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FOREWORD BY YB PUAN YEO BEE YIN

Minister of Energy, Science, Technology, Environment and Climate Change (MESTECC)

I feel privileged to be here today on the occasion of the Official Opening of the **6th International Biotechnology Symposium**. I would like to extend my gratitude to Universiti Malaysia Sabah and the Biotechnology Research Institute who have taken the initiative of hosting this important event which serves as a platform for the promotion of biotechnology in Malaysia. The theme of the symposium, **"Biotechnology in Sustainable Development Goals"** highlights the aspirations of the global community as outlined in the United Nations Millennium Development Goals 2015, which have since then, been translated into the Sustainable Development Goals (SDG) and officially known as "Transforming our World: The 2030 Agenda for Sustainable Development".

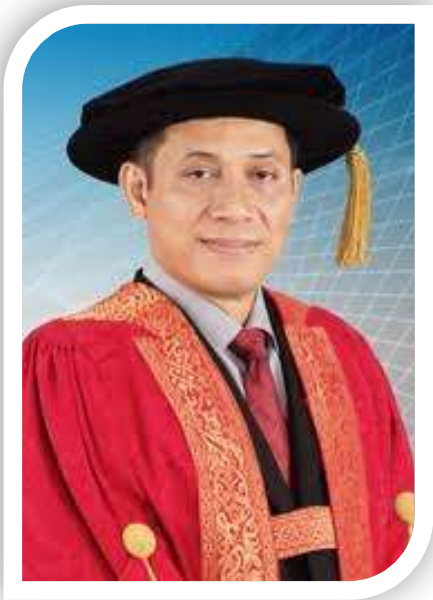
Biotechnology and the life sciences will have a significant impact on the realization of the seventeen goals stated in the SDG document which include, among others, Good Health and Well Being, Sustainable Cities, Communities and Industry; Innovation and Infrastructure. Malaysia strongly supports the SDG and has initiated several measures to translate the goals of the SDG into a tangible reality.

The Ministry of Energy, Science, Technology, Environment and Climate Change (MESTECC) has been the foundation upon which the Biotechnology industry in Malaysia has been established, evolved and developed over the past decade. In 2005, Malaysia established the National Biotechnology Policy (NBP) that aimed to turn the biotechnology sector into one of the key economic drivers in the nation, contributing 5% of the nation's GDP by 2020. The NBP was designed to provide a comprehensive roadmap that would foster a conducive ecosystem for accelerated growth in the biotech industry via three five-year phases which encompassed Capacity Building, Science to Business and the current phase which highlights Global Business Presence.

I would like to take this opportunity to thank the scientific community for partaking in the process of developing the national and international biotechnology industry. Your contribution as researchers has led to many discoveries which are being capitalized by industry to spur the economy towards sustainable development. I encourage you to pursue this path which will lead to new discoveries and can be translated into innovations which will benefit mankind.

Thank you

FOREWORD BY
PROF. DATUK DR. D. KAMARUDIN D. MUDIN
Vice Chancellor of Universiti Malaysia Sabah



I take this opportunity to warmly welcome the delegates to the **6th International Biotechnology Symposium** which is hosted by the Biotechnology Research Institute, of Universiti Malaysia Sabah (UMS).

UMS continues to develop and diversify high-quality teaching and research to propel the nation's higher education to the next level. An academic event like the **6th International Biotechnology Symposium** is one of UMS' continuous efforts to elevate Malaysia's position in the global higher education map.

The UMS vision is to strive to be an innovative university of global standing. Research and Development in Biotechnology represent a critical link between innovation, productivity, health and wealth as they offer quality and sustainability. Following this goal, the **"Biotechnology in Sustainable Development Goals"** is nonetheless a specific, attainable, and relevant issue to be discussed and addressed.

Keeping this in perspective, this symposium offers an international platform for students, researchers and academics from a diverse range of disciplines to participate and share their knowledge, experiences and ideas with their international peers, which will contribute to the development of the scientific and economic strength of our nation from a biotechnology perspective.

MESSAGE FROM DR. ZARINA AMIN

Director of Biotechnology Research Institute, UMS

It gives me great pleasure and honor to welcome all delegates to the **6th International Biotechnology Symposium 2019 (SB6)** organised by the Biotechnology Research Institute, Universiti Malaysia Sabah, which is held on **10th & 11th July, 2019**. Reflecting back over the years, the Biotechnology Symposia have been an integral component in the process of the development of our Institute. Ultimately, it is hoped that this symposium can forge links between scholars and to foster transdisciplinary collaborative research between all Malaysian's biotechnology stakeholders (researchers, lecturers, students, industrialists and bureaucrats) as well as from abroad.

It is said that "Living organisms always react and respond to their environment, while the environment continues to change and challenge living organism". Acknowledging this, this year the symposium will feature the theme of **"Biotechnology in Sustainable Development Goals"**. It is our hope that during the two days symposium, the presentations can stimulate discussion and innovative thinking that would be able to address effective and sustainable strategies to face global challenges to secure major issues including human health, food security, and biodiversity. We feel encouraged by the overwhelming level of support which you, the delegates have demonstrated by your participation. I hope this symposium can be a platform for participants and academic institutions to build and expand our regional and global connections. I would like to thank and congratulate Assoc. Prof. Dr. Kenneth Francis Rodrigues, the Chairman and all the organising committee members for ensuring the symposium run smoothly with a great success. We are delighted to welcome you to the **6th Biotechnology Symposium 2019.**

MESSAGE FROM ASSOC. PROF. DR. KENNETH FRANCIS RODRIGUES

Chairman of the Organising Committee of the 6th International Biotechnology Symposium

I take this opportunity to welcome the delegates to the **6th International Biotechnology Symposium.** It is my honor and privilege to represent the organising committee at this symposium.

The impact of anthropogenic activities on the environment have become a major cause for concern among the global community. Recent incidents of environmental pollution, at the national and international levels have highlighted the fact that we as a species are driving the process of environmental degradation and climate change.

The United Nations Sustainable Development Goals, have served as a rallying point for the global community and for scientists to direct their attention towards resolving the challenges posed by rapid industrialization and habitat destruction. The theme of the symposium "**Biotechnology in Sustainable Development Goals"** highlights the spirit which drives this important gathering.

I wish to thank each and every one of the international and national delegates who have made an effort to grace this event and to remind the community of the need for greater environmental awareness supported with cogent action.

I extend my thanks to our sponsors for their generous support in making this event possible. I wish to thank the Director of the Biotechnology Research Institute, Dr. Zarina Amin for her guidance and to the members of the organising committee and their respective teams who have provided unqualified support to this event.

OPENING CEREMONY OF THE 6TH INTERNATIONAL BIOTECHNOLOGY SYMPOSIUM (SB6) 2019

Date : **10 July 2019 (Wednesday)**
Time : **8.00 am**
Venue : **Ballroom 2 & 3, The Pacific Sutera Hotel, Kota Kinabalu, Sabah**

8.00 am : Arrival of delegates and guests for registration

8.30 am : Arrival of Principal Officers and Head of Departments of Universiti Malaysia Sabah

8.45 am : Arrival of **YBhg. Prof. Datuk Dr. D Kamarudin D Mudin, Vice Chancellor, Universiti Malaysia Sabah**

8.50 am : Arrival of **YB Puan Yeo Bee Yin, Minister of Energy, Science, Technology, Environment & Climate Change (MESTECC)**

9.00 am : Event start

- National Anthem & State Anthem singing
- Do'a Recital
- Welcoming Speech by **Dr. Zarina Amin, Director, Biotechnology Research Institute, Universiti Malaysia Sabah**
- Speech by **YBhg. Prof. Datuk Dr. D Kamarudin D Mudin, Vice Chancellor, Universiti Malaysia Sabah**
- Opening Speech by **YB Puan Yeo Bee Yin, Minister of Energy, Science, Technology, Environment & Climate Change (MESTECC)**
- Presentation of Souvenirs
- Photo Session
- Coffee Break

9.45 am : Estimate to End

CLOSING CEREMONY OF THE 6TH INTERNATIONAL BIOTECHNOLOGY SYMPOSIUM (SB6) 2019

Date : **11 July 2019 (Thursday)**
Time : **4.40 pm**
Venue : **Ballroom 2 & 3, The Pacific Sutera Hotel, Kota Kinabalu, Sabah**

4.40 pm : Event start

- Closing Remarks by **Assoc. Prof. Dr. Kenneth F. Rodrigues Chairman of the 6th Biotechnology Symposium (SB6) 2019**
- Presentation of Award
  - Travel Grant Award
  - Best Oral Presenter Award
  - Best Poster Presenter Award
- Lucky Draw
- Coffee Break

5.30 pm : Estimate to End

SCIENTIFIC PROGRAM

DAY 1 (WEDNESDAY, 10 JULY 2019)		
	SESSION 1 **Chairperson: Prof. Dr. Michael Wong**	
09:45	**KEYNOTE 1** Genomics and Genetics of Breast Cancers in Malaysia **Prof. Datin Paduka Dr. Teo Soo-Hwang**	
10:45	**PLENARY 1** The Ethics of Stem Cell Research **Prof. Dr. Misao Fujita**	
	BALLROOM	**PARALLEL ROOM**
	Chairperson: **Prof. Dr. Michael Wong**	**Chairperson:** **Assoc. Prof. Dr. Teoh Peik Lin**
11:25	Intragenic *ERG* Deletion in Three Malaysian Childhood B-cell Precursor Acute Lymphoblastic Leukaemia Patients **Nor Soleha Mohd Dali**	Antibiotic Discovery in the Abyss **Henry Llyod Stennett**
11:40	Variability of the Flavonoid Metabolites in *Carica papaya* Leaves by Liquid Chromatography-Mass Spectrometry and Multivariate Data Analysis **Norazlan Mohmad Misnan**	Insecticidal Effects of *Chromolaena odorata* Against Rice Brown Planthopper, *Nilaparvata lugens* (Stål.) **Nor Ilya Binti Mohd Zaki**
11:55	Acetohydroxyacid Synthase Gene Serine (653) Mutation Confers Imidazolinone Herbicides Resistance in Malaysian Weedy Rice **Rabiatuladawiyah Ruzmi**	Waste Engine Oil Biodegradation by an Oil-Utilising Fungus, *Aspergillus* sp. in a Stirred Tank Bioreactor **Nurshafiqah Jasme**
12:10	The Development of a Peptide-Based Gene Delivery System: In Vitro Evaluation of a GL-1 Peptide Library **Khairul Azfar Kamaruzaman**	Development of Immobilized System for Rhamnolipid Production by *Pseudomonas aeruginosa* USM-AR2 **Nur Ardhani Mohammed Zulkhifli**
12:25	-	Antioxidant and Antimicrobial Activity of Edible Active Food Coating Prepared with Bioplastic Based Bacterial Cellulose **Joko Sulistyo Soetikno**
12:40	Preliminary Fungal Diversity Study of Limestone Caves in Sabah, Malaysia **Ibrahem Ghani Wasti**	Thermal Treatment of High Moisture Content Biomass Using Dairy Manure **Sitty Nur Syafa Binti Bakri**
12:55	**POSTER SESSION & LUNCH**	
	SESSION 2 **Chairperson: Assoc. Prof. Dr. Mohamad Iqbal**	
14:00	**PLENARY 2** Bioprocess for Biorefinery Enzymes Production in Semi-Industrial Scale: From Soil Isolate to Bulk Powder **Prof. Dr. Hesham Ali El Enshasy**	
14:40	Methyl Jasmonate Elicitation on Kesum (*Persicaria minor* Huds.) Leaf Triggered Proteome Changes Related to Defense and Growth **Wan Mohd Aizat Bin Wan Kamaruddin**	
14:55	Suppression of *Ganoderma boninense* and Potential Induced Resistance Involved in the Biocontrol of *Ganoderma* Disease by *Streptomyces nigrogriseolus* GanoSA1 in Oil Palm Seedlings **Syariffah Muzaimah Syed Aripin**	
15:10	The Allelopathic Effects of *Etlingera coccinea* on Seed Germination of Weedy Rice **Nurfitri Harman**	
15:25	Recombinant Bromelain from MD2-Pineapple: A Model Pipeline for Translational Genomic Research **Cahyo Budiman**	
15:40	Ex-Situ Degradation of Palm Oil Using Natural Seawater and Identification of Bacterial Consortium **Tamothran Muthaliar Arularasu**	

15:55	Electrochemical Voltammetric Determination of Alkoxy Substituted p-Cyano Stilbene Schiff Bases on Au-ITO Electrode as Potential Application in E-DNA Sensor **Hanis Mohd Yusoff**
16:10	Antibacterial Screening of Mangrove Extract Library: Accelerating Drug Discovery from Indonesian Biodiversity **Kholis Abdurachim Audah**
16:25	**POSTER SESSION & REFRESHMENT**
17:30	**End of Day 1**

DAY 2 (THURSDAY, 11 JULY 2019)	
	SESSION 3 **Chairperson: Dr. Zarina Amin**
09:00	**KEYNOTE 2** Infectious Diseases and Sustainable Development Goals **Prof. Datuk Dr. Asma Ismail**
10:00	**REFRESHMENT**
10:20	**PLENARY 3** Microbial Polymer: Polyhydroxyalkanoates (PHAs) as Potential Biomaterial for a Sustainable Tomorrow **Prof. Dr. Amirul Al-Ashraf Abdullah**
11:00	**PLENARY 4** GMOs and Sustainable Agriculture **Prof. Dr. Rahman Milan**
11:40	The Influences of Giving Extracted of Dogfruit Seed (*Pithecellobium lobatum* Benth.) Ethanol to Reduce Blood Glucose Level of Male White Rat (*Rattus novergicus*) of Sprague Dawley Strain Induced with Aloxane **Evi Kurniawati**
11:55	Reconstruction of the Metabolic Biosynthetic Pathway of *E. fuscoguttatus* in Response to *V. vulnificus* Using Metabolomics Approach **Syarul Nataqain Baharum**
12:10	Bioactive Compound Characterization and Evaluation from Endophytic Fungi of Batang Tepus (*Etlingera coccinea* (Blume) S. Sakai and Nagam) **Mohamad Iswandy Ibrahim**
12:25	*Aurantiochytrium* Sp. SW1 Biomass as n-3 Fatty Acids Source in Fish Feed **Herryawan Ryadi Eziwar Dyari**
12:40	**POSTER SESSION & LUNCH**
	SESSION 4 **Chairperson: Dr. Cahyo Budiman**
14:00	**PLENARY 5** Cryo-EM Structures of Ribosomes and Viruses **Assoc. Prof. Dr. Shashi Bhushan**
14:40	Effect of Pectin Biodegradation with *Aspergillus niger* on Total Flavonoid Content of Leaf, Peel, and Lower Grade Fruit of *Citrus limon* L. **Muhammad Yusuf Abduh**
14:55	Optimization of Pullulan Production by *Aureobasidium pullulans* Using Response Surface Methodology **Daniel Joe Dailin**
15:10	Discovery of Simple Sequence Repeat Markers via Transcriptome Analysis of *Baccaurea motleyana* **Khairun Hisam Nasir**
15:25	Morphological and Protein Changes on Acanthamoeba Cyst in Relation to Trehalase Enzyme Exposure **Fatimah Binti Hashim**
15:40	Immobilization of RGD Peptide onto the Surface of Nano-poly(3-hydroxybutyrate-co-4-hydroxybutyrate) Scaffold Fabricated by a Combination of Electrospinning/ Aminolysis Method **Chai Meng Jun**
15:55	Effect of LEDs Light Exposure on Biomass and Growth of *Hibiscus rosasinensis* Callus and Cell Suspensions Cultures **Ooi Saik Huey**

16:10	Characterization the Stability of Allergenic Tropomyosin from Mud Crab, *Scylla olivacea* **Rosmilah Misnan**
16:25	The Effects of Selected Lactic Acid Bacteria Fermentation on the Bioactivity of Mature Coconut Water **Izuddin Abdul Rahman**
16:40	**CLOSING CEREMONY/BEST PRESENTER AWARDS/REFRESHMENT**
17:30	**End of Conference**

ORAL PRESENTATIONS

POSTER PRESENTATIONS

Keynote 1

Genomics and Genetics of Breast Cancers in Malaysia

Teo Soo Hwang
Cancer Research Malaysia, 2nd Floor, Outpatient Centre, Sime Darby Medical Centre, Selangor, 47500 Subang Jaya

Breast cancer is the most common cancer globally, with 2 million women diagnosed and 600,000 individuals dying of breast cancer in 2018. In Asia, breast cancer is increasing in incidence rapidly because of changes in reproductive and lifestyle factors, and today, more women die of breast cancer in Asia than in Europe or North America. Whilst early detection of breast cancer is possible through mammography, there is neither the justification nor funding to support population-wide screening of breast cancer, except in high income Asian countries like Japan, Korea and Singapore. In the absence of such population-wide screening, the most feasible approach may be to offer screening to those at highest risk. In my talk, I will present review what we know about genetic and lifestyle factors which are associated with an increased risk to breast cancer in Asian women, and the impact of such research on risk stratified approaches to screening in Asian women. In the second part of my talk, I will describe what we know about the subtypes of breast cancer based on the genomic and transcriptomic profiles of breast tumours, focusing on how in depth characterisation of Malaysian tumours has led to suggest of treatment possibilities. Together, I aim to provide an update on our efforts in applying the latest technological advances to the understanding of breast cancer in Asian women so that we can identify better ways to prevent, screen for and treat this disease.

Plenary 1

The Ethics of Stem Cell Research

Misao Fujita
Uehiro Research Division for iPS Cell Ethics, Center for iPS Cell Research and Application, Kyoto University

When making rules for new scientific technologies such as iPS/ES cell technologies, it is important to understand the general public's attitude, reflect this societal attitude in policy formulation, and share and examine ethical issues in society. In this presentation, we will present as an example questionnaire surveys[1)2)] that clarifies the attitude of the general public and researchers on animal-human chimeric embryo research and suggest that a clear presentation of the aims and significance of the research is important for increasing the level of acceptance of the general public. Furthermore, we will also touch upon the meaning of linking survey results to policy discussions, as well as the importance of outreach activities. Insofar as time allows, we will introduce a similar questionnaire survey that we had carried out on the research of the creation of artificial gametes. In order to connect attitude surveys to policy, it is important to carry out research based on questions closely related to the ongoing discussions, and have ways to bring survey findings to the place where the policy is discussed.

1) Sawai T, Hatta T, Fujita M. Public attitudes in Japan towards human-animal chimeric embryo research using human induced pluripotent stem cells. Regen Med 2017; 12: 233-48.

2) Sawai T, Hatta T, Fujita M. The Japanese generally accept human-animal chimeric embryo research but are concerned about human cells contributing to brain and gametes. Stem Cells Transl Med 2017; 6: 1749-50.

Plenary 2

Bioprocess for Biorefinery Enzymes Production in Semi-Industrial Scale: From Soil Isolate to Bulk Powder

Hesham A. El Enshasy
Institute of Bioproduct Development (IBD), Universiti Teknologi Malaysia (UTM), Johor Bahru, Johor, Malaysia.

Lignocellulases group of enzymes are the key biocatalysis in second generation biorefinery. They play important role in the first step of pro-biorefinery in the conversion of lignocellulosic non-fermentable feedstock to lower molecular weight fermentable sugars for the production of wide range of biological compounds. In green chemistry bioprocess, enzymes are considered as the major cost in the overall biorefinery process in replacing the current non-environmental friendly practice of using acid/alkali and heavy metals. However, it is necessary not only to have enzymes of wide substrate range and operation under extreme conditions in terms of temperature and pH but should be also available at competitive price. In this presentation, two complete platforms for production of two key enzymes in biorefinery industries. First, production of lignin degrading enzymes from new local fungal isolate. This presentation will provide a comprehensive overview on the application of different enzymatic systems in biorefinery. In addition, industrial platform for enzyme production for xylanases and lignin peroxidases using recombinant and non-recombinant biofactories will be presented in details.

