worm eggs in goats and sheep respectively. Sheep had higher positive samples for tapeworm eggs specifically Moniezia spp. at 22.62% (19 out of 84) while goats at 9.51% (39 out 410). In this study, goats had higher worm infectivity even though they are browsing animals. Sheep are grazing animal thus they have a higher tendency of ingesting worm eggs causing infection. Overall results of this study indicate that the occurrence of gastrointestinal helminthiasis in small ruminants in Perak were still high. Therefore, farmers should be alarmed and push for proper worm management in order to reduce the potential exposure to infection.

Keywords:
Gastrointestinal helminthiasis; goats; sheep; round worm; tape worm
Abstract No: 12981

Trypanosomiasis Cases Received in Veterinary Research Institute (VRI), Ipoh, Perak in 2019

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Abstract

Trypanosomosis is a disease in vertebrates caused by parasitic protozoan trypanosomes of the genus *Trypanosoma*. Malaysia is endemic with Trypanosomiasis caused by *Trypanosoma evansi* which causes low productivity and mortality in cattle and deer. The objective of this study is to determine the occurrence of trypanosomiasis in livestock from cases submitted to the Veterinary Research Institute, Ipoh, Perak. It is one of the notifiable diseases listed by Department of Veterinary Services (DVS), Malaysia. A total of 158 whole blood samples from deer (n1 = 109) and cattle (n2 = 49) from several government farms were submitted from January to December 2019. Blood samples were subjected to buffy coat and thin blood smear methods for examination and detection for blood protozoans. The result indicates 11.9% of deer (13 out of 109) and 12.2% of cattle (6 out of 49) blood samples were positive with *Trypanosoma spp*. The highest trypanosomiasis cases in deer were detected in March 2019 with seven cases, while five cases for cattle in October 2019. Our findings showed that the number of trypanosomiasis is higher in cattle compared to deer. Trypanosomiasis can be controlled by regular fogging to reduce the biting flies’ vector. As buffaloes can harbor trypanosomes without showing any clinical signs, the farm management should minimize the risk of cattle and deer grazing nearby by taking the necessary precautions.

Keywords:
Trypanosomiasis; cattle; deer
Abstract No: 12982

Preliminary Survey of Coccidiosis in Chicken Farms in Perak

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Abstract

Coccidiosis is a common intestinal parasitic disease in domestic fowls. The etiological agent in chicken usually known as *Eimeria* spp. The species is host-specific and parasitize specific intestinal region of the chicken. The infected chicken may develop clinical sign such as in appetite, emaciation, diarrhea, ruffled feathers, anemia and bloody feces. The objective of this study is to detect presence of coccidia oocysts in chicken farms in Perak. A total of 69 chicken fecal samples were collected in 12 farms from various districts such as Kinta, Tapah and Batang Padang commencing from March to July 2019. The samples were processed by simple floatation method in Parasitology Laboratory, Veterinary Research Institute (VRI), Ipoh, Perak. Out of 69 samples, 33 (47.8%) were positive with coccidia oocyst by microscopic examination under 100 x magnification. Our results showed that almost half of the samples were positive for coccidiosis. For future work, species identification of coccidian parasites and its prevalence rate in poultry farms would help for the management of disease.

Keywords:
Coccidiosis; domestic fowls; floatation method; coccidia oocyst
Abstract

A growing body of evidence suggests that exposure to Toxoplasma gondii infection may be regarded as a risk factor for schizophrenia. Nonetheless, the association between toxoplasmosis and schizophrenia is still controversial. Therefore, this study aimed to investigate differences in T. gondii seroprevalence and demographic profiles between seropositive patients with schizophrenia spectrum disorders and controls. The presence of circulating T. gondii DNA was also screened. A total of 109 patients and 109 healthy controls from Hospital Canselor Tuanku Muhriz, Cheras were recruited. The diagnosis of schizophrenia was made based on the Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition (DSM-V). The presence of T. gondii antibodies and DNA were determined using an indirect ELISA and nested-PCR, respectively. The socio-demographic data was analyzed using descriptive statistics. Overall, no significant difference in seropositivity of T. gondii between schizophrenia patients (24%) compared to control subjects (32%) (P=0.2273). Nevertheless, the median serointensity of anti-T. gondii IgG antibody was significantly higher in controls (1.12±32.31) compared to patients (0.67±3.96) (P<0.001). Demographic data showed significant differences in age group, race, education level, occupation and family history of psychiatric illness (all P<0.05). No significant differences were observed between clinical features and seropositivity. Of the 26 seropositive patients, only one (3.8%) was positive by PCR. In conclusion, our data showed that toxoplasmosis is not associated with established schizophrenia. Our findings are to be interpreted with caution, because of the small sample size, the heterogeneity of enrolled patients and the observational nature of the study. Further studies are needed to better define the clinical features correlated to the seropositivity status in the established schizophrenia spectrum disorder patients.

