Specific MicroRNAs Among Milk Siblings: An Epigenetics Approach Towards Understanding the Basis of Milk Kinship

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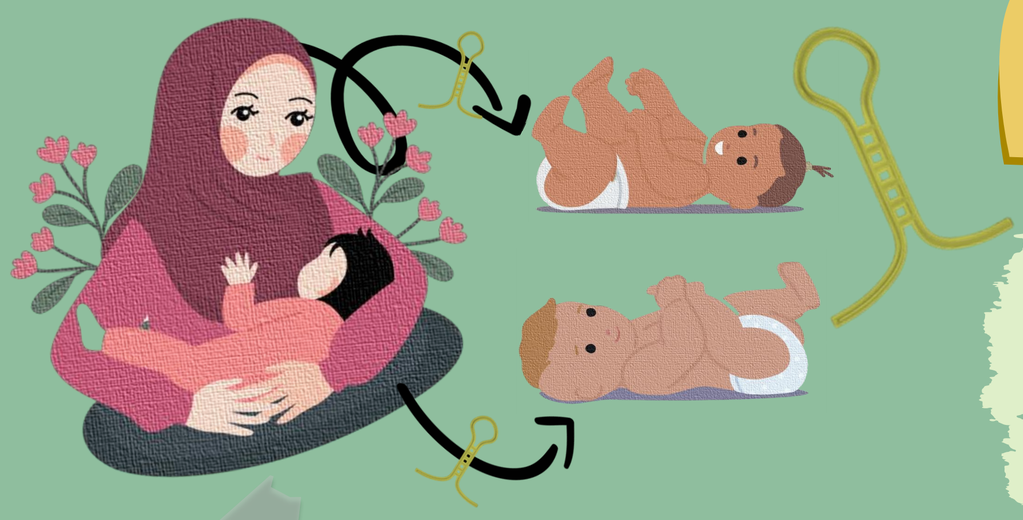
ABSTRACT

Introduction: Milk kinship is an Islamic belief described as a relationship established when infants receive breast milk from non-biological mothers. This form of kinship is said to bear a very close resemblance to blood relation whereby the recipients' infants are regarded as milk siblings to the biological children of the breastfeeding mother. Any future marriage between these individuals is forbidden likewise between the recipient infant and the nursing mother herself as they are thought to have a form of consanguinity. The consanguinity formed by virtue of milk sharing might be due to the composition of human breast milk, especially milk microRNAs that are responsible for epigenetic modulation of gene expression. miRNAs can regulate gene expression by modulating genome-wide epigenetic status of genes, and similarly-shared genes might be the basis that has led to milk kinship formation. Thus, the objective of the present study is to identify potential lactation-specific miRNAs that are similarly shared among milk siblings and their nursing mothers. **Methods:** The study began with molecular extraction of milk RNA from the nursing mothers and cell-free plasma RNA from all milk siblings and their nursing mothers. The RNAs extracted from both sample types were further analyzed using NanoString nCounter® miRNA Panel Analysis (NanoString Technologies, Seattle, WA) to measure the abundance of individual miRNAs biomarkers present within the samples. **Expected Outcomes:** This study is expected to provide scientific explanation that could divulge the secrets behind milk kinship establishment with thorough presentation on the lactation-specific miRNAs shared between milk siblings. Hence, the way for future research would be paved, making the development of milk kinship identification tool possible.

Milk kinship ,culturally defined as relation that formed after feeding of an infant from woman who was not their birthing or biological mother.

- It creates radhaa'ah kinship which is similar relationship established by blood relation.
- Both milk infant and the biological child to the breastfeeding mother are considered milk siblings (*Mahram*) and are thought to have a form of consanguinity.
- Genetic materials (microRNAs) in human breast milk could be the major factor for milk kinship establishment due to their function in epigenetic regulation and gene expression modulation (Abdelkarim & Ahmed, 2018).
- There is a chance that these miRNAs could be similarly transferred to infants via breastfeeding (Melnik & Schmitz, 2017) and possibly alter the genetic composition of both infants and leave similar epigenetic mark and epigenotype (Indrio et al, 2017; Lonnerdal, 2019; Linner & Almgren, 2020).



- **MicroRNAs** are highly conserved short non-coding RNA molecules (18-25 nucleotides).
- It regulates the functions of other genes, instead of being translated.
- In other words, they are genes that modulate other protein-coding genes.
- Modulating gene expression and involve in epigenetic regulation.

OBJECTIVES

1. To determine the miRNAs that are similarly shared among milk siblings.
2. To identify the miRNAs that are similarly detected in mother's milk and milk sibling's blood.
3. To evaluate the miRNA expression patterns in milk siblings due to breast milk intake by the same milk mother during the first two years and above of milk sibling's life.
4. To identify whether same lactation-specific miRNAs can be found in milk siblings older than 2 years of age.

METHODOLOGY

Samples Collection

1. Whole Blood (Infants & Mothers)
2. Human Breast Milk

Plasma Preparation

Total RNA Extraction

1. Plasma
2. Human Breast Milk

RNA Quantification

Quality check before analysis

NanoString nCounter miRNA Analysis

Data Analysis

FINDINGS

Milk Siblings of 6 Months

Group 1

Milk Infant 1 (Plasma) — miRNAs detected= 26
Biological Offspring 1 (Plasma) — miRNAs detected = 25
→ **17 similar miRNAs** identified
Breastfeeding Mother 1 (Milk) — miRNAs detected= 58
→ **10 similar miRNAs** identified

Group 2

Milk Infant 2 (Plasma) — miRNAs detected= 26
Biological Offspring 2 (Plasma) — miRNAs detected = 23
→ **18 similar miRNAs** identified
Breastfeeding Mother 2 (Milk) — miRNAs detected= 58
→ **10 similar miRNAs** identified

Milk Siblings of 4 Years Old

Group 3

Milk Infant 3 (Plasma) — miRNAs detected= 68
Biological Offspring 3 (Plasma) — miRNAs detected= 31
→ **23 similar miRNAs** identified
Breastfeeding Mother 3 (Milk) — miRNAs detected= 84
→ **16 similar miRNAs** identified

Milk Siblings of 8 Years Old

Group 4

Milk Infant 4 (Plasma) — miRNAs detected = 30
Biological Offspring 4 (Plasma) — miRNAs detected= 27
→ **14 similar miRNAs** identified
Breastfeeding Mother 4 (Milk) — miRNAs detected= 41
→ **9 similar miRNAs** identified

1. hsa-let-7b-5p
2. hsa-miR-223-3p
3. hsa-miR-873-3p
4. hsa-miR-23a-3p
5. hsa-miR-378e

These miRNAs were found in all milk siblings across all age categories from 6 months, 4 years old to 8 years old

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6th International Conference on Molecular Biology and Biotechnology 2023 (ICMBB2023)

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Message from MSMBB President (Prof. Dr. Lau Yee Ling)

On behalf of the Malaysian Society for Molecular Biology & Biotechnology (MSMBB), I am pleased to welcome you to the 6th International Conference on Molecular Biology and Biotechnology, held in conjunction with the 29th Scientific Meeting of the MSMBB. Our focus is on transdisciplinary research, an area that has gained considerable interest in recent years, involving academia, society, and funding agencies. This conference provides a platform for experts and students from various fields to discuss and share ideas, using viable approaches to tackle current challenges in areas including agriculture, aquaculture, medicine, forensics, the environment, industry, food, and nutrition.

Here are some important figures for this year's program. We received 101 submissions from nine countries. A highly skilled and dedicated scientific committee conducted a thorough review process and selected the papers to be included in the program. The program includes 53 oral presentations, 30 e-poster presentations competing for the "Best Poster" Award, and an additional 18 e-poster presentations in the non-competitive category.

I would like to express my gratitude to the Organizing Committee for their hard work, dedication, and commitment over the past year. We are honored to have two distinguished keynote speakers, Professor Emeritus Dr. John Beardall (Monash University, Australia) and Professor Dr. Abhi Veerakumarasivam (Sunway University, Malaysia), along with other plenary and invited speakers sharing their insights with us. We also extend our thanks to our sponsors, Collaborative Drug Discovery, Analisa Resources (M) Sdn Bhd, Unggul Medik Sdn Bhd, Next Gene Scientific Sdn Bhd and Aspire Biosains PLT, for their support.

Lastly, I would like to thank the authors who contributed their best research to the 6th ICMBB and the attendees for making this conference possible. We hope that you will find this year's program both exciting and rewarding, and that it will provide a fruitful opportunity for discussions with colleagues from around the world. Enjoy the conference!

Message from ICMBB2023 Chairperson (Asst. Prof. Dr. Michelle Soo Oi Yoon)

The Malaysian Society of Molecular Biology and Biotechnology (MSMBB) is proud to announce the 6th International Conference on Molecular Biology and Biotechnology 2023 (6th ICMBB2023) in conjunction with the 29th Scientific Meeting of MSMBB.

On behalf of the Organizing Committee, I would like to extend a warm welcome to our participants from local and international universities, speakers and sponsors. My deepest appreciation to our distinguished speakers for kindly accepting our invitation; we are indeed honoured to have exceptional international and local experts gracing our conference.

The theme for this year's online conference, 'Transdisciplinary Research: Where Nobody Gets Left Behind' was specially conceived to reflect the dynamism of research, that is moving very steadily towards addressing societal changes. To accommodate a new era where different disciplines are relevant for high-impact research, transdisciplinarity is of importance to support a long-term balance. It is pertinent that science is geared towards solving problems to ensure the development of effective interventions to meet the needs of the industry, most importantly by involving stakeholders. Science via research should be focused on giving back to the society through applications that improve daily life. Hence, this conference brings together knowledge and expertise from various fields of science namely Agriculture, Environmental Studies, Medicine, Food, Aquaculture, Forensic Sciences and Nutrition.

I hope that ICMBB2023 will provide an arena for participants to connect with like-minded researchers for the main purpose of discovering and exchanging knowledge, generating new ideas and establishing collaborations to initiate our theme.

This conference has materialised as the product of amazing commitment by the Organizing Committee to whom I am extremely fortunate to work with. A special mention to our sponsors from Collaborative Drug Discovery (CDD), Analisa Resources, Next Gene Scientific, Aspire Biosains and Unggul Medik - thank you for your support.

I wish all participants a fulfilling and enriching experience at this conference. My hope is that this conference will serve as a driving force for future conference themes and inspire continued progress in the field of molecular biology and biotechnology.

Conference Programme

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<tr><td>0830 – 0855</td><td colspan="2">Participants log in to Zoom (Hall 1)</td></tr>
<tr><td colspan="3">ICMBB 2023 Opening Ceremony, Keynote Session & Technical Talk</td></tr>
<tr><td>0855 – 0900</td><td colspan="2">Welcome by Master of Ceremony & House Rules
Asst. Prof. Dr. Chew Yik Ling (UCSI University, Malaysia)</td></tr>
<tr><td></td><td colspan="2">Opening Remarks
Asst. Prof. Dr. Michelle Soo Oi Yoon (UCSI University, Malaysia)
Chair of the 6th ICMBB 2023</td></tr>
<tr><td>0900 – 0930</td><td colspan="2">Keynote 1:
Chair: Assoc. Prof. Dr. Siti Sarah Othman (Universiti Putra Malaysia, Malaysia)

Transdisciplinary Research and Paradigm Shifts: Some Reflections Based on a Career in Biology
Prof. Emer. Dr. John Beardall
Monash University, Australia</td></tr>
<tr><td>0930 – 0950</td><td colspan="2">Technical Talk:
Chair: Assoc. Prof. Dr. Siti Sarah Othman (Universiti Putra Malaysia, Malaysia)

CDD Vault: A Research Informatics Platform for Enabling Biotech Collaborations
Dr. Eric Gifford
Business Development Scientist, Collaborative Drug Discovery (CDD), USA</td></tr>
<tr><td rowspan="3">0950 – 1000</td><td colspan="2">Lucky Draw I
Photo Session</td></tr>
<tr><td colspan="2">Participants dispersing to Hall 1 and Hall 2</td></tr>
<tr><td>HALL 1</td><td>HALL 2</td></tr>
<tr><td>CONCURRENT SESSION 1</td><td>Agricultural / Aquaculture Biotechnology & Molecular Biology I
Chair: Dr. Tan Boon Chin
(Universiti Malaya, Malaysia)</td><td>Medical / Forensic Biotechnology & Molecular Biology I
Chair: Assoc. Prof. Dr. Lionel In Lian Aun
(UCSI University, Malaysia)</td></tr>
<tr><td>1000 – 1035</td><td>Plenary 1:
Accelerating Adoption of Molecular Technologies for Plant Health and Crop Biosecurity through a Transdisciplinary Approach
Hon. Prof. Dr. Rofina Yasmin Othman
Universiti Malaya, Malaysia</td><td>Plenary 2:
Precision Medicine - Critical Clinical Gaps
Prof. Dr. Wong Tin Wui
Universiti Teknologi MARA, Malaysia</td></tr>
</table>

Note: Zoom links for HALL 1 and HALL 2 are embedded in the table. Kindly click on the session to join the Conference.

1035 – 1100	**Invited 1:** **Forest Genetic Resources Management using DNA Technology** *Dr. Lee Soon Leong* *Forest Research Institute Malaysia, Malaysia*	**Invited 2:** **The Emergence of Rotaviruses of Zoonotic Origin in Sarawak, Malaysia** *Assoc. Prof. Dr. Tan Cheng Siang* *Universiti Malaysia Sarawak, Malaysia*
1100 – 1125	**Invited 3:** **Oil Palm Leaf Transcriptomes Reveal Their Possible Link to Embryogenesis Potential** *Dr. Ooi Siew Eng* *Malaysian Palm Oil Board, Malaysia*	**Invited 4:** **Small Non-Coding RNAs in Neuron Development and Communication: A View from the Axon Side** *Asst. Prof. Dr. Federico Dajas-Bailador* *University of Nottingham, United Kingdom*
1125 – 1130	**Short Break**	**Short Break**
CONCURRENT SESSION 2	**Oral Presentations** *Chair: Asst. Prof. Dr. Baskaran Gunasekaran* *(UCSI University, Malaysia)*	**Oral Presentations** *Chair: Assoc. Prof. Dr. Pung Yuh Fen (University of Nottingham Malaysia, Malaysia)*
1130 – 1140	**O1: Understanding the Oil Palm Pathogen, *Ganoderma boninense* from Multi-Omics Studies** *Dr. Izwan Bharudin* *Universiti Kebangsaan Malaysia, Malaysia*	**O8: Cancer Cell-Derived PDGFB Stimulates mTORC1 Activation in Renal Carcinoma** *Ts. Dr. Saiful Effendi Syafruddin* *Universiti Kebangsaan Malaysia, Malaysia*
1140 – 1150	**O2: DNA Fingerprinting of Commercial MATAG Coconut Production and Genetic Purity Testing** *Ms. Siti Dalila Muaz* *Sime Darby Plantation Technology Centre Sdn Bhd, Malaysia*	**O9: Chemical Profiling of Paddy Husk and its Inhibitory Activity against Human Salivary Gland Cancer** *Dr. Entesar Ahmed Al-Azazi* *Universiti Sains Malaysia, Malaysia*
1150 – 1200	**O3: Bacterial Diversity of Rhizosphere Soils of *Pteris vittata* Growing in Arsenic-Rich and Natural Mineral Soils** *Mr. Aminu Salisu Mu'azu* *Universiti Sains Malaysia, Malaysia*	**O10: Potassium Channel Kv1.3 Restricts Dengue Virus Replication in HEK293 Cells** *Dr. Suzana Misbah* *Universiti Malaysia Terengganu, Malaysia*
1200 – 1210	**O4: Are Flowers Attractive to the Insect Parasitoid, *Pediobius imbreus* of the Oil Palm Bagworm, *Metisa plana*?** *Ms. Ong Chin Yin* *Universiti Tunku Abdul Rahman, Malaysia*	**O11: Amelioration of Streptozotocin-Nicotinamide-Induced Diabetes and Oxidative Stress in Rats by *Centella asiatica* Aqueous Extract** *Mr. Faris Fathullah Suhaili* *Management and Science University, Malaysia*

1210 – 1220	**O5: Degradome Sequencing Reveals miRNA159-Directed Cleavage Site in *GAMYB-like* Gene During Pineapple (*Ananas comosus*) Fruit Development** *Ms. Nur Shadrina Mohd Shahrel* *Universiti Malaysia Sabah, Malaysia*	**O12: The Analysis of Interleukin-1 Alpha (IL-1α) and High Mobility Group Box 1 (HMGB1) Expression in Tumor Tissues of Colorectal Cancer Patients** *Ms. Suha Azizan* *Universiti Malaya, Malaysia*
1220 – 1230	**O6: The Effect of Soil Physicochemical Properties Towards the Community of Soil Invertebrates at Different Plantation Agriculture in Kota Belud, Sabah** *Ms. Elfiorena Farrel Timpas* *Universiti Malaysia Sabah, Malaysia*	**O13: MEF2C Transactivates the Expression of Growth-Promoting KLF6 in Renal Carcinoma** *Ms. Nurul Nadia Mohamad Zamberi* *Universiti Kebangsaan Malaysia, Malaysia*
1230 – 1240	**O7: Effect of Feeding Probiotics, Phytobiotic, and Prophytobiotic on Egg Quality, Total Lipid Content, and Fatty Acid Composition of Egg Yolks of Laying Hens** *Mr. Muhammad Naim Rosli* *Management and Science University, Malaysia*	**O14: Expression of Virus-Like Particles (VLPs) by Mammalian Cells as an Alternative for SARS-CoV-2 Virus** *Mr. Amir Muhaimin Akmal Shukri* *Universiti Teknologi MARA, Malaysia*
1240 – 1255	Q&A Panel	Q&A Panel
1255 – 1400	**Lunch Break**	
CONCURRENT SESSION 3	**Medical / Forensic Biotechnology & Molecular Biology I**	**Medical / Forensic Biotechnology & Molecular Biology I**
	Oral Presentations *Chair: Assoc. Prof. Dr. Choi Sy Bing (UCSI University, Malaysia)*	**Oral Presentations** *Chair: Assoc. Prof. Ts. Dr. Khor Goot Heah (Universiti Teknologi MARA, Malaysia)*
1400 – 1410	**O15: Micronutrient Deficiency and Its Association with ADHD and Academic Performance of Primary Public-School Students in Kabul City, Afghanistan** *Mr. Ziauddin Azimi* *Universiti Teknologi MARA, Malaysia*	**O22: Population Genetic Structure and Breeding Pattern of Bed Bug Infestation in Iraq** *Mr. Hussein Ali Baqir* *University of Kerbala, Iraq*
1410 – 1420	**O16: Evaluation of Fibrinogen-Depleted Human Platelet Lysate in Mesenchymal Stromal Cells Expansion** *Ms. Kee Li Ting* *Universiti Kebangsaan Malaysia, Malaysia*	**O23: Separation of Cordycepin and Adenosine in Aqua Extract of Cultured *Cordyceps militaris (CM)* using HPLC** *Ms. Nurul Huda Syed Ibrahim* *Universiti Sains Malaysia, Malaysia*

Note: Zoom links for HALL 1 and HALL 2 are embedded in the table. Kindly click on the session to join the Conference.

1420 – 1430	**O17: Cloning of Plasmid for Compatible Gene Expression in Cyanobacteria** *Ms. Pavitra Nandagopal* *Universiti Teknologi Malaysia, Malaysia*	**O24: The Effects of Trans Fat Diet Intake on Biochemical Parameters and Global DNA Methylation in Offspring of In-utero BPA Exposed Rats** *Ms. Hala FS Abulehia* *Universiti Teknologi MARA, Malaysia*
1430 – 1440	**O18: Cyanobacteria as a Source of Anticancer Compounds: Evaluation of Toxicity, Antioxidant Activity, Total Phenolic and Flavonoid Contents** *Ms. Reem Abdulsalam Dawood Al-Nedawe* *Universiti Putra Malaysia, Malaysia*	**O25: *In Vitro* Anti-Herpes Virus Activity of Thymoquinone** *Ms. Rasha Saleh Ali Ba Surra* *Management and Science University, Malaysia*
1440 – 1450	**O19: Identification of SARS-CoV-2 Omicron Variant by Oxford Nanopore Sequencing in a Tertiary Institution, Malaysia** *Ms. Norazimah Tajudin* *Universiti Teknologi MARA, Malaysia*	**O26: A Duplex Reverse Transcription Loop-Mediated Isothermal Amplification Based Lateral Flow Dipstick (RT-LAMP-LFD) as a Simple Rapid Molecular Diagnostic Tool to Detect SARS-CoV-2 Nucleocapsid and Envelope Gene** *Mr. Derich Shalbie Simon* *Universiti Malaysia Sabah, Malaysia*
1450 – 1500	**O20: Cloning, Expression and Purification of Recombinant Multicopper Oxidase Laccase from *Pseudomonas putida* B4** *Ms. Suzana Adenan* *Universiti Pendidikan Sultan Idris, Malaysia*	**O27: Development of Multiplex Real-Time PCR for Simultaneous Detection of 10 Viruses Causing Encephalitis** *Ms. Sharifah Aliah Diyanah Syed Hussin* *Universiti Teknologi MARA, Malaysia*
1500 – 1510	**O21: Combination Treatment of Chitosan Loaded Thymoquinone Nanoparticles and Hyperthermia Reduced the Size and Cell Viability of Osteosarcoma Spheroids** *Ms. Halimatun Saadiah Abdul Wahab* *Universiti Teknologi MARA, Malaysia*	**O28: Optimization on Maceration Extraction, Isolation, and Characterization of Polymethoxyflavones from *Kaempferia parviflora*** *Mr. Mohammad Aidiel Md Razali* *Management and Science University, Malaysia*
1510 – 1525	Q&A Panel	Q&A Panel
1525 – 1530	**Short Break** **Participants to join Breakout Rooms for e-Poster Presentation**	

Note: Zoom links for HALL 1 and HALL 2 are embedded in the table. Kindly click on the session to join the Conference.

POSTER Q & A CONCURRENT SESSIONS	**Breakout Room A (Professional)** *Chair: Assoc. Prof. Dr. Siti Hamimah Sheikh Abdul Kadir (Universiti Teknologi MARA, Malaysia)*	**Breakout Room B (Professional)** *Chair: Asst. Prof. Dr. Baskaran Gunasekaran (UCSI University, Malaysia)*	**Breakout Room C (Student)** *Chair: Assoc. Prof. Dr. Dharmani Devi Murugan (Universiti Malaya, Malaysia)*	**Breakout Room D (Student)** *Chair: Dr. Teo Wee Fei Aaron (Universiti Malaya, Malaysia)*	**Breakout Room E (Student)** *Chair: Asst. Prof. Dr. Lam Ming Quan (Universiti Tunku Abdul Rahman, Malaysia)*
1530 – 1630	**PC01:** Dr. Sew Yun Shin	**PC06:** Dr. Hamizah Shahirah Hamezah	**SC01:** Mr. Jerrald Quek Jia Weai	**SC07:** Ms. Hadeel Mohamed Khalaf	**SC13:** Ms. Low Zhi Xuan
	PC02: Dr. Emelda Rosseleena Rohani	**PC07:** Ms. Hasliza Hassan	**SC02:** Ms. Nur Shamiyrah Ramzy Rameshan	**SC08:** Ms. Fong Gui Ying	**SC14:** Mr. Wong Zhenpei
	PC03: Asst. Prof. Dr. Arshad Jawed	**PC08:** Dr. Murni Nazira Sarian	**SC03:** Ms. Chong Sook Kee	**SC09:** Mr. Wan Alif Afiq Wan Nor Ruddin	**SC15:** Ms. Syarifah Faezah Syed Mohamad
	PC04: Ms. Khoo Evie	**PC09:** Dr. Siti Hajar Adam	**SC04:** Ms. Nurul Nadia Mohamad Alias	**SC10:** Mr. Ibraheam Ahmad Mohammad Tarawneh	**SC16:** Mr. Ghazanfer Ali
	PC05: Assoc. Prof. Dr. Rohazila Mohamad Hanafiah	**PC10:** Dr. Muhammad Dawood Shah	**SC05:** Mr. Muhammad Amirul Husni Samsulrizal	**SC11:** Ms. Christina Chong Shook Cheng	**SC17:** Ms. Farashakira Najiah Aszrin@Asrin
	PC12: Assoc. Prof. Dr. Zalinah Ahmad	**PC11:** Dr. Nur Adibah Mohidem	**SC06:** Ms. Rozana Shahirah Ramle	**SC12:** Ms. Thenmoli Govindasamy	**SC18:** Ms. Thai Quynh Mai
1630	**End of Day 1**				

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DAY 2: 8 June 2023, Thursday		
0830 – 0855	Participants log in to Zoom (**Hall 1**)	
0855 – 0900	Welcome by Master of Ceremony & House Rules *Dr. Lau Yin Yin (UCSI University, Malaysia)*	
Keynote Session		
0900 – 0930	**Keynote 2:** *Chair: Prof. Dr. Lau Yee Ling (Universiti Malaya, Malaysia)* **Bridging the Trust Deficit in Science: Embracing our Social Responsibility** *Prof. Dr. Abhi Veerakumarasivam* *Sunway University, Malaysia*	
0930 – 0940	**Lucky Draw II** **Participants dispersing to Hall 1 and Hall 2**	
	Hall 1	**Hall 2**
CONCURRENT SESSION 4	**Environmental Biotechnology** *Chair: Assoc. Prof. Dr. Crystale Lim Siew Ying* *(UCSI University, Malaysia)*	**Industrial, Food & Nutritional Biotechnology** *Chair: Assoc. Prof. Dr. M.S. Kanthimathi Subramaniam* *(Chief Editor of Asia Pacific Journal of Molecular Biology & Biotechnology)*
0940 – 1015	**Plenary 3:** **Transdisciplinary Research for a More Prosperous Future: The Highlights of the 2022 Report of the *Lancet* Countdown on Health and Climate Change** *Prof. Dr. Meisam Tabatabaei* *Universiti Malaysia Terengganu, Malaysia*	**Plenary 4:** **Functional Food: Food That is "Almost-Illegal"** *Prof. Dato' Dr. Azhar Mat Easa* *Universiti Sains Malaysia, Malaysia*
1015 – 1040	**Invited 5:** **Characterization and Genetic Analyses of Heterocyclic Compounds Metabolizing Strain BS19 Isolated from Antarctic Soil** *Assoc. Prof. Dr. Azham Zulkharnain* *Shibaura Institute of Technology, Japan*	**Invited 6:** **Crafting a Jigsaw Puzzle Piece to Address Vaginal Infections via Provaginobiotics** *Assoc. Prof. Dr. Leslie Than Thian Lung* *Universiti Putra Malaysia, Malaysia*

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1040 – 1105	**Invited 7:** **Microbial Bioremediation of Waste Canola Oil by Cold Adapted Antarctic Bacterial Community** *Assoc. Prof. Dr. Siti Aqlima Ahmad* *Universiti Putra Malaysia, Malaysia*	**Invited 8:** **Interactions between Transglutaminase-Treated Plant and Dairy Protein in Protein-Rich Beverages and Gels** *Dr. Sangeeta Prakash* *The University of Queensland, Australia*
1105 – 1130	**Invited 9:** **Potential of Halophiles for Face Mask Waste Degradation in Marine Environment** *Asst. Prof. Dr. Lam Ming Quan* *Universiti Tunku Abdul Rahman, Malaysia*	**Invited 10:** **Does Spray Drying Affect the Functionality of Probiotic? A Case Study on *Pediococcus acidilactici*** *Dr. Putu Virgina Partha Devanthi* *Indonesia International Institute for Life Sciences, Indonesia*
1130 – 1135	**Short Break**	**Short Break**
CONCURRENT SESSION 5	**Oral Presentations** *Chair: Assoc. Prof. Dr. Crystale Lim Siew Ying* *(UCSI University, Malaysia)*	**Oral Presentations** *Chair: Assoc. Prof. Dr. M.S. Kanthimathi Subramaniam* *(Chief Editor of Asia Pacific Journal of Molecular Biology & Biotechnology)*
1135 – 1145	**O29: Antarctic Psychrotolerant Bacterial Response to Cold Temperature** *Prof. Dr. Clemente Michael Wong Vui Ling* *Universiti Malaysia Sabah, Malaysia*	**O35: Metabolic and Genome Engineering of Microbial Chassis for Synthetic Biology and Industrial Biotechnology Applications** *Dr. Ahmad Bazli Ramzi* *Universiti Kebangsaan Malaysia, Malaysia*
1145 – 1155	**O30: Development of Species-Specific eDNA primers for Detection of Invasive *Cichla* Species in Malaysia** *Dr. Adibah Abu Bakar* *Universiti Pendidikan Sultan Idris, Malaysia*	**O36. Effect of Pectinase and Cellulase on the Yield, Physicochemical Properties and Sensory Preferences of Jackfruit Straw Juice** *Dr. Fan Hui Yin* *Universiti Malaysia Sabah, Malaysia*
1155 – 1205	**O31: Utilization of Diesel Oil by Soil Bacteria in Shake Flask System** *Dr. Fazilah Ariffin* *Universiti Malaysia Terengganu, Malaysia*	**O37: Optimization for the Green Synthesis of Silver Nanoparticles Using *Hibiscus cannabinus L.* (Kenaf) Leaves Extract** *Ms. Jess Ong Wei Ting* *UCSI University, Malaysia*

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1205 – 1215	**O32: Biosynthesis and Optimization of Terpolymer p(3hb-co-3hv-co-4hb) using Glycerine Pitch as a Sole Carbon Source** *Mr. Musa Ibn Abbas* *Universiti Sains Malaysia, Malaysia*	**O38: Potential Use of Fruit By-Products as a Source of Prebiotic and Functional Ingredients for Locally Isolated Probiotic Lactic Acid Bacterium, *Lactobacillus pentosus* A6 *In Vitro*** *Ts. Dr. Roslina Jawan* *Universiti Malaysia Sabah, Malaysia*
1215 – 1225	**O33: Tropical Soil Bacterial Diversity** *Ms. Grace Lau Xin Hui* *Universiti Malaysia Sabah, Malaysia*	**O39: *In Vitro* and *In Silico* Investigation of Antimicrobial Activity of Silver Nanoparticles Synthesized Using *Streptomyces* sp. PBD 311B** *Ms. Hemalatha Murugaiah* *Quest International University Perak, Malaysia*
1225 – 1235	**O34: Oil-Degrading Ability of Immobilized *Bacillus cereus* and *Pseudomonas aeruginosa* on PVDF/CTA Membrane** *Mr. Fam Kae Yuan* *UCSI University, Malaysia*	**O40: Green Synthesis of Silver Nanoparticles using *Kaempferia parviflora* Rhizome Extract** *Ms. Alya Khaizura Azman* *Management and Science University, Malaysia*
1235 – 1250	Q&A Panel	Q&A Panel
1250 – 1400	**End of Day 2**	
1400 – 1700	**MSMBB AGM (Open to MSMBB Members only)**	

DAY 3: 9 June 2023, Friday	
0830 – 0840	Participants log in to Zoom (**Hall 1**)
0840 – 0845	Welcome by Master of Ceremony & House Rules *Asst. Prof. Dr. Chew Li Lee (UCSI University, Malaysia)*
0845 – 0900	**Presentation by EduSTEM Winners** *Chair: Assoc. Prof. Dr. Wang Seok Mui (Universiti Teknologi MARA, Malaysia)* **STEM FOOD Fun – Learning the Art of Science through the Science of Food: Future-casting the Science 'Classroom' through an Inquiry-based Pedagogy** *Assoc. Prof. Dr. Crystale Lim Siew Ying (UCSI University, Malaysia)* **Microbial Sterilization, Culture and Inoculation Kit for E-learning (STERILIZATX)** *Mr. Mohamad Fhaizal Mohamad Bukhori (Universiti Malaysia Sarawak, Malaysia)* **Food Science (STEM) to Combat Climate Change and World Hunger** *Asst. Prof. Dr. Tan Choon Hui (UCSI University, Malaysia)*