Plenary 3

Microbial Polymer: Polyhydroxyalkanoates (PHAs) as Potential Biomaterial for a Sustainable Tomorrow

A.A. Amirul[1,2,3*], K.H. Huong[1], R. Hema[4], S. Vigneswari[5], I.M. Syafiq[2], H. Norhafini[2], G. Tana Porani[1]
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**email address: amirul@usm.my*

Polyhydroxyalkanoates (PHAs) is a group of biopolymers that exhibit complete biodegradability and biocompatibility. Poly(3-hydroxybutyrate-*co*-4-hydroxybutyrate) [P(3HB-*co*-4HB)] is among the PHAs that exhibits desirable properties for applications in the medical and pharmaceutical industries. This has encouraged the development of various healthcare-related products such as in cardiovascular, wound healing, orthopedic, drug delivery and tissue engineering applications using the copolymer. Three bacteria that capable of producing P(3HB-*co*-4HB) copolymer have been isolated from Malaysian environment and identified as *Cupriavidus malaysiensis* USMAA1020, *Cupriavidus malaysiensis* USMAA2-4 and *Cupriavidus malaysiensis* USMAHM13. The bacteria produced P(3HB-*co*-4HB) with 4HB monomer compositions ranging from 10 – 95 mol% using various carbon precursors such as γ-butyrolactone, 4-hydroxybutyric acid and 1,4-butanediol, 1,6-hexanediol and 1,8-octanediol. These copolymers exhibited a wide range of physicochemical properties, which depends on the monomeric compositions and type of carbon sources. Particularly, an elastomeric P(3HB-*co*-4HB) was produced from USMAA1020 strain, with an elongation-at-break of 1,637% which represents a novel characteristic. The P(3HB-*co*-4HB) derived from microorganisms is biocompatible and produces inert by-products upon in-vivo degradation. However, as with most biopolymers, the surface of P(3HB-*co*-4HB) is hydrophobic with less recognition sites for cell attachment. Therefore, surface modifications were performed to promote cell-biomaterial interaction for better cell proliferation. This was done by incorporating collagen to enhance the surface architecture of P(3HB-*co*-4HB) scaffolds that closely mimicking the cell environment. The P(3HB-*co*-4HB)/collagen blend scaffolds with bioactive surface were developed for tissue engineering and also as biodegradable wound dressing.

Keywords: Biopolymer; PHA, P(3HB-co-4HB), biomaterial.

Plenary 4

GMOs and Sustainable Agriculture

Abd Rahman Milan and Azwan Awang
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Agriculture is a key component structure for survival for human kind. Nevertheless, the capacity of conventional agriculture to produce food for sustaining increasing human population become a daunting task particularly under the climate changed environment. The invention of GMOs with desired traits through genetic engineering has brought so much promises for our future survivability. The rate of adoption has been tremendous since its first introduction in 1996 by the farmers, including those in developing countries have rip a lot of benefits through planting of GMOs. Currently, even though a lot of GMO foods already consumed by the people without realizing it especially in Malaysia, the development of this product in agriculture are still at the lower phase. Most GMOs are field crops (maize, cotton, soybeans), others are horticulture crops (fruits, vegetables, flowers) and less are livestock. Moreover, consumers tend to be associated product from agriculture biotechnology as GMO and always associated with the bad things. In Malaysia, under the National Biotechnology Policy (2005), biotechnology events and activities are regulated and administered by one Department under Ministry of Water, Land and Natural Resources (KATS) known as National Biosafety Board (NBB) and Genetic Modification Advisory Committee (GMAC). This paper will discuss on the concept of sustainable agriculture and how GMOs fit into the concept. Furthermore, we will look the status of GMO development, hurdles, and opportunity as well in Malaysia.

Plenary 5

Cryo-EM Structures of Ribosomes and Viruses

Shashi Bhushan
School of Biological Sciences, NTU Singapore

Ribosomes are the dynamic protein synthesis machineries of the cell. They may exist in different functional states in the cell. Therefore, it is essential to have structural information on these different functional states of ribosomes to understand their mechanism of action. I will present single particle cryo-EM reconstructions of the *Mycobacterium smegmatis* 70S ribosomes in the P/P state (with P-tRNA), trans-translating state (with tmRNA), and hibernating state (with HPF) resolved to 3.4, 12.5, and 4.1 Å, respectively. The high-resolution structure of the P/P state reveals various rRNA and r-protein extensions in *M. smegmatis* ribosome and suggests how these mycobacterial features can be exploited as the potential drug targets. Structure of the trans-translating state suggests a conserved bacterial rescue mechanism of stalled ribosomes. A comparison of the P/P state to the hibernating state provides possible functional insights about the Mycobacteria-specific Helix 54a rRNA segment. Structure reveals a Mycobacteria-specific H54a-bS1 interaction which seems to prevent subunit dissociation and degradation during hibernation without the formation of 100S dimer. This indicates a new role of bS1 protein in 70S protection during hibernation in mycobacteria in addition to its conserved function during translation initiation. Zika virus has recently emerged as a global threat. The rapid spread of the virus need fast development of effective therapies. While development of a vaccine against Zika might takes many years, monoclonal antibodies could be used as a potential immunotherapy option for Zika-infected individuals. We have determined a 3D structure of Zika in complex with a potent neutralizing antibody. Cryo-EM reconstruction of the Fab-Zika complex validate the design model and reveals insights into the mechanism of antibody neutralization.

OP02

Intragenic *ERG* Deletion in Three Malaysian Childhood B-Cell Precursor Acute Lymphoblastic Leukaemia Patients

Nor Soleha Mohd Dali[1], Nursaedah Abdullah Aziz[1], Durar Aqilah Zamri[1], Betty Ho L. S.[2], James Lee, J. H.[2], Nazzlin Dizana Din[3], Azly Sumanty Ab Ghani[4], Wan Amal Hayati Wan Hasan[4], Julia Abdullah[1], Nor Rizan Kamaluddin[1], Ezalia Esa[1], Yuslina Mat Yusoff[1] and Zubaidah Zakaria[1]

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ERG-related leukaemia is a B-cell precursor acute lymphoblastic leukaemia (BCP-ALL) subtype characterised by highly recurrent *ERG* intragenic deletions. *ERG*-related patients have remarkably favorable outcome despite a high incidence of unfavorable *IKZF1* aberrations. To systematically characterise the intragenic *ERG* deletion in Malaysian paediatric acute lymphoblastic leukaemia patients. High-resolution single nucleotide polymorphism (SNP) 6.0 array test was carried out on the genomic DNA of three Malaysian childhood BCP-ALL patients (P1, P2, P3) diagnosed in 2016 and 2017. The raw data was analyzed using Chromosome Suite Analysis (ChAS) software. SNP array results were validated using Multiplex Ligation-dependent Probe Amplification (MLPA). Three pediatric patients, one aged 14 (P1) and two aged 10 (P2 and P3), presented with symptomatic anemia. Initial full blood count showed leukocytosis with bicytopenia. Physical examination revealed hepatosplenomegaly. Diagnostic bone marrow aspiration in each patient revealed the presence of 90%, 97% and 56% lymphoblast cells, respectively, consistent with diagnosis of BCP-ALL. SNP array analysis revealed intragenic *ERG* deletion in all three patients. Besides this deletion, each patient also has secondary aberrations including *IKZF1*, *CDKN2A* and *CDKN2B* deletions (P1 and P3), *PAX5* and *ETV6* deletions (P3), and 1q amplification (P2). These finding were confirmed by MLPA. Despite the coexistence of intragenic *ERG* deletion with secondary aberrations, all patients achieved remission after standard chemotherapy treatment. The coexistence of ERG deletion with secondary aberration have favourable outcome in BCP-ALL patients.

Keywords: SNP array, MLPA, B-ALL, *IKZF1*, *CDKN2*

OP3

Variability of the Flavonoid Metabolites in *Carica papaya* Leaves by Liquid Chromatography-Mass Spectrometry and Multivariate Data Analysis

Norazlan Mohmad Misnan[1], Low Kah Hin[2], Adlin Afzan[1], Mohd Isa Wasiman[1] and Ami Fazlin Syed Mohamed[1]

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Carica papaya leaves are widely reported to contain many bioactive metabolites including flavanoids, which their concentrations may vary with respect to leaves maturity and the plant sexual reproduction type. The present study aimed to evaluate the characteristic metabolites and to explore variability of flavonoid content in the leaf extracts using liquid chromatography-mass spectrometry coupled with pattern recognition techniques. A total of twenty-four metabolite compounds including twelve flavonoids, four hydroxycinnamic acids, three alkaloids, one coumarin and four organic acids have been identified; six of the dominant flavonoids were quantified and subjected to multivariate analyses. Both principal component analysis and hierarchical cluster analysis were showed distinct flavonoid contents according to shoot, young and old leaf samples. Despite part of variation was originated from the sexual type, old leaves are generally associated with lower flavonoids content whereas young leaves could be discriminated from shoot samples in terms of clitorin, rutin, and nicotiflorin concentrations. The variability of the flavonoid composition may affect the pharmacological properties of the related phytopharmaceuticals.

Keywords: Classification, Chemometrics, Fingerprinting, Metabolomics, Maturity

OP04

Acetohydroxyacid Synthase Gene Serine (653) Mutation Confers Imidazolinone Herbicides Resistance in Malaysian Weedy Rice

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Overuse of the imidazolinone herbicides (IMI-herbicides) in the Clearfield Production System (CPS) has led to the evolution of IMI-resistant weedy rice (*Oryza sativa*) in Malaysian rice fields. The biochemical and molecular basis of resistance to IMI-herbicides were investigated in three populations of field-reported resistant (R) weedy rice (populations A, B, and C), a susceptible weedy rice population (S), an imidazolinone-resistant rice cultivar (IMI-rice), and a susceptible local rice cultivar (MR219). The acetohydroxyacid synthase (AHAS) gene covering potential mutation sites in these populations was amplified, sequenced, and compared. AHAS enzyme extracted from the shoots of all populations were incubated with IMI-herbicides imazapic and imazapyr for *in vitro* AHAS enzyme inhibition assay. The sequence of the 2011 base pair AHAS gene fragment shows that the S and MR219 were 99% similar. Meanwhile, AHAS nucleotide sequences of R populations and IMI-rice were identical, where the same amino acid substitution of Ser-653-Asn was revealed in both populations when compared to S. *In vitro* enzyme assay shows that the AHAS enzyme extracted from R populations and IMI-rice were less sensitive to IMI-herbicides in comparison to S and MR219. Cross-resistance to imazapic and imazapyr was also observed in R and IMI-rice populations in this assay. It is concluded that the sole dependence on IMI-herbicides in the CPS package by rice growers has resulted in target-site mutation at the Ser^{653} codon. The AHAS enzyme assays also proved that the target-site insensitivity is the predominant mechanism of resistance in weedy rice resistant to IMI-herbicides in Malaysian CPS rice fields.

Keywords: herbicide resistance mechanism, target-site mutation

OP05

The Development of a Peptide-Based Gene Delivery System: *In vitro* Evaluation of a GL-1 Peptide Library

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Gene therapy is a promising technique that introduces exogenous genes or oligonucleotides to treat diseases through gene expression or gene silencing. However, genes (DNA and RNA) are very fragile and are prone towards degradation within the human system. The delivery of genes requires the usage of a vector / delivery system to protect and to navigate across the biological barriers for an efficient therapeutic response. The vast majority of delivery systems utilized in clinical trials are mainly viral vectors. As of 2019, only 0.2% of gene therapy clinical trials have reached phase 4 signifying the slow development in producing a safe marketable treatment. The focus has shifted towards developing a working non-viral gene therapy delivery system. Our effort focuses on developing a peptide - based system, as it is easy to synthesize and customise to overcome specific biological barriers for efficient therapeutic response. A small GL-1 peptide library consisting of different types of modifications (lipidation and dimerization) were synthesized through solid phase peptide synthesis (SPPS) and assessed *in vitro* (gene binding, cellular uptake, cytotoxicity and gene knockdown/silencing) to determine which modification had the best siRNA delivery capacity in HeLa cancer cells. The modified GL-1 peptides displayed higher knockdowns abilities (~ 40%) than wild - type GL-1 with no cellular cytotoxicity issues. The combination of cell penetrating characteristics, lipid moiety and a stabilizing disulfide linkage contributes towards the increase in silencing efficiency. The combination of all modifications as a single entity can further improve its efficiency as a gene delivery system.

Keywords: Gene therapy, non-viral gene delivery, siRNA delivery, gene silencing, HeLa cancer cells

OP07

Methyl Jasmonate Elicitation on Kesum (*Persicaria minor* Huds.) Leaf Triggered Proteome Changes Related to Defense and Growth

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Kesum (*Persicaria minor* Huds.) has been frequently utilized in traditional cuisine as it exhibits pungent smell as well as possessing high antioxidant property. Previous studies have shown that this herbal species produced significant physiological changes during stresses including increasing its secondary metabolite production. One of the stress-response hormone that may regulate this is methyl jasmonate (MeJA) hormone. However, the molecular regulation upon such stress in kesum has not been adequately reported. Hence, the aim of the study is to profile the proteome of kesum leaf elicitated with MeJA to elucidate the protein changes associated with this hormonal cue. We believe that this is the first proteomics study on such non-model species particularly using the label-free quantification of SWATH-Mass Spectrometry (MS) approach. Both 1D and 2D-information dependent acquisition (IDA) followed by SWATH-MS were performed which successfully profiled a comprehensive proteome coverage of 751 proteins. Forty proteins were found to be significantly different between control and MeJA-treated samples. The modulated levels of these proteins suggest that the hormone invoked proteins related to defense and recovery response but suppressed proteins involved in growth and development. Furthermore, comparison with our previous transcriptome work also suggest that these proteins can be post-translationally regulated under stress. In conclusion, our proteomics analysis has successfully profiled proteins from this herbal species which could reveal new insights onto the molecular regulation upon MeJA elicitation.

Keywords: herb; label-free; LC-MS/MS, proteomics; systems biology

OP08

Suppression of *Ganoderma boninense* and Potential Induced Resistance Involved in the Biocontrol of *Ganoderma* Disease by *Streptomyces nigrogriseolus* GanoSA1 in Oil Palm Seedlings

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Ganoderma disease of oil palm, caused by *Ganoderma boninense* is a common destructive disease for oil palm especially in Southeast Asia. The disease, without proper control will lead to severe economic damage. A *Streptomyces* isolate, designated GanoSA1, which was identified earlier as *Streptomyces nigrogriseolus* showed distinctive inhibitory activity against *G. boninense* PER71 *in vitro* and *in plantae*. The incidence of *Ganoderma* disease, severity of foliar symptoms, and dead seedlings percentage were significantly reduced in seedlings treated with *Streptomyces* GanoSA1 formulation. The production of indicators of induced systemic resistance (ISR) such as polyphenol oxidase, peroxidase, phenylalanine ammonia-lyase, chitinase and ß-1,3-glucanase were detected in the leaf and root tissues of oil palm. There are significant increases in total production of all enzymes on seedlings treated or untreated with *Streptomyces* GanoSA1 powder. Overall findings of this study suggest that associations of this strain may not only enhance the growth quality of oil palm seedlings but also reduce *Ganoderma* incidence.

Keywords: actinomycete, basidiomycete, nursery, artificial inoculation, disease reduction.

OP09

The Allelopathic Effects of *Etlingera coccinea* on Seed Germination of Weedy Rice

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Etlingera coccinea or locally known as tuhau is a local Sabahan delicacies and usually are only used for consumption. The stem is usually consumed and has a distinctive odour. This study seeks the possible allelopathy characteristic of *Etlingera coccinea*, as a new ecofriendly weedicide, in combating the growth of the notorious weed infestation in rice paddy. The presence of potential allelopathic compounds in the leaf extracts were determined by using standard Colour Test and Thin Layer Chromatography (TLC). Extractions were carried out using methanol, ethyl acetate and hexane. Allelopathic components such as terpenoid, flavonoid, saponin and tannin were detected in the leaf extracts. To evaluate the ability of *E. coccinea* extracts to suppress the growth of weedy rice (*Oryza sativa* complex), *in vitro* bioassay was carried out. The results showed significant suppression of weedy rice seed germination at 0.1g/ml for all leaf extracts except for the hexane extract. The ethyl acetate leaf extract being the strongest as germination percentage was 0%. This study suggests that *E. coccinea* has significant source of allelopathic properties that act as plant growth inhibitors. However, the origin and persistence of the allelopathic effects need further research to determine its effect on agricultural crops.

Keywords: Allelopathy, *Etlingera coccinea, Oryza sativa* complex, Thin Layer Chromatography (TLC), Plant Growth Inhibitor

OP10

Recombinant Bromelain from MD2-Pineapple: A Model Pipeline for Translational Genomic Research

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Currently, there are numerous genomic discoveries of promising genes for industrial applications. However, attempts to further translate these discoveries towards commercialization remain a challenge. Earlier, whole genome sequencing of MD2 pineapple revealed the presence of cysteine proteases bromelain (MD2-bromelain), which is known to have many versatile industrial applications. This study describes our attempts to develop a pipeline for genomic translational research using the MD2-bromelain as a target model. The first stage involved the development of molecular strategies of the expression system for the production of MD2-bromelain in a heterologous expression system. A combination of codon optimization, synthetic gene and solubilizing-tag was successful in producing MD2-bromelain in a soluble form. The second stage involved the development of a single step purification system, which successfully yielded 150 mg/L of pure MD-2 bromelain. This pure bromelain was confirmed (stage 3) to be active with a specific activity of 1.5 U/mg and k_{cat}/K_M of 250 uM/s. In the fourth stage, the MD2-bromelain was confirmed to exhibit at least two industrial enzyme phenotypes of anti-cancer activity towards A549 and MCF-7 cancer cell lines and meat tenderizing activity. Further genetic improvement on the properties of MD2-bromelain revealed that the first round of mutation had increased the enzyme stability by about 4 °C. Lastly, we highlight the strategies used on the packaging of MD2-bromelain for further downstream applications. Our attempt here provides a successful biotechnological approach to push recombinant MD2-bromelain closer towards industrial applications in the near future.

Keywords: Bromelain, Heterologous expression, cysteine proteases, genomic translation, pineapple

OP11

Ex-Situ Degradation of Palm Oil Using Natural Seawater and Identification of Bacterial Consortium

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Palm oil industry is among the most important commodities industry in Malaysia where Malaysia dominates 39% and 44% of global palm oil production and exports respectively. Most of the palm oil exports to various countries are done via sea-shipping which increases the risk towards marine pollution in form of oil spillage from vessels. Degradation studies are important in establishing baseline data which is instrumental for mitigation planning and policy making. Seawater samples were collected at Johor Port, Klang Port and Kuantan Port. Degradation of crude palm oil (CPO) and crude palm kernel oil (CPKO) in natural seawater was investigated using modified shake flask method as described by OECD Guidelines for Testing Chemicals, OECD TG 306 (Biodegradability in Seawater). Dissolved organic carbon (DOC) was measured at selected interval along with measurement of colony forming unit (CFU) counts. Identification of bacterial population was determined using 16S-rDNA sequencing. Furthermore, changes in the free fatty acid (FFA) composition in palm oil supplemented seawater was determined using gas chromatography (GC-FID). Changes in the CFU together with DOC level and FFA indicated substrate utilization by bacteria. A total of 14 bacterial strains were isolated at the end of the test and the lipolytic activity was determined where 10 strains exhibited lipolytic activity. The outcome of this study will enable us to better understand the degradation of palm oil products in seawater and provide a starting frame point to the relevant authorities in palm oil, transportation and environmental agencies to formulate the action plan in the event of spill in marine environment.