Keywords:
Toxoplasma gondii; toxoplasmosis; schizophrenia; serointensity; seroprevalence
Burden and Geographical Distribution of Plasmodium Infections in Balochistan Province of Pakistan: A Trend Analysis of Malaria Cases over a Period of Seven Years

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Abstract

Pakistan bears a high burden of malaria cases despite tremendous achievements in both the malaria case management and prevention activities over the period of time. The purpose of this study was to conduct a trend analysis of plasmodium species prevalence, incidence of malaria cases and geographic distribution of malaria species in Balochistan. The aggregated, annual malaria data of seven years (2013 to 2019) were obtained for the 30 districts of Balochistan province of Pakistan from the provincial Directorate of Malaria Control Program Quetta through formal request. All the cases of the malaria are diagnosed at public sector health facilities on the basis of WHO-recommended methods of microscopy or rapid diagnostic tests. The summery sheets received from all of the districts through Malaria Information System, the main digital reporting system are compiled at provincial office for individual year. Population data for the districts were extrapolated at a growth rate of 2.3% annually from the census of 1998 for the years 2013 to 2017 and annual growth rate of 3.37% from census 2017 for year 2018 and 2019. The cumulative mean test positivity rate was 10.76 in province. This varied from high endemic districts being 25.8 to 2.1 for the low endemic districts. The test positivity rate was consistent over the period of all seven years. Plasmodium falciparum and plasmodium vivax were the most prevalent species. The mean falciparum rate was 29.56 over the year of seven years, with an increasing trend from 28.23 in 2013 to 42 in 2019. This trend was seen for most of the districts which had very high falciparum rate in 2018 and 2019 and this trend is consistently high (>50) for some of the districts. Similarly, annual parasite incidence rate had a slight increasing trend through the years, being highest (API=9) in 2019. The findings from this analysis showed high burden of disease and trend showed that disease burden is far high from national targets set for the year 2020. High burden of the most dangerous species falciparum and its increasing trend is alarming and reflects serious threat which needs strengthening the preventive strategies.

Keywords:
Malaria; Balochistan; rate; geographical distribution
RAPID ORAL PRESENTATION – STUDENT COMPETITION

Abstract No: 13011

A Comparative Study of Anopheles Diversity in a Virgin and a Degraded Forest in Sabah

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Abstract

Anopheles mosquitoes are known to cause life-threatening human malaria. These mosquitoes are abundant in the Sabah forest which is known for its rich biodiversity. Surveillance of mosquitoes deep within the forest cover is important to reduce the probability of eco-tourists and forest workers from getting any infectious diseases from the mosquitoes. An investigation was carried out in Sepilok Forest Reserve (SFR) and Danum Valley Forest Conservation Area (DVCA) to compare the diversity of Anopheles mosquitoes in both areas. Mosquito magnet traps were placed within the forest area for three consecutive nights to collect Anopheles mosquitoes. We collected from DVCA a total of 137 Anopheles mosquitoes and from SFR 67 individuals. Both areas common Anopheles species which are Anopheles montanus and Anopheles balabacensis. The estimated diversity of Anopheles species was marginally higher in SFR than DVCA collections, that is 9 and 6 Anopheles species respectively. Anopheles balabacensis, Anopheles barbirostris and Anopheles latens found in SFR are malaria vectors. DVCA has more Anopheles spp., namely Anopheles asiaticus (67.15%) is the dominant species followed by Anopheles maculatus (11.68%), Anopheles balabacensis (8.76%), Anopheles barbumbrosus (4.38%), Anopheles montanus (4.38%) and Anopheles jamesii (3.65%). Moreover, SFR has more Anopheles vectors. Information on the presence of various Anopheles species in virgin forest (DVCA) and degraded forest (SFR) will provide informed strategy when the need arises to implement control measures in these areas.