0900 – 0905	**Participants dispersing to Hall 1 and Hall 2**	
	Hall 1	**Hall 2**
CONCURRENT SESSION 6	**Agricultural / Aquaculture Biotechnology & Molecular Biology II** *Chair: Asst. Prof. Dr. Michelle Soo Oi Yoon* *(UCSI University, Malaysia)*	**Medical / Forensic Biotechnology & Molecular Biology II** *Chair: Assoc. Prof. Dr. Jamal Houssaini* *(Universiti Teknologi MARA, Malaysia)*
0905 – 0940	**Plenary 5:** **Feed-Based Vaccination in Aquaculture: Current Advancements, Challenges, and Opportunities** *Prof. Dr. Mohammad Noor Amal Azmai* *Universiti Putra Malaysia, Malaysia*	**Plenary 6:** **Stem Cells in Regenerative Medicine and Cancer** *Dr. Thamil Selvee Ramasamy* *Universiti Malaya, Malaysia*
0940 – 1005	**Invited 11:** **Can miRNA Regulation be used as a Diagnostic Tool in Shrimp Biohealth Monitoring?** *Prof. Dr. Subha Bhassu* *Universiti Malaya, Malaysia*	**Invited 12:** **Advances and Challenges in Forensic DNA Analysis** *Pn. Nor Aidora Saedon* *Forensic Science Analysis Centre* *Department of Chemistry, Malaysia*
1005 – 1030	**Invited 13:** **Prevalence of Antibiotic Resistance Bacteria in Aquaculture Sources in Johor, Malaysia** *Assoc. Prof. Dr. Nor Azimah Mohd Zain* *Universiti Teknologi Malaysia, Malaysia*	**Invited 14:** ***In Silico* and *In Vitro* Studies of Mauriporin-Derived Anticancer Peptides** *Dr. Tang Yin Quan* *Taylor's University, Malaysia*
1030 – 1055	**Invited 15:** **Fine Bubble Technology Application for Intensive Aquaculture** *Dr. Diana Chan* *Aquaculture Innovation Centre, Singapore*	**Short Break**
1055 – 1100	**Short Break**	

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CONCURRENT SESSION 7	**Oral Presentations** *Chair: Asst. Prof. Dr. Michelle Soo Oi Yoon* *(UCSI University, Malaysia)*	**Oral Presentations** *Chair: Assoc. Prof. Dr. Nazefah Abdul Hamid* *(Universiti Sains Islam Malaysia, Malaysia)*
1100 – 1110	**O41: The Effect of Supplementation of *Lactococcus lactis* Strain as Probiotic on the Growth and Survival of *Litopenaeus vannamei*** *Prof. Dr. Tengku Haziyamin Tengku Abdul Hamid* *International Islamic University Malaysia, Malaysia*	**O47: Characterizing *Enterobacter hormaechei* from a Clinical Sample in Sabah: Insights from Whole-Genome Sequencing and Bioinformatics Analysis** *Assoc. Prof. Dr. Mohammad Zahirul Hoque* *Universiti Malaysia Sabah, Malaysia*
1110 – 1120	**O42: Development of an Orally Administered Lactococcal-Based Vaccine against *Streptococcus agalactiae* Infections in Tilapia Fish** *Ms. Wong Kuan Yee* *UCSI University, Malaysia*	**O48: Genetic of Different Strains as Potential Factor in Methicillin Resistance Level Determination in Methicillin-Resistant *Staphylococcus* species** *Dr. Abdul Rahim Abdul Rachman* *International University of Malaya-Wales, Malaysia*
1120 – 1130	**O43: Genomic Study of Prebiotic-Hydrolysing Enzymes from Potential Probiotic *Bacillus velezensis* FS26 with *In Vitro* Validation** *Mr. Muhamad Firdaus Syahmi Sam-On* *Universiti Putra Malaysia, Malaysia*	**O49: Lipidomics Analysis of Skeletal Muscle in Aging Rats** *Dr. Tan Jen Kit* *Universiti Kebangsaan Malaysia, Malaysia*
1130 – 1140	**O44: The Effect of BAP, NAA and Kinetin Treatments on Micropropagation of *Zingiber officinale* var. Bentong (Bentong Ginger)** *Ms. Lisa Amiera Rosli* *International Islamic University Malaysia, Malaysia*	**O50: The Effects of *Kaempferia parviflora* Extract on Anthropometrical, Nutritional and Lipid Profile Parameters on Rats Fed a High-Fat Diet** *Mr. Mohamad Hisham Hashim* *Management and Science University, Malaysia*
1140 – 1150	**O45: Unlocking Hub Genes and Key Pathways Associated with Combined Stresses Using Modular Co-Expression Network Analysis in Rice (*Oryza sativa* L.)** *Ms. Izreen Izzati Razalli* *Universiti Kebangsaan Malaysia, Malaysia*	**O51: RU-615 Reduces Fibronectin Deposition in Dexamethasone-Induced Human Trabecular Meshwork Cells Through TGFβ1-SMADs Signalling Pathway** *Ms. Amy Suzana Abu Bakar* *Universiti Teknologi MARA, Malaysia*

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1150 – 1200	**O46: Optimization of Extraction and Antioxidant Activities of *Kaempferia parviflora* Rhizome** *Ms. Adibah Hayati Mohd Sanadi* *Management and Science University, Malaysia*	**O52: Investigating the Neuroprotective Effect of Estrogenic Compounds in an MPP+-Induced *In Vitro* Model of Parkinson's Disease** *Ms. Nishat Anan* *Monash University Malaysia, Malaysia*
1200 – 1210	Q&A Panel	**O53: The Effects of Environmental Enrichment Conditioning on Memory and Learning in Chronic Social Defeat Stress Mice** *Ms. Nur Adzreen Shamsul Adzmi* *Management and Science University, Malaysia*
1210 – 1225	**Short Break**	Q&A Panel
1225 – 1230	**Back to Hall 1**	
Prize Presentations & Closing Ceremony		
1230 – 1245	*Master of Ceremony:* *Asst. Prof. Dr. Chew Li Lee (UCSI University, Malaysia)* Lucky Draw III Awards Ceremony • MSMBB EduSTEM Awards 2023 • MSMBB STEM TikTok Video Challenge Awards 2023 • MSMBB Best Scientist Awards 2023 • ICMBB Best Poster Awards	
	Closing address by the President of MSMBB, Prof. Dr. Lau Yee Ling	
END OF CONFERENCE		

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E-Poster Presentation and Q&A Sessions

The e-Poster judges will be asking their questions to the participants during these Q&A sessions. If you have any questions about their research, you can get in contact with them using Zoom's private chat function during these sessions.

Day 1 (7th June 2023)

Time	e-Poster Presentation (Breakout Rooms)				
	Breakout Room A (Professional) *Chair: Prof. Dr. Siti Hamimah Sheikh Abdul Kadir (Universiti Teknologi MARA, Malaysia)*	**Breakout Room B (Professional)** *Chair: Asst. Prof. Dr. Baskaran Gunasekaran (UCSI University, Malaysia)*	**Breakout Room C (Student)** *Chair: Assoc. Prof. Dr. Dharmani Devi Murugan (Universiti Malaya, Malaysia)*	**Breakout Room D (Student)** *Chair: Dr. Teo Wee Fei Aaron (Universiti Malaya, Malaysia)*	**Breakout Room E (Student)** *Chair: Asst. Prof. Dr. Lam Ming Quan (Universiti Tunku Abdul Rahman, Malaysia)*
1530 – 1537	**PC01:** Identification of Key Starch Biosynthesis Genes Across Malaysian Rice Varieties with Varying Amylose Contents **Dr. Sew Yun Shin** Malaysian Agricultural Research and Development Institute (MARDI), Malaysia	**PC06:** Modulation of Tocotrienol-Rich Fraction on Brain Proteome Profiles and Cognitive Function in APP/PS1 Mice **Dr. Hamizah Shahirah Hamezah** Universiti Kebangsaan Malaysia, Malaysia	**SC01:** Foodborne Pathogens in Leafy and Non-leafy Vegetables **Mr. Jerrald Quek Jia Weai** Universiti Tunku Abdul Rahman, Malaysia	**SC07:** Molecular Detection of *Acinetobacter baumannii* Isolated from Human Clinical Specimens **Ms. Hadeel Mohamed Khalaf** Universiti Sains Malaysia, Malaysia	**SC13:** Cyclodextrin Inclusion Complex of Tetrahydrocurcumin Augments Solubility and *In Vitro* Anticancer Activity against Colorectal Cancer **Ms. Low Zhi Xuan** UCSI University, Malaysia

1537 – 1544	**PC02:** Utilizing Metabolite Analysis for Understanding Recalcitrant Behavior of Desiccated Mangosteen Seeds **Dr. Emelda Rosseleena Rohani** Universiti Kebangsaan Malaysia, Malaysia	**PC07:** Dynamic Changes in the Oil Palm (*Elaeis guineensis* Jacq.) Mesocarp Proteome during Development and Ripening **Ms. Hasliza Hassan** Malaysian Palm Oil Board (MPOP), Malaysia	**SC02:** The Effectiveness of Brown Rice in Glycaemic Control among Diabetes Mellitus Type 2: A Systematic Review of Clinical Trials **Ms. Nur Shamiyrah Ramzy Rameshan** Universiti Sains Islam Malaysia, Malaysia	**SC08:** Bacterial-fungal Diversity in Pigeon Faecal Samples Around UTAR Kampar Campus – A Pilot Study **Ms. Fong Gui Ying** Universiti Tunku Abdul Rahman, Malaysia	**SC14:** Molecular Characterization of LIC10280, a Novel Putative Virulence Factor of *Leptospira interrogans* **Mr. Wong Zhenpei** Universiti Sains Malaysia, Malaysia
1544 – 1551	**PC03:** Circumventing Oxygen Limitations in Industrial Fermentation, a Metabolic Engineering Approach **Asst. Prof. Dr. Arshad Jawed** Jazan University, Saudi Arabia	**PC08:** Neuroprotective Effect of Ethanolic Extract of *Polygonum Minus* Protects on Differentiated Human Neuroblastoma Cells (SH-SY5Y) against H_2O_2 - Induced Oxidative Stress **Dr. Murni Nazira Sarian** Universiti Kebangsaan Malaysia, Malaysia	**SC03:** Revealing *In Silico* Protein-Protein Interactions between Bacterial Leukotoxin from *Aggregatibacter Actinomycetemcomitans* and Human Integrin **Ms. Chong Sook Kee** UCSI University, Malaysia	**SC09:** Specific microRNAs Among Milk Siblings: An Epigenetics Approach Towards Understanding the Basis of Milk Kinship **Mr. Wan Alif Afiq Wan Nor Ruddin** International Islamic University Malaysia, Malaysia	**SC15:** Bibliometric Analysis of MicroRNAs Associated with Chronic Myeloid Leukemia **Ms. Syarifah Faezah Syed Mohamad** Universiti Teknologi MARA, Malaysia

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1551 – 1558	**PC04:** Analysis of *Salmonella* Brancaster Isolated from Chicken in Malaysia by Multilocus Sequence Typing **Ms. Khoo Evie** Veterinary Research Institute (VRI), Malaysia	**PC09:** Effects of *Barringtonia racemosa* Aqueous Extract in Male Reproductive Function in Streptozotocin-Nicotinamide (STZ-NA)-Induced Diabetic Rats **Dr. Siti Hajar Adam** Universiti Pertahanan Nasional Malaysia, Malaysia	**SC04:** Presence of Residual Nucleic Acids in Streptavidin from Three Isolation Methods **Ms. Nurul Nadia Mohamad Alias** Universiti Sains Malaysia, Malaysia	**SC10:** Antimicrobial Effect of *Aronia melanocarpa* Extractions on *Elizabethkingia anopheles* and *Elizabethkingia meningoseptica* **Mr. Ibraheam Ahmad Mohammad Tarawneh** Management and Science University, Malaysia	**SC16:** Impact of Climate Change and Invasive Species on Native Biodiversity and eDNA a Next Generation Biomonitoring Tool **Mr. Ghazanfer Ali** Universiti Malaya, Malaysia
1558 – 1605	**PC05:** Gene Expression Analysis of Methicillin-Resistant *Staphylococcus aureus* Treated with Silver Nanoparticles-Kaempferol (AgNPs-K) **Assoc. Prof. Dr. Rohazila Mohamad Hanafiah** Universiti Sains Islam Malaysia, Malaysia	**PC10:** Gas Chromatography and Mass Spectrometry Profiling and The Antiparasitic Potential of Borneo Fern **Dr. Muhammad Dawood Shah** Universiti Malaysia Sabah, Malaysia	**SC05:** Molecular Modelling and Dynamics of Kaurene Synthase Involved in *Stevia Rebaudiana* (Accession MS007) Terpene Biosynthesis **Mr. Muhammad Amirul Husni Samsulrizal** International Islamic University Malaysia, Malaysia	**SC11:** Identification and Antimicrobial Resistance Profiling of Clinical Bacteria Isolated from Breast Infection Patients in a Malaysian Tertiary Hospital **Ms. Christina Chong Shook Cheng** UCSI University, Malaysia	**SC17:** Effect of *Centella asiatica* L. Aqueous Extract on Male Reproductive Function in Streptozotocin-Nicotinamide (STZ-NA)-Induced Diabetic Rats **Ms. Farashakira Najiah Aszrin@Asrin** Management and Science University, Malaysia

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1605 – 1612	**PC12:** Chemopreventive Effects of Germinated Rough Rice Crude Extract in Inhibiting Azoxymethane-Induced Aberrant Crypt Foci Formation in *Sprague-Dawley* Rats **Assoc. Prof. Dr. Zalinah Ahmad** Universiti Putra Malaysia, Malaysia	**PC11:** Identifying Hotspots of Tuberculosis Cases in Gombak, Selangor, Malaysia **Dr. Nur Adibah Mohidem** Universiti Sains Islam Malaysia, Malaysia	**SC06:** Elucidation of Vitamin D Deficiency with Caries, Periodontitis, and Oral Cancer: A Systematic Review **Ms. Rozana Shahirah Ramle** Universiti Teknologi MARA, Malaysia	**SC12:** *Enterocytozoon Hepatopenaei*, a Microsporidian Parasite Infection in Shrimp: Diagnostics Strategies in Ensuring Safe Biosafety and Biosecurity for Sustainable Aquaculture **Ms. Thenmoli Govindasamy** Universiti Malaya, Malaysia	**SC18:** Searching for AChE Inhibitors from Natural Compounds by using Machine Learning and Atomistic Simulations **Ms. Thai Quynh Mai** Ton Duc Thang University, Vietnam

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E-Poster and Video Presentation Links

The e-posters and their video presentations can be accessed via the links provided below.

E-POSTER PROFESSIONAL CATEGORY (COMPETITION)			
PC01	Identification of Key Starch Biosynthesis Genes Across Malaysian Rice Varieties with Varying Amylose Contents **Dr. Sew Yun Shin** Malaysian Agricultural Research and Development Institute (MARDI), Malaysia	Poster	Video
PC02	Utilizing Metabolite Analysis for Understanding Recalcitrant Behavior of Desiccated Mangosteen Seeds **Dr. Emelda Rosseleena Rohani** Universiti Kebangsaan Malaysia, Malaysia	Poster	Video
PC03	Circumventing Oxygen Limitations in Industrial Fermentation, a Metabolic Engineering Approach **Asst. Prof. Dr. Arshad Jawed** Jazan University, Saudi Arabia	Poster	Video
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PC06	Modulation of Tocotrienol-Rich Fraction on Brain Proteome Profiles and Cognitive Function in APP/PS1 Mice **Dr. Hamizah Shahirah Hamezah** Universiti Kebangsaan Malaysia, Malaysia	**Poster**	**Video**
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PC09	Effects of *Barringtonia racemosa* Aqueous Extract in Male Reproductive Function in Streptozotocin-Nicotinamide (STZ-NA)-Induced Diabetic Rats **Dr. Siti Hajar Adam** Universiti Pertahanan Nasional Malaysia, Malaysia	**Poster**	**Video**
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E-POSTER STUDENT CATEGORY (COMPETITION)			
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SC18	Searching for AChE Inhibitors from Natural Compounds by using Machine Learning and Atomistic Simulations **Ms. Thai Quynh Mai** Ton Duc Thang University, Vietnam	Poster	Video

E-POSTER (NON-COMPETITION)		
EP01	Preliminary Results of the Role of MicroRNA-150-5p in the Pathogenesis of Human Multiple Myeloma **Dr. Ivyna Bong Pau Ni** Institute for Medical Research (IMR), Malaysia	Poster
EP02	Lectin Staining for Detection of Sialic Acid Residues on Cell Surface of Wild Type Chinese Hamster Ovary (CHO) and HeLa Cells **Dr. Salina Abdul Rahman** Institute for Medical Research (IMR), Malaysia	Poster
EP03	Association between School Environment and Adolescents Body Mass Index in Selected Secondary Schools **Dr. Shashikala Sivapathy** UCSI University, Malaysia	Poster
EP04	Molecular Characterisation of *Orientia tsutsugamushi* Identified from a Scrub Typhus Case in Malaysia **Assoc. Prof. Dr. Wang Seok Mui** Universiti Teknologi MARA, Malaysia	Poster
EP05	Prevalence of HSV-1: From Malaysia to Asia Through a Meta-Analysis **Dr. Eric Chong Tzyy Jiann** Universiti Malaysia Sabah, Malaysia	Poster

EP06	Molecular Docking of Annonaceous Acetogenins with Bcl-xL Protein **Dr. Wan Noraini Wan Sulaiman** Universiti Sains Islam Malaysia, Malaysia	**Poster**
EP07	Detection of *tanB* gene *Streptococcus gallolyticus* subspecies *gallolyticus* in Stool of Colorectal Cancer Patients **Assoc. Prof. Dr. Hairul Aini Hamzah** International Islamic University Malaysia, Malaysia	**Poster**
EP08	*In Vivo*, *In Vitro* and *Ex Vivo* Experimental Models of Diabetic Retinopathy: A Historical Review and Current State-of-The-Art **Asst. Prof. Dr. Muhammad Zulfiqah Sadikan** Manipal University College, Malaysia	**Poster**
EP09	EVNol SupraBioTM Attenuates Prostate Epithelial Changes by Regulating the Sex Hormone in Sprague-Dawley Rats **Dr. Izatus Shima Taib** Universiti Kebangsaan Malaysia, Malaysia	**Poster**
EP10	Knowledge, Attitude and Practices of Sun Protection Measures among University Students in Kuala Lumpur **Asst. Prof. Ts. Dr. Eugenie Tan Sin Sing** UCSI University, Malaysia	**Poster**
EP11	Lapatinib-Induced Changes in *Bifidobacterium bifidum* through Alteration of Tight Junction Proteins in Caco-2 Intestinal Monolayer Model: A Review **Dr. Wan Nor I'zzah Wan Mohamad Zain** Universiti Teknologi MARA, Malaysia	**Poster**

EP12	Ethyl Methane Sulphonate Treatment of Eggplant (*Solanum melongena* cv. Surya) Induces a Novel Mutation in the *MFT-2* Gene **Ms. Ranjita Subramaniam** Universiti Malaysia Sabah, Malaysia	**Poster**
EP13	Impaired Mitochondrial Dynamics in Patient with Energy Deficiency **Ms. Fatimah Diana Amin Nordin** Institute for Medical Research (IMR), Malaysia	**Poster**
EP14	*In Silico* Multimerization of Aptamers Targeting Dengue Envelope Domain III as Potential Dengue Diagnostic Antigens **Ms. Nur Aida Laili Mislan** Universiti Teknologi MARA, Malaysia	**Poster**
EP15	Screening of Putative Leptospira Virulence Factors Using a Yeast Growth Inhibition Assay **Mr. Fong Jing Heng** Universiti Sains Malaysia, Malaysia	**Poster**
EP16	Identification of Microbial Population in Sabah Tea Kombucha Pellicle and Its Potential as a Source of Probiotic for Broiler Chicken **Ms. Nurul Farhana Nasir** Universiti Malaysia Sabah, Malaysia	**Poster**
EP17	The Pentacyclic Triterpenoid of *Centella asiatica* Induces Apoptosis in T-Cell Leukaemia; *In Vitro* Flowcytometry Analysis **Dr. Norodiyah Othman** Institute for Medical Research (IMR), Malaysia	**Poster**
EP18	Spontaneous *F9* Gene Mutation in Haemophilia B Patients in Malaysia from 2014-2022 **Mr. Lam Kah Yuen** Institute for Medical Research (IMR), Malaysia	**Poster**

KEYNOTE ABSTRACTS

Keynote 1

Prof. Emer. Dr. John Beardall
(Monash University, Australia)

Transdisciplinary Research and Paradigm Shifts: Some Reflections Based on a Career in Biology

John Beardall*

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Science has a long history of trans-disciplinary collaborations. When researchers from different specialities have come together the resulting new insights have often been responsible for some of the most important advances in science. On the other hand, focus and compartmentalization in science are critical to the development of excellence in a particular field. In this presentation, I will discuss the benefits of transdisciplinary research vs operating in 'silos' and how approaches that build bridges between individuals operating in different silos can lead to paradigm shifts in scientific thinking, as well as 'value-adding' to more specific projects. Using my own experiences as examples, I will consider the obstacles to successful collaborative research and what is required, at both the personal and institutional levels, to make for successful associations, both within academic research and across links with industry.

Keywords: interdisciplinary research, silos, transdisciplinary research

Keynote 2

Prof. Dr. Abhi Veerakumarasivam

(Sunway University, Malaysia)

Bridging the Trust Deficit in Science: Embracing our Social Responsibility

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The recently launched National Biotechnology Policy 2.0 is an affirmation of the relevance of biotechnology as a major contributor to socio-economic growth and national security. Over the past decades, there have been significant investments to strengthen our biotechnology landscape; especially in building human capital and infrastructure. Nevertheless, the sustainability of the biotechnology ecosystem is dependent on the successful delivery of local solutions that effectively address the various challenges such as food security, pandemic resilience and climate crisis. The successful translation of potential into impact is driven by various factors that extend beyond our research-fueled knowledge base. Effective collaboration and communication across the quadruple helix of academia, industry, government and society is critical towards ensuring that biotechnology solutions are available, accessible, affordable and culturally acceptable. Although, trust is the fundamental quality that binds the complex interactions within the science-policy-society nexus, there appears to be a widening trust deficit across most institutional and societal levels. Recognising these evolving realities as well as the complex nature of policymaking and societal engagement, the scientific community needs to embrace their greater social responsibility. The role of a scientist is no longer confined to conducting accurate and reliable research. Since advances in biotechnology depends on public funds, affects policy decisions, and presents benefits and risks to society, scientists have a social responsibility to play diverse roles such as that of a knowledge broker, solution provider, communicator, ethicist and advocate for social justice. The collective ability to harmonise our professional and social responsibilities is critical towards realizing the full impact of biotechnology in the country.

Keywords: bridging, trust deficit, science, social responsibility

PLENARY ABSTRACTS

Plenary 1

Hon. Prof. Dr. Rofina Yasmin Othman

(Universiti Malaya, Malaysia)

Accelerating Adoption of Molecular Technologies for Plant Health and Crop Biosecurity through a Transdisciplinary Approach

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A key principle of ensuring plant health and crop biosecurity is the integration of strategies and practices to prevent, control or at least minimize the introduction and spread of new, emerging or reemerging pathogens. Massive biological databases including phenotypic and genomic databases, increasingly rapid molecular diagnostic technologies, the exciting prospect of the use of AI for predictive analytics and the development of powerful gene manipulation strategies to develop resistance, represent the new arsenal in the pathogen arms race. So how fast are we integrating these strategies for our own crop security and what could be the constraints for their immediate adoption?

Keywords: molecular technologies, plant health, crop biosecurity, transdisciplinary approach

Plenary 2

Prof. Dr. Wong Tin Wui

(Universiti Teknologi MARA, Malaysia)

Precision Medicine – Critical Clinical Gaps

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The personalised perspective of precision medicine involves patient's omics/healthcare assessment with therapy customized in accordance with the individual health status. More than one drug may be prescribed and delivered at variable doses and delivery kinetics to different target sites of action. As such, an ideal dosage form is preferably can be dispensed flexibly with the required drug dose. It is able to carry two or more drugs in a single dosage form, deliver the drugs with the desired kinetics, can possess same or different drug release kinetics, and may engage different drug-specific delivery strategies. The dosage form ideally should be characterized by 100 % drug bioavailability. This presentation highlights the recent drug delivery innovations from nano-to-macroscales for skin, pulmonary and oral applications from the perspectives of material design, dosage form development, and technology device application to realize the true meaning of personalized therapy. Specifically, critical clinical gaps in cancer omics analysis for precision medicine development will be discussed with reference to nanomedicine design against the profiles of cancer cell target and metabolizing enzyme.

Keywords: cancer, drug delivery personalized therapy, precision medicine

Plenary 3

Prof. Dr. Meisam Tabatabaei
(Universiti Malaysia Terengganu, Malaysia)

Transdisciplinary Research for a More Prosperous Future: The Highlights of the 2022 Report of the *Lancet* Countdown on Health and Climate Change

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Climate change threatens to undermine the last 50 years of gains in public health, with more intense and frequent extreme weather and weather-related events, increased heatwave exposure, alteration in the spread of infectious diseases, and exacerbated poverty and mental ill-health. Beyond avoiding the worst impacts of climate change, accelerated climate action could bring immediate and substantial benefits for human health, with cleaner air, healthier diets, and more liveable cities. The Lancet Countdown: Tracking Progress on Health and Climate Change exists to monitor this transition from threat to opportunity. We are a global collaboration of over 300 leading experts from academic institutions and UN agencies across the globe, bringing together climate scientists, engineers, energy specialists, economists, political scientists, public health professionals and doctors. Each year our findings are published annually in the medical journal The Lancet ahead of the UN climate change negotiations. Our data makes clear how climate change is affecting our health, the consequences of delayed action and the health benefits of a robust response. A health-centred response to the multiple, compounding crises the world is facing provides a renewed opportunity to secure a healthier, safer future. Such a response would see countries taking urgent action, and prioritising policies that deliver immediate benefits to public health, and that help build a more resilient, healthier future. Meanwhile, climate change adaptation will deliver more robust health systems which can deliver the care people need to overcome the negative impacts of future disease outbreaks, extreme weather events and geopolitical conflicts. These routes would contribute to a safe, resilient future in which people around the world can not only survive, but thrive.

Keywords: transdisciplinary research, climate change, health, climate change mitigation, climate change adaptation

Plenary 4

Prof. Dato' Dr. Azhar Mat Easa

(Universiti Sains Malaysia, Malaysia)

Functional Food: Food That is "Almost-Illegal"

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Functional food goes beyond providing nutrition and encompasses natural or processed foods that contain biologically active compounds. When present in defined, effective, and non-toxic amounts, these compounds have been clinically proven and documented to offer health benefits for the prevention, management, or treatment of chronic diseases. Although functional food is a marketing term not explicitly defined or acknowledged in food acts and regulations, it holds substantial potential in the future. To convert regular food into functional food, it is essential to subject the functional food ingredients to several scientific processes. These include phytonutrient analysis to establish the health link, preclinical *in-vivo* and *in-vitro* screening, and ultimately clinical trials to validate the functional food ingredients' efficacy and safety. As scientific research and understanding progress, it is anticipated that most conventional foods will be transformed into functional food, catering to the growing demand for health-promoting and disease-preventing food choices. By incorporating functional food into our diets, we can go beyond basic nutrition and harness the potential of biologically active compounds to support our overall well-being and combat chronic diseases. As the field of functional food continues to advance, it opens up new possibilities for personalized and targeted nutrition interventions to enhance health outcomes and improve public health.

Keywords: functional food, beyond nutrition, bioactive compounds, health benefits, marketing term

Plenary 5

Prof. Dr. Mohammad Noor Amal Azmai

(Universiti Putra Malaysia, Malaysia)

Feed-Based Vaccination in Aquaculture: Current Advancements, Challenges, and Opportunities

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Vaccination has been used to control disease outbreaks among cultured fresh and marine fishes. Demands for commercially available fish vaccines is predicted to increase in the future due to the intensification of the aquaculture, increasing disease outbreaks, reducing antibiotic application and industry acceptance. In Malaysia, aquaculture vaccine research and development are progressing, where most studies focused on bacterial fish diseases, including vibriosis, streptococcosis and aeromoniasis. Most of the farmers in this country are from small to medium-sized scales, thus vaccine application should be practical and cost effective to the local farmers – introducing the idea of feed-based vaccination. However, efficacy of feed-based vaccine is sometime questionable and "vaccinated fish" need time for acceptance from the publics and even farmers. Several vaccines against bacterial fish diseases have been developed and patented in Malaysia. However, none of it has been commercialized and available to be used at least for the local farmers. This presentation describes the current advancement of feed-based vaccination in controlling bacterial fish diseases, while discussing the challenges and opportunities of the feed-based vaccination application Malaysia – towards food safety and security.

Keywords: bacterial fish diseases, feed-based vaccination, advancement, challenges, opportunities

Plenary 6

Dr. Thamil Selvee Ramasamy

(Universiti Malaya, Malaysia)

Stem Cells in Regenerative Medicine and Cancer

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Stem cells are increasingly used to model human disorders, employed as a tool in drug discovery and leveraged for their therapeutic value. In our lab, we have successfully developed stem cell-derived organoids or 3D cultures of the miniature liver, brain, and cartilage along with cancer stem cell models to explore many aspects of biology- molecular and cellular mechanisms, drug testing systems and transplantable cellular resources. From the perspective of regenerative medicine, we have developed a multiple-cell system using stem cells to study both degenerative diseases and characterise the therapeutic value of stem cells as single and combination therapy as potential treatment modalities for various degenerative conditions. In order to make stem cell transplantation a success, we have been developing rejuvenation strategies for ageing stem cells and expanding their therapeutic value by improving the stem cell bioprocessing pipeline in collaboration with industrial partners. While one arm of the lab is focusing on regenerative medicine, the other arm is dedicated to developing cancer stem cell models and key regulatory targets through integrated multi-omic bioinformatics analysis and targeted regulators that will enable the targeting of the resistant population in a tumour, therefore eradicating cancer. In this talk, I will highlight how we can leverage stem cell biology to understand disease mechanisms, modelling the diseases and leverage their potential for realising regenerative medicine, along with how stem cell may answer some of your research questions and produce a work with high scientific merit.

Keywords: regenerative therapy, aging and ageing associated degenerative diseases, cancer stem cells, integrated OMICs, disease modelling

TECHNICAL TALK ABSTRACT

Technical

Dr. Eric Gifford

(Business Development Scientist, Collaborative Drug Discovery (CDD), USA)

CDD Vault: A Research Informatics Platform for Enabling Biotech Collaborations

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CDD Vault, a next generation drug discovery informatics platform, helps users to work more efficiently by making all data related to the molecules, biologics, or other entities of interest accessible and analyzable to the team members who need it. In this 15-minute talk, we will introduce Collaborative Drug Discovery's CDD Vault and how this platform reduces the complexity of storing, managing, and generating actionable insights from the wide range of data stored in a team's CDD Vault. We will also introduce the publicly accessible tools: CDD Visualization https://www.collaborativedrug.com/cdd-visualization/ and CDD Public Datasets https://www.collaborativedrug.com/public-access/ with an emphasis on how scientists can access and use these tools to advance their own research.

Keywords: CDD Vault, drug discovery, research data management

INVITED TALKS ABSTRACTS

Invited 1

Dr. Lee Soon Leong

(Forest Research Institute Malaysia, Malaysia)

Forest Genetic Resources Management using DNA Technology

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Illegal harvesting of forest resources poses a significant threat to the sustainability of forest ecosystems. At the Forest Research Institute Malaysia (FRIM), comprehensive DNA profiling and barcoding databases of important forest plant species have been developed since 2009 for species identification, timber tracking and source of origin identification. A total of 366 populations throughout Malaysia and about 15,000 individual samples were used to establish the species, population and individual identification databases. The species identification database can be used to establish the taxonomic classification of a suspected timber, whereas the population identification database can be used to reveal the source of origin up to population level. If the DNA profile of a suspected timber matches that of its original stump, by using the individual identification database, a random match probability can be estimated using subpopulation-cum inbreeding model to rule out the possibility of matching due to chance. For the application of these DNA databases, four standard operating procedures (SOPs) of DNA forensics for wood tracking were developed. The availability of DNA databases of important forest plant species together with FRIM's SOP of DNA forensics for wood tracking enhances the capacity of forest officials to curb the problem of illegal logging, while supporting the industries through plant species authentication. Besides, these databases have also been used to develop various conservation and management guidelines to strike a balance between conservation and utilisation of forest genetic resources.