Keywords: Marine pollution, dissolved organic carbon, microbial population, crude palm oil, crude palm kernel oil

OP12

Electrochemical Voltammetric Determination of Alkoxy Substituted p-Cyano Stilbene Schiff bases on Au-ITO Electrode as Potential Application in E-DNA Sensor

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Three compounds of alkoxy substituted p-cyano stilbene Schiff bases with three different carbon chain (n= 3, 6, 9) have been successfully synthesized and chemically modified on the indium tin oxide coated gold (Au-ITO). The volumetric behavior of those compounds on Au-ITO were investigated using cyclic voltammetry (CV) to study the surface behavior. The surface of ITO glass were coated with gold followed by alkoxy substituted p-cyano stilbene Schiff bases. The fabrication of electrode was done via self-assembled monolayer (SAMs) method. The coated Au-ITO were immersed in solution of alkoxy substituted p-cyano stilbene Schiff bases with concentration 1.0 x 10^{-5} M for 3 hours and were dried in air. Electrochemical measurements of all prepared fabricated electrode were performed using cyclic voltammetry. There are three electrode involved were fabricated electrode as a working electrode, platinum wire as an auxiliary electrode and Ag/AgCl as reference electrode. Potassium chloride (KCl) and ferrocyanide ($K_4Fe(CN)_6 \cdot 3H_2O$) were used as electrolyte in the measurement. The electrochemical behavior of Au-ITO electrode fabricated with alkoxy substituted p-cyano stilbene Schiff bases gave effect to the electron transfer. The result showed changed of current when alkoxy substituted p-cyano stilbene Schiff bases are deposited on the substrate. This could be a promising molecules that can be applied in E-DNA sensor.

Keywords: biosensor, spacer in E-DNA sensor, electrochemical detection, aldehyde, imine

OP13

Antibacterial Screening of Mangrove Extract Library: Accelerating Drug Discovery from Indonesian Biodiversity

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Humans are at a continuous battle against different types of diseases, so that extraordinary effort to accelerate drug discovery has become a necessity. Indonesian biodiversity is abundant natural resources that can be utilized as potential drug sources. Mangroves are among potential plant medicine that grow nearly at all Indonesian coastlines. The aim of this study was to evaluate the potential of mangrove extracts (extract library) as antibacterial agents. In this study, eight mangroves species were used. There were 16 samples collected from different parts of the plants such as leaf, bark or root. Four types of solvents with different polarity were used producing 64 extracts. Disk diffusion method was used for antibacterial screening using five bacterial strains. There were 37 extracts showed antibacterial potential with the lowest and the highest recorded inhibition index were 0.0283 and 1.8983, respectively. The highest inhibition index was recorded for ethyl acetate extract of root of *Bruguiera gymnorrhiza* (77 Ea) screened against *Escherichia coli*. The second highest inhibition index was 0.7867 recorded for leaf of water extract of *Avicennia marina* (84 A) screened against *Staphylococcus aureus*. Phytochemical analysis of the extracts were also evaluated. The majority of samples showed saponin and tannin in considerable amount. This supported the data that mangrove extracts were potential as antibacterial agents.

Keywords: Antimicrobial, drug discovery, drug resistant, extract library, Indonesian biodiversity.

OP14

The Influences of Giving Extracted of Dogfruit Seed (*Pithecellobium lobatum* Benth.) Ethanol to Reduce Blood Glucose Level of Male White Rat (*Rattus novergicus*) of *Sprague Dawley* Strain Induced with Aloxane

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Diabetes mellitus (DM) is a chronic disease caused by body inability to produce or properly use insulin hormone effectively. DM is marked with polyuria, polydipsia, polyphagia, followed with blood glucose increase. DM patients Indonesia in 2000 were 8.4 million people, and it was fourth ranks in the world. Dogfruit is one of plants able to reduce blood sugar content, but it may cause acute renal failure because it contains djenkolid acid. To diagnosis acute renal failure, renal function examination is conducted by measuring urea and creatinine levels. This was an experimental research with *Post Test Only Control Group Design*. Samples were 25 male white rats (*Rattus novergicus*) from *Sprague dawley* strain with 200-500 grams body weight, 3-4 months, and they were divided into 5 groups. The result showed that one way ANOVA test derived p <0,05 This indicated that the administration of ethanol from extract of dogfruit seed influenced blood glucose level.

Keywords: Aloxan, Dogfruit, Glucose.

OP15

Reconstruction of the Metabolic Biosynthetic Pathway of *E. fuscoguttatus* in Response to *V. vulnificus* Using Metabolomics Approach

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Brown-marbled groupers are categorized as an “almost threatened” species due to their high market demand. The challenge in the aquaculture industry for the import/export of groupers are the increasing rate of fish mortality due to pathogenic infection. This research utilises the metabolomics approach, an emerging omics technology with advances in various analytical techniques and data analysis tools, to study the immune response of *E. fuscoguttatus* infected with *V. vulnificus*. We harvested the immune organs, specifically the gills, liver and spleen using a methanol/chloroform/water extraction method and the samples were analysed using LC-MS to establish its metabolic profiles. Omics data was analysed using Profile Analysis software and then subjected to various multivariate analyses using SIMCA P+ and Metaboanalyst. Compounds identification were carried out by using available databases; METLIN, Massbank and KEGG. Comparison between the control and survived-infected groups showed most of the metabolites that are involved in the immune response are amino acids. Glutamine, alanine, phenylalanine and tyrosine were particularly present in elevated intensities in survived-infected gills while leucine and aspartic acid were present in elevated intensities in survived-infected liver. This research manages to highlight the roles of these amino acids in the fish immunity by mapping the pathways that correspond to these metabolites. The findings of this study can be used to enhance the fish feed formula in order to strengthen the immunity of the fish which in turn will reduce the mortality of farmed groupers and improve the current rate of grouper export.

Keywords: disease, vibriosis, grouper, metabolite profiling, immune organs

OP17

Bioactive Compound Characterization and Evaluation from Endophytic Fungi of Batang Tepus (*Etlingera coccinea* (Blume) S. Sakai and Nagam)

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Endophytes are microorganisms that live within plants for at least a part of their life cycle without causing any visible manifestation of disease. The endophytic fungi from plants have several potentials such as a role to promote plants growth and give defence through various mechanism. Cultivation of endophytic fungi from inner stem of *Etlingera coccinea* for the study of bioactive compound with potentially for human use in food and pharmaceutical industries. In addition, this study also attempts to obtain all the features of bioactive material present from the extracts of endophytic fungi. Seven endophytic fungi obtain after isolation form inner stem of the *Etlingera coccinea* and the cultivation with the potato dextrose broth (PDB) for the purpose of bioactive compounds production. The production of bioactive compound from endophytic fungi of inner stem of *Etlingera coccinea* indicate that there was a compound or substance contain and resembles the antioxidant compounds. The antioxidant and antimicrobial assay, enzyme quantification and cytotoxicity assay also use to study the bioactive compound obtain from the endophytic extract. The cultivation of the endophyte from *Aspergillus sp.* to produced bioactive compound reveal the present of tannins, terpenoids, reducing sugar, flavonoids and alkaloids after undergoing compound screening. The total phenolic (TPC) and flavonoid content (TFC) was high for both of the assay. The Fourier Transform Infrared Spectroscopy (FTIR) mostly describe the substance as aliphatic carboxylic acid, alkynes disubstituted, primary aliphatic alcohol, aliphatic primary amides, and inorganic phosphates. The gas chromatography mass spectroscopy (GCMS) reveal the present of compounds such as linoleic acid, propionic acid, ethyl oleate and other. The Brine shrimp lethality assay for cytotoxicity of the extract show that there was negative finding after certain concentration. The compound isolated and characterized from endophytic fungi obtain from inner stem of *Etlingera coccinea* mostly revealed the antioxidant activity after compare with biological activities include antibacterial and antifungal which is weak for both assays. This study suggests that the compounds linoleic acid from *Aspergillus sp.* as the endophytic fungi obtains from inner stem of our sample has a potential and prospect as a source of bioactive compounds which resembles an antioxidant substance.

Keywords: Endophytic fungi, *Etlingera coccinea*, antioxidant activity, linoleic acid, bioactive compound characterization.

OP18

Aurantiochytrium sp. SW1 Biomass as n-3 Fatty Acids Source in Fish Feed

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Aquaculture is among the biggest user of fish oil. The industry heavily depends on fish oil as a source of n-3 polyunsaturated fatty acids (PUFAs) in fish feed to promote fish growth. Due to the increasing demand for fish oil, overfishing for its raw materials has driven aquaculture towards an unsustainable practice. *Aurantiochytrium* sp. SW1 (SW1) is an oleaginous marine protist that produced a high level of n-3 PUFAs. Recently, our research group managed to enhance its n-3 PUFA production further especially the docosahexaenoic acid production. Our objective is to measure the potential of SW1 biomass as the replacement for fish oil in aquaculture fish feed. We conducted a 100-day nutritional feeding experiment on red tilapia (*Oreochromis* sp.) with SW1 biomass as the alternative n-3 PUFA source (fish oil as control) in the feed to determine its effect on growth rate, survivability and feed conversion ratio. The results indicate the differences in all parameters (specific growth rate, feed conversion ratio and survival rate) between both groups (SW1 biomass and fish oil) are not significant. This finding suggests the potential of *Aurantiochytrium* sp. SW1 to replace fish oil and provides an innovative means to develop environmentally and socially sustainable aquaculture feeds.

Keywords: Oleaginous protist, tilapia, lipid, growth, aquaculture.

OP19

Effect of Pectin Biodegradation with *Aspergillus niger* on Total Flavonoid Content of Leaf, Peel, and Lower Grade Fruit of Citrus limon L.

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Extraction yield of total flavonoid from lemon waste may be increased by biodegradation of pectin. This research was conducted to examine the effect of pectin biodegradation of lemon leaf, peel, and lower grade fruit using solid-state fermentation towards the yield of pectin, crude flavonoid, and total flavonoid content. Fermentation was carried out with the help of *Aspergillus niger* at 30℃ for 3, 5, 7, and 9 days of cultivation time. Pectin was extracted from the fermentation broth using citric acid. Crude flavonoid was extracted using maceration and stirred about 500 rpm at 50℃ for 40 minutes. Total flavonoid content was analyzed using a spectrophotometer. The optimum cultivation time of *Aspergillus niger* with leaf and peel was 9 days with a pectin yield from lemon leaf was 0.43% dry weight and the pectin yield from lemon peel was 0.04% dry weight. As for the lower grade fruits, a cultivation time for 7 days showed an optimal result with a pectin yield of 0.08% dry weight. The total flavonoid content in the leaf increased up to 94.3% (1.06 mg of the quercetin equivalents per g of substrate), in the peel increased up to 42% (0.12 mg of the quercetin equivalents per g of substrate), in the lower grade fruit increased up to 48% (0.021 mg of the quercetin equivalents per g of substrate).

Keywords: *Aspergillus niger*, flavonoid, lemon, pectin, solid-state fermentation.

OP20

Optimization of Pullulan Production by *Aureobasidium pullulans* Using Response Surface Methodology

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Biopolymer generated by microorganism is usually water-soluble gum which have innovative and unique physical characteristics. Pullulan is a biodegradable and water soluble exopolysaccharide synthesized by the yeast-like fungus *Aureobasidium pullulans*. Pullulan has extensive applications in pharmaceutical, cosmetic, biomedical applications and food industries because of its advantageous chemical and physical properties. Therefore, there is need to produce pullulan in high amount to cater the demand. In this study, production medium was optimized for high pullulan production. Different production media from previous literatures were screened for efficient pullulan production. The medium selected undergo optimization process using response surface methodology to optimize the medium components for pullulan production using *Aureobasidium pullulans*. Sucrose, yeast extract and K_2HPO_4 were found to have significant effects on pullulan production and optimized. The steepest ascent experiment was adopted to determine the optimal region of the medium composition.

Keywords: *Aureobasidium pullulans*, Pullulan, Optimization, Production, Medium

OP21

Discovery of Simple Sequence Repeat Markers via Transcriptome Analysis of *Baccaurea motleyana*

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Baccaurea motleyana Müll. (Rambai) is a underutilized fruit and is native to Peninsula Malaysia, Indonesia and Thailand. In this study, a total of 54,779 unigenes identified from rambai transcriptome were used for simple sequence repeat (SSR) analysis by MISA (MIcroSAtellite). A total of 20,420 SSRs were found to be distributed within 37.27% of the total unigenes. Mononucleotide repeats represented the main type, accounting for 64.04%, followed by trinucleotide repeats (20.28%) and dinucleotide repeats (19.94%). Gene annotation to seven databases has successful ratio of 68.53% (NCBI protein sequences), 53.68% (NCBI nucleotide sequences), 27.43% (Kyoto Encyclopedia of Genes and Genome Ortholog), 56.0% (SwissProt), 52.44% (Protein family), 53,99% (Gene Ontology) and 26.44% (Kluster of Orthologous group) respectively. The rambai SSR will be applied in genetic diversity study of rambai accession in MARDI's germplasm.

Keywords: *Baccaurea motleyana* Müll, rambai accessions, next gene sequencing, est-ssr, functional annotation.

OP22

Morphological and Protein Changes on *Acanthamoeba* Cyst in Relation to Trehalase Enzyme Exposure

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The cystic form of dormant *Acanthamoeba* resist towards many drugs and antibiotic due to its ecto and endocyst layer of the cell wall comprised of trehalose. This study was conducted to characterize and analyse the morphology and protein expression pattern of *Acanthamoeba* cyst when exposed to trehalase enzyme. Dose response, microscopy and protein analyses were employed to determine the changes of the *Acanthamoeba* cyst when treated with trehalase enzyme. Results showed that the optimum trehalase enzyme activity towards *Acanthamoeba* cyst was 2.2 unit and the IC50 values for DTT was 0.37mM. Light microscopy observation revealed the size of *Acanthamoeba* cyst after treatment is larger than untreated cyst and appeared with large vacuole and the ectocyst layer become thinner. Meanwhile, formation of small blebbing can be seen on the cyst surface. Fluorescence microscopy observation indicated the interruption occurred at the cell wall integrity of *Acanthamoeba* cyst as yellow to red colour of cytoplasmic region were observed when stained by impermeable dye propidium iodide. Accumulation of organelles inside the cell also can be seen. Proteolytic activity indicated by the inhibition of protein bands ranged from 10 kDa to 250 kDa while bands of protein expressed ranged from 13 kDa to 220 kDa. Additionally, the bands produced by trehalase enzyme alone was ranged from 50 kDa to 240 kDa. This study showed that proteolytic activities in trehalase-treated *Acanthamoeba* cyst was similar with positive control (DTT). This research findings proved that trehalase enzyme had similar effect with DTT which able to degrade the cell wall structure of *Acanthamoeba* cyst and might contribute to the anti-cystic activity on *Acanthamoeba* cyst.

Keywords: Trehalose, DTT, membrane integrity, cell wall and protein

OP23

Immobilization of RGD Peptide onto the Surface of Nano-poly(3-hydroxybutyrate-*co*-4-hydroxybutyrate) Scaffold Fabricated by a Combination of Electrospinning/Aminolysis Method

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Polyhydroxyalkanoates (PHA) is a microbial biopolymer produced via bacterial fermentation under limited nitrogen and excess carbon conditions. Among various types of PHAs, P(3HB-*co*-4HB) had gained great attentions due to their biodegradability, biocompatibility and non-cytotoxicity. However, P(3HB-*co*-4HB) is hydrophobic. Therefore, in order to increase the cell-scaffold interactions and to enhance the cell proliferation, P(3HB-*co*-4HB) copolymer was fabricated into nano-fibers via electrospinning and surface modification was carried out by increasing the porosity of the scaffold and introducing macromolecules in the form of RGD peptides. RGD peptide is a tri-amino acid sequence which is highly effective in cell adhesion and cell-extracellular matrix interactions for efficient biomaterial applications. The main focus of this study is to immobilize RGD peptides on electrospun P(3HB-*co*-4HB) nanofibers scaffold in enhancing the surface properties. Aminolysis was carried out by covalently bonding the amino group onto the electrospun nanofibrous scaffold using 1,6-hexanediamine. The NH_2 active sites created were further immobilized with RGD peptides via a cross-linking reagent, glutaraldehyde. The incorporation of RGD peptides on nano-P(3HB-*co*-4HB) was determined by ninhydrin assay. The immobilization of RGD peptides onto the surface of the P(3HB-*co*-4HB) nanofibrous scaffold was characterized using Fourier transform infrared spectroscopy (FTIR) and organic elemental analyser (CHN analysis). The results proved that RGD peptides were successfully immobilized on nano-P(3HB-*co*-4HB) matrix. The AFM result obtained further proved that the porosity of the surface was enhanced by the elcetrospinning and aminolysis method.

Keywords: Biopolymer, electrospun nanofibers, RGD peptide, aminolysis, electrospinning.

OP24

Effect of LEDs Light Exposure on Biomass and Growth of *Hibiscus rosa-sinensis* Callus and Cell Suspensions Cultures

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This study assesses the effect of LEDs light exposure on biomass and growth of *Hibiscus rosa-sinensis* callus and cell suspensions cultures. Callus and suspensions were exposed to different ratios of LEDs light. The light intensity was set to maximum and photoperiods were set as either 16-h or 24-h. Cell suspension cultures were initiated from callus in optimised MS liquid medium supplemented with 4.5 mg/L of NAA + 30 g/L sucrose. Newly initiated callus from the cell suspensions were then introduced into optimized solidified agar MS medium supplemented with 8.0 mg/L of NAA + 30 g/L sucrose. The fresh and dry callus and cells suspension biomass and the growth index were determined by weighing cells technique. The growth kinetics of *Hibiscus rosa-sinensis* callus and cell suspensions followed a general growth pattern of sigmoid curve. Based on the growth curve, the optimum growth time of cell suspensions subculture were found to be 18 days and callus was subcultured every four weeks. 100% white LED light and 50% red and 50% blue LEDs light cell suspension produced largest biomass.

Keywords: Ms. Medium, cell culture, cell growth curve, fresh and dry weight, wavelength.

OP25

Characterization the Stability of Allergenic Tropomyosin from Mud Crab, *Scylla olivacea*

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Scylla olivacea is considered as one of the most important and commercially valuable aquaculture species in Malaysia. However, it was also declared as a significant allergenic crab among local atopic patients. Tropomyosin, the major allergen has been previously identified by proteomics approach. Therefore, this study was conducted to further characterize the stability of allergenic tropomyosin from *S. olivacea* after subjected to common thermal and chemical treatments. Protein extracts were prepared from the untreated and treated muscle tissues. The protein bands were then fractionated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). The allergenic tropomyosin was detected by immunoblotting using sera from crab-allergic patients. Overall, compared to the tropomyosin in the untreated crab, the intensities of tropomyosin band in the majority of treated crabs were significantly increased. However, in some treated crabs including boiled and salted, the intensities were unchanged. The SDS-PAGE results were in line with the immunoblotting results. The tropomyosin bands can still be detected in all treated crabs but with different intensities. IgE binding smears were revealed in some of the treated crabs particularly in the fried and vinegar treated crabs. As a conclusion, this study indicated that tropomyosin is stable to the thermal and chemical treatments tested. It still has the ability to induce IgE binding reactions but at varied capacities. These results will serve as a platform to improve the management of crab allergic patients worldwide.

Keywords: Allergen, SDS-PAGE, immunoblotting, thermal, chemical, stability.

OP26

The Effects of Selected Lactic Acid Bacteria Fermentation on the Bioactivity of Mature Coconut Water

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The demand for coconut water is high due to its unique taste and health benefits. The health benefits are due to the bioactivity of the coconut water, which contains many bioactive compounds. However, the water from the coconut can easily turn bad and become unpalatable, especially in the case of naturally fermented coconut water by microbes, such as lactic acid bacteria (LAB). This in turn also affects the level of bioactivity of the coconut water, which could be deteriorating. This study investigated the effects of fermentation by selected LABs over 24 hours on the bioactivity of mature coconut water. The bioactivity analyses include looking at the changes in inhibitory effects on angiotensin-converting-enzyme (ACEI), acetylcholinesterase (AChEI), elastase (anti-elastase effect), and free radicals (anti-oxidant effects). The results showed improvements in ACEI, AChEI, anti-elastase, and anti-oxidant of as much as 7%, 68%, 45%, and 11%, respectively, after optimized fermentation. The improvements suggested that fermentation by *L. acidophilus* and *L. brevis* could be beneficial despite the unpalatable taste of fermented coconut water. Further work can be done to develop a more palatable drink from the fermentation of LAB on mature coconut water.