Keywords:
Anopheles mosquitoes; vector; surveillance; forest; control
Abstract No: 12979

Exploring the Biochemical Basis of Insecticide Resistance in *Aedes albopictus* from Sabah, Malaysia

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Abstract

There has never been a statewide dengue vector insecticide resistance assessment and related mechanisms in Sabah, Malaysia, although it is one of the top five states that contributed the most dengue cases in Malaysia. Therefore, this study aimed to pioneer a statewide dengue vector insecticide resistance evaluation program in Sabah and characterize the potential biochemical mechanisms associated with resistance. Larvae and adults of *Aedes albopictus* were tested against various insecticides based on the WHO standard protocol. Subsequently, they were subjected to enzymatic assays such as esterases (ESTα and ESTβ), mixed function oxidases (MFO), glutathione-S-transferase (GST) and insensitive acetylcholinesterase (AChE). The bioassays revealed that *Ae. albopictus* was resistant towards organophosphates, organochlorines and carbamates. Biochemical assessment also disclosed a relatively high activity of ESTα, ESTβ, MFO and AChE. In regards to AChE assay, after the inhibition of propoxur, most populations were either heterozygous resistant (RS; 30-70% remaining enzyme activity) or homozygous resistant (RR; > 70% remaining enzyme activity). When enzyme levels of field populations were compared to reference strain, most field populations exhibited resistance ratios (RR) of > 1, which is indicative of resistance. In Pearson’s correlation analysis of survivability rate of adults of *Ae. albopictus* against insecticides with enzyme activities, AChE and GST showed significant correlation with most insecticides, except pyrethroid class. As for *Ae. albopictus* larvae, chlorpyrifos and fenitrothion showed significant correlation with ESTα and ESTβ. In addition, survivability rates of larvae against fenitrothion, fenthion and temephos, were also significantly correlated with AChE, MFO and GST activities, respectively. In short, this study has established a baseline reference of insecticide resistance and the potential biochemical related resistance mechanisms in Sabah. The alarming resistance spread and discovery of potential biochemical resistance mechanisms, should prompt responsible authorities to execute more robust and effective control plan in future.

Keywords:
*Aedes albopictus; Sabah; insecticide resistance; detoxification enzyme*
Abstract No: 13002

**The Involvement of Glutathione S-Transferase Enzyme Upon Xenobiotic Challenges in *Aedes albopictus* Mosquito**

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**Abstract**

At present, insecticide resistance in *Aedes* mosquito is the major issue that threatens the sustainability of vector control strategy. Being a member of multifunctional intracellular enzymes involved in the detoxification of endogenous and xenobiotic compounds, glutathione s-transferases (GST) mediated resistance is considered to be one of the predominant mechanism of insecticide resistance in mosquito species. In this study, the role of enzymatic activity of GST in *Aedes albopictus* under xenobiotic challenges were investigated. The profiling of susceptibility status and GST enzymatic activity of *Ae. albopictus* from all districts throughout Penang towards xenobiotics (malathion and permethrin) were elucidated. Lower resistance ratio (RR50) of malathion compared to permethrin were detected in all field collected strains. There is an elevation in the total protein content as well as the enzymatic activity of GST in all field collected strains of *Ae. albopictus* compared to the susceptible control strain (p<0.05). Next, time-dependent (6 hours, 12 hours and 24 hours) induction of GST enzymatic activities under xenobiotic challenges (sub-lethal concentration) were investigated. Total protein contents (µg) and enzymatic activities of GST were most elevated when the larvae were exposed to 24 hours of acute permethrin and malathion treatments (p<0.05) compared to the larvae which have been exposed to the insecticides for 6 hours and 12 hours (p<0.05). The data obtained suggests the involvement of GST in the defense mechanisms against organophosphate and pyrethroid challenges.