Keywords: DNA barcoding, DNA profiling, short tandem repeat (STR), DNA forensics, conservation genetics

Invited 2

Assoc. Prof. Dr. Tan Cheng Siang
(Universiti Malaysia Sarawak, Malaysia)

The Emergence of Rotaviruses of Zoonotic Origin in Sarawak, Malaysia

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Introduction: Rotavirus is a common viral agent that causes acute gastroenteritis in children, particularly those under five years old. In Malaysia, rotavirus vaccination is not part of the National Immunisation Programme, but is available through private clinics and hospitals. Despite the World Health Organization's recommendation for continuous rotavirus surveillance, data on rotavirus prevalence in Malaysia is limited. This lack of information may have underestimated the need for a national rotavirus vaccination programme. This study aimed to assess the genetic relatedness of Sarawak rotavirus strains to global strains, and to determine the antigenic coverage and epitope compatibility of the Sarawak rotavirus serotype with the Rotarix and RotaTeq vaccines using in silico analysis. **Methods:** Stool samples were collected from 89 pediatric patients (under five years old) with acute gastroenteritis at private hospitals in Kuching, Sarawak from 2019-2021. The presence of rotavirus was confirmed using reverse transcription-polymerase chain reaction, and positive samples were analyzed using nucleotide sequencing. Phylogenetic analyses and epitope compatibility assessments were performed to determine genetic relatedness and antigenic coverage. **Results:** Analysis revealed the presence of G1P[8] (1/13; 7.7%), G3P[8] (3/13; 23%), G9P[4] (1/13; 7.7%), G9P[8] (3/13; 23%), G9P[X] (1/13; 7.7%), GXP[4] (1/13; 7.7%), and GXP[8] (3/13; 23%) in the stool samples. All wild-type Sarawak rotavirus strains, except for G1, exhibited variations in their phylogenetic and antigenic epitope characteristics. **Conclusion:** The current Rotavirus vaccines may not provide optimal protection against severe Rotavirus gastroenteritis due to genotype, phylotype and significant epitope mismatches.

Keywords: Rotavirus, paediatric vaccines, molecular epidemiology, genotype, Malaysia

Invited 3

Dr. Ooi Siew Eng

(Malaysia Palm Oil Board, Malaysia)

Oil Palm Leaf Transcriptomes Reveal Their Possible Link to Embryogenesis Potential

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Introduction: The low somatic embryogenesis rate from leaf explants remains a pressing issue in oil palm clonal propagation in Malaysia. This bottleneck continues to plague the oil palm cloning industry, which inadvertently increases operational costs through the necessary sampling of numerous ortets to achieve target production of clonal plantlets. The physiological state of plants prior to tissue culture may be relevant to the response of the plants in culture. **Methods:** For the purpose of transcript quantification, 3'mRNA sequencing was conducted on leaf tissues sampled from selected mother palms (ortets) from two tissue culture agencies, followed by real time quantitative PCR on a larger sample size. **Results:** Transcriptomics analysis revealed several differentially expressed genes (DEGs) in leaf tissues of embryogenic ortets. Clustering analysis based on expression of these DEGs suggests their potential in differentiating the fecundity of the ortets. Quantitative PCR results from selected significant DEGs on more samples suggest that these DEGs may discriminate between non-, low and high embryogenesis groups. Following that, linear discriminant analysis was able to produce more distinct clustering of the ortets corresponding to the three embryogenic categories. **Conclusion:** The expression of several candidate genes identified from differential transcriptomics analysis may be useful in discriminating potentially highly embryogenic from non- and low embryogenic ortets via the use of linear discriminant analysis or possibly other supervised learning algorithms.

Keywords: transcriptome, discriminant analysis, cloning, oil palm, embryogenesis

Invited 4

Asst. Prof. Dr. Federico Dajas-Bailador
(University of Nottingham, United Kingdom)

Small Non-Coding RNAs in Neuron Development and Communication: A View from the Axon Side

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Introduction: Neurons have highlighted the needs for decentralized gene expression and specific RNA function in somato-dendritic and axonal compartments, as well as in intercellular communication via extracellular vesicles (EVs). We identified a highly complex and differentially localized content of sncRNAs in axons and EVs during early neuronal development of cortical primary neurons and in adult axons in vivo. This content goes far beyond miRNAs and includes most known sncRNAs and precisely processed fragments from tRNAs, sno/ snRNAs, Y RNAs and vtRNAs. **Methods:** Our work has used compartmentalised microfluidic cultures of cortical primary neurons to explore the sub-cellular localisation of small non-coding RNAs and investigate their functional relevance in neuron development and communication via EVs. **Results:** Although miRNAs are the major sncRNA biotype in whole-cell samples, their relative abundance is significantly decreased in axons and neuronal EVs, where specific tRNA fragments (tRFs and tRHs/tiRNAs) mainly derived from tRNAs Gly-GCC, Val-CAC and Val-AAC predomi- nate. Using compartmentalised microfluidic neuronal cultures, we identified local roles for axonal miRNAs, where the repression of local protein synthesis controls axon development and growth. Removal of this repression in the axon triggers local translation of GSK3β protein and subsequent transport to the soma, where it can impact axonal growth. Our current work has explored the capacity for EVs to mediate transfer of miRNAs to control axon development. **Conclusion:** The existence of these complex sncRNA populations that are specific to distinct neuronal subdomains and selectively incorporated into EVs, equip neurons with key molecular tools for spatiotemporal functional control and cell-to-cell communication. These results demonstrate how the axonal small non-coding RNAs can regulate local protein translation in the axon to mediate neuron-neuron communication and retrograde signalling to the soma, amplifying neuronal responses that influence axon development.

Keywords: axon, neuron, development, non-coding RNAs, miRNAs

Invited 5

Assoc. Prof. Dr. Azham Zulkharnain

(Shibaura Institute of Technology, Japan)

Characterization and Genetic Analyses of Heterocyclic Compounds Metabolizing Strain BS19 Isolated from Antarctic Soil

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Introduction: Increased human activity in Antarctica has led to increased risk of environmental pollution. Oil spills, which contains a variety of harmful compounds, including polycyclic aromatic hydrocarbons (PAHs) and heterocyclic compounds, can severely endanger the pristine ecosystem of the continent. PAHs are known to be carcinogenic and mutagenic, while heterocyclic compounds are also toxic to marine life. The application of bioremediation in Antarctica is challenging due to the harsh climate and the need to use native bacteria. The main objective of this study is to isolate heterocylic compound metabolizing bacterium for bioremediation in Antarctica. **Methods:** Isolation was conducted by enrichment culturing method using carbazole as sole carbon source. Isolate was characterized biochemically and genetically before subjected to whole genome sequencing and expression analyses. **Results:** A single isolate, designated as strain BS19, was capable of removing 75% of carbazole after 15 days of culture at 15°C. Whole genome sequencing resulted in incomplete genome of 4.77 Mb with the lowest GC content among *Sphingobium* sp. strains. The gene clusters for complete metabolism of carbazole as carbon source and energy were indentified, and the expression analyses were conducted. Carbazole degradation gene cluster was highly conserved when compared to other previously reported strains. **Conclusion:** This is the first report on carbazole metabolizing bacterium isolated from Antarctica continent. Genetic analyses showed strains BS19 may be able to utilize wide range of xenobiotics, with promising potential for bioremediation applications in Antarctica and other cold climate regions.

Keywords: carbazole, bioremediation, Antarctic bacterium

Invited 6

Assoc. Prof. Dr. Leslie Than Thian Lung

(Universiti Putra Malaysia, Malaysia)

Crafting a Jigsaw Puzzle Piece to Address Vaginal Infections via Provaginobiotics

Leslie Than Thian Lung*

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Probiotics are live microorganisms which when administered in adequate amounts confer health benefits on the host. They are typically known as the good microorganisms that are found in fermented food like yogurt, tapai, kefir and kimchi. Fermented food has been hypothesised to be in existence for over 10,000 years. It is not until the beginning of 1900s where the concept of 'probiotics' is formally propounded by a Nobel Laureate Russian scientist named Elie Metchnikoff. He observed that the rural Bulgarian peasants had a longer life span which he attributed it to the consumption of fermented dairy products contributed by the "Bulgarian bacillus". Since then, probiotics have been applied not just as part of health food for good living but also to address human diseases. Taking cues from the benefits of probiotics and the growing knowledge of close relationship on the role of microbiota in human health and diseases, we explore the idea and potential of vaginal probiotics, or we term it as provaginobiotics to address vaginal infections (VI). Vaginal infections are common among women whereby about 75% of them have had at least one infection in their lifetime. Although the treatment of vaginal infections is considered straightforward, about 5-8% of these women would experience recurrent vulvovaginitis (rVV). Unresolved VI and rVV contribute to significant morbidity and also predispose women to HIV infection, infertility, and poor pregnancy outcomes. In this presentation, I will share about our experience in discovering lactic acid bacteria (LAB) strains and exploring their potential applications for women's health and well-being particularly on addressing VI.

Keywords: lactic acid bacteria, microbiota, probiotics, vaginal infections, women's health

Invited 7

Assoc. Prof. Dr. Siti Aqlima Ahmad

(Universiti Putra Malaysia, Malaysia)

Microbial Bioremediation of Waste Canola Oil by Cold Adapted Antarctic Bacterial Community

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Cooking oils are used for culinary purposes around the world, including at the science stations in Antarctica. Canola oil and canola margarine are the usual dietary fats in most Antarctic stations for food preparation and thus generate waste cooking oil. One solution to remove the waste cooking oil is through the bioremediation by using microorganisms. In this study, a bacterial community from sample BS14 showed both high bacterial growth and a high degradation rate of waste canola oil (WCO). Using one factor at a time method, the most effective microbial community examined was able to degrade 94.42% of WCO (from an initial concentration of 0.5% (v/v)) within 7 days. Meanwhile, using the response surface method, 94.99% degradation of WCO was achieved in 6 days. Furthermore, preliminary screening results for biosurfactant was positive, whereby the biosurfactant was produced in concentrations of up to 13.44 mg/mL in the presence of WCO, after optimisation. The optimum values for each factor were determined using a three-dimensional contour plot generated in a central composite design, where it was determined that a combination of 0.06% salinity, pH 7.30 and 1.55% initial substrate concentration led to the highest biosurfactant production when using WCO. The efficiency of WCO biodegradation achieved in this study provides support for the development of practical strategies for efficient bioremediation in the Antarctic environment. This study could help inform the development of large-scale bioremediation applications, not only for the degradation of WCO, but also of other hydrocarbons in the Antarctic by utilising the biosurfactants produced by BS14.

Keywords: bioremediation, biodegradation, hydrocarbon, biosurfactant, Antarctica

Invited 8

Dr. Sangeeta Prakash
(The University of Queensland, Australia)

Interactions between Transglutaminase-Treated Plant and Dairy Protein in Protein-Rich Beverages and Gels

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Protein-rich foods deliver potent nutrition in a small serving, but protein choice and concentration can disrupt food texture, challenging the industry and posing risks to those with swallowing difficulties. To address these issues, we present a protein-rich plant-dairy blend with concentrated plant proteins and explore enzymatic cross-linking techniques to improve milk and plant protein interaction and transform texture. Our blend combines 3.5% protein milk with varying amounts of pea and oat proteins, resulting in milk-pea (11% protein) and milk-oat (9% protein) mixtures. After heating the proteins at 85ºC for 20 minutes, we incubated them with different amounts of microbial transglutaminase enzyme at 50ºC for 1 hour. Gel electrophoresis demonstrated extensive cross-linking in the milk-pea mixture, eliminating unreacted fractions reserved for transglutaminase. The spectrophotometric analysis confirmed a significant decrease in ε-NH2, indicating a synergistic reaction between milk and pea proteins through enzymatic cross-linking, surpassing individual counterparts and the milk-oat mixture. Fourier-transform mid-infrared spectroscopy revealed protein side chains contributing to cross-link formation between milk and pea proteins. An enzyme concentration of 10 U showed enhanced milk-plant protein interaction compared to 5 U, with 20 U necessary for milk-pea gel formation. The resulting cross-linked milk-pea blend exhibited a thick consistency due to resilient bonds in the protein-rich matrix, allowing the production of functional beverages with abundant amino acids from dairy and plant proteins. However, cross-linking caused phase separation in the milk-oat blend, resolved through shear mixing before enzyme addition for a stable texture. Enzymatic cross-linking effectiveness depends on protein type, concentration, thermal denaturation, and enzyme solubility in high-protein systems. Thus, the industrial application requires careful optimisation while considering manufacturing costs.

Keywords: pea protein isolate, oat protein concentrate, milk protein concentrate, transglutaminase, enzymatic crosslinking

Invited 9

Asst. Prof. Dr. Lam Ming Quan

(Universiti Tunku Abdul Rahman, Malaysia)

Potential of Halophiles for Face Mask Waste Degradation in Marine Environment

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The COVID-19 pandemic has a profound impact worldwide. The extensive usage of face mask has generated tons of waste in a short period of time and predicting at least a twofold increase in related waste by 2030. Single-used face mask, which made up of polymeric substances including polystyrene, polypropylene, and polyethylene, are recalcitrant and can be emergent sources of microplastic pollution in the marine ecosystem. There are some microorganisms which could produce relevant enzymes to degrade the complex carbon-to-carbon backbone and utilise the carbon source in the face mask waste as nutrient. Therefore, the search for salt-loving halophiles with ability to degrade face mask are important. In this study, a halophilic microbial population originated from mangrove forests with potential to degrade face mask waste was investigated using -omics approach. The previously sequenced genomes of halophilic microorganisms, including *Meridianimaribacter* sp., *Robertkochia* sp., *Mangrovimonas* sp. were encoded with genes that may participating in the microplastic degradation. The encoded amidase, serine hydrolases, alkane monooxygenase, fumarylacetoacetase, and homogentisate dioxygenase have the potential to depolymerise the building blocks of face mask structure. In addition, a number of annotated genes, including esterases, lipases, and serine proteases could possibly act on the surface of face mask to increase its hydrophilicity. Collectively, this work provides insights and serves as an initiative for development of face mask waste degrading strategy in the marine environment.

Keywords: face mask waste, halophilic bacteria, microplastic waste management, microplastic degrading enzymes

Invited 10

Dr. Putu Virgina Partha Devanthi

(Indonesia International Institute of Life Sciences, Indonesia)

Does Spray Drying Affect the Functionality of Probiotic? A Case Study on *Pediococcus acidilactici*

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Probiotics are commonly used as dietary supplements and functional food ingredients in the form of powder, capsule, or tablet prepared using spray drying. However, spray drying can expose probiotics to stress, which can damage their functionality. This study investigated strategies to mitigate the negative effects of spray drying on probiotics by varying inlet temperatures (120◦C, 150◦C, and 170◦C) and whey protein isolate (WPI): gum arabic (GA) ratios (1:1, 3:1, 1:3) using *Pediococcus acidilactici* as a model probiotic. Results showed that the inlet temperature significantly affected cell viability, with the highest viability achieved at 120°C and the lowest at 170°C. All encapsulated *P. acidilactici* maintained viable cell counts of 5.24–6.75 log CFU/g after gastrointestinal tract simulation, with the smallest log reduction (0.3 log cycles) observed at a WPI:GA ratio of 3:1 and inlet temperature of 150◦C. All samples containing different WPI:GA ratios maintained sufficient viability (>7 log CFU/g) during the first three weeks of storage at 25◦C. Adherence rate on HT-29 cells and bile salt deconjugation activity of *P. acidilactici* was not significantly affected by spray drying. However, spray drying was shown to reduce *P. acidilactici* antimicrobial activity, with inlet temperature 120°C maintaining higher activity compared to the other temperatures. On the other hand, spray drying significantly ($p<0.05$) increased milk coagulation, acidification, and curd yield compared to non-spray dried *P. acidilactici*, with no significant effect observed from the spray drying conditions. These findings suggest that selecting an appropriate spray drying conditions can improve probiotics' viability and functionality.

Keywords: *Pediococcus acidilactici*, spray drying, probiotics, starter culture, microbial encapsulation

Invited 11

Prof. Dr. Subha Bhassu

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Can miRNA Regulation be used as a Diagnostic Tool in Shrimp Biohealth Monitoring?

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Introduction: Shrimps have been battling with infections that causes mortality and have faced economic loses in many decades In our study we proposed the innate system of immune mechanism have their ability to control and mitigate the infection in a systematic manner. MicroRNA (miRNA) is an endogenous small non-coding RNA that post-transcriptionally regulates the protein-coding genes. It involves various biological regulatory mechanisms in organisms such as cell differentiation, proliferation, immune responses, development, apoptosis, and others. **Methods:** In our infections disease challenge using in-vivo studies, we have traced the host response towards infection using miRNA and supported the results with other evidence. **Results:** These miRNAs are key regulators in energy metabolism that ensures the survival and adaptations of shrimps in response to infections. **Conclusion:** we have identified three (3) miRNA that acts as a mediator to either regulate the host responses or enhance the replication of diseases during infection. Therefore, the emerging of miRNAs could be potential candidates for establishment of diagnostic tool in numerous infectious diseases, a potential biohealth monitoring platform to ensure food safety part of food security.

Keywords: infectious disease, diagnostic biomarkers, biohealth monitoring

Invited 12

Puan Nor Aidora Saedon

(Forensic Science Analysis Centre, Department of Chemistry, Malaysia)

Advances and Challenges in Forensic DNA Analysis

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Forensic DNA analysis in Malaysia had gone through a tremendous advancement at every process since it was first launched in 1995. It used to be the RFLP techniques using radioactive isotopes with heavy lead jacket to the HLA DQα and straight to PCR-STR technique. From the hands on extraction via organic or Chelex, it has progressed to automated platform via Solid Phase Extraction (SPE) methods. Nowadays the SPE is bundled in cartridges and all that needs to be done, is to cut the samples with minimal pre-treatment and in the latest technique available; the extraction step is totally eliminated. Since the extraction step has been shortened, the technology is no longer about the ability to extract but the quality of the extracted DNA. The quantitation process is coupled with extraction to ensure sufficient amount of extracted DNA as well as the ability to detect male DNA and the rate of degradation. The amplification process in a single multiplex has increased from 9 to 24 loci for individual identification. Last but not least, interpretation of DNA profiles especially DNA mixtures is another laborious task for Forensic DNA scientists worldwide. The latest innovative technology is the elimination of extraction, quantitation and amplification process; i.e the crime sample is placed into the cartridge and in 1 hour, the DNA profile at 24 loci is generated. The Next Generation Sequencing (NGS) technique also emerged with the ability to generate results for >150 loci in a single multiplex which promised the ability to determine not only the colour of the eye and hair but also the ancestry of an individual. This advancement in forensic DNA analysis is then utilized to expedite the body identification cases so that the deceased is returned back to the rightful families for proper burial. Although it has progressed tremendously, there are still numerous challenges directly impacted on the quality of the samples submitted which leads to inability to generate interpretable DNA profiles, such as climate, storage conditions and sampling procedures. We may have the latest innovative technology in Forensic DNA analysis but it is futile when these destructive challenges are not dealt with accordingly. The applications of these techniques on different types of body identification cases will be discussed.

Keywords: DNA forensics, DNA extraction, RapidHit

Invited 13

Assoc. Prof. Dr. Nor Azimah Mohd Zain

(Universiti Teknologi Malaysia, Malaysia)

Prevalence of Antibiotic Resistance Bacteria in Aquaculture Sources in Johor, Malaysia

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Introduction: The intensive use of antibiotics in aquaculture results in the proliferation of antibiotic. **Methods:** Antibiotic resistant bacteria from six different aquaculture sources were isolated. These isolates were tested for antibiotic resistance against seven antibiotics via the disc diffusion method. Finally, phenotypic and genotypic identification via 16S rRNA sequencing and phylogenetic analysis were carried out. **Results:** The results show that 58 out of 118 bacterial isolates are resistant to multiple antibiotics. The highest isolate resistance was observed towards rifampicin (89.66%), followed by ampicillin (79.31%) and sulfafurazole (67.24%). The isolates with multiple antibiotic-resistant (MAR) index values with more than 20% were subjected to 16S rRNA gene sequencing. **Conclusion:** The majority of the bacterial strains exhibit multiple antibiotic resistance, indicating that they were isolated from highly contaminated sources based on the tested water qualities profiles.

Keywords: antibiotic resistance, multiple antibiotic resistance, aquaculture sources, MAR index value, 16S rRNA gene sequencing

Invited 14

Dr. Tang Yin Quan
(Taylor's University, Malaysia)

In Silico and *In Vitro* Studies of Mauriporin-Derived Anticancer Peptides

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Introduction: Cancer is the second leading cause of death globally, and drug-resistance cancer cells make treatments difficult. Several studies have showed that cationic peptides may be potential candidates for anticancer therapeutics. This study aimed to discover new potential anticancer peptides (ACPs) derived from mauriporin peptide (from the scorpion *Androctonus mauritanicus*). **Methods:** The study was conducted in two phases; *in silico* analysis followed by *in vitro* validation of the biocomputational results. *In silico* analysis resulted in a set of short ACPs (via amino acid modification) with high hydrophibicity. All ACPs were chemically synthesized for subsequent *in vitro* functional assessment through cytotoxicity (MTT) assay, apoptosis detection assay (Annexin/PI assay and western blot) and gene expression profiling by RT^2 profiler PCR arrays. **Results:** The findings suggested that the parental peptide M1 and its derivative (M1-A^2) selectively inhibited the proliferation of PC-3, HT-29 and A549 cells without interrupting normal cells. Both M1 and M1-A^2 showed good binding efficacy with Bcl-2, Bcl-xL and Mcl-1 that are essential for their anti-apoptotic functions. Moreover, activation of p53-independent intrinsic apoptosis by M1 and M1-A^2 was observed by the activation of caspase-9 in p53-null and mutant cell lines, as well as low LDH leakage at 24 hours. **Conclusion:** This study provides insights into the development and design strategy of peptide fragment-based drug, which can be further explored in screening potential anticancer peptide targeting cancer.

Keywords: anticancer, peptide, *in silico*, venom

Invited 15

Dr. Diana Chan

(Aquaculture Innovation Centre, Singapore)

Fine Bubble Technology Application for Intensive Aquaculture

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Fine bubble technology has been shown to have diverse applications in many industries ranging from agriculture production to wastewater treatment. Its uniqueness lies in the bubbles' high oxygen carrying capacity which is important in supporting animal and plant growth. With the world population growing at a rapid pace, aquaculture is rapidly overtaking wild capture fishery in providing a protein source suitable for meeting the nutritional needs. Fine bubble technology could play an important role in supporting aquaculture industry be it in sustainable intensive aquaculture farming for enhancing food security or in post-harvest technology.

Keywords: fine bubble technology, aquaculture

ORAL ABSTRACTS

O1

Understanding the Oil Palm Pathogen, *Ganoderma boninense* from Multi-Omics Studies

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Introduction: Palm oil is one of the most important oil-producing crops in the world as it contributes ~31% of the world's vegetable oil and fat supply. However, the sustainability of oil palm plantations is threatened by basal stem rot (BSR) disease caused by the phytopathogenic fungus, *Ganoderma boninense*. To date, knowledge of how this fungus mates and infects oil palm is very limited. **Methods:** The genomic and transcriptomic data from the infection analysis were downloaded from the public database. Besides, our group has generated the transcriptomic data from three different fungus growth stages: monokaryon, dikaryon and mating junction. All data were utilised to uncover both research questions. **Results:** We have successfully verified that this fungus harbouring the tetrapolar mating system by having two mating loci, *mat*A and *mat*B. The *mat*A genes contain homeodomain 1 (HD1) and homeodomain 2 (HD2) whereas *mat*B consists of 10 putative pheromone receptor genes, a *Ste3* gene and 4 putative pheromone precursor genes. Genome mapping against *G. boninense* showed two unlinked mating-type loci located at two different scaffolds. Moreover, the sequence of the *mat*A and *mat*B genes was poorly conserved. Besides, we also identified several genes which were postulated that play an important role during the infection such as cerato-platanin (CP). **Conclusion:** Few CP genes were up-regulated during the *G. boninense* infection. The results from these studies lay the foundation for understanding *G. boninense* infection in the oil palm host.

Keywords: *Ganoderma boninense*, genomic, oil palm pathogen, transcriptomic, virulence factors

O2

DNA Fingerprinting of Commercial MATAG Coconut Production and Genetic Purity Testing

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Introduction: MATAG is a hybrid coconut derived from the cross between maternal Malayan Yellow Dwarf or Malayan Red Dwarf variety and Paternal Tagnanan variety. The hybrid, which is high yielding and precocious, is highly sought after for commercial replanting in Malaysia. The recent release of the reference genome of coconut has become an enabler to develop DNA markers, such as Single Nucleotide Polymorphism for marker-assisted breeding and fingerprinting. To improve the current phenotyping precision, we evaluated genetic stratification and purity of the commercial MATAG hybrid and its parent stocks using SNP markers. **Methods:** A total of 768 published SNP were identified to be informative based on the genetic clustering and STRUCTURE analyses of 192 selected palms (57 MYD, 50 MRD, 25 Tagnanan and 60 MATAG) using targeted genotyping by sequencing method, namely SeqSNP. **Results:** Four main clusters formed accordingly to the three parental varieties and their MATAG hybrid. Interestingly, 23 and two off-type MATAG palms were assigned in MRD and MYD clusters, respectively, and two off-type MYD palms were found in the MATAG cluster. These off-type palms were then morphologically confirmed in the field. For cost saving, informative SNP were further reduced to 125 by dropping those markers in strong linkage disequilibrium and they were eventually translated to a PCR-based SNP panel for breeding and commercial seed production. To date, Sime Darby Plantation is maintaining authentic parent stocks (1,255 productive palms and 12,256 seedlings) to produce high-quality MATAG seeds. The current genetic purity ranges between 90% to 95%. **Conclusion:** The application of SNP-based fingerprinting can significantly improve screening precision for authentic MATAG seeds.

Keywords: MATAG, MYD, MRD, Tagnanan, SNP

O3

Bacterial Diversity of Rhizosphere Soils of *Pteris vittata* Growing in Arsenic-Rich and Natural Mineral Soils

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Introduction: Soil is essential for the survival of various microbes, and arsenic pollution can greatly disrupt microbial activity in the soil. *Pteris vittata* can grow in arsenic-polluted soils due to its ability to accumulate high levels of metals in its fronds. This research investigated the diversity, composition, and metagenomic functions of the bacterial population in the rhizosphere zone of *P. vittata* growing in arsenic-rich compared to natural mineral soils. **Methods:** Next-Generation Sequencing (NGS) was used to assess the composition and functions of the soil bacterial communities. The amplicon sequencing targeting the 16S rRNA V3-V4 region was conducted using the Illumina approach. **Results:** The analysis of the filtered reads revealed that the phylum *Actinobacteria, Proteobacteria, Chloroflexi, Gammatimonadetes,* and *Firmicutes* were more abundant in As-rich than natural soils. While *Acidobacteria, Verrumicrobia, Planctomycetes, Myxococcota*, and *Bacteroidetes* were more abundant in natural mineral soils. **Conclusion:** The results revealed that the arsenic-rich soils were richer in species but less diverse than the natural mineral soils. Many intricate bacterial taxa were observed in arsenic-rich compared to the natural mineral soils.

Keywords: bacterial diversity, rhizosphere soils, 16S rRNA, arsenic, *Pteris vittata*

O4

Are Flowers Attractive to the Insect Parasitoid, *Pediobius imbreus* of the Oil Palm Bagworm, *Metisa plana*?

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Introduction: The oil palm bagworm, *Metisa plana* is a leaf defoliating insect, which can reduce the yield of oil palm production and cause crop losses. Beneficial flowers are being grown in oil palm plantations to attract insect parasitoids, which will then parasitise the bagworms. *Pediobius imbreus* (Hymenoptera: Eulophidae) is one of the insect parasitoids of *M. plana.* However, knowledge in the preference of *P. imbreus* towards beneficial flowers is limited. **Methods:** We performed (1) a Y-tube olfactometer bioassay on *P. imbreus* female towards different beneficial flowers, and (2) analyzed the volatile organic compounds that attract the *P. imbreus* females. **Results:** A total of 655 parasitoids were collected from plantations from August 2022 until January 2023, and 11.16 % of these parasitoids were identified as *P. imbreus*. The results from the Y-tube olfactometer experiments on three flowers, namely *Cassia cobanensis, Bidens pilosa,* and *Antigonon leptopus* showed that the *P. imbreus* females were significantly attracted to *B. pilosa* ($P = 0.0002$) followed by *C. cobanensiss* ($P = 0.0060$) and *A. leptopus* ($P = 0.4652$) in significance ($P > 0.05$). Gas chromatography-mass spectrometric analysis of the volatiles from these three beneficial flowers has revealed some of the chemical compounds. **Conclusion:** *P. imbreus* has different preference towards different flowers, which infers that the insect parasitoids select different flowers for nutrition and shelter. The information may help the farmers to select the kinds of flowers to be planted to maintain the parasitoid population and sustainably control bagworm infestation.

Keywords: insecta, flowers, olfactometry, gas chromatography-mass spectrometry

O5

Degradome Sequencing Reveals miRNA159-Directed Cleavage Site in *GAMYB-like* Gene During Pineapple (*Ananas comosus)* Fruit Development

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Introduction: *In silico* computational analysis can provide predictive identification of microRNAs (miRNAs) and their target genes, however the main criterion used to distinguish between regulated and non-regulated genes is that the targeted transcripts (mRNA) will undergo degradation. MiR159 in pineapple targeted and silenced the expression of the *GAMYB-like* family transcription factor, which played a crucial role in flower development and gibberellin (GA) signalling in cereal aleurone cells, as demonstrated in *Arabidopsis* and rice. Here, we aim to provide first-hand empirical data on miR159 regulation of its putative target *GAMYB-like* and its relevance to pineapple fruit development. **Methods:** Degradome sequencing (with Illumina HiSeq 4000) was used to identify over-represented 5'ends (miRNA cleavage sites) inside mRNAs. We discovered that miR159 was consistently expressed in all three biological replicates of the degradome libraries, and the *GAMYB-like* family transcription factor gene was detected in MD2 pineapple using RT-qPCR. Then, a modified 5'-rapid amplification of cDNA ends (5'-RACE) technique was used to validate the target gene cleaved by miR159. **Results:** The results showed that the predominant cleavage site in *GAMYB-like* gene was at position 11 from the 5' end of the miR159 complementary region. Gene Ontology (GO) analysis indicated that the miR159 target genes were involved in various cellular processes during fruit development. **Conclusion:** These findings confirmed that *GAMYB-like* family transcription factor is an authentic target of miR159 and demonstrated the key role of miRNAs in regulating the expression of target genes, providing insights into the mechanisms underlying MD2 pineapple fruit development.

Keywords: degradome sequencing, microRNAs, miR159, *GAMYB*-like transcription factor, pineapple fruit

O6

The Effect of Soil Physicochemical Properties Towards the Community of Soil Invertebrates at Different Plantation Agriculture in Kota Belud, Sabah

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Introduction: This study was conducted to investigate the community composition of soil invertebrates in agriculture areas in Kota Belud, Sabah. **Methods:** Pitfall traps method along 30-meter line transect were applied to collect samples of soil fauna and Berlese-Tullgren funnels were used to extract soil microarthropods from soil samples. Soil samples were collected at three different agricultural area located at Kota Belud, Sabah; rubber (Kg. Sarang), oil palm (Kg. Dudar), and paddy (Kg. Timbang). **Results:** A total of 108 soil samples and 474 individuals of soil invertebrates were collected and analyzed accordingly. All soil samples from each agriculture soil were subjected to selected soil physical and chemical analyses. These analyses included measurements of moisture content, soil texture, and pH for physical parameters, and soil nutrient content and organic matter for chemical characteristics. Physicochemical parameters of the soil were measured to observe the effect on the soil invertebrate's composition. The association of soil physicochemical properties with all the invertebrate's taxa was statistically analyzed through Cannonical Correlation Analysis (CCA). **Conclusion:** Observing the result gained from this study, it is important to consider the activity in the soil layer that affects the existence and survival of soil invertebrates. Given their importance in maintaining life, proper attention should be paid to enhance the presence of soil invertebrates, especially in Sabah which is one of the food crops producing states in Malaysia.