Keywords: Coconut water, lactic acid bacteria, fermentation, bioactivity.

OP27

Preliminary Fungal Diversity Study of Limestone Caves in Sabah, Malaysia

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Despite Borneo being a biodiversity hotspot there have been no studies conducted on the mycobiota of its limestone caves. The ecological implications of cave fungi must be evaluated in order to maintain the integrity of the cave ecosystem when exposed anthropogenic changes. Four limestone caves in Sabah had been selected as ideal study sites. Gomantong and Madai caves represented anthropogenically active caves, and Balambangan and Keruak caves represented anthropogenically non-active caves. The aims of this study were to isolate and characterize the microfungi in speleothem surfaces, cavern water, dead arthropods, and bat guano between caves. A total of 21 speleothem, 13 samples, and 11 samples were obtained from all four caves. Only Gomantong caves yielded arthropod cadavers, in which arthropods from three genera were collected. The highest average CFU count for speleothem was 141.1 $CFUcm^{2-1}$ per isolate, cavern water was 248.15 $CFUml^{-1}$, guano had 2750.00 $CFUg^{-1}$, and dead arthropods had 1.11 CFU per cadaver. Morphological and molecular methods were utilized in attempt to identify all isolates to at least the genus level. A total of 85 distinct MTUs were identified from 195 pure isolates, where 75 isolates (47 species) received molecular confirmation of identification after DNA extraction, amplification, and sequencing. An average of 4.43 distinct species per specleothem site, 4.08 distinct species per water sample, 3.17 species per guano site, and 1.11 distinct species per dead arthropod were recorded. In order of decreasing frequency, the genera of fungi identified include *Penicillium*, *Aspergillus*, *Fusarium*, *Paecilomyces*, *Trichoderma*, *Pestalotiopsis*, *Blastomyces*, *Isaria*, and *Verticillium*.

Keywords: Mycology, Ecology, Speleology, Ascomycetes, Biodiversity.

OP28

Antibiotic Discovery in the Abyss

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It is essential that we discover and develop new antibiotics to tackle antibiotic resistance. Recent years have seen revived interest in culture-dependent methods for discovery - screening rare bacteria from unexplored environments for their ability to inhibit the growth of pathogens.[1] The deep sea is vast, rich in biodiversity, and one of the few 'pristine' environments on the planet.[2] The extremophilic bacteria from this niche are likely metabolic innovators that evolved differently to terrestrial species, making them attractive sources of novel natural products.[3, 4] Our aims include: (i) characterising the microbiome of deep sea sponges, which have never been investigated before; (ii) culturing deep sea bacteria and screening them for antibiotic production; (iii) genome sequencing and mining of producers to delineate the biosynthesis of novel antibiotics. This interdisciplinary project involves microbiology, bioinformatics, and analytical chemistry techniques. Initial screening identified two 'hits'. Recently I completed an 'OSMAC'[5] screen of our isolates and found six strains that produce antibiotics under specific culture conditions. The genomes of these bacteria have been sequenced with Illumina and Nanopore technologies, and several active molecules have been purified. Our hit rate (1.6%) is higher than estimated for other environments,[6] indicating that deep sea sponges are a powerful source of biodiversity. Future work will involve linking natural products to biosynthetic gene clusters, and transferring these clusters to heterologous hosts for larger scale production of antibiotics for method of action and efficacy studies.
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[5] Romano, S. Marine Drugs 2018, 16(7), 244, [6] Baltz, R. Journal of Industrial Microbiology & Biotechnology 2006, 33(7), 507-513

Keywords: Natural products, genome mining, OSMAC, bioinformatics, deep sea bacteria.

OP29

Insecticidal Effects of *Chromolaena odorata* Against Rice Brown Planthopper, *Nilaparvata lugens* (Stål.)

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Brown planthopper (BPH), *Nilaparvata lugens* (Stål), is one of the most destructive insect pests that damages rice plants by sap-sucking and acts as a vector to several rice viruses. Predominant reliance on synthetic chemicals has led to adverse effect on human, animals and environment. The aims of this study were to evaluate the insecticidal effect of leaf extract from *Chromolaena odorata,* further formulate a bio-insecticide from *C. odorata* in controlling the BPH. Dried leaf from *C. odorata* was extracted in methanol by normal soaking extraction (NSE) method. Extracted compounds were then analysed by Gas Chromatography-Mass Spectometry (GC-MS). Bioassay was performed in five series of concentrations to determine the lethal concentration (LC_{50}) that cause 50% of mortality. Bio-insecticide formulation from the plant extract was carried out using the combination of Palm Kernal Oil Effluent (PKOE) and Emersens in different ratios consist of 5% *C. odorata* methanol leaf extract. Several compounds identified by GC-MS analysis were α-Cubebene, (E)-Caryophyllene, Caryophyllene oxide, Phytol, 9,12-Octadecadienoic acid (Z,Z)-, Squalene, Stigmasterol and β-Amyrin which poses insecticidal activity. During bioassay, the LC_{50} value was recorded at 977ppm that cause 50% mortality at 72 hours after treatment. The obtained formulation (5% extract) was stable at 25°C for 90 days and 54°C for 14 days, which meet the FAO requirements for bio-insecticide formulation. In conclusions, *Chromolaena odorata* methanol leaf extract has potential to be developed as bio-insecticide due to its ability to kill the BPH at low concentration.

Keywords: weed species, plant extract, methanol, normal soaking extraction (NSE) bio-insecticide.

OP30

Waste Engine Oil Biodegradation by an Oil-Utilising Fungus, *Aspergillus sp.* in a Stirred Tank Bioreactor

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Oil pollution is an environmental problem of growing importance. One of the obstacles in this process is the bioavailability of many fractions of the oil. The hydrocarbon-degrading microorganisms produce biosurfactants of diverse molecular size and chemical nature where these surface-active materials increase the surface area of hydrophobic water-insoluble substrates and increase their bioavailability, thus enhancing the fungal growth and the rate of bioremediation. In this study, *Aspergillus sp.*, a local fungal isolate was used to degrade waste engine oil in stirred tank reactor (STR). Its oil biodegradation ability was evaluated through cell hydrophobicity, biosurfactant production and emulsification activity. The microbial adhesion to the hydrocarbon (MATH) assay was used to assess the surface cell hydrophobicity of the fungus. Biosurfactant production and emulsification activity were determined by oil spreading test (OST) and emulsification assay, respectively. The results indicate that the isolate showed remarkable removal activity of the waste engine oil. The removal efficiency of waste engine oil reached 56.4% on the 6th day of cultivation. The highest surface cell hydrophobicity (MATH) at 80.3% was observed during 3 days of cultivation. The highest biosurfactant and emulsification activity occurred during 2 days of cultivation, which were 30 mm and 48.3%, respectively. The results implied that this strain served as biosurfactant producer and exhibited an adequate level of emulsification activity on hydrocarbon substrate. Besides, this strain also can induce high cell surface hydrophobicity, which increasing the direct physical contact between cells and poor water-soluble substrates.

Keywords: Bioremediation, Fungi, Cell hydrophobicity, Biosurfactant, Emulsification activity.

OP31

Development of Immobilized System for Rhamnolipid Production by *Pseudomonas aeruginosa* USM-AR2

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Pseudomonas aeruginosa USM-AR2 is a local Gram-negative bacterium that is able to utilize immiscible substrates, including waste cooking oil to produce rhamnolipid. The current study focuses on developing an optimal immobilized system to prolong the cells viability of *Pseudomonas aeruginosa* USM-AR2 for rhamnolipid production. The study was initiated using free cells to determine the stationary phase of cell growth prior to immobilization by entrapment. Cells at the stationary phase were cultivated in different media supplemented with 2% (v/v) waste cooking oil, namely nutrient broth, minimal salt medium, minimal salt medium without nitrogen, and complex medium to select the optimal medium for rhamnolipid production. Cells were immobilized in 6% (w/v) polyvinyl alcohol with 2% (w/v) alginate hydrogels. Immobilized cells were assessed in shake flask system with different cell loading capacity and hydrogel to medium ratio. Optimal immobilized cells were cultivated in a 180 cm^3 custom-designed fluidized bed reactor, with an aeration rate at 0.6 vvm. Rhamnolipid production by free and immobilized cells were compared. Immobilized system was successfully optimized using 3% (w/w) cell loading capacity, cultivated in minimal salt medium, with 1:20 hydrogel to medium ratio in shake flask and 1:5 hydrogel to medium ratio in fluidized bed reactor. Rhamnolipid production by free cells was 0.9 g/L after 5 days of batch cultivation. In contrast, rhamnolipid production by immobilized cells ranged between 0.8 – 1.6 g/L after 80 days of cultivation for 15 cycles of repeated batch culture. These results show that immobilization of *Pseudomonas aeruginosa* USM-AR2 cells in polyvinyl alcohol-alginate hydrogels maintains cell viability and allows continuous rhamnolipid production throughout the prolonged cultivation.

Keywords: Cells entrapment, polyvinyl alcohol-alginate hydrogels, cells loading capacity, hydrogels to medium ratio, fluidized bed reactor.

OP32

Antioxidant and Antimicrobial Activity of Edible Active Food Coating Prepared with Bioplastic Based Bacterial Cellulose

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The present study was related to edible active food packaging and coating prepared with biodegradable plastic based bacterial cellulose and its influence to extend self life of fresh-cut fruit and vegetable, and determination of its antioxidant and antimicrobial activities of the bio-plastic film as food packaging and coating. The bio-plastic film prepared from bacterial cellulose derived from culture of *Acetobacter xylinum* on waste coconut water. Edible active food packaging and coating based bacterial cellulose were prepared by incorporating polyphenol extract of *Moringa oleifera* leaves and acidophilin suspension derived from *Lactobacillus acidophilus* that. Antioxidant and antimicrobial activities of the bio-plastic were carried out on fresh-cut fruits stored at 4°C. Radical scavenging activity of polyphenol extract-incorporated bio-plastic film was measured against DPPH and showed significantly higher ($p<0.05$) than that of control bio-plastic film, while acidophilin incorporated bio-plastic film showed high antimicrobial activity against *Salmonella typhimurium*, *Staphilococcus aureus*, *Escherichia coli*, *Leisteria monocytogenes*, and *Bacillus cereus.* The active phenolic groups and acidophilin on the bio-plastic film surface could explain the differences in antioxidant and antimicrobial efficacy of the edible active packaging and coating materials. This novel alternative methods were antioxidant and antimicrobial active food packaging and coating, whose main advantage is that it can provide sustained release of antioxidant and antimicrobial agents during food storage.

Keywords: bio-plastic, edible active packaging, coating, antioxidant, antimicrobial.

OP33

Thermal Treatment of High Moisture Content Biomass Using Dairy Manure

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Livestock manure could be reused as an alternative source for biomass feedstock and making value-added product. A raw manure heat-treatment is challenging due to its high moisture content. Our previous study reported the possibility to apply heat-treatment to a high moisture raw dairy manure using an industrial rotary kiln combustion type reactor. We found that at least three cycles of non-continuous heat treatment were required to complete treatments both at 250 °C and 300 °C, while four cycles were needed at 200 °C. Due to non-continuous steps, it was difficult to determine the thermal reaction occurred on high moisture content dairy manure inside the reactor. Here, we anticipated that drying and decomposition mechanism processes were strongly involved based on the characteristics and properties of solid torrefied manure. A detailed study is demonstrated in this present work, where a continuous heat treatment of high moisture content dairy manure conducted inside a laboratory oven. We found that some amount of water remained at the transition point of drying to decomposition process. A mathematical model is established to explain the mechanism. The model estimated the starting time of decomposition process through the transition boundary at the end of drying process. Based from the model, we manage to estimate the decomposition process occurred inside the industrial rotary kiln reactor. In addition, we understand that some amount of water remained at the transition of drying to decomposition process. This study will be beneficial in adaptation of torrefaction method using high moisture content dairy manure.

Keywords: Dairy manure, High moisture content, Rotary kiln reactor, Temperature effect, Torrefaction

PP01

Preliminary Study of Temporal Variation in Floral Scent Emission from *Phalaenopsis bellina* Flowers, Endemic Orchid from Sabah

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Flower scent emission is a part of volatile organic compounds and important to deter florivorous insects. Flower of *P. bellina* was internationally known for its lovely appearance and emit a strong, sweet fragrance with citrousy aroma. However, the variation of volatile organic compound in floral scent emission of this species are still not been studied. To investigate the influence of timing on the *P. bellina* floral scent emission, chemical compounds under two different timing were identified using Solid Phase Micro Extraction (SPME) technique and Gas Chromatography-Mass Spectrometry (GC-MS). The sampling time has been performed during the morning (9.00-9.30 am) and afternoon (3.00-3.30 pm). Results revealed that the numbers and chemical compounds variation significantly influenced by different timing of emission. Approximately, 75 metabolites have been identified where terpenoid compounds contribute significantly toward aroma of this plant. Overall floral scent emission of P*. bellina* had the largest chemical compounds in the morning (41) and the number decreased to 34 compounds in the afternoon. In the morning, sesquiterpenes (23.33%) and monoterpenes (29.82%) were the dominant scent compounds, whereas 44.54% (sesquiterpenes) and 43.91% (monoterpenes) detected in the afternoon. α-farnesene (19.56%), 2,6-bis(1,1 dimethylethyl)-4-(1-0)oxopropyl)phenol (15.47%) and 5-isopropyl-2,4-imidazolidinedione (9.89%) contributed proportion to the scent in the morning. Meanwhile, α-farnesene (44.08%), linalyl anthranilate (9.20%) and linalyl formate (5.60%) accounted for the highest compounds in the afternoon. The current preliminary profile of *P. bellina* could provide potential for use in flavor and perfumery industry in the future.

Keywords: SPME, GC-MS, terpenoid, monoterpene, sesquiterpene.

PP02

Effect of Different Polymer Concentrations on Porosity and Pore Size Characteristics of Microsphere Based Polymeric Microemulsion

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Microspheres have been a biotechnological interest owing to their low density and high permeability which made them highly potential in the field of separation, drug delivery system and chromatography. Microspheres from different polymers namely polystyrene, polyethylene, polyvinyl alcohol, polypropylene and polycaprolactone were synthesized in this study. Oil/water emulsification extraction/evaporation technique was employed by dissolving the polymers into their respective organic phase under continuous stirring to form microemulsion prior evaporating the organic phase.The polymerization was carried out at different polymer concentrations (35 wt% , 30 wt% , 20 wt% and 10 wt%). Particle size and homogeneity were observed using inverted microscope while surface functional group was analysed using Fourier-transform infrared spectroscopy (FTIR) analysis. Resulting particle size showed that the average particle size reduced as the polymer concentration decreased at all tested polymers. At the highest (35 wt%) and lowest (10 wt%) polyethylene concentration, the average particle diameter were determined at 24.2 µm and 15.4µm, respectively. Polycaprolactone resulted 24.20 µm average particle diameter size at 35 wt% and 13.13 µm at 10 wt%, while polystyrene obtained 29.70 µm at 35 wt% then decreased at 10 wt% with 15.46 µm. Polypropylene declined from 24.20 µm at 35 wt% to 15.17 µm at 10 wt%. However, polyvinyl alcohol point out a negative results at 35 wt% then positive results at 10 wt% with 13.56 µm. The findings of this study suggested that polymer concentration affects particle size and porosity of the microspheres which these resulted microspheres can be deployed as a template in monolith fabrication.

Keywords: microemulsion, microsphere, polystyrene, monolith template.

PP03

Isolation and Characterization of Phosphate Degrading Bacteria from the Tropical Rainforest Soil of Danum Valley, Sabah

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Symbiotic relationships between soil microbial communities and tropical plants may be responsible for phosphorus partitioning and nutrient uptake. Danum Valley tropical rainforest is known for its biodiverse ecosystem and is hypothesized to harbor novel microorganisms producing phosphatase that can thrive in the complex soil condition. This study aims to screen and characterize novel phosphate degrading bacteria from the tropical rainforest soil. The soil samples were collected from the Danum Valley Conservation experimental study site. Phosphatase degrading bacteria were then screened using the Pikovskaya Agar selective media. The screening results yielded five colonies, designated as PDB1, PDB2, PDB3, PDB4 and PDB5, displaying halo zone, with average of diameter of 10mm. Further, amplification and analysis of 16S rDNA region reveled that these colonies showed high identical to *Bacillus sp.*, *Pseudomonas oryzyhabitans*, *Paenibacillus sp*. and two strains of *Staphylococcus pasteuri*. Interestingly, *Paenibacillus sp*. is a promising biofertilizer and is currently used in the global agriculture industry. Accordingly, *Paenibacillus sp.* was then selected for further characterization using Gram staining and observed under Scanning Electron Microscope (SEM). The Gram staining revealed that *Paenibacillus sp*. is Gram negative bacteria with rod shape, which is in good agreement with SEM result. This study provides an early insight of an excellent phosphate degrading bacteria for agriculture and reforestation industry obtained from Danum Valley. Further study on the specific activity of phosphatase will be carried out in order to determine its actual ability to solubilize phosphate compound in soil.

Keywords: Paenibacillus, Sabah, Soil Microbes.

PP04

Enhanced Catalytic Stability and Reusability of β-Galactosidase Immobilized on Polymethacrylate Monolith

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Enzyme immobilization offers promising route for enhanced enzymatic stability and reusability in comparison with its free counterpart. Lower risk of product contamination besides preserving enzyme from harsh chemical and environmental conditions such as extreme pH and raised temperature are further advantages of the technology. This study evaluated the stability of immobilized enzyme on polymethacrylate monolith at different pH (3-10) and temperature (20-70°C) and its reusability up to 10 cycles. Different immobilization techniques including physical, covalent and cross-linking were also compared. The optimum pH for physical binding was pH 7 (1.484 U) while pH 8 was observed as optimum condition for both covalent binding (2.050 U) and cross-linking (0.589 U) techniques, similar to the optimal activity for free enzyme (2.292 U). The immobilized enzyme via physical and cross-linking demonstrated distinguished performance at 30 °C with activity determined at 2.065 U and 0.893 U, respectively while covalent was most favourable at 40°C (2.522 U). The covalent-bound enzyme was able to retain 40 % of its initial activity after four operation cycles. In contrast, the crosslinked-enzyme merely retained its 20 % activity but consistent up to 10 cycles. These findings show the immobilized enzyme may be pertinent for various enzyme-catalysed bioprocessing application.

Keywords: β-galactosidase, stability, reusability, monolith.

PP05

Transcriptome Sequencing Reveals Key Genes Associated to Juvenile Hormone (JH) Biosynthesis Pathway in Malaysian Stingless Bee, *Heterotrigona itama*

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Utilization of *Heterotrigona itama* in Malaysia and Indonesia for stingless bee honey production has pushed for more deep research to support sustainable propagation of colonies to feed the young industry. The aim of this study was to conduct transcriptome analysis from *H. itama* queen larva and identify a conserved regulatory pathway associated to queen development. In this work, we employed Illumina Hiseq RNA sequencing platform to sequence transcripts extracted from a developing queen larva and the data produced was subjected to bioinformatics analyses. Up to 99,370,410 clean reads were generated, 55,135 unigenes were produced and 8,526 unigenes were successfully annotated based on seven databases (Nr, Nt, KO, Swissport, Pfam, GO and KOG). Annotation of the *H. itama* genes showed the highest percentage of matches to bumblebee group (69%) and followed by honeybee group (19%). KEGG classification further divided the genes into five major metabolic pathways including cellular processes, environmental information processing, genetic information processing, metabolism and organismal systems. About one third of annotated genes were involved in metabolism and they were further clustered into 12 sub-pathways with insect hormone biosynthesis (IHB) as one of these sub-pathways. We further screened 19 transcripts belonging to the IHB pathway and two unigenes were proven to be participating in juvenile hormone biosynthesis pathway – a master regulatory pathway in queen development. From this study, the data provide a fundamental and useful sequence resource for *H. itama* genomics study especially on queen differentiation, which will better facilitate our understanding on molecular regulation in caste determination.