**Keywords:** *Ae. albopictus*; GST enzymatic activity; susceptibility status; xenobiotic challenge; metabolic induction; detoxification enzyme
Abstract No: 12985

Acceptable Knowledge and Awareness of Malaria among Orang Asli Temiar in Pos Kuala Betis, Kelantan

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Abstract

Malaysia is on track towards malaria elimination. However, several cases of malaria still occur in the country. Contributing factors and communal aspects have noteworthy affects in any malaria elimination activities. Thus, assessing the community’s knowledge, attitudes and practices (KAP) and evaluating the community living conditions towards malaria are essential. A household-based cross-sectional study was conducted in five villages of Orang Asli Temiar in Pos Kuala Betis, Gua Musang, Kelantan in July 2019. Demographic, socio-economic and KAP data on malaria were collected using a standardized questionnaire and analyzed using descriptive statistics. Overall, 536 individuals from 208 households were interviewed. Household indoor residual spraying (IRS) coverage and bednet ownership were 100% and 89%, respectively. Houses were typically made of wood walls and floors (47%), with corrugated iron roofs (92%). While nearly all individuals (98%) were aware that malaria is transmitted by mosquitoes and applied bednets at night (95%), only 50% were aware that bed nets are used to prevent the infection. The most common practice when suspected of malaria was seeking treatment at the health facilities (71%), followed by self-purchase of medication from local shops (13%), traditional healing (11%) and self-healing (6%). With regard to potential zoonotic malaria, about 47% individuals reported seeing monkeys nearby and 20% reported entering nearby forest within the last 6 months. We conclude that most populations living in the villages have an acceptable level of knowledge and awareness about malaria. However, the positive attitudes and practice in relation to managing illness against malaria require marked improvement.

Keywords:
Malaria; Orang Asli; knowledge; attitude; practice
Abstract No: 13026

Mermithid Parasitism of Black flies in Peninsular Malaysia

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Abstract

Mermithid parasitism in black flies (Simuliidae) has been recorded extensively and is often associated with gynandromorphism in black fly adults. The discovery of mermithid parasites in the black fly population at Mount Pulai, Johor marks the first recorded instance of this phenomenon in Peninsular Malaysia. In the initial sampling, only one species, S. trangense was infected with mermithids while the other three species present, S. angulistylum, S. bishopi and S. cheongi were uninfected. Twelve gynandromorphs of S. trangense were also described for the first time in Malaysia. However, recent sampling suggests that all four species present at the study site are susceptible to infection through microscopic examination of black fly larvae. Further work will be carried out to characterize the prevalence of mermithid infection in this black fly population and to identify if temporal variation in abiotic factors may affect this prevalence.

Keywords:
Black fly; Simuliidae; mermithids; parasitology; Malaysia
Investigation Presence of GIP in A Nursing Home in Kajang, Malaysia

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Abstract

Gastrointestinal parasite (GIP) infection is a major health concern in many developing countries which affects 3.5 billion individuals all over the world. Old people are susceptible towards GIP infections due to lower immunity as they aged. GIP infection has negative impact on autonomy, functionality and quality of life of the elderly community. This study was carried out to investigate presence of GIP among geriatric community in a nursing home in Kajang. Around fifteen (n=15) individuals participated in this study voluntarily and questionnaire survey on for demographic data (age, gender, medical condition) were carried out prior to stool collection. Their stool samples were collected and stool sedimentation technique was used to isolate the GIP. The samples were stained with Trichrome stain and acid fast stain. Next, the stained slide was examined under oil immersion lens (100x magnification) to detect GIP. Out of 15 participants, 13 were positive for either/both Blastocystis spp. (n=12; 80%) or Cryptosporidium spp. (n=9; 60%). Single infection with Blastocystis spp. was 27% (n=4), single infection with Cryptosporidium spp. was 7% (n=1). Participants aged between 70-84 years old (n=6; 40%) had the highest infection, followed by age class of 40-54 (n=3; 20%) and age 55-69 (n=4; 27%) respectively. In total, infected male was five (n=5) where else female was eight (n=8). It was also recorded four elderly participants had diarrhea in a period of one month. This finding showed GIP was detected among the elders living in a nursing home in Kajang, but only a few showed symptoms of illness like diarrhea. However, the presence of GIP among these tenants could lead to transmission to others. Further study is needed to explore presence of GIP among care takers in the home, as they pose as potential vector to transmit GIP to others under their care.