Keywords: soil invertebrates, agriculture, physicochemical, CCA, composition

O7

Effect of Feeding Probiotics, Phytobiotic, and Prophytobiotic on Egg Quality, Total Lipid Content, and Fatty Acid Composition of Egg Yolks of Laying Hens

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Introduction: Probiotics, prebiotics, and natural products can replace antibiotic growth promoters in the poultry industry for sustainable agriculture and public health preservation. This study aimed to evaluate the effect of feeding probiotic, phytobiotic, and prophytobiotic on egg quality, total lipid content, and fatty acid composition of laying hens at 20-35 weeks of age. **Methods:** Ninety-six Lohmann Brown hens, 20 weeks of age, were randomly allocated to four dietary treatments: Ctl (basal feed), Pr (basal feed + 0.01% *B. amyloliquefaciens*), Phy [basal feed + 1.0 mL lemon myrtle essential oil (LMEO)/kg basal feed] and PrPhy (basal feed + 0.01% *B. amyloliquefaciens* + 1.0 mL LMEO/kg basal feed). The egg quality, total lipid and fatty acid content were analyzed every 4 weeks. The egg lipid content was determined gravimetrically, while fatty acid compositions were analysed using gas chromatography. **Results:** Pr, Phy, or PrPhy supplementation did not exert a detrimental effect on the egg quality (haugh unit, relative weights of the albumen and yolk, specific gravity, shell thickness, and yolk color) of laying hens. No significant ($P<0.05$) change was observed in the total lipids of eggs among the treatment groups. However, the supplementation of Pr, Phy, or PrPhy significantly ($P<0.05$) decreased the total saturated fatty acids and increased total unsaturated and polyunsaturated fatty acids, total omega 3 and 9 levels in the eggs. **Conclusion:** These findings indicated that supplementation of Pr, Phy, or PrPhy in the hen diet can improve the fatty acid compositions of eggs without affecting the egg lipid and quality.

Keywords: probiotic, phytobiotic, egg quality, total lipid content, fatty acid

O8

Cancer Cell-Derived PDGFB Stimulates mTORC1 Activation in Renal Carcinoma

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Introduction: Clear cell renal cell carcinoma (ccRCC) is a hypervascular tumor, characterized by the inactivation of *VHL* tumor suppressor gene and mTOR signalling pathway hyperactivation. The pro-angiogenic factor PDGFB, a transcriptional target of super enhancer-driven KLF6, can activate the mTORC1 signalling pathway in ccRCC. However, the mechanisms of PDGFB-mediated mTORC1 activation in ccRCC remain elusive. Herein, we investigated whether ccRCC cells are able to secrete PDGFB extracellularly and stimulate mTORC1 signalling activity in a paracrine manner. **Methods:** We first generated PDGFB-targeted and PDGFB-overexpressing ccRCC cells. Then, culture media from these cells and the previously established KLF6-engineered ccRCC cells were subjected to PDGFB ELISA. Next, phosphorylated ribosomal S6 Western blot was perfomed to test whether KLF6 overexpression, PDGFB overexpression or secreted PDGFB were able to stimulate mTORC1 activity in the KLF6-repressed cells, which had impaired mTORC1 activity. **Results:** We found that ccRCC cells secreted PDGFB extracellularly and the level of PDGFB secretion was positively correlated with the expression of intracellular KLF6 and PDGFB. The reintroduction of either KLF6 or PDGFB was able to sustain mTORC1 signalling activity in the KLF6-repressed cells. We further demonstrated that conditioned media of PDGFB-overexpressing ccRCC cells was able to re-activate mTORC1 activity in these KLF6-repressed cells. **Conclusion:** Cancer cell-derived PDGFB can mediate mTORC1 signalling pathway activation in ccRCC, consolidating the link between the KLF6-PDGFB axis and the mTORC1 activity in ccRCC. This additional jigsaw is vital for the construction of comprehensive ccRCC molecular dependency map for the development of efficient ccRCC diagnostic or therapeutic strategies.

Keywords: renal cancer, mTOR signalling pathway, PDGFB, KLF6, CRISPR/Cas9

O9

Chemical Profiling of Paddy Husk and its Inhibitory Activity against Human Salivary Gland Cancer

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Introduction: Global agriculture produces tens of millions of tons of paddy husk every year. Paddy husk is an inedible agriculture waste obtained during the process of rice milling. Previous studies reported that it contains inhibitory potential due to the presence of phytochemicals that possess anti-cancer properties. The main aim of this study is to identify the presence of anti-cancer-related phytochemicals in paddy husk aqueous methanol extract and elucidate its inhibitory effects against human submaxillary salivary gland epidermoid carcinoma cells (HTB-41). **Methods:** Chemical profiling of paddy husk aqueous methanol was done by using GC/MS analysis while the inhibitory activity (IC_{50}) against HTB-41 cells was calculated by using the Trypan Blue Exclusion Assay (TBEA). **Results:** Paddy husk aqueous methanol profiling analysis shows the presence of vitamin E such as tocopherol which possessed anti-cancer properties. Paddy husk aqueous methanol elucidated inhibitory activity on HTB-41 cells where an IC_{50} dose of 200 µg/ml managed to reduce cell viability to 50.5%. This extract act in a tumor-selective manner since the cytotoxicity test showed no significant changes (88.90%) in cell number and viability after treatment. **Conclusion:** The presence of vitamin E in paddy husk aqueous methanol successfully showed inhibitory effects on the human salivary cancer cell line while it acted in a tumor-selective manner by not inducing any significant changes in human gingival fibroblast cell (HGF-1).

Keywords: paddy husk, chemical profiling, salivary gland cancer, agriculture waste, cytotoxicity

O10

Potassium Channel Kv1.3 Restricts Dengue Virus Replication in HEK293 Cells

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Introduction: Dengue is a mosquito-borne viral disease that represents a significant public health threat. The disease is caused by infection with dengue virus (DENV). During infection, recent findings have suggested the significant role of membrane protein channels controlling cellular ion homeostasis. Such channels include the voltage-gated potassium channel Kv1.3, capable of restricting DENV entry into host cells. The interplay of DENV-Kv1.3 proteins and the specific mechanism facilitating this event however, remain unclear. **Methods:** Our previous yeast two-hybrid interactomes has identified DENV non-structural protein 2A (NS2A) interacting with Kv1.3. The protein-protein interaction was confirmed by a luminescence-based mammalian interactome (LUMIER) assay, co-immunoprecipitation, and *in silico* analysis. The importance of Kv1.3 was further tested in HEK293 cells by analyzing the DENV yield following Kv1.3 channel blockade. **Results:** The experimental data showed that DENV NS2A significantly interacts with Kv1.3 channel protein. This is supported by *in silico* analysis demonstrating an excellent binding affinity between the viral NS2A and Kv1.3. Interestingly, we observed an increase in DENV replication following Kv1.3 channel inhibition in HEK293 cells, suggesting dysfunctional Kv1.3 promotes DENV replication in cellular host. **Conclusion:** Functional Kv1.3 is vital in controlling potassium influx, which restricts DENV replication in host cells. Thus, the channel could serve as a promising target for intervention and management of dengue infection.

Keywords: dengue virus, non-structural 2A protein, Kv1.3, potassium channel, infection

O11

Amelioration of Streptozotocin-Nicotinamide-Induced Diabetes and Oxidative Stress in Rats by *Centella asiatica* Aqueous Extract

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Introduction: Medicinal plants have played a crucial role in the treatment of diverse diseases. It is believed that medicinal plants are compatible with the human body and have fewer adverse effects than pharmaceuticals. *Centella asiatica* leaves aqueous extract (CALE) was used to evaluate the effects on biochemical parameters and oxidative stress in streptozotocin-nicotinamide (STZ-NA)-induced diabetic rats. **Methods:** DM was induced in male Sprague-Dawley rats by a single intraperitoneal injection of NA (100 mg/kg) 15 minutes prior to STZ (55 mg/kg). The diabetic rats were orally administered with CALE (250 and 500 mg/kg/day) and glibenclamide (0.6 mg/kg/day) for 35 days. The body weight and feed and water intake (FWI) were monitored daily, while fasting blood glucose (FBG) levels were measured weekly. The changes in biochemical parameters were assessed and antioxidant biomarkers were evaluated on enzyme immunoassays to determine treatment effectiveness. **Results:** Diabetic rats demonstrated a significant ($P<0.05$) reduction in body weight and FWI but an elevation in FBG levels. Compared to the disease control (STZ+NA) group, CALE treatment groups significantly ($P<0.05$) reversed the elevated levels of FBG. Serum liver and renal parameters, and lipid profile of CALE-treated diabetic groups were significantly ($P<0.05$) improved as compared to the STZ+NA group. The total superoxide dismutase, glutathione peroxidase, and catalase activities of serum and liver of CALE-treated diabetic groups significantly ($P<0.05$) higher, but malondialdehyde activity significantly ($P<0.05$) lower compared to STZ+NA group. **Conclusion:** The CALE has the potential to ameliorate hyperglycaemia, hyperlipidaemia, and oxidative stress.

Keywords: diabetes mellitus, *Centella asiatica*, antidiabetic, antioxidative, STZ-NA-induced diabetic rats

O12

The Analysis of Interleukin-1 Alpha (IL-1α) and High Mobility Group Box 1 (HMGB1) Expression in Tumor Tissues of Colorectal Cancer Patients

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Introduction: Colorectal cancer (CRC) is the third most prevalent cancer globally, with low overall survival rates and poor prognosis mainly due to late diagnosis. This calls for the exploration of new biomarkers in improving the detection of CRC. Damage-associated molecular patterns (DAMPs) including interleukin-1 alpha (IL-1α) and high mobility group box-1 (HMGB1) are crucial mediators of inflammation, implicated in the CRC pathogenesis. Our previous *in-vitro* work demonstrated that IL-1α promotes tumour growth and stimulates the production of pro-metastatic mediators, while HMGB1 only has the latter capability. Here, we investigated the expression of these DAMPs in CRC patients' tumour tissues. **Methods:** 38 tumour samples and their corresponding non-tumour adjacent tissue (NAT) were obtained from Universiti Malaya Medical Center (UMMC) and DAMPs were stained via immunohistochemistry (IHC). A semi-quantitative IHC analysis using ImageJ Fiji software was used to quantify and analyze the tissue sections. **Results:** The expression of both IL-1α (17.27% ± 1.705) and HMGB1 (30.91% ± 2.417) was significantly upregulated in CRC tumour tissues compared to NAT. Notably, the expression of IL- 1α was significantly upregulated in tumour tissue for stage I (19.33% ± 2.99), II (15.75% ± 2.92), and III (16.91% ± 2.95), while HMGB1 was only significant in stage III (37.82% ± 3.20). Interestingly, positive correlation was discovered in HMGB1 with distant metastasis. **Conclusion:** These results suggest that IL-1α and HMGB1 could serve as potential diagnostic and prognostic markers for CRC. Further works in increasing the sample size are underway to increase statistical power.

Keywords: interleukin-1 alpha (IL-1α), high mobility group box 1 (HMGB1), colorectal cancer, biomarker, immunohistochemistry

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O13

MEF2C Transactivates the Expression of Growth-Promoting KLF6 in Renal Carcinoma

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Introduction: Kruppel-like factor 6 (KLF6), a super enhancer-driven transcription factor, is at the epicentre of a cellular signalling loop that links several hallmark features of clear cell renal cell carcinoma (ccRCC). CRISPR/Cas9-mediated KLF6 targeting impaired ccRCC cells growth in-vitro and in-vivo, which were in line with the reported cancer cells high dependency on super enhancer-driven genes. However, little is known about regulatory elements that establish the large super enhancer region spanning the KLF6 locus and drive high expression of this gene in ccRCC. **Methods:** Herein, we performed DNA motif analysis on ccRCC H3K27ac and p300 ChIP-Seq data and found MEF2 family binding motif at the KLF6 promoter. Subsequent analyses revealed MEF2C as the putative KLF6 transactivator and to validate this, we repressed MEF2C in ccRCC cells using CRISPRi and RNAi approaches. Then, we assessed KLF6 expression and MEF2C binding signals at the KLF6 promoter region in the MEF2C-engineered ccRCC cells via qPCR and MEF2C ChIP-qPCR, respectively. **Results:** We found that KLF6 expression level positively correlated with the expression of MEF2C. Moreover, MEF2C ChIP-qPCR confirmed the binding of MEF2C at the KLF6 promoter region. This was corroborated by the upregulation of KLF6 expression upon reintroduction of exogenous MEF2C in MEF2C-targeted ccRCC cells. **Conclusion:** Our results have thus far shown MEF2C binding at the KLF6 super enhancer region and its role as direct KLF6 upstream transcription regulator. Lastly, this study paves the way for further dissection of KLF6 super enhancer landscape establishment, which the long-term aim is to construct a complete ccRCC molecular dependencies map.

Keywords: KLF6, MEF2C, renal cancer, CRISPR/Cas9, super enhancer

O14

Expression of Virus-Like Particles (VLPs) by Mammalian Cells as an Alternative for SARS-CoV-2 Virus

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Introduction: Virus-like particles (VLPs) have numerous applications in advanced medical research since they are non-infectious due to the absence of viral genetic materials. These applications include vaccine technology advancement, diagnostic kits development, therapeutic improvement and specific drug carrier. To date, SARS-CoV-2, is still classified as Risk Group 3 pathogen, which requires the use of a Biosafety Level 3 (BSL-3) facility for any laboratory work involving viral propagation. Therefore, the aim of study is to construct the SARS-CoV-2 Delta variant virus-like particles (SDV-VLPs), which allow fundamental and advanced studies to be conducted in any institutions without the BSL-3 facility. **Methods:** The recombinant DNA carrying the genes encoding for SARS-CoV-2 Delta variant structural proteins (spike, membrane and envelope) and enhanced green fluorescence protein (eGFP) was constructed into expression vector pcDNA3.1(+). Transfection into Vero 76 African green monkey kidney cell line was performed, followed by the Neomycin selection assay 96 hours later, for 24 days. Transfected cells were then harvested and subjected to immunofluorescence, immunoperoxidase and Dot blot. **Results:** The transfected mammalian cells appeared green fluorescence when viewed under fluorescence microscopy, which indicate the expression of SDV-VLPs. The Neomycin-selected VLPs-expressing cells were positively detected in all immunoassays conducted, which confirmed the presence of SDV-VLPs. **Conclusion:** This study shows that the SDV VLPs was successfully expressed by the mammalian expression system, which could provide a groundwork for further research and development of VLPs-based vaccines, therapeutic agents, diagnostic kits and targeted-drug carrier to mitigate the current implications related to viral infections and future outbreak.

Keywords: SARS-CoV-2, virus-like particles, expression, mammalian cells

O15

Micronutrient Deficiency and Its Association with ADHD and Academic Performance of Primary Public-School Students in Kabul City, Afghanistan

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Introduction: Several health issues, especially in developing countries, are primarily caused by childhood micronutrient deficiency. This research aimed to identify micronutrient deficiencies and their relationships to attention deficit hyperactivity disorder (ADHD) and academic performance (AP) among primary public-school students in Kabul City, Afghanistan. **Methods:** Three-hundred and fifty-eight primary public-school students were recruited from five schools in Kabul City, with an average age of 7.7 years. Plasma samples were tested to determine the micronutrient content. The AP and ADHD-T questionnaires were translated from their original English forms, and the factorial structure, validity, and reliability of the scales were assessed to evaluate children's ADHD and AP. **Results:** Vitamin D (95%), vitamin B12 (73.96%), calcium (100%), vitamin A (33.6%), zinc (24.23%), and folic acid (5.1%) deficiencies were present in these students. The APQ-Dari and ADHD-T-Dari exhibited high internal consistencies, great content and face validity. For APQ-Dari, Cronbach's alpha was 0.97. The overall Cronbach's alpha for the ADHD-T-Dari scale was 0.898, while the subscales had 0.851 and 0.847, respectively. The children showed inattention (16.8%), hyperactivity/impulsivity (29.9%), and ADHD (21.5%), while the male students scored higher than the female. Vitamin D and vitamin B12 deficiencies were associated with ADHD. Low family income and illiterate parents had a significantly positive correlation with ADHD. ADHD and AP had a negative relationship. **Conclusion:** School-age children have micronutrient deficiencies; lack of vitamin D and vitamin B12 have been linked to ADHD. Micronutrients had no apparent influence on children's AP, while ADHD had a strong impact on AP.

Keywords: micronutrient deficiency, ADHD, academic performance, primary public-school students

O16

Evaluation of Fibrinogen-Depleted Human Platelet Lysate in Mesenchymal Stromal Cells Expansion

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Introduction: Human platelet lysate (hPL) is proposed as a replacement for fetal bovine serum (FBS) for in vitro cell growth in accordance with good manufacturing practice (GMP) criteria. Nonetheless, hPL contains fibrinogen and other coagulation factors which causes gel formation during cell culture. Heparin is commonly added to avert this problem but it is mainly animal derived, and it can only minimize the chance of gel formation. Therefore, this study is conducted to propose an alternate approach for fibrinogen-depleted hPL (Fd-hPL) preparation for the expansion of mesenchymal stem cells (MSCs) without heparin. **Methods:** hPL was prepared by double freeze-thaw of expired human platelet concentrates. Heparin-hPL (H-hPL) and fibrinogen- depleted-hPL (Fd-hPL) were prepared by adding heparin to hPL or adding calcium salt to hPL to precipitate and eliminate the fibrin clot, respectively. The concentration of calcium, fibrinogen, and growth factors in H-hPL and Fd-hPL were evaluated. H-hPL and Fd-hPL were studied for their effects on umbilical cord-MSCs (UC-MSCs). **Results:** Fd-hPL had significantly greater calcium concentrations and lower fibrinogen levels than H-hPL. Both H-hPL and Fd-hPL did not show significant differences in the concentration of BDNF, TGF-1, and PDGF-BB, but Fd-hPL showed a decreased concentration of VEGF. Fd-hPL remains the feature of UC-MSCs because it had no effect on cell viability, proliferation, multilineage differentiation potential, or surface marker expression. **Conclusion:** Fd-hPL promoted in vitro MSC expansion without impairing cell characteristics and it has the potential to be used as a replacement for FBS in the MSCs expansion without xenogenic components.

Keywords: human platelet lysate, fibrinogen, calcium, mesenchymal stem cell, primary cell culture

O17

Cloning of Plasmid For Compatible Gene Expression In Cyanobacteria

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Introduction: Cyanobacteria are referred as emerging microbial host that is suitable for eukaryotic transgene expression. The demand of flavanone-based drugs and supplements in pharmaceutical and nutraceutical industries has been increasing and became the major factor on the extensive studies in flavonoids potential applications. However, there is no expression plasmid used for production of flavanone in cyanobacteria. **Methods:** PCR was used to amplify *CHI* and *CHS* genes for insertion into pSyn_6. pSyn_6 was linearized by using NdeI for *CHI* insertion whereas CHI-pSyn_6 was linearized by using BamHI-HF for *CHS* insertion. The quality of genes and linearized vectors, pSyn_6 and *CHI*-pSyn_6 were analysed using agarose gel electrophoresis. *CHS* and *CHI* were assembled using seamless cloning method and transformed into *E. coli* DHB10B strain. The positive transformants were confirmed by using nucleotide sequencing. **Results:** One expression plasmid, *CHS-CHI*-pSyn_6 was cloned for expression of plant transgenic genes in cyanobacteria. This plasmid consists of an integration site, NS1 that allows homologous recombination between neutral site vector and *Synechococcus elongatus* PCC7942 chromosome and strong constitutive promoter, psbA gene which drive high level expression of gene of interest. In addition, the expression plasmid also carried Sp (spectinomycin) resistance gene. The size of *CHS-CHI*-pSyn_6 is approximately 6.3 kbp. **Conclusion:** One expression plasmid, *CHS-CHI*-pSyn_6 that might be compatible for gene expression in cyanobacteria has been successfully transformed into *E. coli* DH10B. This study will provide better understanding on application of expression plasmid with neutral site for metabolic engineering of eukaryotic genes into microbial hosts.

Keywords: cyanobacteria, expression plasmid, neutral site

O18

Cyanobacteria as a Source of Anticancer Compounds: Evaluation of Toxicity, Antioxidant Activity, Total Phenolic and Flavonoid Contents

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Introduction: Cyanobacteria (blue-green algae) are a diverse group of photosynthetic, prokaryotic microorganisms found in fresh and marine waters. As a natural and rich source of bioactive molecules, cyanobacteria have major benefits with a broad range of biological activities including antimicrobial, antiviral, anticancer, antioxidant and anti-inflammatory properties. Nowadays, many experiments on cyanobacteria have shown promising potential as a new anticancer therapy. In this study, three cyanobacterial species namely *Anabaena* sp., *Microcystis* sp., and *Desertifilum* sp. extracted by methanol and chloroform were evaluated for their total phenolic contents (TPC), total flavonoid contents (TFC), cytotoxicity and antioxidant activity. **Methods:** TPC and TFC were analysed spectrophotometrically while 2,2-diphenyl-1-picrylhydrazyl (DPPH) and ferric reducing antioxidant power (FRAP) assays were carried out to determine the antioxidant activity. The extracts were also tested to evaluate their toxicity level using *Artemia salina* lethality assay. **Results:** The results showed that the methanolic extract of *Desertifilum* sp. contains the highest amount of TFC (126.65±3.76 mg QE/g), TPC (19.89±1.56 mg GAE/g), and the highest antioxidant activity through FRAP assay (32.55±2.39 mg GAE/g), while *Microcystis* sp. showed the highest antioxidant potential through DPPH assay (54.04±0.347 %). Besides, all the extracts showed low toxicity against *Artemia salina*. **Conclusion:** This study revealed that *Desertifilum* sp. is an excellent source of natural products from cyanobacteria which could be explored further for its potential in becoming a new anticancer treatment as it has low toxicity, and high TPC, TFC and antioxidant activity.

Keywords: antioxidant, cyanobacteria, cytotoxicity, total flavonoid, total phenolic

O19

Identification of SARS-CoV-2 Omicron Variant by Oxford Nanopore Sequencing in a Tertiary Institution, Malaysia

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Introduction: The SARS-CoV-2 Omicron variant is the predominant variant which continue to surge since it emerges in Malaysia in December 2021. The identification of SARS-CoV-2 variants has been well established with next gene sequencing techniques which produce information on the virus genome and its classification. Nanopore Sequencing however able to provide real time sequence information to aid in the clinical diagnosis in a very short turn around time. This study aims to use Nanopore Sequencing to identify Omicron variant in patients admitted in a tertiary institution, Malaysia. **Methods:** Fifty-three samples of SARS-CoV-2 collected in February until June 2022 were subjected to whole genome sequencing using the Nanopore technique protocol- the Midnight Primer and Rapid Barcoding library kit before sequence using MinION MK1c within 16hours overnight. The fasta file then retrieved from MinKNOW software after basecalling and analysed using Epi2Me bioinformatic platform. The Nextclade and Pangolin results were generated to produce the variant calling. **Results:** Out of 53 genome, the sublineage is BA.1.1 (12), BA.1.1.7 (1) were detected in February and March 2022 and classified in Nextstrain Clade 21K. In addition, sublineage BA.2 (19), BA.2.3 (15) and BA.2.10 (6) were categorized in Nextstrain Clade 21L found throughout February until June 2022. **Conclusion:** Nanopore Sequencing is a third-generation sequencing technology that offer simple, fast and less laborious method in identifying variant of SARS-CoV-2. From this results, BA.2 sublineage has been outcompeting previously dominant BA.1 as the result of rapid transmission within six month time.

Keywords: SARS-CoV-2, Nanopore, Omicron, whole genome sequencing, variant

O20

Cloning, Expression and Purification of Recombinant Multicopper Oxidase Laccase from *Pseudomonas putida* B4

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Introduction: Laccases are blue multicopper enzymes (EC 1.10.3.2), oxidizing both phenolic and non-phenolic substrates, by reducing four-electron of oxygen to produce water. In biotechnology sectors, laccases are important in organic synthesis, lignin degradation, bioremediation and pharmaceutical industries. **Methods:** In this paper, molecular studies were done in order to get a novel multicopper oxidase (MCO) laccase from *Pseudomonas putida* B4. The process involved PCR, cloning of recombinant MCO into PGEX4T-1 expression vector and purification through affinity chromatography by using 1 mL Glutathione Sepharose Fast Flow (GSTrap FF) resin. **Results:** Recombinant protein of MCO/PGEX4T-1 was expressed in *E. coli* BL21 DE3, induced with 1 mM IPTG, at 37 °C for 16 hours. The intracellular laccase with size ~54 kDa was purified to homogeneity. Anthracene assay was done to study enzyme activity with 5.00 U/mL detected from purified laccase. **Conclusion:** In future, this purified laccase are important findings that can be used in characterizing the laccase properties such as laccase stability in certain conditions such as its stability at high temperatures and extreme pHs. The study of laccase crystal structure from purified laccase is also important in order to explore in depth characteristics of laccase secondary and tertiary structures.

Keywords: laccase, polycyclic aromatic hydrocarbons, *Pseudomonas putida*, biodegradation, purification

O21

Combination Treatment of Chitosan Loaded Thymoquinone Nanoparticles and Hyperthermia Reduced the Size and Cell Viability of Osteosarcoma Spheroids

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Introduction: Osteosarcoma which develop mostly in adolescents is a malignant bone tumor with stagnant survival rate among patient due to the inadequate improvement in standard therapies. Three-dimensional (3D) culture system can mimic the cells behaviour, morphology and physiology in vitro. The antiproliferative effects of thymoquinone (TQ) on colon, breast, lungs, and osteosarcoma made it the best candidate for this study. Dual-encapsulation of synthesized chitosan nanoparticles (CNPs) containing L-ascorbic acid and TQ (CNP-LAA-TQ) into nanoparticles can increase drug delivery and limit the undesirable cytotoxicity. Meanwhile, combination of hyperthermia with CNP-LAA-TQ resulted in a better outcome as CNP-LAA-TQ heating can increase drug bioavailability and provide sustained drug release over longer duration. Therefore, this study aims to look at the cell viability of osteosarcoma (MG-63) spheroids after first treatment and second treatment. **Methods:** 3D culture was performed using spotting method on a 96-well collagen scaffold plate with seeding density of 20,000 cells/spot. On day 3, the spheroids were treated with CNP-LAA-TQ concentration of 5000ug/mL (IC_{50}) for 48h and recovered for 24hours at 37°C followed by another treatment using the same concentration of CNP-LAA-TQ (5000ug/ml) for 48 hours and recovered for another 24hours at 37°C. Spheroids size was measured using Image J software and cell viability assay was performed after each treatment. **Results:** MG-63 spheroids size was significantly reduced after combination treatment with hyperthermia during second treatment compared to first treatment. **Conclusions:** This showed that CNP-LAA-TQ with combination of hyperthermia are dose and time-dependent as exposure of MG-63 to CNP-LAA-TQ can sensitize and kill some of the spheroids during 1st treatment and kill cells more effectively in 2nd treatment.

Keywords: chitosan nanoparticles, thymoquinone, 3D culture, osteosarcoma, hyperthermia

O22

Population Genetic Structure and Breeding Pattern of Bed Bug Infestation in Iraq

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Introduction: Bed bug concerns have increased over the past three decades due to a sharp increase in bed bug infestations in human dwellings. Unfortunately, there is little information about the bed bug population throughout Iraq, and no studies have been conducted on the genetic structure and breeding pattern of bed bugs in Iraq. **Methods:** A total of 140 individuals were collected from 14 infested sites thoroughly inspected in eight governorates in Iraq. This study aimed to use microsatellites marker to conduct a genetic characterization of *C.hemipterus* populations, to accurate the efficacy of the markers used to characterize the genetic structure of *C.hemipterus* populations in Iraq, and to evaluate the inbreeding pattern, genetic differentiation, and gene flow among the sampled populations. **Results:** The number of alleles varied from 6 to 18 across seven microsatellite loci. There was a significant difference in the number of alleles present at each locus between and within the populations. The average observed and expected heterozygosity among all populations was 0.730 and 0.175, while 0.173 and 0.673, respectively. Based on polymorphic information criteria, the markers with a value >0.5 were highly polymorphic. High genetic differentiation was detected (F_{ST}= 0.772). The bed bug populations showed strong inbreeding, with highly positive coefficients of inbreeding (F_{IS}=0.761). **Conclusion:** The study offers information about bed bug population structure and active and passive dispersion factors. This data is needed to plan, implement, and monitor bed bug control measures that reduce the local population, discourage further invasions, and spread the problem beyond the regions that have been treated.

Keywords: population genetics, bed bug, Iraq, breeding pattern

O23

Separation of Cordycepin and Adenosine in Aqua Extract of Cultured *Cordyceps militaris (CM)* using HPLC

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Introduction: In this research paper, the significant highlight is on a type of highland mushroom called *Cordyceps militaris (CM)*. The sample used in this study is cultured *CM*. The targeted bioactive compound is Cordycepin and Adenosine where Adenosine is the analogue of Cordycepin. **Methods:** Cordycepin was extracted from the stroma powder of *CM* which was macerated in distilled water for 48 hours and was filtered using filter paper. The filtrate was collected and freeze dried to ensure no moist in the extract powder. The extract powder was later sub-fractioned using Snake-Skin dialysis tubing with molecular weight cut off of 35kDa. The extract was then used for High Performance Liquid Chromatography (HPLC) using two pure compounds as references, namely Cordycepin and Adenosine (both from TCI Chemicals). The column used to run the experiment is Zorbax Eclipse Plus C18, 4.6x150mm with the flow rate of 0.75 mL/min in 1% Acetonitrile as solvent. **Results:** The bioactive compound, Cordycepin was clearly distinguished and the peak was observed at 5.572 minute with an area count of 5745.5. Adjecently, the retention time for Adenosine was observed at 4.606 minute while the area count was 78. **Conclusion:** Cordycepin and Adenosine peaks were separated and clearly observed at different retention time in the presence of the pure compounds as references through HPLC analysis.

Keywords: cordycepin, adenosine, maceration, sub-fraction, HPLC

O24

The Effects of Trans Fat Diet Intake on Biochemical Parameters and Global DNA Methylation in Offspring of In-utero BPA Exposed Rats

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Introduction: Bisphenol A (BPA) is one of the most commonly reported environmental endocrine-disrupting chemicals (EDCs). Exposure to BPA during critical windows such as pregnancy is known to affect the programming of metabolically active tissues in offspring, which increases the susceptibility of the individual to chronic metabolic diseases later in adult life. Programming does not contribute to direct chronic disease, but it changes the physiological conditions of the organism, so it handles the postnatal environment differently, for instance in unhealthy lifestyle such as excessive trans-fat diet (TFD) intake. In our study, we aimed to investigate the effect of prenatal BPA exposure with postnatal TFD intake on biochemical parameters and global DNA methylation expression on adult SD rat offspring. **Methods:** Eighteen pregnant rats were divided into three groups: control (CTL), vehicle tween 80 (VHC), and BPA (5 mg/kg/day) from PD 2 to PD 21; then their weaning rats were fed normal diet (ND) or trans-fat diet (TFD) from PNW 3 to PNW 14. Glucose, insulin, lipid profile and global DNA methylation expression were measured. **Results:** The study has displayed that there was no significant difference between groups in relation to biochemical parameters including glucose, insulin, and lipid profiles ($p>0.05$). Furthermore, the study findings have shown a significant increase in global DNA methylation in BPATFD group rat offspring. **Conclusion:** prenatal BPA exposure with postnatal TFD in offspring may affect global DNA methylation in adulthood, and the effect may be more aggravated in late adulthood.

Keywords: Bisphenol A, endocrine-disrupting chemicals, trans-fat diet, programming, DNA methylation

O25

In Vitro Anti-Herpes Virus Activity of Thymoquinone

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Introduction: Thymoquinone (TQ) has demonstrated broad-spectrum activities and has also been shown to exhibit inhibitory effects against a variety of viruses. The aim of this work is to evaluate the potential antiviral efficacy of TQ, the major bioactive component of *Nigella sativa* oil, against herpes simplex virus type 1 (HSV-1) and type 2 (HSV-2). **Methods:** Antiviral activity against HSV was studied by determining the 50% cytotoxic concentration (CC_{50}) and the half-maximal viral inhibition effective concentration (EC_{50}). The selectivity index (SI) of the compound was also determined as a parameter to indicate the *in vitro* antiviral activity of the TQ by the ratio of CC_{50} to EC_{50}. The viral load and protein expression were analysed using qPCR and western blot. **Results:** Our findings showed that CC_{50} of the tested compound was moderate with no or weak antiviral activity with SI<10. However, a significant decrease in viral load was observed. Western blot analysis indicated that TQ treatment decreased the level of viral glycoprotein B expression. **Conclusion:** This study suggests that even though TQ has weak antiviral activity with low SI, it demonstrated potent inhibitory effects on HSV DNA replication by reducing viral load. These effects imply that this compound may be considered a promising treatment for HSV post-infection; however, further studies, such as *in vivo* evaluations, are required for the development of an effective anti-herpetic drug.