Keywords: Caste development, molecular biology, transcriptome, corbiculate bee, Meliponini, eusocial insect.

PP06

DNA Extraction and Amplification of a Metabarcode Gene Ribulose-Bisphosphate Carboxylase (*rbcL*) from Malaysian Stingless Bee (*Heterotrigona itama*) Propolis

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Stingless bee propolis has different biological properties and chemical compositions depending on species of plants it originates, thus it is important to relate propolis to its botanical source. Through metabarcoding, the botanical sources of propolis can be profiled based on DNA constituent present in the sample. However, optimization work to amplify a metabarcode sequence has to be conducted beforehand; hence, the aims of this study is to determine the best method to extract the DNA and PCR-amplify the metabarcode gene from propolis. In this work, we used two methods (CTAB-based extraction and commercial kits) to extract total DNA from hexane-prewashed propolis of *Heterotrigona itama*. Polymerase chain reaction (PCR) method was employed to amplify *rbcL* region from the purified DNA by using gene specific primer set. Based on the result, *rbcL* region (~620 bp) was successfully amplified in all of the extracted DNA samples. From this, we showed that DNA is retrievable and the *rbcL* region is PCR-amplifiable from *H. itama* propolis, thus giving access to deciphering botanical sources of stingless bee propolis via metabarcoding.

Keywords: Amplicon sequencing, Meliponini, polymerase chain reaction.

PP07

Characterization of the Saxitoxin Biosynthetic Starting Gene, sxtA in the Toxic Dinoflagellate *Pyrodinium bahamense* var. *compressum*

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Harmful algal bloom (HAB) has become a frequent phenomenon in coastal waters of West Sabah where one of the causative organisms is the toxic dinoflagellate, *Pyrodinium bahamense* var. *compressum*. Previous studies have well elucidated the genes responsible for the toxin production in several dinoflagellates such as *Alexandrium sp*. and cyanobacteria, however little is known for the major tropical PST-producing dinoflagellate; *Pyrodinium bahamense* var. *compressum*. In this study, we focused on the unique starting gene of saxitoxin biosynthesis sxtA, which includes two domains; SAM-dependent methyltransferase, sxtA1 and the class II aminotransferase coding gene, sxtA4. Through BLAST analyses, it was found that the gene sxtA1 and sxtA4 in *Pyrodinium bahamense* var. *compressum* share high sequence similarity and identity with sxtA domains of other STX-producing dinoflagellate. Besides that, phylogenetic analyses also revealed close relationships of both the sxtA1 and sxtA4 genes with the other genes from other STX-producing dinoflagellates. Hence, our work helps broaden the knowledge underlying toxin production in *Pyrodinium bahamense* var. *compressum* for future works.

Keywords: paralytic shellfish poisoning, SAM-dependent methyltransferase, class II aminotransferase, harmful algal blooms, toxic dinoflagellate.

PP08

Identification of Probiotic-Related Genes from *Pediococcus acidilactici* Through Genome Sequencing

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Pediococcus acidilactici is a species of lactic acid bacteria (LAB) which is used in food fermentation and bioprocessing. The aim of this research is to assemble and annotate the short-read sequences of a genome of a *Pediococcus acidilactici* strain isolated from fermented beef for identification of genes attributed to probiotic properties. Initial steps for genome assembly were quality control, trimming of the raw sequenced genome using FastQC and Trimmomatic. *De novo* genome assembly was performed with SPAdes, while genome annotation was done by using Prokka and RAST. Genome assembly produced 239 contigs with length of 1,954,278 bp. The N50 reported was 31,626 with G+C content of 42.06%. A number of probiotic related genes were identified. For example, cholylglycine hydrolase and xylulose-5-phosphate phosphoketolase are responsible for fermentation process and gastrointestinal resistance, whereas efflux pump Lde gene and teichoic acid production genes involve in antibiotic resistance and adhesion ability. These functional genes identified can attribute to the probiotic properties of the *P. acidilactici* strain. Further validation of these genes and genomic comparison between different species or strains can be done in future research in order to identify the niches of probiotic bacteria.

Keywords: *Pediococcus acidilactici*, beef meat, *de novo* assembly, genome annotation, probiotic genes.

PP09

Characterization of Biofilm-Forming Soil Bacteria Isolated from the River Basin, Kelantan

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Bacteria can exhibit into two different forms, the planktonic and biofilm forms. They are ubiquitous in the environment, particularly in soil system. In contrast to their planktonic forms, bacteria within biofilm improve the survival rate under growth-limiting conditions via the process of aggregation involves the production of Extracellular Polymeric Substances (EPS) and biofilm. The self-produced polymeric matrix provides a shield for the maintenance and propagation of bacterial cells in the soil. The matrix, in turn, provides stability to soils and reduce soil loss during flooding. We investigated the biofilm formation ability in 49 isolates from the Kelantan River Basin (KRB). DNA ribotyping was performed to ascertain the identity of environmental isolates. Subsequently, the bacterial isolates were cultured in static microtiter plates to identify biofilm formation using crystal violet assay. Our findings revealed 7 types of isolates from KRB which demonstrated the ability to form biofilm in vitro by forming a halo and biomass at the surface and air-liquid interface of microtiter plates along with the increased in optical density (OD) reading. The OD values were measured spectrophotometrically at 420nm which represented the quantity of biofilm formation. The current data may facilitate better insight into the understanding of bacterial survival and growth which influence the extent of bacterial survival under adverse environment and contribute to soil stability.

Keywords: DNA ribotyping, crystal violet assay, optical density (OD) values, soil aggregation, soil stability.

PP10

Characterization of the Natural Product in *Ficus lepicarpa* (Moraceae) using GC-MS

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Ficus lepicarpa commonly known as 'Saraca fig' or locally known as "ara kayan", "ombuwasak", "tombuasak" and "litotobow" in Malaysia has been traditionally used by the local people as a vegetable dish, as a tonic and to treat ailments such as fever and ringworm. The present investigations comprise an estimation of total phenolic and flavonoid content accompanied by an important *in vitro* antioxidant assay like DPPH-radical scavenging activity and reducing power of *F. lepicarpa* leaves extracts and characterization of the natural products in *F. lepicarpa* was done using the gas chromatographic-mass spectrometric (GC-MS) technique. GC-MS analysis of methanol extract of the leaves of *F. lepicarpa* indicated the presence of different bioactive compounds such as hexadecanoic acid methyl ester (0.11%), phytol (0.13%), squalene (2.85%), sitosterol (4.44%), 12-Oleanen-3-yl acetate, (3.alpha.) (21.09%), lupeol (4.16%) and amyrin (2.62%). The total phenolic content of *F. lepicarpa* was 58.85±0.04 mg Gallic Acid Equivalence/g and total flavonoid 44.31±0.10 mg Catechin Equivalence/g) contents. *F. lepicarpa* possessed strong antioxidant capacity though it was lower than that of standard Ascorbic acid. Results showed that *F. lepicarpa* possesses strong antioxidant activity and also contains some important bioactive compounds that justify its medicinal properties as used in ethnomedicine.

Keywords: natural product, ethnomedicine, antioxidant, total phenolic, total flavonoid.

PP11

Effect of Hot Water Treatment on Seed Germination and Protein Profiles of Sabah Tr-8 Rice (*Oryza sativa*) Variety

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Hot water treatment is commonly used for seeds disinfection and to stimulate seed germination. Our study aims to investigate the effect of hot water treatment with different water temperature and length of immersion period on the germination and seed proteins profiles of Sabah TR-8 rice. Seeds were immersed into hot water treatment at 26 (control), 45, 50, 55 and 60°C for 10, 30 and 60 minutes. Treated seeds were germinated at 28°C and arranged according to Randomized Complete Block Design with 3 replications. Germination percentage were measured on 14 days after sowing and the results were subjected to ANOVA and post hoc analysis. All treatments and their interaction showed a significant effect on the germination percentage. Seeds treated under control, 45 and 50°C resulted in nearly 100% germination regardless of length of immersion period. Similar results were found in seeds treated at 55 and 60°C for up to 30 minutes and 10 minutes, respectively. However, germination percentage decreased to 70% and 26% when seeds were exposed to 55°C for 60 minutes and 60°C for 10 minutes, respectively. Seeds treated at 60°C for 60 minutes showed only 3% germination. Thus, the lethal temperature-50 (LT_{50}) of hot water treatment range from 55 to 57°C for 30 minutes and 58 to 60°C for 60 minutes. The LT_{50} will be reference for screening heat tolerant rice in our next studies. Additionally, soluble seed proteins were extracted from treated seeds and separated on 12.5% SDS-PAGE. Several protein bands were found varied.

Keywords: Paddy, heat stress, seed emergence, SDS-PAGE, North Borneo.

PP12

Effect of Various Extraction Protocols on Spidroin Structure and Protein Composition of Malaysian *Nephila pilipes* Dragline Silk

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The dragline silks from giant orb-weaving spiders are exceptionally tough which now became a model organism for studies of its protein structures and physical properties for future's new biomaterial development. Among the all-known giant spiders, *Nephila pilipes* has shown higher extensibility. Their web can last up to two years due to its unique mechanical properties. Thus, the current study focuses on examining the effect of three protein extraction protocols on *Nephila pilipes* dragline silk spidroin structure and its protein composition. Our results support previous studies that the lithium bromide (LiBr) solvent was the most effective dissolving agent among all. The two major proteins of dragline silk were successfully detected on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) visualization while microscopic analysis on Scanning Electron Microscope (SEM) reveals the immediate deformation of the spidroins. It was due to the high concentration and acidic content of this solvent that gave the greatest and immediate impact on denaturing the highly stable, hydrophobic, and insoluble dragline spider silk fibroin protein and thus the best extraction solvent for isolation protocol of total protein from the spider silk spidroin.

Keywords: spider silk protein, golden orb web spiders, insoluble proteins, major ampullate silk, denaturing agent.

PP13

Identification and Characterisation of MicroRNAs and Its Regulation During Fruit Ripening in Pineapple

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MicroRNAs (miRNAs) are a class of small, usually with 19 to 24 nt in length. It is found endogenously within the cell and does not code for any protein. However, it participates in regulating the level of mRNA transcript through cleavage or translational inhibition, creating an effect called gene silencing. MicroRNAs have been proven to be essentials for major biological and physiological developments in plants. It is postulated that miRNA may also play an important role in the mechanism of ripening in the non-climacteric fruit, pineapple. Here we report a complete list of pineapple miRNA obtained from high-throughput small RNA sequencing. In this study, high-throughput sequencing (Illumina platform) was used for the construction of sRNA libraries from pineapple fruit and leaves. Bioinformatics pipeline developed through the manipulation of comparative genomics strategy revealed that 579,179 reads were homologous to 153 miRNAs (from miRBase), comprising of 41 miRNA families. Subsequent bioinformatics analyses based on a sequence homology search, found 19 potential miRNA targets. The results indicate that most pineapple miRNAs are involved in pineapple growth and development, stress response, cell differentiation, and other biological and physiological processes. In order to decipher the gene regulation associated with pineapple development mediated by miRNA, the gene quantification approach, stem-loop RT-qPCR was utilized. A total of 34 miRNAs displayed significant differential expression between different stages of fruit ripening. The discovery of these miRNAs demonstrates the crucial role it plays in gene regulation during pineapple ripening. This research is supported by The Ministry of Higher Education of Malaysia through a Fundamental Research Grant Scheme (FRG0488-2018).

Keywords: MicroRNA, Pineapple, small RNA Sequencing, Fruit Ripening, Non-climacteric.

PP14

Development of a Headspace Solid Phase Microextraction-Gas Chromatography-Mass Spectrometry Protocol for the Detection of Volatile Organic Compounds Released from *Ganoderma boninense* and Oil Palm Wood

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Basal stem rot disease caused by white rot fungus *Ganoderma boninense* is a major threat to the oil palm industry and thus detection of infections at early stage in development is desirable. In this study, a headspace solid phase microextraction (HS-SPME) method coupled with gas-chromatography mass-spectrometry (GC-MS) was developed and optimised to analyse the volatile organic compounds (VOCs) released from *G. boninense* cultures and infected oil palm wood. Several factors affecting the HS-SPME extraction efficacy were investigated; 0.25 g of sample crushed powdered in liquid nitrogen was shown to be the most useful preparation procedure, while fiber divinylbenzene/carboxen/polydimethylsiloxane (DVB/Car/PDMS) was shown as the optimum extraction phase. The optimised method was capable of sampling VOCs with high reproducibility from three type of sample groups: *G. boninense* mycelium, oil palm wood, and oil palm wood colonised by *G. boninense*. This preliminary study led to tentative identification of several VOCs, including alcohols, alkanes, volatile acids, ketones, aldehydes, esters, sesquiterpenes, and polycyclic aromatic hydrocarbon groups. Aliphatic compounds with eight carbon atoms, such as 1-octen-3-ol, 3-octanone, 1-octanol, and (E)-2-octenal were the most abundant constituents of the *Ganoderma* sample, whereas furfural and hexanal were the major compounds detected in oil palm wood.

Keywords: *Elaeis guineensis*, *Ganoderma boninense*, GC-MS, HS-SPME, Volatile organic compounds.

PP15

Cloning, Expression and Purification of a Conserved Hypothetical Proteins Related to Stress Response in Psychrophilic Bacteria, *Pedobacter cryoconitis*

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Pedobacter cryoconitis is an extremophilic bacteria that produce many biologically important proteins, especially those related to stress response. One of these proteins is Ga_HP2, a 38 kDa conserved hypothetical proteins containing zinc-binding dehydrogenase domain. Structural zinc-binding site in dehydrogenase was previously described to be crucial for the protein stability of mammalian alcohol dehydrogenase. However, there are still very limited information about their structure and function, especially in extremophiles. This is largely due to the difficulty to achieved high quality proteins that is required for crystallization work and other structural biology studies. The present study aims to clone and purify Ga_HP2 proteins in preparation for structural biology studies. The in vitro analysis of Ga_HP2 will be conducted, in which the proteins will be cloned, expressed in *Escherichia coli*, and purified through his-tag and gel filtration. *P. cryocinitis* were freshly grown from glycerol stock and the genomic DNA extraction was conducted using Qiagen DNeasy DNA extraction kit. PCR amplification was performed using the primers, Ga_HP2F 5'−ggt−gat−gat−gat−gac−aag−atg−aaa−gca−atc−3' and Ga_HP2R 5'−gga−gat−ggg−aag−tca−tta−aat−tct−gat−tac−ag−3'. Recombinant DNA was constructed using Thermo Scientific aLICator pLATE51 ligation independent cloning and expression system. Protein expression of recombinant Ga_HP2 shows overexpressed soluble expression at 16°C. His-tag purification and subsequent gel filtration successfully purify the soluble proteins to more than 90% purity. The purified Ga_HP2 proteins will provide a high-quality specimen for crystal screening and X-ray crystallography to elucidate the protein structure and function.

Keywords: Extremophilic bacteria, Zinc-binding dehydrogenease domain, Ligation Independent Cloning (LIC), his-tag purification, gel filtration.

PP16

Characterisation of Structure and Function Relationship of Heat Shock Protein 20-like Chaperones in the Psychrophilic Yeast, *Glaciozyma antartica*

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Studies have shown that molecular chaperones acquire the abilities to prevent proteins from thermal degradation and refold denatured proteins to their functional stage in low temperature. Extensive studies on small heat shock proteins (sHSP) ranging from mammals, yeasts, plants and bacteria have elucidated their vital role in promoting thermotolerance and preventing protein aggregation in cells. The sHSPs help to maintain protein homeostasis by interacting with partly unfolded, aggregate-prone proteins to prevent cell damage. However, discovery on psychrophilic organisms are still in the infancy level. The exclusive ability of psychrophilic sHSP to function efficiently at low temperature offers a great opportunity for scientists to study the relationship between the protein function and structure in terms of stability, flexibility, dynamic conformation. Hence, this study aims to determine the function of HSP20 chaperones from *Glaciozyma antartica* and investigate the relationship between the molecular structures of HSP20 and the thermal adaption. In this study, all 4 target HSP20 genes from *G. antartica* were successfully amplified from total RNA. Currently, 2 genes were verified by sequencing and cloned into pET32 Ek/LIC plasmid. The expressions of the recombinant proteins were conducted under heterologous *E. coli* expression system. Protein expression was done in 37°C where the 2 target genes managed to be expressed in soluble proteins and purified using nickel affinity chromatography. Future work will focus on functional characterisation of all *G. antarctica* HSP20 target of interest and gene expression analysis related to thermal response. The findings of this study are expected to provide more insight into the thermal protection mechanism of HSP20.

Keywords: chaperones, small heat shock proteins, psychrophilic, thermotolerance, HSP20.

PP17

Cloning, Expression and Purification of HSP70 from Psychrophilic Yeast, *Glaciozyma antarctica*

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The 70 kilodalton heat shock proteins (HSP70) family are ubiquitous and highly conserved ATP-dependent molecular chaperone that is involved in protecting cells from various stresses. HSP70 chaperone protein are the central components of cellular network in protein folding mechanisms. They involve in folding of newly synthesize proteins, protection of hydrophobics regions of denatured proteins, regulation of apoptosis, the immune response, and several other cellular processes. Many have studied the correlation between structure and function of the HSP70 but the knowledge specifically in psychrophilic yeast under low energy environment still remain indefinite. The goal of this project is to produce and purify a recombinant form of Hsp70 from *Glaciozyma antarctica* (Ga_HSP70-1) for structural analysis and biochemical assays. We have successfully cloned Hsp70 into a pET32-Ek/LIC vector (Novagen) and expressed in BL21(DE3) cells. The soluble proteins were successfully obtained by manipulating the temperatures and inducer. We have successfully extracted and purified it using an immobilized metal affinity chromatography (IMAC). We are now ready to begin the structural and functional analysis. Insight into the structure of Ga_HSP70-1 should help in understanding the mechanism which allow it to function in low energy environment.

Keywords: chaperone, psychrophilic, structure, low energy.

PP18

Clinacanthus nutans as Potential Advanced Glycation End Products Inhibitors

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In prolong hyperglycaemia, the formation of advanced glycation end products (AGEs) from a non-enzymatic glycation reaction between reducing sugars and proteins are greatly accelerated. Accumulations of these AGEs in body tissues have been associated with the onset of many diabetes mellitus complications and other age related diseases. Considering the potential use of *Clinacanthus nutans* (Burm.f.) Lindau (Acanthaceae) in diabetic patient, the present study aimed to assess the phytochemical composition of the leaves extract and to investigate its ability to inhibit the formation of AGEs. Four aqueous-ethanolic extracts of *C. nutans* were tested with a fluorescence-based assay. The percentage of AGE inhibition at 5 mg/mL extract increased in the following order; water, 30% ethanol, 70% ethanol and 100% ethanol extract. The inhibitory activity of 100% ethanol extract (IC_{50}= 80.18 ± 11.6 mg/mL) was 60 folds higher than water extract. Quantifications of the three flavone glycosides markers (clinacoside, isoschaftoside and schaftoside) using HPLC-DAD were performed to examine the association of these chemical markers with the inhibitory activity. The results showed that the amount of all markers was inversely related to the inhibitory activity and for the most promising extract (100% ethanol), these markers were indeed below the limit of quantitation. As the flavone glycosides were not responsible for the inhibitory activity, deep metabolome comparison between active and inactive extract via mass spectrometry and molecular networking along with bioassay-guided fractionation is currently being accessed to identify the potential AGE inhibitors.