Keywords:
Gastrointestinal parasite (GIP); nursing home; geriatric community; Malaysia
Abstract No: 13027

**Molecular Identification of Hookworm Infections in Humans and Domestic Animals among the Negrito (indigenous) population in Malaysia**

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**Abstract**

Studies on hookworm infections among the Negrito Orang Asli population in Malaysia are scarce, and most of the previous findings have relied on microscopic examination without specific-species identification. This study aimed to investigate the current hookworm infections in humans and the potential of zoonotic transmission among the Negrito population using the molecular approaches. Overall, a total of 367 human and 59 animal stool samples (i.e. dogs and cats) were included in this study. After extraction of the DNA, a two-step semi-nested PCR was used to amplify ITS-2, 5.8S and 28S rRNA genes of *Necator americanus* and *Ancylostoma* spp. Positive samples were then sequenced to confirm the species of hookworm. Samples with positive *A. ceylanicum* species were then subjected to the amplification of *cox1* gene of *A. ceylanicum*, sequenced and analyzed phylogenetically for haplotype characterization. Of the 367 Negrito participants, 86 (23.4 %) were positive with hookworm infection and, *N. americanus* was identified as the predominant species (77/86; 89.5 %). No *A. duodenale* was detected in this study. Interestingly, *A. ceylanicum* (animal hookworm) was also found in 32/86 (37.2 %) of human samples. For animal stools, all samples (100 %) were found to be positive with hookworm, dominated mostly by *A. ceylanicum* species. *Ancylostoma caninum* were also identified in two of the animal samples. Further phylogenetic analysis revealed *A. ceylanicum* from both human and animals’ samples were clustered within the same zoonotic clade indicating zoonotic transmission in Negrito population. Therefore, effective control measures for hookworm infections should be implemented in this population.

**Keywords:**
Hookworm; Negrito; animals; molecular; *Necator americanus*; *Ancylostoma* spp.; zoonotic
Abstract No: 13010

An Investigation of the Prevalence of Bovine Fasciolosis in a Dairy Farm in Klang, Selangor

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Abstract

Bovine fasciolosis study in Malaysia is scarce and regionally done. This neglected endoparasitic infection causes risk of significant economic loss to the ruminant livestock industry worldwide and perilous towards human public health. An investigation was done in December 2019 to determine the fasciolosis status at a dairy farm located in Klang, Selangor and the availability of gastropod fauna as intermediate host. The farm is handled by a smallholder farmer in oil palm cultivation site for goats and cattle dairy production. Ten fecal samples were collected from ten female mixed breed cattle, age ranging from eight months to eight years for their Fasciola sp. eggs presence in the feces. The eggs of Fasciola gigantica were found in six (60%) of them diagnosed by using FlukefinderÒ sedimentation technique. The clinical signs observed from the cattle signalment include the pelvic bones appearance and loss of weight. Two species of freshwater snails namely Lymnaea auricularia and Sinotaia sp. have been lured approximately 300m from the farm in a water stream nearby a lake that could be responsible for the fasciolosis in those cattle playing role as intermediate host for Fasciola sp. development. Along the distance, the area is identified as grazing area for those cattle. Positive fasciolosis alongside with the symptoms in Klang indicates the need for broader spectrum of bovine fasciolosis study especially in Malaysia to initiate better control measure to keep the prevalence low and sustain the economic development.

Keywords:
Fasciolosis; freshwater snail; Lymnaea; Sinotaia; Fasciola gigantica
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Evaluating the Risk Factors of Human G6PD Genetic Variants and Filipino Beta
Thalassemia in acquiring *Plasmodium knowlesi* infection in Sabah, Malaysia