Keywords: herpesviruses, *Nigella sativa*, thymoquinone, antiviral activity

O26

A Duplex Reverse Transcription Loop-Mediated Isothermal Amplification Based Lateral Flow Dipstick (RT-LAMP-LFD) as a Simple Rapid Molecular Diagnostic Tool to Detect SARS-CoV-2 Nucleocapsid and Envelope Gene

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Introduction: To slowdown the spread of COVID-19, it is crucial to identify and isolate infected individuals at early infection. However, existing diagnostics are either costly, time-consuming, or exhibit varying levels of accuracy. Moreover, SARS-CoV-2 variants mutate at primer binding sites can evade detection by current PCR-based tests. To address this issue, a duplex reverse transcription loop-mediated isothermal amplification coupled with a lateral flow dipstick (RT-LAMP-LFD) technique holds promise as a fast and user-friendly molecular test. **Methods:** LAMP primers were developed from conserved regions of the Nucleocapsid (N) and Envelope (E) genes of SARS-CoV-2. DNA and RNA templates were produced by cloning genes into pJET1.2 vector and transcribed using T7 RNA polymerase. RT-LAMP assays were performed using optimized LAMP protocol using *Bst* 3.0 DNA polymerase on synthesized RNA template. To test the sensitivity, 1:10 serial diluted recombinant plasmids were used. The specificity of the assay was assessed by conducting a test on plasmids containing genes from other coronaviruses; SARS-CoV, MERS-CoV and IBV. The findings were analyzed by gel electrophoresis, colorimetry, and Lateral Flow Dipstick (LFD). **Results:** The optimized protocol detected the control plasmids within 10 minutes but is more sensitive with time. A 30-minute LAMP reaction was as sensitive as PCR. Moreover, the designed primers are highly specific and only amplified the targeted regions. Additionally, duplex RT-LAMP reaction targeting two regions was successfully visualized on LFD with two test lines. **Conclusion:** The use of LAMP-LFD is potentially a straightforward, specific, and sensitive method for rapid molecular diagnosis of COVID- 19.

Keywords: nucleocapsid gene, envelope gene, RT-LAMP, SARS-CoV-2, lateral flow dipstick

O27

Development of Multiplex Real-Time PCR for Simultaneous Detection of 10 Viruses Causing Encephalitis

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Introduction: Encephalitis is the inflammation of the brain parenchyma, typically caused by viral infections. About 4.3 million people were affected and resulted in 150,000 deaths worldwide in 2015. Clinical diagnoses such as neuroimaging and electroencephalogram only reveal the disease but not the causative agents. Most laboratory diagnoses are time-consuming, less specific and sensitive. A rapid diagnosis allows timely treatment and reduces overall patient morbidity and mortality. This research provides a method allowing the simultaneous detection of several common viruses causing encephalitis. **Methods:** Specific primers and probes were designed for 10 viruses from *Herpesviridae*, *Flaviviridae*, *Picornaviridae*, and *Paramyxoviridae* families, namely Echovirus 7, herpes simplex 1, dengue, Zika, measles, cytomegalovirus, Epstein-Barr, chikungunya, respiratory, and coxsackie A16 viruses. Optimisations were conducted using singleplex qRT-PCR on chemically synthesised positive control template, followed by two panels of multiplex qRT-PCR based on Fluorescent Amplitude Modulation Method (FAMM), Asymmetric PCR with melting curve analysis, and Multiplex Probe Amplification with 3' end phosphorylated primers combined with melting curve (MPA-MC) analysis. **Results:** The specificity of primer and probes were 97-100% using *in silico* validation; and the optimal PCR conditions and limit of detection for each virus were determined. Most viruses showed high expressing ability, but echovirus 7 and respiratory syncytial virus considered as low expressing targets. Results showed that MPA-MC was capable of detecting and differentiating viruses in both panels without any cross-amplification. **Conclusion:** The newly developed multiplex qRT-PCR panel offers an alternative cost-effective method for the rapid detection of viral encephalitis compared to conventional methods.

Keywords: viral encephalitis, multiplex qRT-PCR, FAMM, asymmetric PCR, MPA-MC

O28

Optimization on Maceration Extraction, Isolation, and Characterization of Polymethoxyflavones from *Kaempferia parviflora*

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Introduction: Polymethoxyflavones (PMFs) are a unique flavones group typically found in citrus fruits. Widely used in traditional medicines and therapies, the PMFs demonstrate potent biological activities and therapeutical potential. Interestingly, *Kaempferia parviflora* rhizome or kunyit hitam originated from southeast Asia and possessed abundant bioactive PMFs. **Methods:** The PMFs from *Kaempferia parviflora* were extracted, isolated, and identified. Optimization on maceration extraction was carried out at different solid-to-solvent ratios (1:10, 1:20, 1:30, 1:40, 1:50), solvent-solvent ratio (40%, 60%, 80% & 95% ethanol) and extraction duration (1, 2 & 3 days) to determine the optimum yield of the crude *Kaempferia parviflora* extract. The crude extract was subjected to thin-layer chromatography and liquid-liquid fractionation. The fractions were purified by column chromatography to isolate the PMFs compound. Identification of PMFs was elucidated through ^{1}H-NMR, ^{13}C-NMR, MS, and FT-IR. **Results:** Solid-to-solvent ratio of 1:40, 60% ethanol, and one day extraction period produced the highest crude extract percentage yield (12.03%, 12.43% & 9.46%). The R_f value of PMFs from the crude extract was compared with the standard 5,7-Dimethoxyflavone (R_f = 0.21), 5,7,4'-Trimethoxyflavone (0.16), 3,5,7-Trimethoxyflavone (0.26) and 3,5,7,4'-Tetramethoxyflavone (0.22). Fractionation of crude extract yield n-hexane fractions (H_1-H_{22}; 8.7832 g) and chloroform fractions (C_1-C_{13}; 24.5610g). The PMFs structure was confirmed through spectral analysis and comparing spectroscopic data based on literature. **Conclusion:** Major PMFs were successfully identified and may contribute further to elucidating the biological activities of the bioactive compounds in *Kaempferia parviflora* extract.

Keywords: *Kaempferia parvifora*, maceration, optimization, characterization, polymethoxyflavones

O29

Antarctic Psychrotolerant Bacterial Response to Cold Temperature

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Introduction: Many species of *Cryobacterium* have been isolated from cold environments. However, it is unclear how these psychrotolerant bacteria survive and adapts to colder temperatures than their optimal growth temperatures. Hence, this project was undertaken to determine the response of an Antarctic *Cryobacterium* sp. SO1 to a temperature 10℃ lower than its optimal growth temperature of 20℃. **Methods:** Two sets of three flasks containing 50 ml of strain SO1 culture were incubated 20℃ (optimal) until they reached the exponential phase of growth, and one set was rapidly exposed to a 10℃ drop (suboptimal). Cell RNA transcripts from the two temperatures were sequenced, evaluated, and compared. **Results:** Some cells in the culture died because of the suboptimal cold conditions, while others continued to grow with some adjustments to their gene expression patterns. In dying cells, programmed cell death (PCD) pathways were activated, resulting from severe physical and cellular damage. The cellular components of dying cells acted as an autoinducer for quorum sensing, signaling the cells to adapt to the new normal cold temperature and adjust the expression of an array of genes. Surviving cells adjusted to the colder growth temperature by removing misfolded and inactive proteins and RNA, repairing misfolded RNA, and synthesizing new RNA, which were among the major responses.

Keywords: bacterium, cold-adaptation, gene expression pattern

O30

Development of Species-Specific eDNA Primers for Detection of Invasive *Cichla* Species in Malaysia

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Introduction: Locally known as top predator fishes, peacock bass or cichlids are invasive in Malaysia's freshwater system. Due to the fish's tendency to hide beneath the water's surface, detection probabilities for these fish are typically low, especially when using the traditional capture-survey method. So, a relatively new non-intrusive and quick method that can be used to determine the distribution of these invasive fishes is environmental DNA (eDNA) monitoring. **Methods:** In this research, highly specific primers for *Cichla* species based on mitochondrial DNA (mtDNA) COI gene sequences were developed using Primer-BLAST tool and the specificity of the primers, were thoroughly design using adjusted parameters. An ex-situ test to detect *Cichla* species in water was also employed using digital PCR (dPCR) analysis. **Results:** This study's findings demonstrated that the COI gene is suitable to develop *Cichla* species-specific markers. According to the ex-situ validation results, the developed markers CO1 and CK1 specifically amplified to cichlid species *C. ocellaris* and *C. kelberi*, respectively, demonstrating the specificity of these markers. Absolute fluorescent quantification, which detected the presence of *Cichla* species eDNA in the water sample with a 90% detection confidence, also supported the specificity analysis performed by dPCR. **Conclusion:** The CO1 and CK1 markers were successfully developed and are now suitable for use as eDNA markers for rapid detection of invasive peacock bass species. Thus, eDNA analysis using species-specific markers can be used as a new, quick biomonitoring tool to detect invasive species for the management and conservation of biodiversity.

Keywords: eDNA, *cytochrome oxidase I,* invasive species, peacock bass, biomonitoring

O31

Utilization of Diesel Oil by Soil Bacteria in Shake Flask System

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Introduction: The pollution caused by diesel fuel has emerged as one of the most serious environmental problems worldwide. Diesel oil contaminants have been detoxified using various methods, including physical, chemical, and biological processes. Through the utilization of natural biological activity, the technique known as "bioremediation" makes it possible to degrade pollutants in the environment. Therefore, the present study aimed to isolate and identify soil bacteria that could utilize diesel oil in the shake flask system. **Methods:** Bacteria were isolated from soil samples collected at an automobile workshop that were potentially exposed to hydrocarbon contamination. The soil samples were spread on a selective medium (mineral salt media agar) containing diesel oil as the growth substrate. The bacterial isolates were screened and identified for their ability to utilize diesel oil by culturing in minimal salt media (MSM) supplemented with 1% diesel oil. The treatment was incubated at 37°C at 150 rpm for 24 days. The isolates were characterized based on their growth patterns using colony forming unit (CFU/ml), optical density measurement, and identified using the BBL Crystal Identification Kit and 16S rRNA gene sequencing techniques. **Results:** Two isolated bacteria that could utilize the diesel oil-containing treatment were identified as Pseudomonas and Acinetobacter using BBL Crystal ID Kit. The 16S rRNA gene sequences revealed that these bacterial strains were *Pseudomonas aeruginosa* and *Acinetobacter junii*. **Conclusion:** This study demonstrated that bacterial species isolated from hydrocarbon-contaminated soil could be optimized to be used as potential bioremediation agents for diesel removal.

Keywords: bioremediation, diesel oil, soil bacteria, *Pseudomonas aeruginosa*, *Acinetobacter junii*

O32

Biosynthesis and Optimization of Terpolymer P(3HB-*co*-3HV-*co*-4HB) Using Glycerine Pitch as a Sole Carbon Source

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Introduction: Plastics have become a vital commodity in our lives, resulting in a wide range of items that combine comfort, and quality, and are utilized in packaging, medical, agricultural, and pharmaceutical industries. Polyhydroxyalkanoates (PHAs) are biodegradable, biocompatible microbial biopolymers produced by several bacterial species. Bioplastics like PHAs have proven to be alternative materials to replace synthetic plastics. The most used carbon sources are sugars and oils whose utilization is deemed uneconomical and unsustainable. This research aims to biosynthesis and optimized terpolymer using *Cupriavidus malaysiensis* (USMAA1020). **Methods:** In this study, terpolymer synthesis was accomplished using Shake flask fermentation, PHA analysis using Gas chromatography, terpolymer optimization was conducted using random surface methodology. **Results:** Effects of different concentrations of glycerin pitch, 1-pentanol, 1-4 butanediol, and oleic acid were studied and the highest PHA content was observed in 15g/L glycerine pitch, 0.06wt% C of 1-pentanol, 0.25wt% C of 1-4 butanediol and oleic acid yielded the highest PHA concentration of 4.27 ± 0.81g/L. Improvement was focused on the concentrations of glycerine pitch, oleic acid, and 1-4 butanediol serving as the major carbon sources affecting the terpolymer synthesis. The optimization study has resulted in high PHA concentration 10.5 ± 0.31g/L which indicated an increase in the PHA content when compared to the cultures before optimization 4.27 ± 0.81g/L. **Conclusion:** The results showed the ability of the *C. malaysiensis* (USMAA1020) to convert glycerine pitch to PHAs also provides an alternative carbon substrate that successfully synthesized bioplastic and controls environmental pollution.

Keywords: biodegradable, biopolymer, polyhydroxyalkanoates, bioplastics, terpolymer

O33

Tropical Soil Bacterial Diversity

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Introduction: Bacteria are found in soils, which are vital in various ecological processes such as biogeochemical cycling, improvement of soil quality, plant growth and maintenance of a balanced ecosystem. Despite the increasing knowledge of soil microbial diversity in many regions around the world, there is limited data on the bacterial diversity of the soils in the tropical regions such as Malaysia. Hence, this research was conducted to determine the bacterial population of soils from selected areas in East Malaysia using a metagenomic approach. **Methods:** Three soil samples (n=3) were collected in Kota Kinabalu, Sabah alignment (SaBC access and export license reference nos. JKM/MBS.1000-2/2 JLD.14(92), (93) & (94) and JKM/MBS.1000-2/3 JLD.5(10), respectively. DNA was extracted from the soil samples and used for amplification of the 16S rDNA gene followed by sequencing. **Results:** A total of 39 different bacteria phyla were found in the soil samples. The most abundant phyla in the analyzed soils were *Proteobacteria* (19.90%) followed by *Acidobacteriota* (15.73%), *Actinobacteriota* (12.79%), *Firmicutes* (9.40%), *Chloroflexi* (9.23%), *Planctomycetota* (7.19%), *Verrucomicrobiota* (5.53%), *Myxococcota* (5.43%), *Latescibacterota* (2.72%) and *Desulfobacterota* (2.38%). **Conclusion:** These baseline data generated from the work gave an overview of the predominant groups of bacteria phyla in Sabah soils and can be utilized to monitor the changes in bacterial diversity brought by the environment in the future.

Keywords: bacterial diversity, tropical soil

O34

Oil-Degrading Ability of Immobilized *Bacillus cereus* and *Pseudomonas aeruginosa* on PVDF/CTA Membrane

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Introduction: The application of oil-degrading bacteria has been widely investigated as they are capable of breaking down and metabolizing hydrocarbons present in crude oil and its derivatives. These bacteria play a crucial role in bioremediation of oil spills as they could provide an efficient, cost-effective, and environmentally friendly solution for the clean-up of contaminated sites. **Methods:** The oil-degrading bacteria, *Bacillus cereus* and *Pseudomonas aeruginosa,* were immobilized (3% v/v of 0.7 OD600) onto PVDF/CTA membrane in minimal salt media (MSM). The oil degradation ability of the immobilized bacteria was then tested against their planktonic free cells (3% v/v) by incubating them in 50 ml of MSM containing 0.1% v/v of crude oil for 72 hours at 30 °C and 200 rpm of shaking. GC-FID was used to analyse the rate of crude oil degradation of each sample. **Results:** The results showed that the immobilized *B. cereus* and *P. aeruginosa* were able to remove 44.2% and 26.6% of the crude oil, respectively, while their planktonic free cells removed 64.6% and 41.2% of the crude oil, respectively. **Conclusion:** *Bacillus cereus* performed better than *P. aeruginosa* in oil degradation, while the immobilized bacteria for both species performed less effectively than their planktonic counterparts. These results demonstrated the potential of using membrane immobilized oil-degrading bacteria as a bioremediation solution for oil spill clean-up. Further studies on continuous operation of the immobilized bacteria is needed to ensure the advantage of using PVDF/CTA membrane as the carrier.

Keywords: bioremediation, oil-degrading bacteria, *Bacillus cereus*, *Pseudomonas aeruginosa*, immobilization

O35

Metabolic and Genome Engineering of Microbial Chassis for Synthetic Biology and Industrial Biotechnology Applications

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Introduction: Recent advancement of metabolic engineering and synthetic biology approaches using microbes as chassis has provided a modular industrial biotechnology platform for the development of bio-based chemicals using sugars and lignocellulosic biomass as biofeedstock. **Methods:** Microbial utilization of xylose sugar and enhanced tolerance agains biomass-derived inhibitors such as furfural would enable improved and efficient biomanufacturing process important for industrial biotechnology applications. **Results:** In this work, we will present our recent endeavors in the engineering of model microbial chassis, *Corynebacterium glutamicum* to express recombinant xylonate dehydratase (XylD) that enabled the bacterial growth (OD_{600}=1.9) on 2% xylose minimal medium as opposed that the control strain pXMJ19 that could not grow (OD_{600}=0.2) after 48-H fermentation. To create a stable and plasmid-free expression of XylD, the XylD gene cassette was integrated into the bacterial genome at the chromosomal region of the xylose uptake IolT transporter via homologous recombination. In our efforts to develop a new metabolically-versatile and robust bioproduction host, *Pseumodonas extremaustralis* was engineered to express recombinant furfural reducatase (FucO) where the engineered pFucO strain showed increased tolerance and cell growth (OD_{600}=5.3) compared to pJM105 control strain that was inhibited during 48-H culture. To establish *P. extremaustralis* as bioproduction host, metabolic engineering strategy was employed to introduce DXP-to-limonene biosynthetic pathway genes (DXS, DXR, IDI, GPPS, LimS) that enabled limonene production (3 μg/mL) from glucose following 48-H cultivation. **Conclusion:** In sum, microbial engineering strategies have been successfully implemented in the engineered microbial chassis that provide starting platforms for biomanufacturing applications using biofeedstock as renewable sources.

Keywords: synthetic biology chassis, *Corynebacterium glutamicum*, *Pseudomonas extremaustralis*, genome engineering, industrial biotechnology

O36

Effect of Pectinase and Cellulase on the Yield, Physicochemical Properties and Sensory Preferences of Jackfruit Straw Juice

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Introduction: Jackfruit straws are usually discarded as agricultural waste despite of juice recovery for potential beverage production. Therefore, the effect of cellulase and pectinase on yield, physicochemical and sensory properties of jackfruit straw juice were studied. **Methods:** A total of 5 samples of jackfruit straw slurries treated with different ratios of pectinase (P) and cellulase (C) (ratio of P:C of 2:0 (S1), 1.5:0.5 (S2), 1:1 (S3), 0.5:1.5 (S4), 0:2 (S5)) were prepared, while slurry without enzymatic treatment was used as control sample. All enzyme-treated samples were incubated at 50°C for 2 h and enzymes were inactivated at 90°C for 5 min prior to obtain juice through filtration. **Results:** Juices yielded from all samples were significantly higher (p<0.05) with S3 obtained the highest yield (80.67%±1.15) compared to the control sample (37.33±2.31%). For the physicochemical analyses, all samples were significantly different (p<0.05) from the control sample. S3 showed the highest clarity (0.18Au± 0.001) and the lowest viscosity (44.33cP±0.577). Meanwhile, S5 showed the highest total soluble solids (2.83±0.12). Due to the liberation of polygalacturonic acid during pectin degradation, enzyme-treated samples except S5 showed a lower pH and higher titratable acidity compared to control sample. However, ascorbic acid of all samples did not significantly reduced (p>0.05) after enzyme treatment. Sensory evaluation elucidated a higher preference for appearance of S3 (6.32±1.72), but a higher preference for sweetness (5.16±1.92) and sourness (6.20±1.53) of S5. **Conclusion:** Taken together, results revealed that jackfruit straw juice (S3) treated with pectinase and cellulase at ratio of 1:1 exhibited a better juice quality in overall.

Keywords: jackfruit straw juice, enzymes, yield, physicochemical, sensory

O37

Optimization For The Green Synthesis of Silver Nanoparticles Using *Hibiscus cannabinus L.* (Kenaf) Leaves Extract

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Introduction: With the current search for natural alternatives in nanotechnology, plant extracts have garnered trememendous attention in the synthesis of nanoparticles. However, behavior and characteristics of the nanoparticles formed are highly dependent on the synthesis parameters due to their nanoscale size. **Methods:** In this study, kenaf leaves extract (KLE) was used to synthesise silver nanoparticles (KLE-AgNPs) whereby the effect of different pH, incubation/reaction time and temperature on the formation were analyzed. Additionally, the purification of KLE-AgNPs was also optimized via different centrifugal force. The KLE-AgNPs formed were characterized using UV-vis spectrophotometer, dynamic light scattering (DLS) analysis, FTIR and FESEM-EDX. **Results:** Results shown that KLE-AgNPs with 60.32±2.41 nm in size, -43.03±2.55 mV zeta potential, and low PdI were successfully formed. The optimal conditions were as follows; pH 11, 48 hours incubation time, reaction temperature of 37°C, and centrifugation at 10000*g* for purification. Furthermore, FTIR spectra confirmed the presence of bioactive compounds in KLE that aided in the synthesis as reducing, capping and stabilizing agents. Meanwhile, FESEM-EDX revealed that the KLE-AgNPs were spherical in shape and in the range of 20nm to 55nm. The strongest peak in the EDX spectrum represented silver thereby confirming the successful synthesis of AgNPs using KLE. **Conclusion:** The outcome of this study highlights the importance of identifying various operational factors that could affect the properties of AgNPs and their targeted applications in diverse fields.

Keywords: silver nanoparticles, green synthesis, kenaf leaves, process optimization, nanotechnology

O38

Potential Use of Fruit By-Products as a Source of Prebiotic and Functional Ingredients for Locally Isolated Probiotic Lactic Acid Bacterium, *Lactobacillus pentosus* A6 *In Vitro*

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Introduction: Prebiotics are non-digestible food ingredients that can enhance gut health by increasing the number of beneficial bacteria, improving the balance of gut bacteria, strengthening the gut barrier, and may even reduce inflammation, improve immune function, and lower the risk of some chronic diseases. Probiotic substrate choice varies across strain, making prebiotic selection critical for achieving synbiotic product. Therefore, the objectives of this study are to investigate growth compatibility of *Lactobacillus pentosus* A6 in various types and concentration of fruit-by products based prebiotics. **Methods:** The fermentability of prebiotic samples [powderized freeze-dried watermelon rinds, melon rinds, mango peels, jackfruit peels and sweet tapioca peels at concentration of 1.0, 1.5, 2.0 and 2.5% (w/v) respectively] by *L. pentosus* A6 were tested in batch fermentation. Cell viability, pH and titratable acidity were recorded at before and after 24 h of fermentation. **Results:** Results show that watermelon rinds at 1.5 % (w/v) recorded the highest viable cells number at 4.20 x 10^{10} ± 1.00 CFU/mL while 1 % (w/v) of jackfruit peels recorded the least viable bacterial count at 2.03 x 10^{8} ± 0.58 CFU/mL after 24 h of fermentation. Most of the carbon-free media supplemented with prebiotic displayed a higher viable bacterial count as compared to MRS medium (control). The highest bacterial count recorded the highest reduction of pH. **Conclusion:** The result demonstrated that the types and concentration of prebiotics exhibited significant effect on growth of *L. pentosus* A6. The synbiotic products can be used in the production of functional foods containing prebiotic ingredient or as a supplementation of prebiotic in the diet.

Keywords: lactic acid bacteria, probiotic, prebiotic, agro waste, fruit by-products

O39

In Vitro and *In Silico* Investigation of Antimicrobial Activity of Silver Nanoparticles Synthesized Using *Streptomyces* sp. PBD 311B

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Introduction: Silver nanoparticles (AgNPs) have proven to be a promising avenue to synthesize alternative biomedical agents for the prevention and treatment of infections caused by antibiotics resistant bacteria. The present study highlights the mechanistic approach of AgNPs inhibition against *S. aureus*. **Methods:** AgNPs are synthesized extracellularly using *Streptomyces* sp. PBD311B and the presence of AgNPs were confirmed using UV-Vis spectroscopy. The antimicrobial activity of AgNPs was determined using well diffusion assay. The surface topology of AgNPs treated *S. aureus* was determined using Atomic Force Microscopy. The proteins involved in the synthesis of AgNPs were resolved on SDS-PAGE and analyzed using LCMS/MS. Molecular docking was carried out using Haddock 2.4 to simulate the interaction of the proteins from cell lysate with the membrane protein of *S. aureus*. **Results:** UV-vis spectrum peak formed at 420 nm confirmed the presence of AgNPs. The antimicrobial activity of AgNPs against *S.aureus* was 7.5±0.7 mm. Meanwhile, molecular docking studies indicate the binding interaction of proteins with membrane protein (Sortase A) of *S. aureus*. **Conclusions:** The experimental findings and *in silico* molecular docking studies suggest the antibacterial potential of AgNPs against *S. aureus*.

Keywords: silver nanoparticles, *Streptomyces*. sp., antimicrobial activity, docking, *in silico* analysis

O40

Green Synthesis of Silver Nanoparticles using *Kaempferia parviflora* Rhizome Extract

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Introduction: Due to its numerous applications in different industries, nanotechnology is one of the science technologies that is now garnering attention. Using plants to biosynthesize nanoparticles from metal ions is an environmentally beneficial strategy. The characteristics of a nanoparticle differ from their macroscopic counterparts before they are reduced to the nanoscale. This study aims to optimise the ideal conditions to synthesize green silver nanoparticles (AgNPs) from *Kaempferia parviflora* rhizome extract. **Methods:** The green synthesis of AgNPs was accomplished using the aqueous extract of *Kaempferia parviflora* powder, in which plant biomaterials were used as a reducing and capping agent. Four different parameters were optimized for synthesizing AgNPs, including pH, reaction time, temperature, plant rhizomes concentration, and concentration of silver nitrate. AgNPs were characterized using UV-vis spectroscopy, Fourier transform infrared spectroscopy, transmission electron microscopy (TEM), and energy dispersive X-ray spectroscopy (EDS). **Results:** The AgNPs were synthesized using optimized parameters of pH 11 mixed with 2 mM AgNO3 at 75 °C, mixing ratio of silver nitrate to the volume of supernatant plant extraction of 5:4 ml, and incubation for 24 hours. The maximum absorbance of the UV-vis spectra was at 424 nm. **Conclusion:** The rate reduction of Ag^{+} to Ag^{o} from silver nitrate solution occurs at the optimized parameters within 24 hours. UV–Vis spectroscopy and FTIR analysis confirmed that the *Kaempferia parviflora* AgNPs rhizome extract could be exploited for further biological potential.

Keywords: *Kaempferia parviflora*, green synthesis, silver nanoparticles, optimization

O41

The Effect of Supplementation of *Lactococcus lactis* strain as Probiotic on the Growth and Survival of *Litopenaeus vannamei*

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Introduction: Acute Hepatopancreatic Necrosis Disease (AHPND) or Early Mortality Syndrome (EMS) is a bacterial disease in shrimps caused by pathogen *Vibrio parahaemolyticus*. It has culminated in huge loss in global shrimp production due to mass mortality. A probiotic strain *Lactococcus lactis* strain FA1 was recently isolated from shark intestine, showing inhibition towards the growth of the pathogen. Due to inhibitory potential, the effect of probiotics strain on growth performance of shrimp infected with *V. parahaemolyticus* was evaluated. **Methods:** The probiotic strain was incorporated into feed for juvenile shrimps *Litopanaeus vannamei* for 3 weeks before which they were then challenged with pathogen *Vibro parahaemolyticus*. The study compares 4 shrimp groups: Control (Without any treatment); Group A (Probiotic treated, uninfected); Group B (Probiotic treated, infected) and Group C (No probiotic, infected). The survival and growth performance (weight and length gain) of shrimps were evaluated in the following 30 days. Statistical analyses (ANOVA; Post Hoc Tukey) were used to compare between shrimp groups. **Results:** In general, infected shrimp demonstrated some of the key symptoms of AHPND (pale or white hepatopancreas), transparent body and erratic swimming behaviour. The supplementation of probiotics resulted in a reduced mortality for infected shrimp. The probiotic treated shrimp group significantly (P value< 0.05) showed a better weight gain, compared to both infected and uninfected group. Meanwhile, some of the infected shrimps were able to show recovery from infection. **Conclusions:** This indicated that the strain *Lactococcus lactis* is highly suitable for use as the future probiotic in shrimp aquaculture.

Keywords: Early mortality syndromes (EMS), shrimp probiotics, *Lactococcus lactis*, *Litopenaeus vannamei*

O42

Development of an Orally Administered Lactococcal-Based Vaccine Against *Streptococcus agalactiae* Infections in Tilapia Fish

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Introduction: Tilapia is the second most farmed fish in the world and accounts for 5.1% of total aquaculture production. Unfortunately, streptococcosis outbreaks in tilapia aquaculture have been consistently reported annually causing systemic infections associated with high mortality and morbidity leading to significant economic losses. Currently, existing vaccine candidates against *Streptococcus spp.* are designed for intraperitoneal injections that are not practical and labor-intensive. This has prompted farmers to protect livestock using antibiotics, thus encouraging the emergence of multidrug resistance bacteria. **Methods:** In this study, both surface immunogenic protein (SIP) and truncated SIP (tSIP) protein obtained from *S. agalactiae* were developed as oral vaccine candidates using *Lactococcus lactis* as a live delivery vehicle. Recombinant *L. lactis* expressing SIP and tSIP proteins were constructed and nisin-induced expression of proteins were detected in both intracellular and extracellular protein fractions by western blotting. Juvenile tilapia fishes were immunized orally by coating recombinant *L. lactis* strains on fish pellets. The immunized tilapia fishes were challenged with *S. agalactiae* via submersion. **Results:** The relative percentage survival (RPS) for SIP and tSIP vaccine groups were 50% and 88.89% respectively. Parameters such as quantitative expression of immune genes and sera IgM levels were evaluated between vaccinated and control groups to assess immunogenicity and efficacy. **Conclusion:** Future work will include *in vivo* challenge assessments of this vaccine candidate with adjuvants to boost immunogenicity in tilapia fishes.

Keywords: *Lactococcus lactis*, oral vaccine, *Oreochromis niloticus*, *Streptococcus agalactiae*, surface immunogenic protein (SIP)

O43

Genomic Study of Prebiotic-Hydrolysing Enzymes from Potential Probiotic *Bacillus velezensis* FS26 with *In Vitro* Validation

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Introduction: A genomic study on carbohydrate-active enzymes from *Bacillus velezensis* FS26 was an advanced technique used to predict the capability to utilise prebiotics. Prebiotics are substrates that increase bacterial growth while benefitting the host. Moreover, it contains glycosidic bonds that need to be hydrolysed by beneficial bacteria to deliver their effectiveness in the host. Thus, this study aims to predict the prebiotic-hydrolysing enzymes from the potential probiotic *Bacillus velezensis* FS26 genome with *in vitro* validation. *B. velezensis* FS26 was previously isolated from giant freshwater prawns and regarded as a potential probiotic for aquaculture. **Methods:** The genomic study was conducted by predicting the glycoside hydrolases from the *B. velezensis* FS26 genome using the dbCAN meta server. Additionally, the phenol red carbohydrate assay validated the prebiotic-utilising capability of *B. velezensis* FS26 using three commercial prebiotics, including lactulose, raffinose and inulin. **Results:** The genomic study predicted several enzymes capable of hydrolysing glycosidic bonds in the prebiotic structure, such as α-galactosidase, fructofuranosidase, levansucrase, and β-galactosidase. Moreover, the phenol red carbohydrate assay revealed the capability of *B. velezensis* FS26 to use commercial prebiotics, including lactulose, raffinose and inulin, in contrast to pathogenic *Aeromonas hydrophila* LMG13658 and *Vibrio parahaemolyticus* PKK24. **Conclusion:** *B. velezensis* FS26 showed the promising capability to utilise prebiotics, which could be a potential synbiotic for aquaculture.

Keywords: *Bacillus velezensis* FS26, carbohydrate active enzymes, glycosidic bond, genome, prebiotic

O44

The Effect of BAP, NAA and Kinetin Treatments on Micropropagation of *Zingiber officinale* var. Bentong (Bentong Ginger)

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Introduction: Bentong ginger (*Zingiber officinale* var. *Bentong*) is a valuable local herb grown in highlands of Bentong districts, Pahang. This ginger cultivar has strong aroma, larger and spicier rhizomes, higher pungency, and less fibrous pulp, as compared to domestic ginger. Bentong ginger is also well known for its significant quantities of pharmaceutically important phenolics, such as gingerol and shogaol. However, Bentong ginger cultivation is severely threatened by soil-borne diseases and scarcity of planting materials. Rhizomes that are commercially marketed, is also used as seeds for conventional propagation. Thus, a systematic micropropagation technique could serve as a suitable alternative for effective production of a disease and pest-free Bentong ginger planting materials. **Methods:** Young rhizome shoot buds explants were surface sterilized in 50% sodium hypochlorite, 70% ethanol and 0.2% mercuric chloride. The explants were then cultured in Murashige and Skoog (MS) media fortified with a range of different BAP, NAA and Kinetin concentrations, either alone or in combination. Cultures were maintained at 25±2°C with a 16-h photoperiod under an irradiance of 45 μmol m^{-2} s^{-1} provided by cool white, fluorescent light in growth room. **Results:** Murashige and Skoog (MS) media supplemented with 1.0mg/L BAP and 0.5mg/L NAA resulted in highest number of roots and shoots per plantlet. The *in vitro*-rooted plantlets were then successfully acclimatized. **Conclusion:** The present study's outcome can be adopted for large-scale production of disease-free Bentong ginger planting materials.