Keywords: Belalai gajah; antiglycation agents; phytochemicals; diabetes mellitus; flavone glycosides.

PP19

Biologically Decolorization of Commercial Dye Using Locally Isolated Microorganisms

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Complex biopolymer such as lignin and textile dyes is major pollutants that contribute to the toxicity and unsafe effluent to the environment. By utilizing certain microorganisms, decolorization can be done in cost effective, eco-friendly and fastest way. The present work represents isolation, screening and characterization of three microorganisms isolated from environmental samples and their ability to reduce few commercially available dyes is demonstrated.

Keywords: azo dye; bacilli species; immobilization; aerobic; degradation.

PP20

Mutational Spectrum of *F9* Gene in Haemophilia B Patients in Malaysia

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Haemophilia B is an X-linked recessive inherited bleeding disorder attributed to deficiency in the blood coagulation factor IX protein. Deficiency of the clotting factor is caused by mutation of the *F9* gene. This study aimed to characterise the mutational spectrum of *F9* gene in a representative cohort of haemophilia B patients in the multi-ethnic Malaysian population. A total of 71 samples were studied, consisting of 23 patients and 48 family members. DNA of patients and family members were extracted and screened for *F9* gene mutations by polymerase chain reaction (PCR) and direct sequencing. *F9* gene mutations were successfully identified in all patients. Nineteen point mutations (13 missense, 5 nonsense, 1 silent) and 4 deletions were detected in the patients. These mutations were primarily found at exon 8 (43.5%). Two of the discovered mutations, NM_000133.3:c.230T>G and NM_000133.3:c.40delC are novel mutations, which have not been reported previously in haemophilia B database. This study also led to identification of female carriers in 22 family members. The mutations identified in our local population are heterogenous and the missense mutations are the most prevalent genetic changes. **Conclusion:** These findings will be used to develop a Malaysian mutation database which would facilitate carrier screening and confirmation of haemophilia B diagnosis in the Malaysian population.

Keywords: X-linked, Factor IX, Mutations, Sequencing, PCR.

PP21

Identification of Unique DNA Sequences from *Salmonella* Serogroup C Genome

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Salmonella bacteria can cause a wide range of diseases such as gastroenteritis, typhoid fever and septicaemia and is receiving a significant public health concern worldwide. Most of the *Salmonella* infection in humans and animals is originated from *Salmonella* serogroups A to E. The identification of *Salmonella* serogroup and serotype using immunological based method have few drawbacks such as a false-positive reaction due to weak and non-specific agglutination between antiserum used and the antigen present on *Salmonella* cell surface. To compensate this drawback, identification of *Salmonella* serogroup and serotype using molecular method can be done by targeting specific DNA sequences present in specific serogroup or serotype. The objective of this study is to detect specific DNA sequences present in *Salmonella* serogroup C genome. In this study, two genome from *Salmonella* serogroup C were extracted and sequenced using Illumina platform (150 Paired End reads). The raw sequenced reads obtained from Illumina sequencer (HiSeq 4000) were trimmed using Trimmomatic software to remove the adapter added during library preparation step. Prior to genome annotation part, the trimmed raw sequenced reads were assemble using SPAdes software. Genome annotation was then conducted using the RAST (Rapid Annotation using Subsystem Technology) server. The resulted contigs from both sequenced genomes were compared with four other genomes from different serogroups (serogroup B, C, D and E) using the CCT (CGView Comparison Tool) software. The comparative genomic analysis reveal the presence of unique DNA sequences in the sequenced genomes. PCR was conducted and the result obtained support this finding.

Keywords: Gene marker, slide agglutination test, whole genome sequencing, subtyping, bioinformatics.

PP22

Enhancement of *Saccharomyces cerevisiae* Growth and Glucose Consumption under Very High Gravity Condition via Fed-Batch Fermentation System Using Sago Hampas as a Substrate

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Very high gravity (VHG) ethanolic fermentation is a new outlook on technology for bioethanol production. However, fermentation of bioethanol in glucose excess of 250 g/L (VHG fermentation), cause the fermentation process to be sluggish and inhibit glucose utilisation. High content of glucose in fermentation medium elevated the osmotic pressure, which has a destructive effect on yeast cells. To minimise the negative effect, fed-batch system was employed to reduce the substrate inhibition and eventually enhance the growth of yeast, *Saccharomyces cerevisiae*. Batch fermentation was conducted as a comparison and both systems have the initial glucose concentration of 250 g/L by using sago hampas hydrolysate supplemented with 5 g/L yeast extract as the substrate. Fermentation process was done in 2-L jar using B-Braun fermenter. In batch fermentation, the highest glucose consumption by *S. cerevisiae* achieved was 151 g/L and the maximum yeast cell concentration recorded was 8.26 x 10^5 cells/mL. When a fed-batch system was performed, yeast are able to consume glucose up to 202 g/L and the highest yeast cell concentration obtained was 16.3 x 10^5 cells/mL. Both glucose consumption and yeast concentration are significantly higher in fed-batch system as compared to batch system.

Keywords: osmotic pressure, sluggish, substrate inhibition.

PP23

Analyses of Frond Sap from Various Growth Stages of the Sago Palm

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As a slow degradable waste, sago fronds need to be utilized and developed into high value products in order to provide benefits to sago farmers and generate new source of income for native people in a short time. This leads to the study of sap from sago frond as a main alternative raw material. In this study, the optimized condition of frond sap as fermentation substrate was studied by analyzing the total volume of sap extracted, total major free sugars, total reducing sugar and starch contents of stored frond sap from different growth stages; *angat burit* and *upong muda* (inner and outer circle frond) of the sago palm. The highest volume of frond sap was extracted from outer circle frond of *upong muda* palm, with an average of 293.33 ± 1.67 mL/kg and 1666.67 ± 11.67 mL/frond. On top of that, sago frond sap has an acidic pH, with glucose as major sugar component and contained various kinds of minerals like calcium, potassium and magnesium. Moreover, sago frond sap at all growth stages contained around 28.32 g/L to 63.48 g/L of reducing sugar composition and 0.32 g/L to 1.11 g/L of starch content. Based on the results obtained within 21 days of storage at -20°C, sap extracted from inner circle frond of *upong muda* palm is the best fermentation substrate as it contains the highest reducing sugar with low starch content. It can be concluded that all stored sago frond saps are suitable and can be used as fermentation substrate.

Keywords: *angat burit*, *upong muda*, sugar, starch, fermentation.

PP25

EST-SSR Marker Discovery and Validation for Ginger (*Zingiber officinale*)

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Malaysia has a vast diversity of herbs species that are widely used as folk medicine and health supplement. Ginger (*Zingiber officinale*) was listed in EPP1 to improve the product quality and marketing efforts to meet the global demand for high-value herbal supplements. In Malaysia, ginger is commercially cultivated in Bentong, Keningau and Tambunan. Halia Bentong especially was highly demanded for domestic and international market such as Hong Kong and Britain. To ensure the ginger cultivated is pure Halia Bentong, ginger authentication using DNA fingerprinting approach was necessary to give China market confidence. Thus, EST-SSR markers for ginger have been discovered and mined based on EST database (*Zingiber officinale*) that was deposited in National Center for Biotechnology Information (NCBI). 1,710 EST-SSR markers were mined and 50 EST-SSR markers were selected and designed using BatchPrimer3. These markers were tested on 216 samples of Halia Bentong, Halia Bara and Halia Gunung Karak. Thirty one *Kaempferia sp* samples that shared same family with ginger were also included in this experiment to act as outgroup to the ginger samples that being studied. Out of 50 EST-SSR markers, only 10 markers were polymorphic. Genetic distance for each sample was calculated using PowerMarker V3.25 software based on Nei's genetic distance. A dendogram was generated using NTSYSpc 2.21s software by UPGMA method. The dendogram generated showed the samples were clustered in four main groups. Information of this genetic relationship will help to understand the diversity of ginger collected and the markers can be used for authentication purpose.

Keywords: Herbs, DNA fingerprinting, authentication, Halia Bentong, dendrogram.

PP26

Expression, Purification and Catalytic Properties of Mini Bromelain from MD2 Pineapple

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Bromelain is the major cysteine protease enzyme that presents in the fruits and stems of pineapple (*Ananas comosus*). Whole genome sequencing of MD2 pineapple had revealed 14 genes encoding cysteine protease bromelain with the size ranging from 19 to 40kDa. While large-sized of cysteine protease bromelain was widely studied, no report, to our knowledge, for the small-sized cysteine protease bromelain. This study aims to determine catalytic properties of a small-sized of cysteine protease bromelain of MD2 pineapple (sBro-MD2). To address, the gene encoding sBro-MD2 with the size of 19 kDa was retrieved from the Genbank, codon optimized, chemically synthesized and inserted into pGS21a plasmid for further expression. Expression at various temperatures yielded the protein to be in inclusion body which was then solubilized using 8 M urea followed by purification using a single step of GST affinity chromatography. The yield of pure sBro-MD2 was about 14 mg of 1L culture. The pure sBro-MD2 was further shown to exhibit remarkable activity towards a synthetic peptide substrate with the specific activity of 0.604 U/mg and catalytic efficiency (kcat/KM) of 2.552 min-1 μM-1. This activity was considerably lower than that of large-sized bromelain which might be due to their structural differences. The study suggests that sBro-MD2 is promising to be further developed as mini cysteine proteases for various applications.

Keywords: Bromelain, heterologous expression, cysteine proteases, purification, catalytic activity, pineapple.

PP27

Electrospraying of Enzyme Suspension: Effect of Buffer Solution on Enzyme Properties in Liquid and Solid Phase

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Electrospraying is a well-established liquid atomization that able to produce monodispersed particles in the sub-micron to nano size range by means of electrostatic forces. In this study, electrospraying of cyclodextrin glucanotransferase (CGTase) enzyme suspension in different type of buffer solution was conducted to investigate the effect of buffer on the enzyme properties before and after electrospray. For this purpose, three types of sample were prepared by mixing 1% v/v CGTase in deionized water (control), phosphate buffer (0.1 M, pH 6), and acetate buffer (0.1 M, pH 6). Prior to electrospray, the samples were subjected to Dynamic Light Scattering (DLS) analysis to examine the enzyme properties (size, distribution) in the liquid phase. Morphology and structural properties of the samples collected after electrospray were analyzed by using a Field-Emission Scanning Electron Microscope (FESEM) and Fourier Transform Infrared (FTIR) spectrometer, respectively. The DLS analysis shows that the enzyme suspended in deionized water has poly-dispersed distribution while enzyme in buffer solutions show improved stability (reduced aggregation) and has smaller size. These results are consistent with the enzyme particle size analyzed by FESEM. Moreover, the FESEM analysis revealed that the enzyme suspended in different buffer exhibited different morphologies while the FTIR analysis shows that the enzyme secondary structure was not affected by the buffer type. Findings of the present study indicate that, by tuning the enzyme properties in the liquid phase, properties of the enzyme in the solid phase can also be controlled without affecting the enzyme secondary structure.

Keywords: cyclodextrin glucanotransferase, electrohydrodynamic atomization, enzyme nanoparticles.

PP28

Molecular Basis of Microbial Consortium-Induced Growth Promotion in *Carica papaya*: Revelation by Transcriptomic Analysis

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A microbial consortium which was previously isolated from different crops rhizosphere displayed an excellent anti-quorum sensing and antagonistic activity against papaya dieback pathogen, *Erwinia mallotivora*. Papaya plants colonized with the microbial consortium showed significant growth promotion as exemplified by increased in root biomass and stem diameter. To elucidate the molecular basis of growth promotion, transcriptome analysis was performed to reveal the changes in gene expression induced by the microbial consortium in the leaves of papaya plants. A total of 73 genes were found differentially expressed which represented 26 up-regulated and 37 down-regulated genes. Key up-regulated papaya genes are (i) Nodulin MtN21/ EaMA like transporter participating in nutrient transport and mobilization; (ii) Xyloglucan endotransglucosylase, GA requiring 3 and RING/ U-Box involved in cell biogenesis, cell growth and development; (iii) CXXS1 associated with cell redox homeostasis; (iv) Bifunctional inhibitor involved in defense and (v) Thioredoxin and oxidative stress 3 involved in tolerance to heavy metal and oxidative stress response. The upregulation of nutrient mobilization and uptake as well as cell biogenesis-related genes could be attributed to plant growth promotion. The bacterial colonization triggered down-regulation of genes coding for transcription factors involved in stress signalling as well as salicylic acid and jasmonic acid responsive genes. Others are genes associated with plant defense against biotic and oxidative stress. Our study presented that the plant growth promotion as observed in papaya could be attributed to the up-regulation of nutrient uptake-associated genes and down-regulation of genes coding for transcription factors of stress signalling.

Keywords: Rhizosphere, colonization, transcriptome, gene expression, leaves.

PP29

Identification of Suitable Carrier for Microbial Consortium Formulation against Papaya Dieback Disease

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Beneficial microbial communities play an important role for optimal functioning of plants through influencing their physiology and development process. They provide the plant with beneficial effects such as enhance mineral uptake, nitrogen fixation, growth promotion and protection against plant pathogens. In previous studies, an effective microbial consortium against papaya dieback disease was successfully identified. This consortium, which was originally isolated from rhizosphere soil of different crops not only increases the physiological parameters of papaya plants such as stem diameter and root biomass but also enhance tolerance of papaya plants to dieback disease in greenhouse trial. In this research, we report the identification of suitable inorganic carrier for development of complete microbial consortium formulation. Among the 3 carrier tested i.e. talcum, zeolite and vermiculite, we found that zeolite is the most appropriate one to be used since it gives the highest cell numbers after storage of 1 to 4 months at room temperature. Commercial applications of microbes either for the improvement of plant health or disease management rely on the development of formulations with appropriate carriers that support bacterial independence for a considerable period. Carriers increase the survival rate of bacteria by protecting them from dryness and death of the cells.

Keywords: Rhizosphere, formulation, inorganic, commercial, disease management.

PP30

Prevalence of Metachromatic Leukodystrophy in Malaysia

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Metachromatic leukodystrophy (MLD; OMIM 250100) is a lysosomal storage disease caused by a deficiency of the arylsulphatase A enzyme (ARSA; EC 3.1.6.8). Affected patients usually presented with muscle wasting and rigidity, convulsions and paralysis, progressive dementia or psychiatric disorder. Our purpose was to estimate the birth prevalence of MLD among races in Malaysia and to compare with the epidemiological data. In this retrospective cross-sectional study, the electronic medical records of all patients with MLD were reviewed for demographic and laboratories findings. Information of the number of live births were obtained from Department of Statistics Malaysia while carrier frequency rate was calculated using online calculator. Between 2012 and 2017, 15 out of 223 patients were diagnosed with MLD in our laboratory. 60% of patients were from Iban ethnicity (n=9) followed by Malay (n=5) and Chinese (n=1). The expected MLD birth prevalence in general population was estimated as 1 in 494,514. However, when look into ethnicity, the estimation prevalence in Ibanese was 1 in 6,981, which is much higher compared to other races. The p.(Pro428Profs*32) mutation was relatively more prevalent among Ibanese compared to non Ibanese (OR=1.3058, $p<0.05$). The carrier frequency rate in Ibanese, Malay and Chinese were 2.37%, 0.21% and 0.72% respectively. Despite the low prevalence of MLD in Malaysia, Ibanese has the highest prevalence compared to other races. Ibanese patients with symptoms should be considered to be screened for MLD for early diagnosis and treatment hence will improve the quality of patients' life.

Keywords: Lysosomal storage disease, Arylsulphatase A, Enzyme assay, Prevalence, Mutation.

PP31

Acaudina molpadioides Enhanced LDL Uptake in HepG2 Cells by Downregulation of PCSK9 Expression

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Acaudina molpadioides has been reported to demonstrate various important bioactivities such as anticoagulation, antithrombosis, anti-hyperglycemia and anticancer. However, its anti-atherosclerotic potential is yet to be explored. Proprotein convertase subtilisin/kexin type 9 (PCSK9) has emerged as the key role in cholesterol homeostasis by enhancing lysosomal degradation of hepatic low density lipoprotein (LDL) receptor resulting in excessive accumulation of LDL-cholesterol plasma level which accelerate atherosclerosis, a leading cause of cardiovascular disease and stroke. In this study, *A. molpadioides* enhanced fractions were subjected to promoter-reporter based functional assay to evaluate the PCSK9 gene expression at transcriptional level. Quantitative real-time polymerase assay and immunofluorescence staining were used to evaluate whether the enhanced fractions increase the uptake of LDL-C by repressing the hepatic mRNA expression of PCSK9. Our findings revealed that *A. molpadioides* supressed the hepatic mRNA PCSK9 expression. LDL-C uptake by LDL-R was also increased by 56.8 % compared to control. Hence, inhibition of PCSK9 by bioactive compounds in *A. molpadioides* could be another promising therapeutic option for PCSK9 and atherosclerosis treatment.

Keywords: atherosclerosis, low density lipoprotein, promoter-reporter based assay, PCSK9 mRNA expression, immunofluorescence staining.

PP32

Cerebrospinal Fluid Oligoclonal Bands: Identification and Distribution in Malaysia From Year 2013 – 2017.

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The detection of oligoclonal bands (OCB) in the cerebrospinal fluid (CSF) is important as it aids in the diagnosis of multiple sclerosis (MS). To date, the most efficient methods for detecting OCB are the techniques using isoelectric focusing (IEF) on agarose gel followed by immunoblotting or immunofixation. The objective of this study was to determine the distribution of CSF OCB cases in Malaysia from year 2013 to 2017. A total of 1087 CSF and corresponding serum samples were received from hospitals in Malaysia from 2013 to 2017. These routine diagnostics samples were subjected to protein electrophoresis by IEF and followed by immunofixation. The test was performed using Hydrasys 2 Scan analyzer according to the manufacturer's instructions. Five classic patterns of CSF and serum were identified in our patients with 7 cases of non-diagnostic profile (1%). 63% of the patients were Type 1 which reported as no bands in either sample. 18% of the patients were Type 2 with OCB in CSF but not in serum indicating local intrathecal IgG synthesis. 1% accounted for Type 3 with OCB in CSF with additional mirror pattern of IgG bands in both samples. 14% of the patients were Type 4 with mirror pattern of IgG band in both samples. 3% of the patients were Type 5 with OCB present in both samples with a "ladder" type pattern. Type 2 was the major positive cases detected in patient with CSF OCB with an increasing trend of positive cases which consistent with the sample number.

Keywords: Multiple sclerosis, electrophoresis, isoelectric focusing, immunofixation, Hydrasys 2 Scan.

PP35

Phylogenetic Study in Elucidating the Diversification Patterns of House Shrew (*Suncus murinus*) in Malaysia

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Due to high phenotypic variation and synonyms of *Suncus murinus*, a study on the systematics of *Suncus murinus* population focusing on Malaysia Borneo samples were conducted by inferring the mitochondrial DNA gene sequences. The aim of this study is to identify the phylogenetic position based on mtDNA cytochrome *b* marker of Malaysian Borneo *S. murinus* population in comparison with other populations from Peninsular Malaysia and other Southeast Asia countries. A total of 56 partial cytochrome *b* gene sequences was used in the phylogenetic interpretation which resulted in distinct grouping of Malaysian Borneo (Sarawak) population from the Peninsular Malaysia population and other Southeast Asia countries. Based on the phylogenetic inferences, Malaysian Borneo *S. murinus* is more closely related to the population from Myanmar, Perak and Sri Lanka compared to the other geographic region. It can be hypothesised that the Malaysian Borneo population can be a considered as a separate subspecies or a new subspecies. Following that, the study was intrigued to pinpoint the diversification route and dispersal events that was undergone by Malaysian Borneo *S. murinus* population. The ancestral range distribution showed that *S. murinus* ancestor in Asia originate from the Indian plate. In conclusion, the findings suggest an early dispersal of the ancestral population to Malaysian Borneo as a result of exposed land bridges and hull fouling. It was shown that the Malaysian Borneo lineages differ from the lineages that occur in the other Sunda plate countries and was directly descended from the Sri Lankan population.