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Abstract

*Plasmodium knowlesi* has become the dominant cause of malaria in Sabah, Malaysian Borneo, now
accounting for >98% of malaria cases. Phenotypic glucose-6-phosphate dehydrogenase (G6PD)
deficiency linked to mutations in the X chromosome was previously reported to be associated with
protection against acquiring *P. knowlesi* infection in a multivariate model. Other
haemoglobinopathies such as thalassemia caused by different genetic polymorphisms are also
known to have protection against other species of severe malaria in endemic regions. To date, no
previous studies have been reported assessing the relationship between G6PD genetic variants and
Filipino β-thalassemia with acquiring *P. knowlesi* infection in Malaysia. In this study, the association
of G6PD genetic variants and beta thalassemia with *P. knowlesi* infection was investigated. Blood
samples were collected from humans enrolled in a prospective malaria study at Keningau and Ranau
districts of Sabah, and comprised 106 *P. knowlesi* mono infection cases (PCR confirmed) and 89
healthy malaria-negative controls. Host DNA was extracted using QIAGEN DNA Mini Kit and
multiplex PCR was conducted to detect G6PD variants (Asian Type) and the Filipino β-thalassemia
deletion. Results demonstrated that 4/106 (3.8%; 95%CI 1.0-9.3) of *P. knowlesi* infected and 11/89
(12.4%; 95%CI 6.3-21.0) of non-infected samples had one of 8 G6PD Asian Type variants known to be
associated with phenotypic enzyme deficiency (OD 0.28 [95%CI 0.09-0.91]; p=0.031). Viangchan
(2.8%) and Coimbra (1.0%) variants were observed among *P. knowlesi* infected samples while in non-
infected, Viangchan (9.0%), Coimbra (2.2%) and Mediterranean (1.1%) were identified. For the
Filipino-β-thalassemia deletion, *P. knowlesi* infected samples had a higher proportion detected (6.2%)
versus healthy controls (3.6%), although this was not statistically significant (p=0.442). In conclusion,
results support the relationship of G6PD genetic variants with protection against acquiring *P.
knowlesi* infection. In contrast, there did not appear to be an association between Filipino-β-
thalassemia and susceptibility to *P. knowlesi* infection. However, this lack of association could be due
to the confounding from other host or parasite factors related to malaria susceptibility. Thus, further
studies, including genome-wide association studies, are needed for a comprehensive understanding
of the role of human genetics in conferring protection against *P. knowlesi* infection.

Keywords:
G6PD; thalassemia; *P. knowlesi*; malaria
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First Report on a Black Fly (Simuliidae) Attracted to Human in Peninsular Malaysia

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Abstract

The adult females of some black fly (Diptera: Simuliidae) species are hematophagous insects that feed on avian and mammals blood including humans. In Peninsular Malaysia, a total of 63 species of black flies have been recorded yet there is no record of human attracted species. In September 2017, two individuals of adult females were attracted to a human during a biodiversity survey conducted at Tasik Kenyir, Terengganu, Peninsular Malaysia. Their blood-feeding activity, however, could not be confirmed because the samples were captured quickly after landing on the forehead of a volunteer. The DNA barcoding COI gene showed that the sample has 96% similarity with Simulium (Gomphostilbia) maleewongae of the Gombakense species-group. This is the first report on human attracted black fly in Peninsular Malaysia. Further morphological analysis is warranted to determine if this is an undescribed species.

Keywords:
Black fly; human attracted; Peninsular Malaysia; Simuliidae
Abstract No: 13036

**Zika Virus Modulates Barrier Function, Inflammatory Response and Junctional Integrity of Brain Microvascular Endothelial Cells**

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**Abstract**

Zika virus (ZIKV) is a mosquito-borne virus with positive single-stranded RNA. Recent outbreak highlighted ZIKV as causative agent for fetal brain damage especially in infected pregnant women. This implicates that the virus has the ability to cross the placental barrier and enter the fetal circulation by crossing of microvascular endothelial cell layer. Therefore, this in vitro study is designed to investigate the infection outcome of ZIKV towards brain microvascular endothelial cells (MECs). Brain MECs were infected with ZIKV at MOI of 1 and 5 and the total RNA was measured employing quantitative reverse transcription-PCR (qRT-PCR) method. The changes in barrier function and membrane permeability of ZIKV-infected brain MECs were determined using electric cell-substrate impedance sensing (ECIS) system. Immune responses of MECs towards ZIKV was determine via analysis of cytokine released and gene expression using one-color gene expression microarray at 1, 3, 6, 12 and 24 hours post infection. The quantitative qPCR results demonstrated that ZIKV was able to infect and replicate in brain MECs at both MOIs. The highest replication rate was detected in the cells at MOI of 5. The ECIS results demonstrated that ZIKV infection enhances vascular leakage by increasing cell membrane permeability through alteration of brain MECs barrier function and disruption of actin cytoskeleton arrangement. The level of cytokines especially CCL2, CXCL10 and VEGF-A were elevated in brain MECs implicating their roles in inducing vascular leakage. This was further supported by high expression of genes that involved in regulation of inflammatory response (TLR4 and ZC3HAV1), actin cytoskeleton (ITGB5, LAMPTOR1, SHROOM2 and SHROOM 3), and adhesion molecules (CEACAM3, CERCAM, JAM2 and CLDN12) which were reflected by microarray and real time gene validation assays. Overall, findings of this study revealed that ZIKV infection could alter barrier function of brain MECs by altering adhesion molecules and induces inflammatory response.