Keywords: *Zingiber officinale, in vitro* culture, Bentong ginger, BAP, NAA, kinetin

O45

Unlocking Hub Genes and Key Pathways Associated with Combined Abiotic and Biotic Stresses Using Modular Co-Expression Network Analysis In Rice (*Oryza sativa L.*)

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Introduction: Understanding molecular mechanisms in plant stress combinations is crucial for unraveling complex interactions in plant responses. In this study, we aimed to identify essential genes and pathways regulating the response to combined stresses in rice. **Methods:** We utilized the Modular Gene Co-Expression Network (mGCN) approach with CemiTool, an R package, to analyze gene expression profiles from four datasets obtained from the Gene Expression Omnibus (GEO) database, representing drought, salinity, tungro virus, and blast pathogen stresses. Gene Set Enrichment Analysis (GSEA) was employed to identify gene classes. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses were conducted to examine the functional enrichment associated with these gene clusters. Additionally, we used the STRING database to map the protein-protein interaction (PPI) network and identified hub genes using the MCC (Maximal Clique Centrality) algorithm. Furthermore, we verified the expression levels of hub genes using quantitative real-time PCR (qRT-PCR). **Results:** We identified highly correlated gene clusters organized into 11, 12, 46, and 14 modules and they highly involved with response to water deprivation, root development, defense response to fungus and biotic stimulus. Our findings revealed six hub genes that were identified as overlapping across all stresses, known to play critical roles in plant signalling pathways, regulating plant immune responses, and involvement in reactive oxygen species (ROS) in stress tolerance response. **Conclusion:** Overall, this study provides insights into the biological significance of combined biotic and abiotic stresses in rice and may contribute to the development of future strategies for rice tolerance improvement.

Keywords: co-expresison network, modular analysis, protein-protein interaction, hub genes, biotic and abiotic stress

O46

Optimization of Extraction and Antioxidant Activities of *Kaempferia parviflora* Rhizome

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Introduction: Traditional herbal plants contribute significantly to human health owing to the abundance of appealing bioactive compounds. Among them is *Kaempferia parviflora* (KP) rhizome, a widely used traditional medication that attracted diverse attention in East and Southeast Asia. The KP extract is rich in flavones derivatives, a subgroup of flavonoids resulting in astonishing biological activities. Nonetheless, the antioxidant activity of the KP extract remained a point of contention as the free radicals scavenging activity of the crude extract is influenced by multiple factors. Therefore, this study aims to optimise several parameters and extraction methods to maximise extraction yields, phenolic and flavonoid content and achieve the highest possible levels of antioxidant activity in the KP extracts. **Methods:** The KP rhizomes were extracted by maceration techniques using different solvent types (ethanol and methanol). The antioxidant activities of KP extract were optimised for different solvent concentrations (70 and 90% V/V), temperature degrees (room temperature and 60 °C), and sample forms (fresh and dried KP) using a Uv-Vis spectrophotometer. All the samples were subjected to Total Phenolic Content (TPC), Total Flavonoid Content (TFC), and 2,2-Diphenyl-1-picrylhydrazyl (DPPH) assay. **Results:** Increasing ethanol concentrations up to 90% enhanced the yield (27.18%), TPC (430.14 ± 19.25), and TFC (694.32 ± 7.33), but not for DPPH where 90% of methanolic extraction exhibited the highest DPPH scavenging activities for both fresh (94%) and dried (86%) KP samples. **Conclusion:** *Kaempferia parviflora* extract is highly valuable for its antioxidant activity under optimal conditions. Extraction methods play a major role in controlling the phytochemical properties of KP rhizome extracts. This study found that 90% of ethanol concentrations affected KP's antioxidant properties by altering antioxidant components and their activities.

Keywords: *Kaempferia parviflora*, antioxidant activities, extraction, flavonoid, phenolic

O47

Characterizing *Enterobacter hormaechei* from a Clinical Sample in Sabah: Insights from Whole-Genome Sequencing and Bioinformatics Analysis

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Introduction: *Enterobacter* spp. are rod-shaped, gram-negative, facultatively anaerobic bacteria. While they are typically non-pathogenic, they can lead to nosocomial infections in humans. The objective of this study is to characterize a local isolate of *Enterococcus* spp., obtained from a clinical sample collected at a tertiary hospital in Kota Kinabalu, Sabah, using a whole-genome sequencing approach. **Methods:** After receiving approval from both the Medical Research Ethics Committee (MREC), Ministry of Health, Malaysia (No. NMRR-19-1770-48622) and the University Malaysia Sabah ethical committee (JKEtika 1/19(26)), the collected samples were cultured for bacteria on blood agar. Subsequently, the bacterial DNA was extracted and characterized by utilizing 16S rRNA sequencing. Once verified, the bacterial genome was sequenced using the Illumina HiSeq 4000 platform. The quality of the sequence reads was checked using FastQC. Finally, the genome was annotated and characterized using PATRIC, which is a comprehensive bioinformatics resource tool for bacteria. **Results:** The whole genome sequencing resulted in 76 contigs, estimating a genome size of 5,023,587 bp, with an average G+C content of 54.88%. The N50 length was 378,113 bp. We identified 4,910 protein-coding sequences (CDS), 74 transfer RNA (tRNA) genes, and 5 ribosomal RNA (rRNA) genes. Among the CDS, there were 829 hypothetical proteins and 4,081 proteins with functional assignments. We also detected 17 putative genes involved in efflux pump and 75 genes that conferred antibiotic resistance. The phylogenetic tree showed that the isolate belongs to *Enterobacter hormaechei*. **Conclusion:** The molecular characterization data obtained from our study could be valuable in the detection of pathogenic microorganisms responsible for Enterobacter spp. infections. Furthermore, this data could expand the use of whole genome sequencing in clinical settings to identify and resolve suspected outbreak cases.

Keywords: *Enterobacter* spp., *Enterobacter hormaechei,* whole genome sequencing, phylogenetic analysis

O48

Genetic of Different Strains as Potential Factor in Methicillin Resistance Level Determination in Methicillin-Resistant *Staphylococcus* species

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Introduction: Methicillin resistance (MR) in *Staphylococcus* species was carried through mobile genetic elements (MGE) called Staphylococcal Chromosomal Cassette mec (SCCmec). However, strain-specific factors may also contribute to resistance characteristics in *Staphylococcus* species. Hence, this study was conducted to analyse different strain factors for the understanding of methicillin-resistant determinants in *Staphylococcus* species. **Methods:** Thirty-five isolates which carry the mecA gene were subjected to typing methods; dru typing and PCR-RFLP of gap genes. Bioinformatics analysis such as phylogenetic tree construction for dru region and cluster analysis of gap-RFLP using GelcomparII were conducted to observe the correlation of different strain factors toward methicillin resistance determination in MRSA and MRCoNS. **Results:** Sixteen MRSA and nineteen MRCoNS were identified by biochemical tests, 30 µg cefoxitin antibiotic disc susceptibility test and mecA gene screening. From 35 MR *Staphylococcus* isolates, 32 isolates (MRSA=13; MRCoNS=19) were positive for dru region amplification by using PCR. Three dru types were detected which are dt11c (MRSA=12; MRCoNS=5), dt10a (MRSA=1; MRCoNS=12) and dt7a (MRCoNS=1). For RFLP analysis, all isolates were positive for gap gene amplification by using PCR and produced 11 different gene sizes after digestion with AluI restriction enzyme and showed an obvious distinct pattern between MR with MIC ≥8 µg/ml and MR with MIC <8 µg/ml. **Conclusion:** Sequence polymorphism in dru and gap genes can be used to differentiate various resistance levels among different *Staphylococcus* species.

Keywords: Methicillin resistance *Staphylococcus* species, dru typing, gap gene, RFLP

O49

Lipidomics Analysis of Skeletal Muscle in Aging Rats

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Introduction: Sarcopemia is the gradual loss of skeletal muscle mass and function with age. Little is know about the changes in the lipidome of skeletal muscle during aging. This study aimed to identify lipidomics changes in skeletal muscle during aging using rats as a model. **Methods:** Male Sprague-Dawley rats were used in this study, and skeletal muscle samples were collected at 6, 12, 21 and 24 months old. Lipids were extracted using the Folch method, and untargeted lipidomics approach was used via liquid chromatography mass spectrometry. MS-DIAL software was utilized for data preprocessing and lipid annotation, and statistical and network analyses were performed using MetaboAnalyst and LION/web Lipid Ontology, respectively. Novel object recognition test was also conducted to assess locomotor activities in the rats. **Results:** The results of the novel object recognition test confirmed that locomotor activities of the rats decreased with age. A total of 1,681 lipid species were detected in the rats' skeletal muscle at different ages, with 1,089 lipids showing significant differences in expression with age. These lipids were classified as monounsaturated and saturated fatty acids, lysoglycerophospholipids, glycerophosphocholines, and glycerophosphoethanolamines, which function mainly as membrane components located at the endoplasmic reticulum and mitochondria. These lipids possess physical or chemical properties that include a headgroup with a positive charge/zwitterion and a positive intrinsic curvature. **Conclusion:** This study's findings suggest that lipid metabolism in skeletal muscle undergoes alterations during aging. These lipids could serve as potential biomarkers to indicate sarcopenia and provide baseline data for better understanding muscle aging.

Keywords: sarcopenia, aging, skeletal muscle, lipidomics, LCMS

O50

The Effects of *Kaempferia parviflora* extract on Anthropometrical, Nutritional and Lipid Profile Parameters on Rats Fed a High-Fat Diet

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Introduction: Metabolic syndrome (MetS) is a constellation of many metabolic disorders, such as hypertension, impaired glucose tolerance, dyslipidemia, and obesity. The widespread of MetS in society, mainly in developing countries is becoming an important health problem. Thus, there is an increasing need to develop new treatments for this pathology disease. The main objective of the present study was to evaluate the MetS-associated alterations developed in high-fat diet (HFD) induced obesity in the rodent model. *Kaempferia parviflora,* or black ginger is a native rhizome plant in Southeast Asia with novel bioactive compounds and health-promoting properties. **Methods:** Male Sprague-Dawley rats were fed ad libitum for 8 weeks with HFD. The rats were then administered two doses of ethanolic extract of *Kaempferia parviflora* (EtKP) at 100mg/kg and 200mg/kg body weight for another 8 weeks. Changes in anthropometry, dietary status, and lipid parameters were measured. **Results:** Rats fed with HFD showed elevation in body weight with a minimum of 20% weight increase and development of white adipose tissue mass compared to normal diet rats. The EtKP administration at 100mg/kg and 200mg/kg body weight significantly decreased weight gain and food intake and improved lipid profiles in obese rats. In addition, the administration of EtKP reduced adiposity by decreasing the white adipose tissue mass and adipocyte size. **Conclusion:** These findings demonstrated that EtKP exhibited anti-obesity effects by suppressing body weight gain and food intake, improving lipid profiles, and reducing white adipose tissue mass in obese rats fed HFD.

Keywords: *Kaempferia parviflora*, obesity, high-fat diet, lipid profile, nutritional changes

O51

RU-615 Reduces Fibronectin Deposition in Dexamethasone-Induced Human Trabecular Meshwork Cells Through TGFβ1-SMADs Signalling Pathway

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Introduction: TGFβ-SMAD pathway has been associated with increased extracellular matrix (ECM) in the trabecular meshwork (TM) leading to aqueous humour outflow resistance and elevation of intraocular pressure (IOP) in primary open-angle glaucoma (POAG). Elevated IOP remains the only modifiable risk factor and treatment target for POAG. RU-615, a derivative of imidazo[1,2-a]benzimidazole has been shown to counteract the steroid-induced increase in IOP. However, whether it affects the deposition of ECM components involves TGFβ-SMAD pathway in the TM, is unknown. This study explored the involvement of TGFβ-SMAD pathway in the effects of RU-615 on the expression of fibronectin (FN) in dexamethasone-treated human TM cells (HTMCs). **Methods:** Primary HTMCs were incubated with 0.1 mM RU-615 with or without 100 nM dexamethasone. The cell lysate and culture media were collected after 3 and 7 days of incubation for gene and protein analysis of FN, TGF-β1, SMAD4 and SMAD7 using real-time polymerase chain reaction (RT-qPCR) and ELISA, respectively. **Results:** RU-615 treatment downregulated the gene and protein expressions of FN by 1.46- and 39.59-fold, respectively; TGF-β1 by 0.48- and 65.47-fold, respectively and SMAD4 by 0.76- and 28.3-fold, respectively and upregulated the SMAD7 by 2.49- and 12.13-fold, respectively in comparison with dexamethasone treated group ($p<0.05$). **Conclusion:** Reduction of fibronectin by RU-615 induced by dexamethasone in HTMCs involved the repression of TGF-β1 and SMAD 4 and enhancement of the inhibitory SMAD 7 signalling. These effects may contribute to IOP-lowering properties of RU-615 leading to ECM reduction and enhancing aqueous humour outflow in the TM.

Keywords: dexamethasone, extracellular matrix, human trabecular meshwork cells, imidazo[1,2-a]benzimidazole, primary open angle glaucoma

O52

Investigating the Neuroprotective Effect of Estrogenic Compounds in an MPP+-Induced *In Vitro* Model of Parkinson's Disease

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Introduction: The higher incidence and severity of Parkinson's disease (PD) in men compared to women suggests a protective role of female sex hormones. Estrogenic compounds are reported to be neuroprotective with their ability to block apoptotic cell death and reduce oxidative stress in different models of brain injury. However, the adverse side effects of the long-term administration of the female endogenous hormone, 17β-estradiol, fueled the exploration of non-steroidal and naturally-sourced phytoestrogens as a safer alternative. This study investigated the neuroprotective potential of 17β-estradiol and the phytoestrogens, Genistein and Resveratrol, against MPP+ (1-methyl-4-phenyl pyridinium)-induced cell death in SH-SY5Y neuroblastoma cells. **Methods:** To characterize MPP+-induced apoptosis in SH-SY5Y cells, changes in the number of apoptotic nuclei, time-dependent production of reactive oxygen species (ROS), and caspase-3 activity were measured. Changes in cell viability were measured after pre-treating SH-SY5Y cells with three different concentrations of each estrogenic compound before the incubation with the MPP+ neurotoxin. **Results:** MPP+ increased the number of apoptotic nuclei, time-dependent ROS production and caspase-3 activity in SH-SY5Y cells. The neuroprotection study showed that a 24-hour pre-treatment of all three estrogenic compounds had no significant neuroprotective effect on SH-SY5Y cell death induced by MPP+. **Conclusion:** While previous studies suggest protective effects of these estrogenic compounds against other PD models, no existing studies have explored the impact of Genistein and 17β-estradiol in SH-SY5Y cells challenged with MPP+. Therefore, future studies can employ alternative *in vitro* and *in vivo* PD models to further evaluate the neuroprotective efficacy of these estrogenic compounds and aid in the search for disease-modifying drugs for this debilitating disease.

Keywords: neuroprotective agents, Parkinson's disease, estrogenic compounds, phytoestrogen, apoptosis

O53

The Effects of Environmental Enrichment Conditioning on Memory and Learning in Chronic Social Defeat Stress Mice

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Introduction: By the year 2023, World Health Organization projected that major depressive disorder would become the leading contributor to the total global burden of disease. Chronic psychological stress have been shown to have a direct effect on synaptic plasticity and stress associated memories, causing a biological predisposition to depression. On the other hand, a growing body of research demonstrates that environmental enrichment, which promotes physical exercise, social engagement, and sensory stimulation, has positive effects on the neurocognition functions. However, there is lack of study done to clarify the effects of environmental enrichment on learning and memory in a chronic social defeat stress (CSDS) model. **Methods:** C57BL/6N mouse were housed in environmentally enriched housing condition for 30 days and later were subjected to daily social defeat stress by a CD1 aggressor mice for a period of 10 days. Force swim test (FST) and tail suspension test (TST) were used to assess depressive-like behaviour. Subsequently, memory and learning functions were assessed by Y-maze and novel object recognition (NOR) tests. **Results:** Environmental enrichment conditioning showed to significantly alleviate depressive-like behaviour in the mice subjected to CSDS. Dysfunction in spatial working memory as well as recognition memory sensitivity induced by CSDS were significantly reduced in mice with environmental enrichment conditioning as compared to CSDS mice without the exposure. **Conclusion:** Data from this study highlights the importance of enriched environmental preconditioning in alleviating memory and learning impairment induced by CSDS.

Keywords: environmental enrichment, social defeat, chronic stress, memory, learning

POSTER ABSTRACTS

PC: Competition Category for Professional
SC: Competition Category for Student
EP: Non-Competition Category for Professional and Student

PC01

Identification of Key Starch Biosynthesis Genes Across Malaysian Rice Varieties with Varying Amylose Contents

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Introduction: There are varying amylose contents (ACs) across Malaysia rice germplasm of which rice ACs are basically classified as very low (<10%), low (10-19%), intermediate (20-24%) and high amylose content (>24%). **Methods:** In this study, we aimed to obtain the expression profiles and to identify starch biosynthesis genes in the whole grain of a selected 10 rice varieties via relative gene expression quantification. These varieties consisted of Pulut Malaysia and Pulut Siding (low AC), MASRIA and MRQ76 (low AC), MR307 and MR297 (intermediate AC) and MRQ74 and MR103 (high AC), where seeds were obtained from MARDI Rice and Paddy Research Centre. **Results:** Expression profiles of a total of 17 genes which involved in the starch biosynthesis pathway were obtained and their values were normalised using reference gene UBQ5, while MRQ76 was used as a reference variety for comparison across varieties. One-way ANOVA with Tukey HSD Post-Hoc analysis showed that significant differences between very low and low AC rice groups were SSS1, PUL, SBE1, SBE3 and AGPL2; very low and intermediate AC rice groups were SSS1, PUL, SBE1, SBE3 and GBSS1; very low and high AC rice groups were SSS1, PUL, SBE1, SBE3 and GBSS1; low and high AC rice groups was PGM (p<0.05). Linear regression analysis predicted that GBSS1 and SBE3 were the significant positive and negative determinant factors for rice grain amylose content, respectively (p<0.05). **Conclusion:** The overall findings from this study provides important information related to rice amylose trait that can be further applied to future cross-breeding or genome editing work in local rice varieties.

Keywords: amylose content, gene expression profiling, rice grain, starch biosynthesis

PC02

Utilizing Metabolite Analysis for Understanding Recalcitrant Behavior of Desiccated Mangosteen Seeds

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Introduction: Mangosteen is well-known for its sweet and exquisite flavour, making it one of Malaysia's most important exports. However, mangosteen seeds do not tolerate desiccation and low temperature and hence loses its viability quickly. This study aims to investigate seed metabolism under different periods of desiccation, which will help develop suitable seed storage methods for recalcitrant seeds. **Methods:** Seeds extracted from the fruits were cleansed before desiccation at different periods (0, 6, 16, 24, and 48 h) in a desiccator with silica gel (140 g). Seeds were then examined for moisture content (drying in the oven at 103 °C for 16 h) and germination to observe the seed survivability. Extraction was done with 80% methanol and 0.1% formic acid. The extracts were subjected to a phytochemical profile for screening. Subsequently, Liquid Chromatography-Mass Spectrometry (LC-MS) will be utilized to provide a complete metabolite profile of each treatment given. **Results:** The moisture content of the seeds declined as exposure prolonged, decreasing from 51.1% (at 0 h) to 32.6% (after 48 h). After six weeks, the highest germination percentage was recorded at 95% for 0 h and 24 h desiccation. In the phytochemical profile, the colour intensity increases as the desiccation period increases. SIMCA analysis of the LC-MS data showed no grouping from the different treatments. **Conclusion:** In conclusion, 24-hour desiccation might be recommended as a feasible strategy for mangosteen seed storage. The metabolites profiled from the chemical analysis may provide critical information helpful in understanding the behaviour of recalcitrant species.

Keywords: desiccation, Liquid Chromatography-Mass Spectrometry (LC-MS), recalcitrant seed

PC03

Circumventing Oxygen Limitations in Industrial Fermentation, a Metabolic Engineering Approach

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Introduction: Apart from respiration, oxygen is required for the regulation of a variety of cellular functions. Oxygen deficiency can alter the function of intracellular proteins, and affect the biosynthesis of specific sets of proteins, as well. The deficiency of oxygen effects the function of global transcription factors. Once the biomass concentration increases in a fermentation process, the broth gets viscous, aeration becomes limited, and the dissolved oxygen (DO) saturation dips severely, thereby reducing the productivity. Co-expression of Vitreoscilla hemoglobin, inducible under oxygen deficient conditions, boosts oxygen production from inside the fermentation medium, overcoming its limitation and restoring recombinant protein productivity. In our study, Vitreoscilla hemoglobin (vitHb) was co-expressed with the Staphylokinase (STK) gene in *E. coli* (BL-21) strain. **Methods:** The culture conditions were optimized simultaneously using Statistical optimization techniques, e.g., Response Surface Methodology (RSM). **Results:** Highest production of intracellular STK was observed at 140.4 mg/L at shake flask level in optimized semi-synthetic medium after 24h. At 5L fermenter level, the production of STK maximized to 372.7mg/L (increase by 23.2%), co-expressing vitHb gene at 30% DO concentration, as against 302.1mg/L without the vitHb at 50% DO saturation. **Conclusion:** Our study provides a simple and convenient way to overcome DO limitations in submerged fermentation processes. It shows enhancement in the recombinant STK production levels by 23%, compared to control (without vitHb gene) that can increase production and make the bioprocess economical at industrial levels.

Keywords: dissolved oxygen, metabolite, microbial hemoglobin, fermentation

PC04

Analysis of *Salmonella* Brancaster Isolated from Chicken in Malaysia by Multilocus Sequence Typing

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Introduction: *Salmonella* Brancaster is a chicken-associated serovar that is increasingly reported in Malaysia. Conventional *Salmonella* serotyping is based on the bacteria's outer membrane lipopolysaccharide O-specific, phase 1 and 2 flagellar H-proteins. The limitation of conventional serotyping is unable to study the genetic and clonal relationships of *Salmonella* of the same serovar. Multilocus sequence typing (MLST) is a DNA sequence-based typing method used to study the genetic diversity and relatedness of the highly diverse *Salmonella.* **Methods:** In this study, we used MLST to examine the sequence type (ST) and genetic diversity of 10 representative *S.* Brancaster isolates from chicken cloacal swabs and raw chicken meat. **Results:** Eight *S.* Brancaster isolates were assigned to ST2133 by the MLST allelic profiles, with exact matches at all 7 loci. The remaining 2 *S.* Brancaster isolates with different allele number at the *aroC* locus were likewise assigned to the closest match ST2133 based on 6 loci. The maximum-likelihood dendrogram constructed from concatenated sequences of the 7 loci divided them into 9 clusters. **Conclusion:** The *S.* Brancaster in the present study revealed clonal diversity, indicating that they were heterogeneous. This study gives an insight into using MLST sequencing data to analyse the clonal relatedness between *Salmonella* of the same serovar, as compared to conventional serotyping.

Keywords: *Salmonella* Brancaster, chicken, multilocus sequence typing, ST2133

PC05

Gene Expression Analysis of Methicillin-Resistant *Staphylococcus aureus* treated with Silver nanoparticles-Kaempferol (AgNPs-K)

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Introduction: Methicillin-resistant *Staphylococcus aureus* (MRSA), a multidrug resistant strain, is known to cause a threat to public health due to its limited therapeutic treatment. Kaempferol (K) is a natural flavonoid that shows antibacterial activities toward MRSA, but its effectiveness is limited due to its low water solubility. Hence, kaempferol were incorporated with silver nanoparticles (AgNPs) to enhance the solubility and antibacterial activity. **Methods:** Thus, this study was done to determine the antibacterial activities and mechanism of action of silver nanoparticles-kaempferol (AgNPs-K) against MRSA by using Next generation sequencing (NGS). NGS has been done to MRSA RNAs treated by AgNps-K. Realtime PCR had been done to validate the results of NGS. **Results:** In this analysis, a total of 1222 genes had been identified. Total number of down-regulated genes was 581. Meanwhile, the number of up-regulated genes was 641. Data analysis of differential expression genes (DEGs) showed that AgNPs-K extracts strongly induced the differential expression ($p<0.05$). KEGG pathway analysis revealed that the AgNPs-K significantly affected biosynthesis peptidoglycan, gene expression, RNA processing, and macromolecule metabolism processes in MRSA. **Conclusion:** Data analysis revealed that multiple mechanisms of action were involved in antibacterial activity of AgNPs-K toward MRSA.

Keywords: MRSA, silver-nitrate, kaempferol

PC06

Modulation of Tocotrienol-Rich Fraction on Brain Proteome Profiles and Cognitive Function in APP/PS1 Mice

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Introduction: Alzheimer's disease (AD) is a neurodegenerative disorder, characterized by a gradual impairment in learning and memory. The pathological hallmarks of AD include the accumulation of amyloid plaques and tau protein neurofibrillary tangles. However, little is known about the effect of vitamin E analogs on AD. Therefore, this study was carried out to evaluate the effect of tocotrienol-rich fraction (TRF), a mixture of vitamin E analogs derived from palm oil on APP/PS1 transgenic mice, a mouse model of AD. **Methods:** APP/PS1 mice were supplemented with TRF orally for a duration of 10 months. Cognitive assessments were evaluated by novel object recognition and Morris water maze tasks. Meanwhile, open field test was conducted to assess the locomotor activity. Proteomics analysis was performed on the mice brain using liquid chromatography tandem mass spectrometry. Immunohistochemistry and thioflavin-S staining were performed to examine the TRF effect on amyloid pathology. **Results:** APP/PS1 mice treated with TRF showed improvements in exploratory activity, learning, and memory as assessed by the behavioral tests. Proteomics analysis showed that TRF altered proteins in the APP/PS1 mice in a brain region-specific manner. TRF modulated the expression of amyloid beta (Aβ) protein in hippocampus. Reduction of Aβ deposition was also observed in the APP/PS1 mice brain. **Conclusion:** TRF supplementation improved exploratory activity, learning and memory abilities in APP/PS1 mice. Amyloid pathology ameliorated with the treatment of TRF. TRF also potentially exerts its neuroprotective effects in APP/PS1 mice brain by modulating proteins involved in various biochemical pathways.

Keywords: Alzheimer's disease, tocotrienol, palm oil, brain, proteomics

PC07

Dynamic Changes in the Oil Palm (*Elaeis guineensis* Jacq.) Mesocarp Proteome during Development and Ripening

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Introduction: Palm oil is an edible vegetable oil derived from lipid-rich fleshy mesocarp tissue of oil palm (*Elaeis guineensis*) fruit and has global economic and nutritional significance. Oil palm fruit ripening is a coordinated process involving complex biosynthetic pathways. While the understanding of oil biosynthesis in plants is growing, more research into the fundamentals of oil biosynthesis in oil palm is still needed. As such, there has been ongoing interest in elucidating the mechanism of oil production in oil palm fruits through proteomic approach. **Methods:** In this study, gel-, combination geLC- and liquid chromatography (LC)-based proteomics were established to investigate the proteome of the oil palm fruit mesocarp at different developmental stages according to week after anthesis (WAA). **Results:** In total, 172 proteins were found to be differentially expressed (p-value <0.01, fold change>5) during the preceding lipid biosynthesis, 392 proteins during lipid biosynthesis and 402 proteins during the ripening phase, respectively. Our results revealed clear metabolic shifts involving glycolysis-related enzymes as well as lipid, amino acid and secondary metabolisms from early stages of fruit development (10 to 16 WAA) throughout maturation and ripening phases (16 to 24 WAA). **Conclusion:** The findings would benefit the development of genetic markers for oil palm breeding programmes and confer better understanding of key processes throughout oil palm fruit development.

Keywords: oil palm, fruit development, ripening, proteomics, mass spectrometry

PC08

Neuroprotective Effect of Ethanolic Extract of *Polygonum Minus* Protects on Differentiated Human Neuroblastoma Cells (SH-SY5Y) against H_2O_2 -Induced Oxidative Stress

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Introduction: *Polygonum minus* Huds (*P. minus*) known as 'kesum' is widely used in traditional medicine. *P. minus* exhibited several medicinal and pharmacological properties. The current study aimed to investigate the neuroprotective effects of *P. minus* on H_2O_2-induced neurotoxicity in SH-SY5Y cells. **Methods:** The neuroprotective effects and mechanisms of *P. minus* ethanolic extracts (PMEE PMEE against H_2O_2-induced neurotoxicity were investigated in the differentiated SH-SY5Y cells through cell cytotoxicity assay. With respect to the nuclear factor erythroid 2-related factor 2/antioxidant response element (Nrf2/ARE), nuclear factor kappa B-cell (NFκB/IκB), and mitogen-activated protein kinase (MAPK) signalling pathways, the influence of PMEE pre-treatment on gene expression levels in differentiated neuronal cells was assessed using quantitative polymerase chain reaction (qPCR). The acetylcholine (ACh) concentration in the culture medium was measured using an enzyme- linked immunosorbent assay (ELISA). **Results:** Our study showed that the PMEE provided neuroprotection against H_2O_2 -induced oxidative stress by activating Nrf2/ARE, NFκB/IκB and MAPK signaling pathways in PMEE pre-treated differentiated SH-SY5Y cells. Meanwhile, the acetylcholine (ACh) level was decreased in oxidative stress-induced treatment group after 4 hours exposure with H_2O_2. **Conclusion:** In conclusion, PMEE may aid in reducing oxidative stress as a preventative therapy for neurodegenerative diseases. The results indicate that PMEE has neuroprotective effects on SH-SY5Y neuroblastoma cells in-vitro.

Keywords: *P. minu*s, neuroprotective, oxidative stress, SH-SY5Y, neurodegenerative disease

PC09

Effects of *Barringtonia racemosa* Aqueous Extract in Male Reproductive Function in Streptozotocin-Nicotinamide (STZ-NA)-Induced Diabetic Rats

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Introduction: Diabetes mellitus (DM) is a chronic metabolic disorder associated with various complications which include derangement in male reproductive functions. *Barringtonia racemosa*, has been studied widely as a complementary intervention in managing DM. However, the effect of *B. racemosa* on the male reproductive system is yet to be elucidated. Therefore, this study aimed to investigate the potential protective role of *B. racemosa* on male reproductive functions in type 2 DM (T2DM). **Methods:** The diabetic rats were administered 250 and 500mg/kg/day body weight of *B. racemosa* aqueous extracts (BRAE) for five consecutive weeks with fasting blood glucose (FBG) and body weight obtained every week. Following sacrifice, testes homogenates were analysed for antioxidant activity levels. The steroidogenic function of the testes was determined by the testosterone and 17β-Hydroxysteroid dehydrogenase III (17β-HSD3) levels. The testes sections were visualized for histopathological changes and sperm count and its morphology was obtained for further evaluation. **Results:** Administration of BRAE ameliorates the FBG level and preserved the testes oxidative stress marker by reducing lipid peroxidation and improve the antioxidant enzyme. This finding is supported by the histopathological finding which reveals amelioration of the structural damage in the testes of diabetic rats treated with BRAE. BRAE also alleviates the steroidogenic function of the testes with significant improvement in testosterone and 17-hydroxysteroid dehydrogenase levels. The sperm count and sperm morphology were improved compared to non-treated diabetic rats. **Conclusion:** *B. racemosa* prevents diabetes-induced male infertility possibly via their antioxidants potential

Keywords: *Barringtonia racemosa,* antidiabetic, antioxidant, male infertility

PC10

Gas Chromatography and Mass Spectrometry Profiling and The Antiparasitic Potential of Borneo Fern

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Introduction: *Nephrolepis biserrata* belongs to the family Nephrolepidaceae and is widely distributed in Borneo. It is traditionally consumed by the locals to treat different diseases. **Methods:** In the current study, we highlighted the phytochemical composition of the solvent extract of the fern through gas chromatography-mass spectrometry (GC-MS). We also investigated the antiparasitic activity of the solvent extract of the fern against the aquaculture parasitic leech, *Zeylanicobdella arugamensis*. **Results:** The GC-MS analysis indicated the presence of phenolics (phenol, benzyl alcohol, 2,4-bis(1,1-dimethylethyl phenol, and catechol), fatty acids (n-hexadecanoic acid and octadecanoic acid), and diterpene alcohol (phytol). Various concentrations of methanol extracts of the fern were tested experimentally against *Z. arugamensis*, resulting in significant anti-parasitic activity, with 100% mortality of parasitic leeches observed. The average time to kill the leeches at concentrations ranging from 25 to 100 mg/ml was 25 to 4 minutes, respectively. **Conclusion:** Our results suggest that the solvent extract of Borneo fern is a good source of secondary metabolites with strong potential as a natural control agent against parasitic leech infestation. However further research is needed to purify and isolate the secondary metabolites of the extract responsible for the antiparasitic activity.