Keywords: Mitochondrial, phylogenetic, house shrew, dispersal.

PP36

Inferring Genetic Relatedness of Sabah Indigenous Ethnic Groups Based on Complete Mitochondrial DNA Hypervariable Region.

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The hypervariable region of the mitochondrial DNA (mtDNA) is highly polymorphic due its rapid mutation rates which approximately 5 to 10 times faster as compared to nuclear DNA. Haplogroup assignment of mtDNA hypervariable regions serves two main goals: firstly, to investigate the genetic relatedness of ethnic group in Sabah and secondly, to postulate the genetic relationship among the Sabah indigenous ethnic groups to neighboring populations from Southeast Asia. This study analyzes the complete mtDNA hypervariable region (HVR), which is 1.15 kbp in length comprising of three hypervariable regions named as HVI, HVII and HVIII. A total of 117 unrelated individuals representing Dusun, Orang Sungai and Bajau Laut were recruited. The DNA sequences of HVR were then compared with the revised Cambridge reference to identify haplogroups. Subsequently, phylogenetic analyses will be conducted. The work is still in the progress of haplogroups identification. In brief, a total of 57 polymorphic variable sites were found in our Sabahan population samples. The outcome of this study might be useful in the field of forensic and molecular anthropology.

Keywords: mtDNA, hypervariable regions, haplogroup, Sabah indigenous ethnic group, genetic relatedness.

PP37

In Vitro and *In Vivo* Biological Control Response of *Streptomyces spp.* Associates with Fusarium Wilt Disease of Banana

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Fusarium wilt disease of banana triggered by *Fusarium oxysporum f. sp. cubense* (FOC) is one of the most destructive banana diseases worldwide and caused massive losses for the farmers due to none satisfactory solutions. Thus, this study aim to evaluate the potential of selected *Streptomyces spp.* (Streptomyces S1, S5, S7 and S12) as biological control agents towards FOC as in vitro and in vivo. Double petri dishes assay was evaluated in vitro. While for in vivo, glasshouse trial and field evaluation were conducted. For glasshouse study, banana seedlings were inoculated with FOC suspension and subsequently treated with *Streptomyces spp*. one week after pathogen inoculation. Besides, field experiment was carried out using randomized complete block design with four replications. A total of 216 banana seedlings with prior treatment of *Streptomyces spp.* formulation were planted in hotspot area. From the result, Streptomyces S12 was recorded to have the highest suppression towards FOC colony with only 0.69cm radius growth compared to control which is 2.58cm. Glasshouse trial also discovered all banana seedlings inoculated with FOC without prior Streptomyces treatment died after 7 days of treatment. Whereas banana seedlings with prior treatment of Streptomyces shown recovery and survived throughout the study. Preliminary field evaluation analysis recorded that S5 showed the highest survival rate with 96.30% compared to the control with only 62.97% survival. This formulation believed to have a great potential and promising biological control effects on controlling Fusarium wilt disease of banana in the future.

Keywords: Fusarium Wilt, Banana, Biological Control, *Streptomyces*.

PP38

Hyptolide from *Hyptis pectinata* Exhibit Remarkable Inhibition Properties Toward the Proteolytic Subunit ClpP of *Plasmodium knowlesi*

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Caseinolytic protease (Clp) is a viable target for development of antimalarial drug. This protein exists in all malaria parasite, including *Plasmodium knowlesi*. Extensive studies on bacterial Clp revealed that this protein is inhibited by a member of lactone group, β-lactone. This compound is known to specifically inhibit proteolytic subunit of Clp (ClpP) in irreversible manner. Meanwhile, studies on the inhibitory properties of the other members remain limited. Recently, hyptolide, which belongs to ∂-lactone member, was isolated from *Hyptis pectinata* and promising to be used as new inhibitor targeting ClpP. Nevertheless, in addition, to our knowledge, study of Plasmodium Clp is so far only limited to *P. falciparium*. This study aims to investigate the inhibition properties of two distinct lactone family towards ClpP of *P. knowlesi* (Pk-ClpP). To address, Pk-ClpP was overexpressed under *Escherichia coli* system and purified. To confirm if Pk-ClpP is inhibited by β-lactone, the proteolytic activity of this protein was measured in the presence of various concentration of β-lactone. The result showed that β-lactone indeed exhibited inhibition towards Pk-Clp with IC50 value of 6.2 nM. Interestingly, when hyptolide was added into the cocktail, this compound also inhibited Pk-ClpP with IC50 value of 2.4 nM. The IC50 values of these two compounds were confirmed to be remarkably lower compared to that of serine protease inhibitor phenylmethyl sulfonyl fluoride (PMSF), with IC50 value of 18.2 nM. This result confirmed that Plasmodium ClpP is inhibited by lactone group and might be promising as a new target for antimalarial drug.

Keywords: *Plasmodium knowlesi,* malaria, lactone group, Hyptolide, *Hyptis pectinata,* Caseinolytic protease.

PP39

A Peptide Labeling Strategy for at Protein Quantification in Oil Palm Root Early Stage of *Ganoderma* Inoculation

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Basal Stem Rot (BSR) disease caused by *Ganoderma boninense* has persisted as the major obstacle with a huge impact to the oil palm industry. However, there's still lack of information on the disease progression in oil palm especially in its root system. Thus, proteomics studies via peptide labelling were accomplished to classify proteins in oil palm root tissues involved through artificial inoculation with *G. boninense* as early as day 3, day 16 and day 32. Three different experimental conditions were employed to the oil palm in this study which includes artificial *G. boninense* inoculation (T1), without inoculation (T2) and absolute control (T3) in the randomized complete block design. Digested peptide was labelled via tandem mass tagging (TMT) labeling kit accordingly and fractionated prior to liquid chromatography mass spectrometry (LCMS/MS analysis via Thermo Scientific™ ORBITRAP Fusion™ Tribid™ Mass Spectrometer. The MS Spectrum was analysed further via Proteome Discoverer Version 2.1 using Oil Palm and Plant UniProt Database. Descriptive statistical analysis was performed to the protein abundance for determining the significantly changes in protein abundance (fold changes of ≥0.7 and ≤-0.8, for upregulated and down reguated, respectively) in the inoculated oil palm root against uninoculated and control samples through Perseus Software version 1.6.2.3. A total of 417, 104 and 182 proteins were regulated in oil palm roots at day 3, day 16 and day 32 post inoculation, respectively. This experiment reveals differentially expressed proteins during early stages of artificial inoculation against the control in oil palm root which involved in different biological activities, molecular functions and cellular components.

Keywords: oil palm, *Ganoderma boninense*, tandem mass tagging, ORBITRAP, artificial inoculation.

PP40

Electrochemical DNA Potential Spacer: Synthesis and Characterization of New p-nitro Stilbene Schiff bases Derivatives

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Various methods were used to find a suitable spacer to the solid surface in E-DNA such as by using the thiolated DNA. In previous studies, Schiff bases and their complexes are multipurpose compounds which are widely used for industrial and biological activities. The purpose of this study is to synthesis three new p-nitro stilbene Schiff bases derivatives in order to overcome few limitations on stability faced by the thiolated compound. 4- amino-4'-nitrostilbene was reacted by condensation with three different aldehydes in ethanol and were recrystallized by hot acetonitrile. The compounds formed were characterized on the basis of spectral analysis such as Fourier transform-infrared spectrometer (FTIR), UV Vis spectrophotometer and nuclear magnetic resonance (NMR). The absorption peak observed near 1250 cm^{-1} and 1020 cm^{-1} indicates the C-O-C stretch of N-(4-methoxy-benzylidene)-4-(4-nitrostyryl)aniline. C=N (secondary aldimine) and N=O (nitro) shows an absorption at 380-385 nm 276-277 nm and respectively. Therefore, this study may open a new opportunity in development of DNA biosensors.

Keywords: biosensor, spacer in E-DNA sensor, electrochemical detection, aldehyde, imine.

PP41

Optimization of Glassy Carbon Electrode for Sibutramine Detection using Electrochemical Sensor

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Overweight and obesity are contemplated as worldwide public health issue. Most obvious solution is by losing weight. Some people choose to take fastest way and neglecting their health by taking so-called slimming products that can easily found everywhere and promoted widely without really engage with the professional as in medical doctor. Sibutramine is the chemical that used to help in losing weight. However, this substance has been banned since 2010 due to the risk it's perceived. Unfortunately, it is still present in some slimming products to date. This research aims to develop an electrochemical method for determination of Sibutramine in slimming products. Glassy Carbon Electrode was used for the analysis of the electrochemical behaviour of Sibutramine under optimal condition. Under optimum condition, cyclic voltammetry (SV) method was able to detect 1 ppm of Sibutramine using phosphate buffer saline (PBS) buffer with pH 2, scan rate of 0.25 V/s and Methylene blue as redox indicator. Further study will be conducted involving modification of glassy carbon electrode with hybrid nanomaterials to detect lower concentration of Sibutramine, thus are very useful to find illegally added of Sibutramine in slimming products.

Keywords: weight loss, glassy carbon electrode, modification, slimming juice, slimming pills.

PP42

Comparison Study of Porcine DNA Extraction Methods in Pharmaceutical Capsules

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The production of pharmaceutical capsules in the medical industry primarily uses gelatin originating from animal tissues; largely from pig skin, bovine hides and cattle bones. Gelatin is a mixture of polypeptides obtained from partial hydrolysis of collagen. The use of porcine-based gelatin contradicts with the Islamic belief that strictly forbids Muslims from consuming pork. Firstly, this project aims to optimize an efficient DNA extraction method by modifying existing methods. Three DNA extraction methods were conducted; commercial kit, the conventional phenol-chloroform (PC), and CTAB method. The extractions were preliminary conducted on vegetable and bovine pharmaceutical capsules from Halalgen Sdn. Bhd. For commercial kit, vegetable capsules had better quality of pure DNA compared to the bovine capsules. For PC method, only the bovine capsules had good quality of pure DNA after troubleshooting. For CTAB method, the modified method resulted in both bovine and vegetable capsules having excellent pure DNA quality. Next, PC method was used on raw meats (chicken, lamb, beef, fish and porcine) for PCR control groups. The extracted DNA from raw meats were run through PCR using a known primer sequence. However, it is still on troubleshooting process as the results obtained are not satisfactory. In conclusion, the CTAB method gave the best quality of pure DNA for extraction of capsules from Halalgen Sdn. Bhd. In the future, the development of extraction methods involving multiple brands of pharmaceutical capsules will be conducted along with PCR (qualitative analysis) and qPCR (quantitative analysis).

Keywords: pig, gelatin, phenol-chloroform, CTAB, PCR.

PP43

Molecular Docking of Bioactive Compounds from *Mangifera odorata* as Cholinesterase Inhibitors in the Treatment of Alzheimer's disease

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The prevalence of Alzheimer's disease (AD), characterized by memory loss and cognitive dysfunction, has increased every year that resulted in a huge economic burden as there is no effective cure for this disease. The existing drugs such as donopezil, tacrine and galantamine used in this disease treatment have adverse side-effects and low in bioavailability. Therefore, the demand in developing natural-derived medicines becomes increasing. In the present study, we aimed to evaluate the anti-AD potential of natural compounds identified from *Mangifera odorata* fruit, or locally known as kuini, by assessing their binding interactions with two AD targets, acetylcholinesterase (AChE, PDB ID: 4EY7) and butyrylcholinesterase (BChE, PDB ID: 4BDS). Through molecular docking, among 78 compounds, decuroside III, eriodictyol and 3,4,2',4',alpha-pentahydroxychalcone exhibited the highest binding affinities with AChE where these compounds interacted with the important residues at peripheral anionic site (PAS) of AChE. For BChE, mangiferonic acid, mascaroside and mangiferolic acid exhibited the highest binding affinities with this enzyme which interacted at PAS and choline binding site. In conclusion, our findings indicated the potential of *M. odorata* compounds as cholinesterase inhibitors for use in the treatment of Alzheimer's disease.

Keywords: Kuini, acetylcholinesterase, butyrylcholinesterase, molecular docking

PP44

Characterization of Nano-Sized Calcium Carbonate ($CaCO_3$) Powder from Chicken Eggshell

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Large quantity of chicken eggshell wastes is available in hatching industry, food processing manufacturers and households. Malaysian consumed about 2.8 million chicken eggs per day. These wastes were able to produce a valuable product of $CaCO_3$ as more than 94% of chicken eggshell is $CaCO_3$ compounds. A simple, eco-friendly and low-cost method without the use of hazardous chemicals were applied to produce nano-sized calcium carbonate ($CaCO_3$ NPs) powder from chicken eggshell wastes. Nano-size $CaCO_3$ powders were characterized using Scanning Electron Microscopy (SEM) and the morphology was of the particles is calcite with rhombohedral structure. Energy Dispersive X-ray Analyzer (EDX) result showed that the $CaCO_3$ NPs had high purity with Carbon, Oxygen and Calcium. Transmission Electron Microscope (TEM) result showed the range of the particles size from 8.52 to 72.2 nm. Comparison studies between standard $CaCO_3$ and eggshell $CaCO_3$ NPs in FT-IR showed that $CaCO_3$ from eggshell was given the same peak with standard $CaCO_3$ (commercial). Nano-size of $CaCO_3$ powders have wide applications in chemical industry, food industry, biomedical, environmental, and as material filler.

Keywords: Comparison; Scanning Electron Microscopy; Energy Dispersive X-ray Analyzer; Transmission Electron Microscope; Fourier-transform Infrared Spectroscopy.

PP45

Effect Shaker Agitation Rate on Fresh Weight of In Vitro MD2 Pineapple Using Liquid Shake Culture

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The present study was conducted to investigate the effect of agitation rate on fresh weight of a pineapple Protocom-like-bodies (PLBs) and shoot. The seven grams of PLBs were cultured in 250 ml Erlenmeyer flask with MS medium and plant growth regulator (1.5 mg/L BAP and 0.2 mg/L NAA). PLBs were growing at different speed of 50, 80, 100, 120 and 150 rpm that placed on an orbital shaker and named as liquid-shake cultures. After 40 days of culture, the speed rate at 100 rpm was the highest in fresh weight at 76 grams. A comparative study of agitation found that 80 rpm was the best speed which enhances both PLBs and shoots formation. The findings in the present study would be helpful for large-scale mass propagation of in vitro MD2 pineapple using this simple and efficient protocol.

Keywords: Pineapple MD2, micropropagation, liquid-shake culture, agitation rate.

PP46

***De novo* Transcriptome Sequencing and Analysis of Differential Gene Expression Among Varieties in Black Pepper (*Piper nigrum* L.) Flower and Fruit Development**

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Black pepper (*Piper nigrum*) is a vital spice crop with use ranging from culinary to pharmacological applications. However, limited genetic information has constrained the understanding of the molecular regulation of flower and fruit development in black pepper. In this study a comparison among three different black pepper varieties, Semengok Aman (SA), Kuching (KC) and Semengok 1 (S1) with varying fruit characteristics was used to provide insight on the genetics in regulation of flower and fruit development. Next generation sequencing (NGS) technology was used to determine the flower and fruit transcriptomes by sequencing on an Illumina HiSeq 2500 platform followed by *de novo* assembly using SOAPdenovo-Trans. The high-quality assembly of 66,906 scaffolds of contigs included 64.4% of gene sequences (43,115) with similarity to one or more protein sequences from the Genbank database. Annotation with Blast2Go assigned 37,377 genes to one or more Gene Ontology terms. Of these genes, 5,874 genes were further associated with the biological pathways recorded in the KEGG database. Comparison of flower and fruit transcriptome data from the three different black pepper varieties revealed a large number of DEGs between flower and fruit of the SA variety. Gene ontology (GO) enrichment analysis further support functions of DEGs between flower and fruit in the categoies of carbohydrate metabolic processes, embryo development and DNA metabolic processes while the DEGs in fruit are the biosynthetic process, secondary metabolic process and catabolic process. The enrichment of DEGs in KEGG pathways was also investigated and large number of genes was found to belong to the nucleotide metabolism and carbohydrate metabolism categories. Gene expression profiles of selected sugar transport and carbohydrate metabolism genes were generated using probe based assays from six different fruit development stages in each of the three black pepper varieties. These results indicate several candidate genes related to the development of flower and fruit in black pepper and provide a resource for future functional analysis and potentially for future crop improvement.

Keywords: Black pepper, NGS, *de novo* transcriptome, flower, fruit, differential gene expression.

PP48

Insecticidal and Repellent Activities of Black Pepper (*Piper nigrum* L.) Extracts Against Two Species of Household Ants

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Piper nigrum L. or commonly known as the black pepper is a perennial climbing vine that belongs to the family Piperaceae. It is a valuable cash crop itself let alone the essential oils and the secondary metabolites that the plant produces. The secondary metabolism of the pepper family is one of the most versatile of the botanical families known. However, the desirability of these essential oils and secondary metabolites need to be explored to fully utilize it. Hence, in the present study, the toxicity effect and insecticidal activity of the dried fruits of *P. nigrum* L. were investigated against two species of common pest ants, namely the longhorn crazy ant (*Paratrechina longicornis*) and the Pharaoh ant (*Monomorium pharaonis*). Three extracts were obtained by solvent extraction and steam distillation. Among the solvent extracts, CPN2 (2%) exhibited the strongest toxicity against *P. longicornis* while CPN (2%) was most toxic against *M. pharaonis*. All three extracts were able to cause complete mortality of the test insects for 24 hours after exposure. In the repellency evaluation, PNEO (2%) showed the most consistent repellency effects against both ant species tested. These results indicate that *Piper nigrum* L. fruit extracts possess natural insecticidal and repellent activities against common household ants.

Keywords: Piperaceae, secondary metabolites, repelling bioactivity, hymenoptera, insect pests.

PP49

The March Towards Development of Mosquito Repellent Based on *Piper nigrum* Linnaeus

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Recently there is growing trend in consumer to choose for skin care products with green-technology which is safer for adults and kids. Since there is high demand in the market for natural products, an intensive study on *Piper nigrum L*. berries and waste (leaves, stem and stalk) have been fully utilized to identify their potential as mosquito repellent. With this, phase titration technique is adopted for the development of micro-emulsion for the first step of product development. The pepper-based DEET-free mosquito repellent is basically made up from oil, water, surfactant and co-surfactant to create a clear or translucent emulsion. Other essential oils are paired up to boost the synergistic effect of the protection time. Furthermore, laboratory testing of mosquito repellent efficiency is conducted in accordance to Malaysian Standard (MS 1497:2007). As a result, no skin irritation such as allergy, eczema, hives or redness is observed between four hours post-application of the formulations. These formulations are proven safe, non-irritant and non-toxic to adults and kids and also effective with re-application within two hours post-application for maximum result. The result is comparable to one of the commercially available mosquito repellent, in which it claimed to give protection up to eight hours. With the success of this project, more demand on pepper cultivation for pepper is foreseen to cater the needs of downstream industry.

Keywords: natural product, DEET-free, product formulation, downstream industry.