**Keywords:**  
Zika virus; Flaviviruses; brain microvascular endothelial cells; barrier function; inflammatory response
Abstract

Despite decades of hard work to control mosquitoes as a part of disease prevention tactics, many countries are still battling to overcome vector-transmitted diseases. Aiming at the disease vectors, the mosquitoes such as *Aedes aegypti* and *Aedes albopictus*, had demonstrated resistance towards the four major classes of chemical insecticides (i.e., organochlorine, carbamate, organophosphate and pyrethroid). The loss of efficacy of these insecticides may cause failure at mosquito-borne disease control and lead to increased disease transmission. There are many alternatives to synthetic and chemical insecticides that await discovery and development. To diversify the choices of vector control and to combat widespread of insecticide resistance in mosquitoes, research in developing novel insecticides with unique modes of action is very much required. *Streptomyces*, as the largest genus of actinobacteria, producing 75-80% of economically important secondary metabolites, displayed noteworthy results in suppressing agricultural pests but there is a lack of study in the case of mosquitoes. Ethyl acetate extract of *Streptomyces* sp. KSF103 was evaluated for larvicidal activity against *Ae. aegypti* and *Ae. albopictus*, in accordance to WHO standard protocol. The larvae were exposed to different concentrations of the formulation along with untreated control. The compound was found to be effective against late third-instar and early fourth-instar larvae of *Ae. aegypti* and *Ae. albopictus*, with LC$_{50}$ values of 45 and 60 µg/mL respectively, on the basis of 24-h exposure. This study showed that the ethyl acetate extract of *Streptomyces* sp. KSF103 may be considered as a novel potent source of mosquito larvicidal agent. The discovery of actinobacteria as insecticides merits further study as potential mosquito larval control agents or as lead compounds.

*Keywords:*
*Aedes; Streptomyces; larvicide*
Molecular Identification of Cyclophyllid families (Cestoda) Found in Rats Based on the Analysis of 18S Ribosomal DNA gene

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Abstract

Studies of rats’ parasites are very important in scientific research as it correlates to the health of animals and humans. Based on previous studies, rats act as reservoir host of the zoonotic cestodes but very little is known regarding the specific cestodes species that infect the rats. Hence, the aim of this study is to identify the cyclophyllidean cestodes infection in rats as hosts. Since molecular-based identification method is imperative to identify the species of cestodes found in rats, mitochondrial 18S ribosomal DNA gene from the cestodes derived from five different host species (\textit{Rattus rattus}, \textit{Rattus tiomanicus}, \textit{Sundamys muelleri}, \textit{Leopoldamys sabanus}, \textit{Maxomys surifer}) was examined. Two species of cestode were collected and identified which are \textit{Hymenolepis diminuta} (n = 6) and \textit{Raillietina} sp. (n = 4). Phylogenetic trees were obtained by constructing Maximum Parsimony (MP) and Neighbour-joining (NJ) using MEGA X software to clarify the cestodes infesting host. Analyses showed that both genera are diverged from each other as \textit{Hymenolepis diminuta} formed its own monophyletic clade and separated from \textit{Raillietina} species. The pairwise genetic distance is highly distinguished between \textit{Raillietina} sp. and \textit{Hymenolepis diminuta} and genetically distinct from the outgroup species \textit{Taenia taeniaeformis}. The results reveal that there are presence of \textit{Raillietina} sp. in rats which is commonly found in small intestines of bird species and can accidentally found in humans. In conclusion, this study records the first list of \textit{Raillietina} sp. infected rats in Peninsular Malaysia. These molecular data can be useful to deeply study intra-specific variation within \textit{Hymenolepis diminuta} and \textit{Raillietina} sp. cestode in the future.

Keywords:
Zoonotic cestodes; rats; 18S rDNA gene; phylogenetic studies