Keywords: secondary metabolites, fern, *Nephrolepis biserrata*, antiparasitic

PC11

Identifying Hotspots of Tuberculosis Cases in Gombak, Selangor, Malaysia

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Introduction: Tuberculosis (TB) incidence is the highest in Gombak among other districts in Selangor, which needs high priority on visualizing disease transmission based on spatial dimension. Therefore, this cross-sectional study aimed to identify the hotspots location of TB cases in Gombak. **Methods:** The sociodemographic data of 3325 TB cases from 1st January 2013 to 31st December 2017 were collected from the MyTB web and Tuberculosis Information System (TBIS) database at the Gombak District Health Office and Rawang Health Clinic. Detailed information includes individual's ID, date of diagnosis, and patient's address. The coordinate of each patient's address was geocoded using Google Earth and then they were georeferenced with base map in AcGIS. Getis-Ord Gi* statistics was applied to identify the hotspots and coldspots of TB cases. This study validated the hotspots by randomly captured pictures on several hotspot locations. **Results:** The map displayed that hotspot locations were consistently located in the southwestern part of the study area, with 99% (136 points) and 95% (65 points) confidence levels. This could be attributed to the overcrowding of inmates in the Sungai Buloh prison located there. Throughout the years of study period, the location of hotspots shifted gradually from the northwestern to the southwestern parts of the district. These hotspot locations also cover the other areas such as apartment, hostel, market, school, and factory. **Conclusion:** This study highlighted the role of hotspot analysis to identify areas with a high TB burden based on high densely populated and vulnerable areas, which helps in improving targeted intervention and public health surveillance.

Keywords: geographic information system, hotspot, map, spatial, tuberculosis

PC12

Chemopreventive Effects of Germinated Rough Rice Crude Extract in Inhibiting Azoxymethane-Induced Aberrant Crypt Foci Formation in Sprague-Dawley Rats

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Introduction: Chemoprevention has become an important area in cancer research due to low success rate of current therapeutic modalities. Diet plays a vital role in the etiology of cancer. This research was carried out to study the chemopreventive properties of germinated rough rice (GRR) crude extract in Sprague-Dawley rats induced with azoxymethane. Germination of rough rice causes significant changes in several chemical compositions of presently bioactive compounds. These compounds may prevent or postpone the inception of cancer. **Methods:** Fifty male Sprague-Dawley rats (6 weeks of age) were randomly divided into 5 groups which were (G1) induced with azoxymethane (AOM) and not given GRR (positive control), (G2) induced with AOM and given 2000mg/kg GRR, (G3) induced with AOM and given 1000 mg/kg GRR, (G4) induced with AOM and given 500 mg/kg GRR, and (G5) not induced with AOM and not given GRR crude extract (negative control). To induce colon cancer, rats received two IP injections of AOM in saline (15mg/kg) for two subsequent weeks. Organs were removed and weighed. Aberrant crypt foci (ACF) were evaluated histopathologically. β Catenin expressions were determined by Western blot. **Results:** Treatment with 2000mg/kg GRR crude extract not only resulted in the greatest reduction in the size and number of ACF but also displayed the highest percentage of nondysplastic ACF. Treatment with 2000mg/kg GRR also gave the lowest level of expression in β-catenin. **Conclusion:** Thus, GRR could be a promising dietary supplement for prevention of colorectal cancer (CRC).

Keywords: chemoprevention, germinated rough rice, azoxymethane, colorectal cancer, aberrant crypt foci

SC01

Foodborne Pathogens in Leafy and Non-leafy Vegetables

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Introduction: The rise in the consumption of fresh vegetables is likely to be a significant factor in the increased incidence of foodborne illnesses. This is due to the fact that vegetable leaves may serve as a reservoir for foodborne pathogens. Moreover, most of the leafy vegetables are minimally processed and consumed raw, which further increases the risk of consuming contaminated food. Thus, the present study aimed to determine and compare the prevalence of several foodborne pathogens, including *Escherichia coli*, *Salmonella* species, *Shigella* species and *Listeria* species in both leafy and non-leafy vegetables. **Methods:** A total of 40 leafy and non-leafy vegetables were purchased from retail markets in Kampar, Perak, Malaysia. The study utilizes standard plate count method to quantify the colony forming units (CFU) of *Escherichia coli*, *Salmonella* species, *Shigella* species and *Listeria* species. **Results:** Results revealed that *Salmonella* spp. (15%) and *Listeria* spp. (15%) had the highest prevalence among the foodborne pathogens followed by *E. coli* (5%) and *Shigella* spp. (5%) in both leafy and non-leafy vegetables. The overall presence of pathogens was low. Salmonella spp. and Listeria spp. was detected more frequently in both leafy (10%) and non-leafy vegetables (5%). The microbial load of the pathogens ranged from log 4.446 to 5.511 CFU/g. **Conclusion:** Overall, leafy vegetables had a higher prevalence of foodborne pathogens than non-leafy vegetables. However, there was no visible trend in terms of microbial load. Therefore, it is imperative that all types of vegetables be appropriately prepared before consumption, especially leafy greens, to ensure safety of the consumer.

Keywords: vegetables, prevalence, *Salmonella*, *Listeria*, *Escherichia coli*

SC02

The Effectiveness of Brown Rice in Glycaemic Control among Diabetes Mellitus Type 2: A Systematic Review of Clinical Trials

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Introduction: High glycemic index (GI) possesses by WR has been implicated to be associated with higher risk of type II Diabetes Mellitus (T2DM). Brown rice (BR), which maintained the presence of bran and germ rice kernel offers superior nutritional benefits as opposed to WR. BR possesses lower GI could be beneficial in managing T2DM. This systematic review was carried out to evaluate the effects of BR on glycemic control among T2DM patients. **Methods:** Data search was conducted from these databases namely Medline, Ebscohost, Scopus, PubMed, Cochrane Central Register of Controlled Trials (CENTRAL), ScienceDirect with specific keywords. All controlled clinical trials published from year 2011 until December 2021 involving adults with T2DM who were consuming brown rice compared to those consuming white rice were included. The study was designed by adhering to the PRISMA guidelines. The primary outcomes analyzed qualitatively and quantitatively were glycated hemoglobin (HbA1c), fasting blood glucose (FBG), postprandial blood glucose levels. **Results:** Three studies met the inclusion criteria stated. Brown rice does improve glycemic control through significant reduction of HbA1c (0.24 to 0.4% reduction), fasting blood glucose level (FBG) (4.72 to 11% reduction) and postprandial plasma glucose level (signification reduction of area under the curve). One of the studies also showed significant reduction of C-peptide levels. **Conclusion:** This systematic review suggested that substitution WR consumption with BR shows improved glycemic control of patients with T2DM. High quality long term clinical studies are still needed to verify these findings on improvement of glycemic control demonstrated by BR.

Keywords: diabetes, brown rice, glycemic control, non-esterified fatty acid (NEFA)

SC03

Revealing *In Silico* Protein-Protein Interactions between Bacterial Leukotoxin from *Aggregatibacter actinomycetemcomitans* and Human Integrin

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Introduction: *Aggregatibacter actinomycetemcomitans*, the primary causative agent of aggressive periodontitis, selectively kills human leukocytes via its membranous leukotoxin (LtxA) which is a pore-forming protein belongs to the Repeat in Toxin (RTX) Family. LtxA recognises the lymphocyte function-associated receptor-1 (LFA-1) on hematopoietic leukocytes. Accustomed activation of LFA-1 is aasociated with the major leukocytic diseases including haematological malignancies and autoimmune disorders. LtxA-mediated cytotoxicity of neutrophils results in the excessive production of hypercitrullinated proteins, which act as neoantigens in Rheumatoid Arthritis (RA). Due to the lack of structural information, it is obscure to deduce how LtxA confers specificity to the activated LFA-1. Structural studies of LtxA are difficult because the recombinant LtxA is expressed as inactive inclusion body in *Escherichia coli*. In silico mining presumatively would yield a deeper insignth on the LtxA-LFA-1 interaction. **Methods:** A protein model of LtxA was generated using AlphaFold2, trRosetta, and i-TASSER. A selected LtxA protein model was then subjected to HADDOCK (High Ambiguity Driven protein-protein DOCKing), along with Human CD18 protein, to examine the interaction between the biomolecular complexes. **Results:** Amongst the 126 amino acid residues in the RTX region of LtxA, about 17 were rigorously implicated in the docking event, and 5 of these are inferred to be responsible for LtxA's target selectivity. **Conclusion:** The computational results revealed the relevant amino acids that might impart host-cell specificity on LtxA. These residues can be targeted as potential mutant locations for in vitro cell assay to further evaluate its functional responsibility. Ideally, the structural information would serve as a blueprint in designing an alternative therapeutic strategy for combating periodontitis and leukocytic disorders.

Keywords: leukotoxin, Repeat in Toxin Family, LFA-1

SC04

Presence of Residual Nucleic Acids in Streptavidin from Three Isolation Methods

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Introduction: Streptavidin (SAV) is a non-glycosylated tetrameric protein that has been widely utilized in biomedical and diagnostics applications. Recombinant SAV (rSAV) can be expressed using *Escherichia coli* host system to high expression level. Nevertheless, accumulation of rSAV in high levels results in the formation of inactive and insoluble inclusion bodies (IBs) which requires efficient downstream processing steps to obtain an active soluble recombinant protein. This process involves isolation of IBs from cell lysates through multiple fractionation steps followed by a solubilization step and refolding step. Recently, the presence of nucleic acids (NAs) in IBs preparation after fractionation is a cause of concern for subsequent protein refolding. Residual nucleic acids that are co-precipitated with IBs were found to have an ionic interaction with the unfolded polypeptides during refolding process resulting in a lower protein yield and increased aggregation. **Methods:** In this study, a series of different treatments were conducted to remove NAs contaminants during IBs preparation. Treatments involve a combination of mechanical and chemical approaches using sonication and extensive washing steps and a biological approach that involves the use of benzonase nuclease. The residual NAs present in IBs and refolded rSAV were quantitated using an optimized real-time PCR. The yield, purity, and activity of the refolded rSAV were characterized using SDS-PAGE and biotin-binding assay. **Results:** The yield of refolded rSAV was found the highest (~73%) when IBs were treated with extensive washing steps. **Conclusion:** Taken together, this study revealed that the presence of residual NAs in refolded rSAV resulted in lower refolding yield.

Keywords: inclusion bodies, *Escherichia coli*, nucleic acids, refolding, streptavidin

SC05

Molecular Modelling and Dynamics of Kaurene Synthase Involved in *Stevia rebaudiana* (Accession MS007) Terpene Biosynthesis

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Introduction: This paper presents the study on protein modelling, substrate docking and molecular dynamics of kaurene synthase involved in *Stevia rebaudiana* MS007 (stevia). Kaurene synthase (KS) is a key enzyme in terpene biosynthesis pathway, and its activity is essential for biosynthesis of the sweetening compounds (i.e stevioside and rebaudioside) in stevia. **Method:** The KS gene was isolated and subsequently characterized using sequence homology and Multiple Sequence Alignment (MSA). The gene was translated and then subjected to protein modeling and molecular dynamics analysis. The molecular modelling approach involved the use of protein modelling tools to analyze the structure of the KS genes. Autodock Tools and Vina was used to perform molecular docking of KS, with ent-copalyl diphosphate ligand (ECDP) and GROMACS for molecular dynamics simulations of the KS enzyme complex. **Results:** Through these analyses, model predicted by AlphaFold was chosen as it has highest ERRAT value: 94.3369. As for substrate docking, 4 modes were generated and mode 1 was chosen as it has the lowest affinity energy (kcal/mol) value which is -10.6 kcal mol^{-1}. In molecular dynamics simulation, KS enzyme was considered a stable enzyme since the RMSD value of the protein was below 4Å. The minimum distance between KS and ECDP was below 3Å which also show its complex interaction was good and strong. **Conclusion:** The results of this study provide insight into the mechanisms of terpene biosynthesis in stevia and can be used to develop biotechnological strategies for improving the production of sweetening compounds in stevia.

Keywords: *Stevia rebaudiana*, molecular dynamic, molecular modelling, terpenoid biosynthesis, GROMACS

SC06

Elucidation of Vitamin D Deficiency with Caries, Periodontitis, and Oral Cancer: A Systematic Review

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Introduction: The relationship between vitamin D deficiency with dental caries, periodontitis and oral cancer is controversial. **Objectives:** This review aimed to systematically evaluate the published literature and summarise the available evidence about the impact of vitamin D deficiency on the oral health diseases mentioned above. **Methods:** For the literature search, PubMed, Web of Science, Scopus and ScienceDirect databases were used with limitations of papers published in English language. The search terms included were vitamin D, periodontitis, oral cancer, and caries. All papers published from January 2017 until November 2022 were included. The PRISMA process was used for the screening and selection studies. **Results:** A total of 3001 studies were identified from the initial search. The association between vitamin D deficiency with caries, periodontitis and oral cancer were assessed in 46 full-text articles. However, due to unmet inclusion criteria, 32 studies were included in this systematic review: 15 studies on caries, 16 periodontitis and one oral cancer. In terms of study quality and risk of bias in individual studies, 27 out of 32 studies were categorized low. A total of 12 studies on periodontitis showed impact of vitamin D deficiency. **Conclusion:** This review reveals majority of the evidence showed an impact of vitamin D deficiency with periodontitis. However, the association of vitamin D deficiency with dental caries was controversial in the findings. Thus, further literature research is required to clarify the impacts of vitamin D deficiency on caries and oral cancer.

Keywords: Vitamin D deficiency, oral health, caries, periodontitis, oral cancer

SC07

Molecular Detection of *Acinetobacter baumannii* Isolated from Human Clinical Specimens

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Introduction: *Acinetobacter baumannii,* a Gram-negative, is well recognized for producing illnesses that are resistant to numerous drugs. The environmental reservoirs of this bacterium are generally unknown and have mainly been isolated from clinical situations. **Methods:** A total of 150 clinical samples included source (urine, sputum, wounds, and burns) were collected from were collected from Iraqi hospitals. This study aimed to isolation and identification *Acinetobacter baumannii* by conventional method like colony morphology, biochemical test and vitik system, in addition using molecular identification by using PCR. **Results:** All specimens were cultured on culture media including MacConkey and blood agar. The identification of the isolated by biochemical test (oxidase, catalase, simmon citrate (growth at 44 ^{0}C in the present of antibiotics) that showed a positive reaction. A total of 20 isolated (9.6%) isolates *Acinetobacter baumannii* were identified. The genomic DNA of *Acinetobacter baumannii* were extract and DNA purification kit also these isolates submitted for amplification to detect the genomic DNA by using specific primer 16s rRNA. **Conclusion:** The study suggests that *Acinetobacter baumannii* isolate capable of growing under selective conditions for initial identification and molecular detection and for the specific isolated strain.

Key words: *Acinetobacter baumannii*, muti drug resistance, Iraq, colony

SC08

Bacterial-fungal Diversity in Pigeon Faecal Samples Around UTAR Kampar Campus – A Pilot Study

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Introduction: Feral Pigeon (*Columba livia*) is a pigeon species that shifts to urban areas. Due to the increasing of pigeon population, pigeon droppings have become a health concern in colonised areas, as they are reservoirs of microorganism potentially pathogenic microorganisms, which could pose a risk of infection especially to immunocompromised individuals. UTAR Kampar campus has become a habitat for pigeons due to the open-air architecture of some buildings. We aim to detect and characterize the faecal bacteria and fungus communities of pigeons via next-generation sequencing (NGS). **Methods:** A total of 56 fresh pigeon faecal samples were collected from different locations in UTAR Kampar campus for total DNA extraction. The diversity of bacteria and fungus were investigated by amplicon sequencing targeting on the 16S rRNA (V3-V4 region) and internal transcribed spacer (ITS 1 region), respectively via MiSeq Illumina Platform with 2 × 250 bp paired-end protocol. **Results:** The bacterial community is dominated by *Escherichia-Shigella* (56%), *Lactobacillus* (14%), *Candidatus Bacilloplasma* (11%) and *Suttonella* (10%), identified to genus level. In contrast, fungal community is more unique to the genus *Kazachstania* (~100%). **Conclusion:** Majority of the bacteria (*Escherichia-Shigella* and *Suttonella*) and fungus (*Kazachstania*) in pigeon dropping are potentially pathogenic microorganism. Identification to species level is to be performed. This study is important to raise public awareness on potential diseases caused by pigeon droppings.

Keywords: *Columbidae*, High-Throughput Nucleotide Sequencing, microbiota

SC09

Specific microRNAs Among Milk Siblings: An Epigenetics Approach Towards Understanding the Basis of Milk Kinship

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Introduction: Milk kinship is an Islamic belief described as a relationship established when infants receive breast milk from non-biological mothers. This form of kinship is said to bear a very close resemblance to blood relation whereby the recipients' infants are regarded as milk siblings to the biological children of the breastfeeding mother. Any future marriage between these individuals is forbidden likewise between the recipient infant and the nursing mother herself as they are thought to have a form of consanguinity. The consanguinity formed by virtue of milk sharing might be due to the composition of human breast milk, especially milk microRNAs that are responsible for the epigenetic modulation of gene expression. miRNAs can regulate gene expression by modulating genome-wide epigenetic status of genes, and similarly-shared genes might be the basis that has led to milk kinship formation. Thus, the objective of the present study is to identify potential lactation-specific miRNAs that are similarly shared among milk siblings and their nursing mothers. **Methods:** The study began with molecular extraction of milk RNA from the nursing mothers and cell-free plasma RNA from all milk siblings and their nursing mothers. The RNAs extracted from both sample types were further analyzed using NanoString nCounter® miRNA Panel Analysis (NanoString Technologies, Seattle, WA) to measure the abundance of individual miRNAs biomarkers present within the samples. **Expected Outcomes:** This study is expected to provide scientific explanation that could divulge the secrets behind milk kinship establishment with thorough presentation on the lactation-specific miRNAs shared between milk siblings. Hence, the way for future research would be paved, making the development of milk kinship identification tool possible.

Keywords: epigenetics, milk kinship, milk miRNA, NanoString

SC10

Antimicrobial Effect of *Aronia melanocarpa* extractions on *Elizabethkingia anopheles* and *Elizabethkingia meningoseptica*

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Introduction: Elizabethkingia is a genus of bacteria described in 2005, includes two human opportunistic species, which are having highly importance in the health care environments, as they are merging pathogens responsible of increased case-fatality rates worldwide. **Methods:** In this study, the antibacterial activity of *Aronia melanocarpa* (black chokeberry) aqueous, ethanolic, and methanolic extracts were tested against different strains (*E. meningoseptica* (IJN), *E. meningoseptica* (NCTC), *and E. anophelis*). Different concentrations of each extract prepared to investigate the antimicrobial sensitivity of these microbes towards each of the extracts' concentrations using agar well diffusion, MIC, and MBC assays. **Results:** Results showed that aqueous extracts did not exhibit any antibacterial effect against *E. meningoseptica* and *E. anophelis*. While methanol and ethanol extracts exhibited very promising and hopeful antibacterial effectiveness against the three tested strains. **Conclusion:** Therefore, this study is suggesting that *A. melanocarpa,* methanolic and ethanolic extracts can be among of choice to prepare future pharmaceutical products, alternative antimicrobial agents, or medical treatments for human pathogenic infectious caused by the antibiotic resistant Elizabethkingia microbes.

Keywords: antimicrobial activity, *Aronia melanocarpa*, *Elizabethkingia meningoseptica*, *Elizabethkingia anophelis*

SC11

Identification and Antimicrobial Resistance Profiling of Clinical Bacteria Isolated from Breast Infection Patients in a Malaysian Tertiary Hospital

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Introduction: Breast abscess and mastitis are common breast infections and up to 40% of breast infections are caused by polymicrobial. The delay in appropriate antibiotic treatment could cause longer hospital stays and higher risk of antibiotic resistance. Furthermore, the antibiotic resistance surveillance data for breast infections in the Malaysian setting is scarce. Therefore, this study aims to identify the prevalence and antibiotic resistance profiles of clinical isolates in breast infection patients in a Malaysian hospital. **Methods:** A total of 27 clinical isolates were collected from breast infection patients admitted to University Malaya Medical Centre (UMMC) Surgery Unit from 1 September 2021 to 31 March 2023. Bacterial identification was performed using 16s rRNA gene sequencing. Disc diffusion and broth microdilution were performed on 27 clinical isolates following standard guidelines. **Results:** *Staphylococcus* constitutes the most prevalent bacteria genus (74.0%), followed by *Streptococcus* (11.1%), *Pseudomonas* (7.4%), *Enterococcus* (3.7%) and *Citrobacter* (3.7%). The majority of the isolates were drug-resistant bacteria (77.7%, n=21). Interestingly, all drug-resistant bacteria were resistant to penicillins group (100%, n=21) which is recommended for breast infection management in Malaysia, indicating that penicillins might not be effective due to the high rates of resistance observed in the study. Alarmingly, 7 isolates were found to be multidrug-resistant (25.9%) and 6 were *Staphylococcus* species. All MDR *Staphylococcus* isolates were resistant to penicillins and fluoroquinolones groups. **Conclusion:** In conclusion, this study is the first to report a high resistance rate of clinical isolates found in breast infection patients, highlighting the need for improved antibiotic stewardship practices in Malaysia.

Keywords: antimicrobial resistance, breast infection, tertiary care

SC12

Enterocytozoon hepatopenaei, a Microsporidian Parasite Infection in shrimp: Diagnostics Strategies in Ensuring Safe Biosafety and Biosecurity for Sustainable Aquaculture

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The emergence of shrimp disease Hepatopancreatic microsporidiosis (HPM) caused by Enterocytozoon hepatopenaei (EHP), a microsporidian parasite has governed so much concern in food safety among consumers. EHP infecting the shrimps remains a silent pathogen preventing optimal shrimp growth. The biggest challenge is its concerns about food safety, which is the main goal in guaranteeing food biosecurity and biosafety. Thus, detecting EHP in infected shrimps is crucial in ensuring food safety in the downstream process. This poster briefly describes the current and suggested future diagnostics methods for detecting EHP infection in shrimp aquaculture. Moreover, interventions with current molecular biology and biotechnology are included in addressing EHP infection in shrimps. Finally, a systematic guideline for shrimp food safety is proposed. Overall, this will be a guide in preventing disease outbreaks in shrimp aquaculture and to ensure food safety.

Keywords: *Enterocytozoon hepatopenaei* (EHP), diagnosis, interventions, food safety

SC13

Cyclodextrin Inclusion Complex of Tetrahydrocurcumin Augments Solubility And *In Vitro* Anticancer Activity Against Colorectal Cancer

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Introduction: Tetrahydrocurcumin (THC), a hydrophobic polyphenolic bioactive substance extracted from turmeric, has been established as a natural anticancer agent. Unfortunately, its sparing solubility (approximately 1.3%) in water and its reduced systemic bioavailability has limited its efficacy. This study explores the use of an organic-based drug delivery approach via encapsulation to circumvent the pitfalls of THC's poor solubility and potentially improve its chemotherapeutic properties. **Methods:** An inclusion complex of THC with β-cyclodextrin (βCD) at a molar ratio of 2:1 was formed and characterized using UV–vis spectroscopy, differential scanning calorimetry (DSC), Fourier transform infrared spectroscopy (FTIR), and scanning electron microscopy (SEM). The inclusion complex's solubility assessment and drug release study were evaluated and compared with pure THC. The anticancer effect of the inclusion complex on colorectal cancer cells (SW480 and HCT116 cells) was investigated by MTT assays, migration assays, Transwell invasion assays, Annexin-V/PI staining assays, and poly adenosine diphosphate-ribose polymerase (PARP) cleavage assays. **Results:** The inclusion complex displayed higher aqueous dispersion (65-fold) and physiochemical characterization confirmed the successful formation of a β-CD inclusion complex encompassing a hydrophobic cavity. Through the presence of an inclusion complex, cell viability was potentially reduced with an SI value > 10 while the apoptosis rate was increased ($p < 0.05$) in vitro. Additionally, the complexation further reduced the migration and invasion capabilities of cancer cells in comparison to pure THC. Both formulations were consistent in terms of caspase 3 activation. **Conclusion:** These findings provide evidence of the potential use of this formulation in rendering hydrophobic agents capable of providing a chemotherapeutic application against colorectal cancers.

Keywords: tetrahydrocurcumin, cyclodextrin, inclusion complex, solubility and colorectal cancer

SC14

Molecular Characterization of LIC10280, a Novel Putative Virulence Factor of *Leptospira interrogans*

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Introduction: Leptospirosis is a zoonotic disease caused by pathogenic Leptospira species. However, the molecular mechanisms of leptospiral pathogenesis are still unclear as many genes related to virulence are still undiscovered. The budding yeast Saccharomyces cerevisiae is a popular eukaryotic model that has been used as an alternative model to identify bacterial VFs that target conserved eukaryotic cellular processes. Previously, our group has identified a protein with unknown function, LIC10280 as potential candidate VFs of Leptospira interrogans from yeast growth inhibition assay. In current study, we will validate the protein LIC10280 as a leptospiral VF, studying molecular characteristics and its function in leptospiral pathogenesis. **Methods:** First of all, in silico analysis is carried out on protein sequence of LIC10280 to predict and analyse its molecular properties, function, and structure. Next, the targeted eukaryotic cellular processes or molecules of LIC10280 will be investigated in the yeast cell model. The conservation of protein LIC10280 among Leptospira species and validation of LIC10280 as the leptospiral VF in mammalian cells model will be determined. Finally, the interaction between LIC10280 and host components will be investigated by in vitro studies. **Results:** Currently, protein LIC10280 is predicted as a secretory protein that contains a signal peptide at the N-terminus of the protein sequence. Only heterologous expression of the full-length sequence of protein LIC10280 shows yeast growth inhibition activity and reduces the viability of yeast cells. The mature protein part of LIC10280 shows nucleus binding properties in the yeast microscopy study. **Conclusion:** This study is still ongoing to identify the possible target molecule(s) or cellular process of protein LIC10280 to better understanding on pathogenesis of leptospirosis.

Keywords: *Leptospira interrogans*, virulence factor, yeast, pathogenesis, leptospirosis

SC15

Bibliometric Analysis of MicroRNAs Associated with Chronic Myeloid Leukemia

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Introduction: MicroRNA (miRNA) is a short non-coding RNA that influences gene expression by post-transcriptional regulation of target messenger RNA (mRNA). The potential roles of miRNAs as either oncogenes or tumor suppressor genes have brought a new dimension to our clinical approach to diagnosing and treating cancer. Aberrant miRNA expression was associated with various cancer, including chronic myeloid leukemia (CML). This study aims to investigate the miRNA research related to CML and to conduct a trend-related research analysis. **Methods:** In a Scopus collection, we analyzed 442 published articles on miRNA related to CML from 2006 to 2023. The network analysis was conducted using the R&R studio software. **Results:** The journal Oncotarget had the highest number of published articles, with an h-index of 12. China had the highest number of total publications, and the institute with the most significant number of publications was Central South University. Li,Y was the leading author in the respective field with an h-index of 15 and a total citation of 1031. Keywords analysis revealed that research on exosomes, autophagy, and chemoresistance was trending after CML and miRNA. Besides, specific miRNAs had emerged concerning differentially expressed genes (DEGs), tyrosine kinase inhibitor (TKI), biomarker, and tumor suppressor. Factorial analysis revealed clusters from the author's keywords associated with biomarkers, acute myeloid leukemia, exosomes, and microRNAs. **Conclusion:** Overall, miRNA-related CML research is still in its infancy due to the low number of original articles published. Hence, collaborations between China, USA, and the United Kingdom might help spread this interest area faster worldwide.

Keywords: microRNA, chronic myeloid leukemia, CML, bibliometric analysis, Scopus

SC16

Impact of Climate Change and Invasive Species on Native Biodiversity and eDNA as a Next Generation Biomonitoring Tool

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Invasive species and climate change have a negative influence on biodiversity and the resilience of ecosystems. More frequent extreme weather occurrences, for example floods and droughts put native species under stress and open pathways for the spread of alien species. Melting sea ice creates fresh shipping corridors and routes for the introduction of invasive species. Invasive species have direct and indirect impacts on local biodiversity. Direct interaction includes predation and competition for resources. Indirect consequences include the spread of diseases to and native species. Invasive species often enter from higher diversity areas and introduce diseases and pathogens not present in the native species range. This might make native species "more exposed" and vulnerable. The emerging species may benefit from this diversity exposure in its invading range. Without controls in their new range their expension may decrease habitat quality, woresen microbial exposures, lower biodiversity, and ultimately affect fishery resources and protected species. In the era of rapid invasion of invasive species Environmental DNA (eDNA) can provide faster and quicker way of monitoring of invasive species and conservation of biodiversity. DNA shed by organisms can be collected from the environmental sample and analyses for conservation and monitoring purposes. eDNA metabarcoding is now recognized as a powerful tool for obtaining comprehensive biodiversity data. Its applications for environmental management are democratizing and include biodiversity surveys, early detection of invasive species, detection and monitoring of rare/protected species and environmental quality assessment based on biodiversity index.

Keywords: invasive species, climate change, environmental DNA

SC17

Effect Of *Centella asiatica* L. Aqueous Extract on Male Reproductive Function in Streptozotocin-Nicotinamide (STZ-NA)-Induced Diabetic Rats

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Introduction: Diabetes mellitus (DM) is a metabolic disorder associated with various complications including derangement in male reproductive functions. *Centella asiatica* (CA) has been studied widely as an alternative herbal intervention in managing DM. However, the effect of CA on male reproductive system has mixed reported findings. Therefore, this study aimed to investigate the effects of CA on testes in type 2 DM (T2DM). **Methods:** For animal preparation, streptozotocin-nicotinamide (STZ- NA) induced adult male rats were administered with 250 and 500mg/kg/day body weight of CAAE for five consecutive weeks. Fasting blood glucose (FBG) and the body weight were obtained weekly. Testes were then removed for antioxidant activity levels analysis. Testes steroidogenic function was determined by the testosterone and 17β-Hydroxysteroid dehydrogenase III (17β-HSD3) levels. Histopathological changes of testes were observed. Sperm count and its morphology were also obtained for further evaluation. **Results:** The administration of CAAE ameliorates the FBG level and weight loss in STZ-NA-induced rats. The oxidative stress marker was preserved in the testes following CAAE treatment, which contradicted with the testosterone and 17β-HSD3 findings as it shows a significant reduction in hormonal levels following administration of CAAE. Sperm count showed reduction with more abnormal morphology compared to STZ-NA-induced rats. The histopathological changes observed more structural damage in the testes of diabetic rats treated with CAAE. **Conclusion:** CAAE ameliorate hyperglycaemia and oxidative stress, however, may cause disruption in the steroidogenic function which could impair overall testicular function in DM. Thus, CA possesses antifertility effect which could give more harm than benefit in T2DM male patients.

Keywords: *Centella asiatica*, antioxidant, antidiabetic, antifertility

SC18

Searching For AChE Inhibitors from Natural Compounds by Using Machine Learning and Atomistic Simulations

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Introduction: Acetylcholinesterase (AChE) is one of the most important drug targets for Alzheimer's disease treatment. In this work, a combined approach involving a Machine Learning model and atomistic simulations was established to predict the ligand-binding affinity to AChE. GraphConv model was selected and utilized to rapidly and accurately screen the natural compound database for potential AchE inhibitors. Then, atomistic simulations including molecular docking and steeredmolecular dynamics simulations were then used to confirm the Machine Learning outcome. Good agreement between Machine Learning and atomistic simulations showed potential compounds to inhibit AChE and was also the basis for taking next steps for optimal drug research in the treatment of Alzheimer's. **Methods:** The four main methods used in the research are computational Machine Learning combined with atomic simulations including docking simulation and steeredmolecular dynamics simulations to find out the binding affinity of compounds with AChE, investigated pharmacokinetic parameters including blood-brain barrier ability and toxicity of compounds to select the most optimal compound. **Results:** Good agreement between ML and atomistic simulations was observed. Twenty compounds were suggested to be able to inhibit AChE. Especially, four of them including *geranylgeranyl diphosphate, 2-phosphoglyceric acid, and 2-carboxy-d-arabinitol 1-phosphate, and farnesyl diphosphate* are highly potent inhibitors with sub-nanomolar affinities. These compounds with log(BB) in the range of −0.59 to 0.00 were able to cross the blood-brain barrier. Moreover, the hERG inhibition index showed that these compounds could not have toxicity to the human body. **Conclusion:** A combined ML/FPL approach was proposed to predict the binding affinity of a ligand to AchE. Overall, our obtained results may stimulate the search potentials drugs for an Alzheimer's disease therapy.