PP50

Improved Production of Gaba and L-Dopa By Optimization of Fermentation Process Parameters Through Response Surface Methodology

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Coconut (*Cocos nucifera* L.) is as a 'versatile tree' due to its multifunctional attributes that have generated a wide range of uses from food to cosmetics, and high value household to industrial products.
Gamma-aminobutyric acid (GABA) and levodopa (L-DOPA) are compounds that can potentially treat hypertension and Parkinson's diseases. The purpose of this study is to optimize the fermentative parameters for GABA and L-DOPA production by *Lactobacillus acidophilus* co-culture with *Lactobacillus brevis* (*LALB*) in mature coconut water (MCW). In this study, we used response surface methodology (RSM) which is central composite design (CCD), where the 3 factors represent the sucrose concentration, culture temperature and incubation time. Best conditions for GABA and L-DOPA production differed. The optimal conditions for producing 369 mg/L GABA in MCW by *LALB* were 1 g sucrose at 37.5°C and 24 h incubation time under static condition while optimal conditions for L-DOPA, 5 g sucrose at 30°C and 36 h incubation time. After RSM optimization, the levels of GABA and L-DOPA significantly increased by 7.6 and 89.4%, respectively, compared to the negative control (non-fermented). In summary, the use of lactic acid bacteria fermentation can enhance the levels of bioactive compounds and improve the functional properties beneficial for health, which could promote the development of products based on MCW. It can be a potential functional drink for treatment of hypertension and Parkinson's disease. This work was most useful to add value to the by-product of coconut milk industry by producing a fermented or cultured drink.

Keywords: Coconut water, lactic acid bacteria, fermented drink, hypertension, Parkinson's disease.

PP51

Analysis of MatK (Maturase K) Sequence Reveal Narrow Genetic Divergence of Malaysian cultivated Taro

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Taro, scientifically known as *Colocasia esculenta* is a widely distributed root crop which can be found from temperate to tropical region of the world. However, the understanding in their genetic divergence still limited. Hence, a study to resolve genetic divergence of Malaysian Taro have been conducted using partial MatK (maturase K) sequences. Analysis of 48 intraspecific Malaysian Taro collection reveal low genetic divergence. Analysis of 877 bp MatK sequences showed only 30 nucleotide sites are variable while the remaining 847 nucleotide sites are conserved. BLAST analysis has been performed to confirm sequence reliability. Blast result showed 100% identity to MatK gene for maturase K with the E-value of 0.0. The sequence analysis also reveals the presence of two haplotypes with the pairwise genetic distance for both haplotype is 0.04 which suggested narrow genetic divergence between both haplotypes. A maximum likelihood dendogram also showed the presence of two clusters followed as the haplotype group. This study provides an insight towards understanding the genetic divergence of Malaysian Taro for DNA barcoding application for conservation management and molecular identification purposes.

Keywords: *Colocasia esculenta*, DNA barcoding, phylogenetic.

PP52

cDNAs Isolation and Identification of New Terpene Synthase from *Phalaenopsis bellina*, Fragrance Orchid of Sabah

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Phalaenopsis bellina (Rchb.f) Christenson is endemic to Borneo. It has been reported as one of the most iconic Phalaenopsis species, due to its attractive fragrance. *P. bellina* flowers contained essential oils, particularly rich with volatile terpenoid compounds, which are critical cues for insect pollinator attraction. However, the biosynthesis of fragrance production and mechanism that regulate fragrance emission have not been well studied. This research was carried to isolate and characterize the partial sequence of the terpene synthase (TPS-1) gene from *P. bellina*. The total RNA isolation was performed using three different commercial kits, (Vivantis, Novelgene, and Analytik Jena) and manual extraction (modified phenol-chloroform method). The RNA was transformed to cDNAs by Reverse Transcription method. The middle region of the terpene synthase 1 (TPS-1) gene was amplified by PCR method using degenerative primers special designed for TPS-1. Amplified DNA fragments were obtained at 1070 bp encoding for 252 amino acid respectively. BLASTX result showed that the sequence of TPS-1 shared the highest identity with partial sequence of terpene synthase- x from *Phalaenopsis bellina* (99.34% identity, E-value=0). Meanwhile, the analysis results of "Interproscan" for domain identification showed that this TPS-1 sequence has a single specific motif (DXXD) for TPS catalyzing cyclization reactions. The phylogenetic tree was designed for comparison with terpene synthase genes from other plant. *P. bellina* TPS-1 sequence was determined to be very close and grouped in a same clade with a partial sequence of TPS-x from *P. bellina* and *P. equestris*. The isolation and characterization of new terpene synthases provides opportunities for detailed functional evaluations of terpene metabolites in *P. bellina*.

Keywords: Partial sequence, Terpenoid, Essential oil, Blastx, Volatiles.

PP53

Microsatellite Makers Reveal Low Levels of Heterozygosity in the Tri-Spine Asian Horseshoe Crab (*Tachypleus tridentatus*) from Tuaran, Sabah

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The biodiversity rich waters of Borneo have for many centuries been able to sustain the tri-spine Asian Horseshoe crab (*Tachypleus tridentatus*). However, latest reports from around the world have indicated a decrease in the number of global populations. The severity of this impact to the loss of genetic diversity in Sabah is yet to be determined. Thus, for the purposes of managing these animals sustainably, studies on the genetic architecture and population structure of the Horseshoe crabs are important. Here, we report some findings of our ongoing work. Samples were collected from Tuaran, Sabah and we used 10 microsatellite markers to determine the level of polymorphism present in the species. All PCR amplicons were resolved using the QIAXcel DNA High Resolution system. The results indicate the presence of between 1-3 alleles per loci. Only one locus (*TTLR151*) was monomorphic across all samples. The Chi-square test and G-square Likehood Ratio test revealed that the population deviates significantly from Hardy-Weinberg equilibrium. In addition, the mean Observed Heterozygosity (0.397) was 17% lower than the mean Expected Heterozygosity (0.480). Both values were considered exceptionally low for a population collected from the wild. We also found that the F_{IS} inbreeding value was high (43%) indicating a population that is moderately inbred and deficient in heterozygosity. The low level of heterozygosity is of concern to us as it is indicative of a loss of genetic diversity. Further sampling will be done to compare the findings with samples from other locations throughout Sabah. This research provides molecular information that will be used in conservation strategies of the Horseshoe Crab population in Sabah. This project was funded by the Fundamental Research Grant Scheme (FRG0483-2018) by the Ministry of Education, Malaysia.

Keywords: Horseshoe crab, *Tachypleus tridentatus*, microsatellite markers, genetic diversity.

PP54

A Multiplex PCR Method for Rapid Identification of Commercially Important Seaweeds *Kappaphycus alvarezii*, *Kappaphycus striatus* and *Eucheuma denticulatum*

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In Malaysia, the red algae, *Kappaphycus alvarezii*, *Kappaphycus striatus* and *Eucheuma denticulatum*, are commercially cultivated for the production of carrageenan. These seaweeds are difficult to identify due to their morphologically plastic nature and absence of diagnostic morphological characters. Genetic approach has been proven to be more reliable and useful as compared to identification made solely on the basis of their physical morphologies. However, molecular characterization of each isolate is time-consuming and a painstaking task as multiple runs of PCR amplification and need to be carried out and the identity of the isolates is only known after sequencing of the PCR amplicons. In this study, we present a simple, one-step molecular method to identify the three eucheumatoid species, *K. alvarezii*, *K. striatus* and *E. denticulatum*. Based on the nuclear ribosomal internal transcribed spacer (ITS) sequence, all the available genetic polymorphisms were reviewed, and three primers were designed. With the combination of these primers in the same PCR, a specific amplicon of distinct size ranging from approximately 140-400 bp is produced for each of the three red algal species. The proposed method is found to be an effective and practical tool to aid in the selection of the desired seaweed seedlings even before they are cultivated and also identification of commercial cultivars correctly.

Keywords: Rhodophyta, nuclear ribosomal DNA, internal transcribed spacer, molecular characterization, red algae.

PP55

Hyptolide Inhibits Proliferation and Induce Apoptosis of Human Breast Cancer Cell Lines (MCF-7)

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The α,β-unsaturated d-lactone (hyptolide) isolated from the leaves of Hyptis pectinata Poit (Lamiaceae) was studied for the development of a potential anticancer drug. This study aimed to investigate the cytotoxicity, antiproliferation and apoptosis induction of hyptolide isolated from *Hyptis pectinata* Poit on human breast cancer cells (MCF-7). 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay was performed to analyze cytotoxic potential of hyptolide whereas Acridine Orange/Ethidium Bromide (AO/EB) staining was used to detect apoptosis. Hyptolide was obtained as crystal at 87-88 °C melting point. Presence of hyptolide was confirmed using LC-MS analysis with a single peak at 9.201 retention time and m/z value of 386. Hyptolide have growth inhibitory activity of MCF-7 cells with IC50 of 31.2 µg / mL. Apoptosis assayed using etidium bromide-acridin orange staining, showed increases in apoptosis. The results conclude that hyptolide possess antiproliferative effects through growth inhibition and apoptosis induction.

PP56

Antioxidant Activity and Total Phenolic in Aqueous Extracts of Selected Mangrove Plant in Sabah

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In recent years, research on medicinal plants has attracted much attention due to their wide range of pharmacological significance. A mangrove is a unique group of vascular plants that able to survive in extreme conditions of the coastal area and may have been assisted by a type of defence metabolites. Six species of mangrove (*Avicennia marina, Bruguiera gymnorrhiza, Ceriops tagal, Rhizohora apiculata, Rhizophora mucronata* and *Xylocarpus granatum*) from different parts were extracted successively with aqueous by maceration process. The aims of this study are to measure quantitatively the total phenolic content and assess the radical scavenging activity of the selected mangrove extracts. All the extracts were subjected to Follin-Ciocalteu method for its phenolic content and DPPH radical scavenging assay for antioxidant activity. The highest total phenolic content was observed in *Ceriops tagal* leaves extract (236.24 mgGAE/g), followed by *Bruguiera gymnorrhiza* stem extract (199.55 mgGAE/g) then *Rhizophora mucronata* root extract (89.15 mgGAE/g). However, the EC_{50} value of all extract cannot be determine because of the inhibition percentage is below 50%. As a conclusion, *Ceriops tagal* leaves extract has high phenolic content with promising bioactive compounds in producing new drugs against anti-bacterial, anti-fungal and anti-diabetic.

Keywords: DPPH radical scavenging assay; Follin-Ciocalteu method, *Avicennia marina; Bruguiera gymnorrhiza; Ceriops tagal; Rhizohora apiculata; Rhizophora mucronata*; *Xylocarpus granatum.*

PP57

Total Phenolic Content and Antioxidant Activity of Ethanolic Extracts of Selected Mangroves from Sulaman Lake Mangrove Forest, Tuaran

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Free radical induced-oxidative stress has led to various damages in the body, causing degenerative diseases such as cardiovascular diseases (CVD) and diabetes. Mangrove plants are potential natural source of micronutrients in neutralizing free radical because their ability to grow in extreme environmental conditions such as high salinity and anaerobic soil. This study aims to evaluate the total phenolic content (TPC) and antioxidant activity (AA) of ethanolic extract from different part (leaves, root and stem) of selected mangrove plants; *Rhizophora mucronata*, *Xylocarpus granatum*, *Avicennia Marina*, *Ceriops tagal*, *Rhizophora apiculata* and *Bruguiera gymnorhiza.* TPC was determined by Folin-Ciocalteu's method while AA was evaluated using 1,1-diphenyl-2-picrylhydrazyl (DPPH) assays. Appreciable quantities of TPC, ranging from 64.57 to 528.58 mg GAE/g while the highest value was found in leaves of *Ceriops tagal* (528.58 mg/g), followed by stem (297.86 mg/g) and leaf (280.99) of *Rhizophora mucronata*. Interestingly, a profound similar trend was found between TPC and AA of respective extracts. The highest antioxidant activity was obtained in leaves of *Ceriops tagal* with EC50 value of 11.39 µg/ml, followed by leaves of *Rhizophora mucronata* (21.45 µg/ml). As a conclusion, study shows that mangrove species are promising antioxidants that would pave the way for further studies on new medicinal uses.

Keywords: Folin-Ciocalteu's method; gallic acid; 1,1-diphenyl-2-picrylhydrazyl (DPPH) assays; mangrove extracts; EC50 value.

PP58

Bioprospection of Natural Antioxidant from Microalgae *Chlorella*, *Chaetoceros* and *Dunaliella*

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The need for sustainable natural antioxidants is increasing in the industrial sector. Photosynthetic microalgae such as *Chlorella*, *Chaetoceros* and *Dunaliella* are antioxidant-producing microalgae and natural carotenoids used to counteract free radicals during photosynthesis. Research objectives were to analyze the bioprospection of microalgae *Chlorella pyrenoidosa*, *Chlorella vulgaris*, *Chaetoceros mulleri* and *D. salina* as source of natural antioxidant. Proximate analysis *C. pyrenoidosa*, *C. vulgaris*, *Chaetoceros mulleri* and *D. salina* were determined. Antioxidant activity these species prepared was performed through DPPH assay. *Chlorella vulgaris* demonstrated a highest antioxidant potential with 272,9 %, followed by *Chaetoceros mulleri* with 72,39 ppm of inhibition, *Chlorella pyrenoidosa* with 70,4,2 % of inhibition, *D. salina* with 35,2 % of inhibition, and *T. chuii* with 52.58 % of inhibition. The results suggested bioprospection of antioxidant in these microalgae which could be potentially applicated further for medicine, feed supplements, and cosmetics industries.

Keywords: DPPH, carotenoid, inhibition, proximate, natural product.

PP59

Screening of Lignin-Degrading Fungi from West Coast Sabah (Malaysia) for Ligninolytic Potential

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Lignin is a complex aromatic polymer that intertwining between cellulose and hemicellulose fibers in plant. Its recalcitrant nature makes it difficult to be degraded thus limited its potential to be utilize as a value-added product. In this work, soil and rotted bark samples collected around West Coast Sabah (Malaysia) were screened for their lignin degrading activity using remazol brilliant blue R (RBBR) assay. The preliminary results showed that these samples have a slight decolourization of RBBR dye thus microbial isolation was done from these samples. Hence, 110 fungi isolates have been successfully isolated and screened for their lignin degrading activity. The results showed that 85 fungi isolates have higher RBBR decolourization compared to *Phanarochaete crysosporium*. We suggest that lignin peroxidase/laccase enzyme ratio played an important role on the decolorization.

Keywords: Lignin, decolorization, RBBR, lignin peroxidase, laccase.

PP60

Bioformulation of *Bacillus altitudinis* P-10 as a Biocontrol Agent against Bacterial Leaf Blight (*Xanthomonas oryzae*) in rice (*Oryza sativa*)

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Bacterial Leaf Blight (BLB) caused by *Xanthomonas oryzae pv oryzae* (Xoo) is one of devastating pathogens which significantly reduces Indonesian rice production. The BLB coping strategy has been carried out with BLB resistant rice varieties and synthetic bactericides which take a long time to establish and have a negative impact on the environment. *Bacillus altitudinis* P-10 isolated from rhizosphere of rice plants had the ability to inhibit the growth of Xoo pathogens *in-vitro*. This bacteria was able to induce growth and resistance of the plant to diseases. Therefore, an appropriate and effective formulation is needed to be made as an effective biocontrol agent. The aims of this study were to determine the bioformulation of *B. altitudinis* P-10 and to analyse the effectiveness of the formulation in suppressing bacterial leaf blight *in-planta*. The method consisted of formulation technology, testing the effectiveness of biocontrol agent formulations and phytochemical tests. Kaolin dan molasses were used as carrier media for bioformulation. The statistical analysis used a completely factorial randomized design with 10 replications. The results showed that bioformulation with kaolin as a carrier media was the most effective formulation in suppressing Xoo attacks compared to molasses as a carried media. The severity of the disease with kaolin media was significantly lower that control and molasses treatment. The kaolin biofomulation was more stable in maintaining the culture of *B. altitudinis* P-10, which was 8.7 x 10^8 at week 8, whereas in molasses medium was 1.1 x 10^7. *B. altitudinis* P-10 in molasses medium was able to produce secondary metabolites of flavonoids, quinone and tannin. The conclusion was *B. altitudinis* P-10 bioformulation with kaolin as a carrier media was better than molasses in preventing the plant from BLB caused by Xoo.

Keywords: *Bacillus altitudinis* P-10, PGPR, Bacterial Leaf Blight, kaolin, bioformulation.

PP61

Ethanol Production from Honey Pineapple (*Ananas comusus*) Waste with Different Temperature Treatment

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Bioethanol is one of energy alternative that can be produced by fermentation using agricultural waste. Honey pineapple (*Ananas comusus*) is a famous agriculture product of Pemalang Regency, Central Java – Indonesia. As an agricultural country, Indonesia produces many agricultural waste. This research aimed to analyze the potential use of honey pineapple waste to produce bioethanol. The rind of honey pineapple was chopped and mixed with aquadest with ratio of 1;2, and then boiled with 70°C and 100°C for 10 minutes. The liquid extract was then used as a fermentation media adden with 0.05% urea. The inoculum used was fermipan. Incubation was done for 10 days in static condition and bioethanol level was measured with pignometer. Result showed that boiling with 70°C produced the highest level of bioethanol with 27.32%, whereas boiling with 100°C was 7.9%. In conclusion, boiling temperature affected the bioethanol production.

Keywords: honey pineapple waste, fermentation, bioethanol.

PP62

Extraction of Cellulose from Oil Palm Empty Fruit Bunch (OPEFB)

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Oil palm empty fruit bunch fiber (OPEFB) is a waste from palm oil mill. It is rich in residual of useful compound such as cellulose and so on. The increasing interest of OPEFB as a source of cellulose is due to its low cost, renewable and abundantly available especially in Southeast Asia region. The objective of the present study was to analyze the effect of bleaching treatment: concentration and period using sodium chlorite ($NaClO_2$) on extraction of cellulose and recovery. Batch process of bleaching was carried out in ratio of 1:50 of fibers to $NaClO_2$ solution within 0.7% to 2%. This followed by analysis of cellulose morphological under SEM and FTIR analysis. The study found that bleaching duration affect cellulose recovery and the highest yield is 54% found to be within 3hr to 6hr of bleaching duration. The concentration of $NaClO_2$ (0.7%, 0.8%, 1.2%, 1.6% and 2.0%) with constant 2 hours of bleaching affected the cellulose yield whereas 0.7% to 0.8% resulted in higher yield of cellulose. FTIR analysis showed no peaks of 1241.27 cm^{-1} (which represent the C = stretching in lignin) in extracted cellulose. Under the SEM analysis, the extracted cellulose has smooth morphological structure compared to raw and untreated OPEFB. The findings of the study suggested that $NaClO_2$ effective as bleacher for the extraction of cellulose and removal of lignin from the OPEFB. In addition, the pretreatment of OPEFB improved cellulose recovery.

Keywords: EFB, cellulose, delignification, bleaching, extraction.

PP63

Transcriptome analysis of *Kappaphycus alvarezii* (Rhodophyta, Solieriaceae) cultured under different light wavelengths and carbon dioxide enrichment

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Transcriptomes associated with the process of photosynthesis and carbon fixation have offered insights into the mechanism of gene regulation in terrestrial plants, yet limited information is available for macroalgae. Intertidal red alga, *Kappaphycus alvarezii*, are exposed to different light conditions (i.e. light spectra and irradiance levels) and carbon dioxide (CO_2) levels during their life cycle as these factors which are rate limiting to photosynthesis change in accordance with the seasons and tidal amplitude. This study aims to examine the underlying mechanisms associated with photosynthesis and carbon fixation under specific light wavelengths: blue light (BL), green light (GL), red light (RL) and white light (WL), and carbon dioxide (CO_2) enrichment. We analysed the effects of light regulation on the aspects of photosynthetic protein complexes and observed that different light wavelengths regulate a similar set of metabolic pathways. Analysis of carbon fixation pathway revealed that the key enzyme-encoding genes involving in C_3 and C_4 pathways were actively transcribed in *K. alvarezii* and suggested the likelihood of a shift in the pathway related to carbon metabolism after acclimation to increased level of CO_2. This information adds to our understanding of molecular mechanisms underlying light-induced responses and inorganic carbon fixation in red algae.

Keywords: gene expression; light regulation; macroalgae; photosynthesis; transcriptome sequencing.

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