Keywords: AChE, alzheimer's disease, docking, FPL, Machine learning

EP01

Preliminary Results of the Role of MicroRNA-150-5p in the Pathogenesis of Human Multiple Myeloma

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Introduction: Multiple myeloma (MM) is a type of haematologic neoplasm characterised by the accumulation of cancerous plasma cells within the bone marrow. MicroRNAs (miRNAs) alteration were shown to have a pivotal role in either progression or suppression of MM. MicroRNA-150-5p (miR-150-5p) was dysregulated in various human cancers including MM; However, its role in MM is unclear. **Methods:** This study aims to investigate the function of miR-150-5p in human MM cells using in vitro cell-based assays. The expression levels of miR-150-5p in MM patients and cell lines were evaluated by RT-qPCR. U266 MM cells were transfected with synthetic miR-150-5p mimics or miRNA mimic negative control. The effect of miR-150-5p mimics on MM cell growth was assessed by cell proliferation assay, while the proportion of apoptotic cells was detected using Annexin V-FITC and PI double staining and flow cytometry analysis. **Results:** miR-150-5p was down-regulated in MM patients (n=13/14) and cell lines (n=6/6). Restoration of miR-150-5p using synthetic miRNA mimics significantly inhibited cell proliferation in U266. Nevertheless, replacement of miR-150-5p did not alter the apoptotic events. **Conclusion:** The present preliminary results implicate that miR-150-5p plays a role as a tumour suppressor and participates, at least in part, in the regulation of MM pathogenesis.

Keywords: multiple myeloma, miR-150-5p, cell proliferation, apoptosis

EP02

Lectin Staining for Detection Of Sialic Acid Residues On Cell Surface Of Wild Type Chinese Hamster Ovary (CHO) And HeLa Cells

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Introduction: Sialic acid plays important roles in human physiology particularly in cell-cell interaction and communication, cell-cell signalling, carbohydrate-protein interactions, cellular aggregation, development processes, immune reactions, reproduction, neurobiology and human diseases. In this study, we investigated the presence of sialic acid on the surface of CHO cells by using rhodamine-linked peanut agglutinin (PNA-Rho) lectin, which binds to Galβ1-3GlcNAc only if the terminal sialic acid is absent. **Methods:** Wild type CHO and HeLa cells were seeded on cover slips in a 24 well plate. Wild type HeLa cells were chosen as a positive control. After overnight incubation, one set of wild type CHO and HeLa cells were treated with neuraminidase to cause release of sialic acid residues from surface glycoproteins and glycolipids. Subsequently PNA-Rho was used to stain all cells and the samples were visualised using fluorescence microscopy. **Results:** Lectin staining without neuraminidase treatment showed no fluorescent labelling. In contrast, following neuraminidase treatment, fluorescent detection of PNA-Rho was detected in both wild type CHO and HeLa cells. This indicating neuraminidase treatment successfully removed sialic acid normally present on cell surface glycans, exposing more galactose residues for PNA-Rh binding. **Conclusion:** In summary, sialic acid residues are found on the surface of both wild type CHO and HeLa cells. Future work will be done to see if these lectins can be used to monitor changes in sialic acid levels on cell surfaces especially when its production is impaired due to mutations.

Keywords: sialic acid, Chinese Hamster Ovary, HeLa, rhodamine-linked peanut agglutinin

EP03

Association between School Environment and Adolescents Body Mass Index in Selected Secondary Schools

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Introduction: Poor dietary habits and low physical activity level were significantly associated with obesity among adolescents. School environment is one of the factors that influences adolescent's eating habits. Hence this study aimed to determine the relationship between school environment and weight status of adolescents. **Methods:** A cross-sectional study with 322 adolescents from selected secondary schools were recruited. The data was collected using self-administered questionnaires, which consisted of sociodemographic characteristics, eating habits, food frequency questionnaire (FFQ) physical activity, whole school environmental mapping and anthropometry measurements. **Results:** The proportion of female were 50.6%, male 49.4% and majority were Chinese adolescents (89.1%). Only two schools had completion rate of more than 60% toward the whole school environmental mapping, which were considered as good school compliance. In FFQ, the most common food and beverage consumed by the adolescents were white rice (14%) and water (33%). The mean score of physical activity level was 2.17±0.72 and most of the adolescents were physically inactive (62%). About 13% of them were categorized as thinness, 64% normal weight, while 16.8% and 6.5% were overweight and obese, respectively. Weight status and the food habit of eating a cake or a dessert at meals was found to be inversely correlated ($r=-0.135$, $p=0.009$). An inverse relationship was found between weight status and the habit of drinking 8 glasses of water daily ($r=-0.127$, $p=0.003$). **Conclusion:** Food habits of adolescents may play a significant role in their weight status. The compliance of schools in terms of school environmental mapping can be improved.

Keywords: adolescents, school environment, body mass index, eating habits, secondary school

EP04

Molecular Characterisation of *Orientia tsutsugamushi* Identified from a Scrub Typhus Case in Malaysia

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Introduction: Scrub typhus is neglected and underdiagnosed in Malaysia. Its epidemiological data and true burden in Malaysia are limited. Epidemiological studies related to scrub typhus are largely on seroprevalence; molecular surveillance has been mostly focused on samples from arthropods. Molecular genotyping is the method of choice for studying the genetic diversity of scrub typhus as it can detect the causative agents at the genomic level. In this study, molecular detection was performed on a febrile patient who presented with eschar, a classical clinical feature of scrub typhus. **Methods:** The blood sample of the patient was subjected to nested-PCR for *Orientia tsutsugamushi*, the causative agent of scrub typhus by detecting the presence of the 56-kDa type-specific antigen (TSA) gene. The amplified product was sequence verified by DNA sequencing followed by phylogenetic analysis. **Results:** BLAST analyses of the 56-kDa TSA showed sequence similarity (608/617 bp, 99%) to *O. tsutsugamushi* strain UT302, which was originally isolated from Thailand. Phylogenetic analysis demonstrated UT302 placed within the clade of TA763, a strain type commonly present in Thailand, and has been seen in Taiwan and Southeast Asia, but not in Japan and Korea. **Conclusion:** Studies on the molecular diversity of rickettsiae in Malaysia are limited. The present study has provided additional molecular evidence of rickettsial infections in Malaysia. Molecular surveillance of rickettsial diseases is important as a better understanding of the circulating strains is useful in the development of diagnostic tests and vaccines to support public health measures in controlling rickettsial infection in this country.

Keywords: *Orientia tsutsugamushi*, scrub typhus, polymerase chain reaction, DNA sequencing, phylogenetic analysis

EP05

Prevalence of HSV-1: From Malaysia to Asia Through a Meta-Analysis

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Introduction: Herpes simplex virus 1 (HSV-1) is known for its neuroinvasive capability and thus increasing the risk of Alzheimer's disease. Therefore, a comprehensive overview of the prevalence of HSV-1 in humans is undoubtedly crucial. This study aims to determine the prevalence of HSV-1 in the Malaysian population, and in Asia through a meta-analysis. **Methods:** The prevalence of HSV-1 was determined from a total of 451 Malaysian volunteers. The data was pooled into a meta-analysis to estimate the prevalence of HSV-1 in Asia. An extensive literature search was performed for relevant studies from the year 2013-2023 to be included in the meta-analysis. The heterogeneity was examined with an I^2 index and a Q-test. Publication bias was assessed using a Funnel plot and Egger's test. **Results:** The Malaysian volunteers exhibited 41.9% of HSV-1 positive. For the meta-analysis, a total of 26 studies with 31464 subjects were included. The pooled prevalence rate was calculated using a random-effect model based on high observed heterogeneity ($I^2 > 96$ and p-value in Q-test < 0.001). In Asia, the prevalence of HSV-1 was 72.4%. When stratified into different regions, the prevalence of HSV-1 was highest in Western Asia (79.1%), followed by East Asia (71.7%), Southeast Asia (64.1%), and South Asia (27.4%). No publication bias was detected in the meta-analysis. **Conclusion:** The meta-analysis suggests that about three-quarters of the Asian population is infected with HSV-1. Since HSV-1 is highly associated with the development of Alzheimer's disease, understanding the underlying mechanism is significantly essential and requires further attention.

Keywords: prevalence, meta-analysis, HSV-1, Alzheimer's disease, Asian populations

EP06

Molecular Docking of Annonaceous Acetogenins with Bcl-xL Protein

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Introduction: Drug discovery is vital in cancer therapeutic and precision medicines. Investigating annonaceous acetogenins (ACGs) from the natural product could be the best strategy to find a new drug candidate for treating cancer. ACGs derived from plants comprise a unique structure that has excellent pharmacological properties, including anticancer. There is still lack of studies on ACGs mode of action in apoptosis induction suggesting Bcl-xL protein to be targeted. It is postulated that ACGs could mimic BH3-only protein at the hydrophobic groove of Bcl-xL protein and inhibit the Bcl-xL reaction. Hence, the objective of the study is to evaluate the ACGs potential, namely, xylomaticin, squamostatin A, and annoreticulin and as a candidate for Bcl-xL inhibitors in the computational study. **Methods:** Three ACGs were assessed through molecular docking study using AutoDock Vina software for their binding interactions and affinities into Bcl-xL protein. **Results:** Of all three ACGs, the complex of xylomaticin/Bcl-xL showed the lowest binding energy (–12.1 kcalmol^{-1}), indicating the strongest binding affinity among all. Meanwhile, the other two ACGs exhibited better binding energies as compared with ABT-737 (– 10.2 kcalmol^{-1}) as a control ligand. Interestingly, these three ACGs formed the same three H-bond interactions with the Bcl-xL protein. They were also interacting with ARG139 residue in the conserved region of the Bcl-xL binding pocket, suggesting the inhibition of this protein. **Conclusion:** The docking results predicted that all tested ACGs have good potential to be developed as Bcl-xL inhibitors that might turn on apoptosis in cancer cells and overcome the multidrug resistance.

Keywords: xylomaticin, squamostatin A, annoreticulin, annomonticin, docking

EP07

Detection of *tanB* gene *Streptococcus gallolyticus* subspecies *gallolyticus* in Stool of Colorectal Cancer Patients

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Background: *tanB* gene encodes for tannase and is specific for *Streptococcus gallolyticus* subspecies *gallolyticus* (SGG). The human gut may be colonized by SGG through zoonotic transmission. Patients with colorectal carcinoma (CRC) have a higher SGG colonization rate than healthy humans. Therefore, the detection of *tanB* SGG in patients with early-stage CRC might be a useful screening tool. We aimed to establish a stool PCR technique without the need for bacterial cultures. **Method:** stool samples were collected from 113 patients, who were referred to SASMEC@IIUM health centre for colonoscopy. Bacterial DNA was directly extracted from the stool specimen before PCR. The PCR optimisation involved two pairs of primers targeting the *tanB* gene. DNA sequences of random samples were deduced by DNA sequencing and further analysed to determine the analytical specificity. The sensitivity of the technique was determined by a 10-fold dilution of a known standard. **Results:** Thirty-three (33) out of 113 patients were diagnosed with CRC. Upon optimization with two CRC samples, primer pair 1 showed a high analytical specificity of the PCR. The sensitivity of the assay reached 10^2 DNA copies/ml. As expected, further testing on all samples resulted in a higher rate of SGG detection in CRC samples (50%; n=16/33) compared to the non-CRC samples (20%; n=16/80). **Conclusion:** The established PCR technique potentially benefits early CRC diagnosis.

Keywords: *Streptococcus gallolyticus*, bacteria, polymerase chain reaction, gene, colorectal cancer

EP08

In Vivo, *In Vitro* and *Ex Vivo* Experimental Models of Diabetic Retinopathy: A Historical Review and Current State-of-The-Art

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Introduction: One of the major microvascular complications of diabetes is diabetic retinopathy (DR), the leading cause of blindness globally. DR prevalence among diabetes patients is 25%, with 6% having a vision-threatening issue worldwide. Chronic hyperglycemia and inadequate glycemic control were found to have a strong connection with DR progression. Given the rising prevalence of diabetes worldwide, a greater number of DR cases are expected in future. To understand the pathophysiological mechanism of DR in humans and to investigate potential novel compounds for therapy, certain types of experimental models are typically used. **Methods:** The online PubMed and Medline search engines were used to collect publications published between 1960 and 2021. This was accomplished by studying the abstracts and full papers of all included sources using a single or combination of keywords, such as diabetic retinopathy, streptozotocin (STZ), *in vivo*, *in vitro* and *ex vivo*. All publications cited were published in English-language. **Results:** Current review provides a comprehensive update on mechanisms, methodologies and pros and cons of various experimental models used in DR research, including *in vitro*, *in vivo* and *ex vivo* models. Among these, *in vivo* model is most preferable due to several limitations in *in vitro* and *ex vivo* such as the absence of a retinal microenvironment and complex retinal isolation. **Conclusion:** Although experimental models can be used to predict treatment mechanisms, they are not always completely and accurately translated to human conditions. To determine whether the treatments are both safe and effective, clinical trials must be conducted.

Keywords: diabetic retinopathy, experimental models, *in vivo, in vitro, ex vivo*

EP09

EVNol SupraBio™ Attenuates Prostate Epithelial Changes by Regulating the Sex Hormone in Sprague-Dawley Rats

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Introduction: Bishenol F (BPF) is one of the Bisphenol A analogues has been found to disturb the male reproductive hormone levels that indirectly affect the morphology of the prostate gland. EVNol SupraBioTM (EV) is a palm oil tocotrienol-rich fractions (TRF) that act as a potent antioxidant however its effect on prostate morphology due to BPF-induced changes in reproductive hormones is remain unclear. Therefore, this study was carried out to evaluate the effect of EV on the morphology of the prostate gland due to changes in reproductive hormones in Sprague Dawley rats induced by BPF. **Methods:** Male Sprague Dawley rats (n=40) were divided into 5 groups: control, EV (EVNolSuprabioTM: 100 mg/kg group), BPF (BPF: 10 mg/kg), BE50 (BPF+EV:50 mg/kg) and BE100 (BPF+EV:100 mg/kg). BPF and EV was administered through oral force-feeding for 28 days. Blood was taken for determination of luteinizing hormone (LH), testosterone and estradiol levels, testes for assessment of Steroidogenic Acute Regulatory (StAR) and Cytochrome 17A1 (CYP17A1) and prostate for histological examination. **Results:** The results showed EV had the potential in increasing the LH and testosterone levels and descreased the estradiol level as compared to the BPF group. Interestingly, the immunohistochemistry findings showed BE groups had the potential in increasing the expression of StAR and CYP17A1 proteins in the Leydig cells. BE100 significantly reduced the thickness of epithelial prostate ($p<0.05$) as compared to BPF group. **Conclusion:** EVNol SuprabioTM has the potential to protect BPF-induced prostate morphology via steroidogenic hormones regulation.

Keywords: endocrine disrupting chemical, bisphenol, steroidogenesis, prostate

EP10

Knowledge, Attitude and Practices of Sun Protection Measures among University Students in Kuala Lumpur

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Introduction: Unprotected exposure to ultraviolet radiation (UV) is an essential risk factor for skin cancer, photoaging, cataracts and immune system suppression. This study aimed to evaluate the sun protection of university students in Kuala Lumpur. **Methods:** This cross-sectional study recruited 261 university students via convenient sampling. The validated sun protection questionnaire was adopted from Janjani et al. (2019). Association between knowledge, attitude and practices and socio-demographics were determined. Furthermore, correlations between knowledge, attitude and practices were determined using Spearman's Rank Order. **Results:** Median scores (interquartile range) of students' knowledge, attitude and practices were 47.50 (12.50), 66.00 (16.00) and 55.90 (15.60) respectively. Scanty students had good levels of knowledge (0.8%), attitude (26.4%) and practices (5.0%). Most of them had poor knowledge (60.9%), moderate attitude (71.3%) and moderate practices (62.5%). Knowledge scores were significantly associated with gender and paternal education. Attitude score was significantly associated with paternal education. Practice score was significantly associated with gender, ethnicity and students' current year of study. Female university students had a significantly better median knowledge score, 50.0 (12.50) vs 47.50 (13.75) for males. Likewise, they had a significantly better practice score, 55.90 (13.00) vs 54.60 (18.20) for males. Knowledge scores were weakly correlated (r=0.224) with attitude scores. Ironically, attitude scores were weak (r=-0.282) and negatively correlated with practice scores; thus, having a better attitude did not translate into sun protection measures. **Conclusion:** Students at universities are oblivious to sun protection measures. Even among those with proper knowledge, the use of sun protection measures is very low.

Keywords: sun protection measures, ultraviolet radiation (UV), university students

EP11

Lapatinib-Induced Changes In *Bifidobacterium Bifidum* through Alteration of Tight Junction Proteins in Caco-2 Intestinal Monolayer Model: A Review

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Introduction: Targeted cancer drug such as lapatinib has been associated with side effects mainly diarrhoea. Lapatinib which targets ErbB1 and/or ErbB2 receptor tyrosine kinases is effective in treating ErbB2+ve breast cancer but as it is delivered over many months, basically meaning diarrhoea is often prolonged, thus impacts significantly on the quality of life (QOL) of cancer patients. Previous studies showed decrease of Bifidobacterium spp in tyrosine kinase inhibitor (TKI)-treated patients with severe diarrhoea, suggesting altered microbial composition, yet the underlying mechanisms remain unknown. This study aimed to gather updated information about lapatinib-induced changes in *Bifidobacterium bifidum* altering tight junction proteins leading to diarrhoea. **Methods:** Google scholar and Pubmed were searched using the keywords *Bifidobacterium bifidum* combined with lapatinib, diarrhoea, intestinal permeability and tight junction proteins from 2018 to date. **Results:** Very few studies on *Bifidobacterium bifidum* and lapatinib or even other targeted drugs were found. Bifidobacterium spp are Gram-positive, anaerobic microorganisms, important in maintaining intestinal homeostasis. *Bifidobacterium bifidum* is one example of Bifidobacterium spp with various functions which include modulating mucosal immune system, production of antimicrobials, and alteration of the intestinal microflora, including strengthening barrier function. Thus, changes of *Bifidobacterium bifidum* induced by lapatinib would possibly modulate the tight junctions leading to increase intestinal permeability hence diarrhoea. **Conclusion:** Understanding the changes that occur in the intestinal epithelium following lapatinib treatment will lead to an ability to target prevention or treatment as well as managing TKI-induced diarrhoea appropriately, ultimately improving patient's QOL and reducing the cost of cancer treatment therapy.

Keywords: lapatinib, *Bifidobacterium bifidum*, intestinal, tight junction proteins, diarrhoea

EP12

Ethyl Methane Sulphonate Treatment of Eggplant (*Solanum melongena* cv. Surya) Induces a Novel Mutation in the *MFT*-2 Gene

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Introduction: Eggplant (*Solanum melongena)* is a crop that holds significant value in terms of nutrition and economy. Despite of high phenotypic diversity, the genetic base of the crop is narrow. Inducing mutations by chemical and physical methods is highly efficient to increase its gene pool. This research aims to produce novel eggplant germplasms via chemical mutagenesis utilizing Ethyl Methane Sulphonate (EMS). **Methods:** Initially, a representative plant kill curve analysis was conducted using locally sourced F1 hybrid eggplant seeds to identify optimal concentration for EMS mutagenesis. Subsequently, the commercial eggplant cultivar, Surya (obtained from the World Vegetable Centre) was treated with 0.7 % EMS. Seeds were then planted up to two generations to produce M2 families. Next, genotypic screening was performed across six *Flowering Locus T/Terminal Flower 1* (*FT/TFL1*) homologs via Pacbio long-reads amplicon sequencing. **Results:** Altogether, we observed 28.9 % germination of the 180 EMS treated seeds and 72.5 % germination of the 40 control seeds. Finally, 16 M2 families were derived from the mutant populations and phenotypically characterized with six controls. Approximately eight members from each of the 16 M2 families were established which amounted to 95 plants. Phenotypic variants were observed and these included dwarfism, chlorophyll deficiency and other altered leaf, fruit and flower traits. Amplicon sequencing of the *FT/TFL1* family of genes revealed a novel EMS induced mutations in one of the homologs i.e. *SmMFT*-2. Further analysis revealed the altered allele was located at the upstream region from the start of the coding sequences. **Conclusion:** The new variants constitute a valuable addition to the biological resources for eggplant, expanding the genetic pool of the crop.

Keywords: eggplant, EMS mutagenesis, *Flowering Locus T* (*FT*), *Terminal Flower 1* (*TFL1*), variants

EP13

Impaired Mitochondrial Dynamics in Patient with Energy Deficiency

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Introduction: Mitochondrial dynamics refers to coordination of mitochondrial fission and fusion processes which maintains their distribution, shape, and size. Mitochondrial dynamics plays an important role in cell cycle regulation and abnormalities have been linked to human pathologies. Patients with energy deficiencies, e.g. Leigh syndrome, may have primary mitochondrial abnormalities which can be inherited through nuclear or mitochondrial genes mutation. This study's purpose is to investigate the role of mitochondrial dynamics in a patient with an energy- deficient condition. **Methods:** Fibroblasts from a 3-month-old male forensic patient with clinical indications of respiratory problems, runny nose, and a presumptive positive complex I/II mitochondrial enzyme deficiency were cultured and harvested for a western blot investigation. Solubilized total protein was extracted, and the concentration was determined by Bradford assay. Samples were probed antibodies with GTPases of the dynamin superfamily. A GAPDH monoclonal antibody was used as a normalization control. Fibroblasts of BJ CRL-2522™ were used as a baseline control. **Results:** Mitochondrial fusion proteins, namely Mfn1, Mfn2 and Opa1 were found to be significantly decreased in this patient's cells compared to wild type (WT) ($p<0.05$). In contrast, mitochondrial fission protein level of Drp1 ($p<0.05$) was observed to be significantly increased compared to WT. This disproportion between fusion and fission proteins might contribute to the mitochondrial abnormality as seen in the patient. **Conclusion:** Our study suggested an impaired mitochondrial dynamics, appeared to affect the mitochondrial fusion and fission processes. Extensive studies, such as immunofluorescent staining are recommended to comprehend the mitochondrial dynamics' function in mitochondrial disorders.

Keywords: mitochondrial fusion, mitochondrial fission, western blot, fibroblasts

EP14

In silico Multimerization of Aptamers Targeting Dengue Envelope Domain III as Potential Dengue Diagnostic Antigens

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Introduction: Dengue infection is prevalent in tropical and subtropical regions and can cause a wide range of symptoms. Early diagnosis and prompt treatment are crucial to prevent complications and reduce the risk of death. Enzyme-linked immunosorbent assay is widely used to diagnose dengue from other viruses. However, direct detection of antigen based on antibodies has several disadvantages such as unstable, batch-to-batch variation, and high production cost. Aptamers are attractive alternatives to antibodies and small molecules in diagnostic and other applications due to their higher binding affinity to a target, stability, lower production cost, and longer shelf life. This study aimed to perform *in silico* aptamer multimerization to increase the binding affinity of aptamers compared to individual parent aptamer units. **Methods:** Discrete aptamer units against dengue envelope protein were retrieved from previous publication. The aptamer units were truncated and refined by rational truncation to retain its secondary structure such as the loop region followed by multimerization where two or more truncated aptamer units were linked together via poly-A linker. The secondary structure of the multimerized aptamer were predicted via MFold software. **Results:** Several refined truncated aptamer units were obtained. *In silico* analysis of the multimerised aptamers indicated the loop region of each aptamer units within a construct were retained, and its binding affinity to target has increased compared to single parent aptamers. **Conclusion:** We have successfully obtained multimerized aptamers with increased binding affinity targeting the dengue develop domain III. These aptamers will be subjected to enzyme-linked apta-sorbent assay for further evaluation and validation of its binding affinity *in vitro*.

Keywords: aptamer, *in silico*, dengue virus, envelope domain III protein, diagnosis

EP15

Screening of Putative Leptospira Virulence Factors Using a Yeast Growth Inhibition Assay

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Introduction: Leptospirosis is caused by the pathogenic *Leptospira spp.* (*L. interrogans*). Leptospira's pathogenicity on the host is determined by its virulence factors. Several Leptospira virulence factors are still to be identified. Yeast s*accharomyces cerevisiae* (S. cerevisiae) is commonly employed as a model organism due to the great degree of conservation of cellular processes between yeast and human cells. The present study is aimed to investigate the effect of virulence factors on the yeast using high-throughput screening method. **Methods:** A total of previously cloned 228 putative Leptospira virulence genes in the yeast expression plasmid were transformed into the yeast *S. cerevisiae*. The transformed yeasts were allowed to grow in the 96-well microplate using synthetic complete minus uracil (sc-ura) media. The yeasts were then induced by growing in sc-ura medium with addition of copper sulphate before taking 600 nm optical density (OD_{600nm}) measurement for 24 hours. From the yeast's growth profile, the cell doubling time ratio was determined to estimate the strength of the yeast growth inhibitory effect. The threshold optical density value derived from the control yeast samples was 1.000. **Results:** There were 32 *L. interrogans'* putative virulence factors were showed cell doubling time ratio greater than 1.000. Three putative virulence factors LIC10280, LIC13053 and LIC20217 were unable to obtain cell doubling time ratio with previously known to show strong inhibitory effect towards yeast. **Conclusion:** Secondary screening for further confirmation of the virulence factors on yeast growth inhibition is recommended. Further proteomic study will be conducted on interaction between the yeast protein and the selected *L. interrogans'* putative virulence factors.

Keywords: leptospira, virulence factors, yeast, high-throughput screening assay

EP16

Identification of Microbial Population in Sabah Tea Kombucha Pellicle and Its Potential as a Source of Probiotic for Broiler Chicken

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Introduction: Malaysia's livestock sector relies on broilers industry. However, feed price fluctuations, disease outbreaks, and market competition have been threatening the broiler industry. To remain competitive and meet the growing demand for broiler products, the industry must innovate to ensure efficient supply chain while improving production quality and quantity. Kombucha produced from sugared black tea (*Camellia sinensis*) by a symbiotic culture of bacteria and yeast (SCOBY), is reported to have probiotic potential. Sabah tea is one of the popular teas used to brew kombucha. A pellicle formed during fermentation is often discarded, which is wasteful as it also contains diverse microbial population with possible probiotic potential. This research aimed to identify the potential probiotic population in Sabah tea kombucha pellicle and its effects on growth performance of broiler chicken. **Methods:** DNA was extracted from the sample to identify its probiotic population using 16S metagenomic analysis. A total of 150 one-day-old Cobb500 were randomly divided into four groups: basal diet (control), BD + 0.05% (T1), BD + 0.1% (T2), BD + 0.2% (T3). Feed intake, weight gain, and feed conversion ratio (FCR) were recorded weekly. **Results:** The results showed the dominant presence of *Komagataeibacter* followed by *Bacillus* and *Bifidobacterium*. T2 and T3 showed steady increased in feed intake throughout the study, with T3 showed significant weight gained as compared to control during week 5 and exhibited the best FCR after 35 day of feeding trial. **Conclusion:** The current study provides promising evidence for the use of Sabah tea kombucha pellicle as a low-cost probiotic supplement for improving the growth performance of broilers.

Keywords: kombucha, probiotics, broiler chicken, growth performance

EP17

The Pentacyclic Triterpenoid of *Centella Asiatica* Induces Apoptosis in T-Cell Leukaemia; *In Vitro* Flowcytometry Analysis

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Introduction: *Centella asiatica* (CA) is a well-known medicinal plant that has numerous biological activities, including anticancer properties. T-cell leukaemia is life-threatening cancer that affects white blood cells in the body and current treatment options often have severe side effects. Therefore, there is a need for new treatments that are effective and have fewer side effects. This study aims to investigate the effects of a pentacyclic triterpenoid derived from CA on promoting apoptosis in T-cell leukaemia. **Methods:** Cells were treated with different inhibitory concentrations (IC_{50}) of triterpenoids (madecassoside; ME, asiaticoside; AE, madecassic acid; MA and asiatic acid; AA) ranging from 10 to 100 μM for 48 hours. Cell apoptosis was determined by double staining with Annexin V-FITC/propidium iodide and detected by flowcytometry. The percentage of cells that are Annexin V positive (early apoptotic) and/or PI positive (late apoptotic or necrotic) can be determined by gating the cells using flowcytometry software. **Results:** MA significantly promoted the highest level of apoptosis (21.51%; 5.08% early and 16.43% late apoptosis) followed by ME (12.88%; 2.64% early and 10.24% late apoptosis), AE (10.41%; 2.80% early and 7.61% late apoptosis) and AA (5.77%; 1.51% early and 4.26% late apoptosis) compared to the untreated cells. Most of the cells treated with cytarabine (positive control) underwent apoptotic (35.66%; 4.35% early and 31.31% late apoptosis) and necrosis (18.35%). **Conclusion:** The CA triterpenoid could serve as a potential therapeutic agent for cancer treatment, and its mechanism of action could pave the way for the development of new anticancer drugs.

Keywords: triterpenoid, *Centella asiatica*, apoptosis, flowcytometry

EP18

Spontaneous *F9* Gene Mutation in Haemophilia B Patients in Malaysia from 2014-2022

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Introduction: Haemophilia B (HB) is an X-linked inherited bleeding disorder caused by deficiency on *F9* gene located at chromosome X, resulting reduced antigen level in plasma or dysfunctional coagulation factor (FIX) protein. Approximately 30% of HB patients show spontaneous mutations on *F9* gene without family history of HB due to the natural changes in the DNA structure during replication, mitosis and meiosis. The objective of this study was to identify the spontaneous *F9* gene mutation in HB patients in Malaysia population. **Methods:** A total of 35 Malaysian families with HB from 2014 - 2022 were screened on *F9* gene by Sanger sequencing. **Results:** 5 out of 35 (14%) families with HB were shown spontaneous *F9* gene mutations on exon 5 (20%) and exon 8 (80%), while 30 families with HB were hereditary mutations. The most frequently spontaneous mutations were point mutations (nonsense; 60% and missense; 20%), follow by frameshift mutation (deletion; 20%). **Conclusion:** Although HB is an inherited disease, it can also occur due to spontaneous mutation. In Malaysia population, the percentage of spontaneous mutation in HB is 14%, which is much lower than other countries.

Keywords: haemophilia B, *F9* gene, spontaneous mutation, coagulation factor protein

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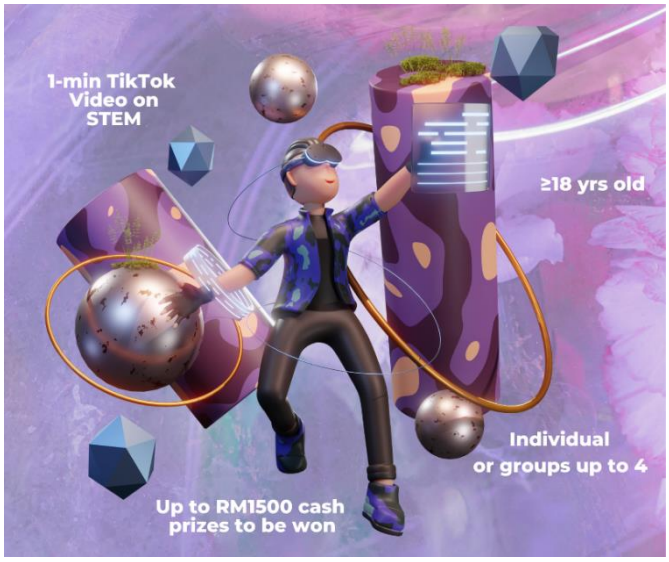
THEME: "#MSMBBeverywhereSTEM"

Everywhere you look, hear and do, you see Science in everything, every day! How does it happen? How does it work? What makes it work?



Some of the questions keep us pondering everything that happened around us. How? Fascinating if we know and understand the role of science, technology, engineering and mathematics revolve and support us daily. Let's help us break down the real science behind everyday activities in our lives!

Be it in the secret of fluffy omelette, does cloud taste like marshmallows, or to even breaking down the string theory!

The submission deadline for this challenge was 25th January 2023 and winners were announced on 15th February 2023. All submissions can currently be viewed on @msmbbofficial instagram account

Objective

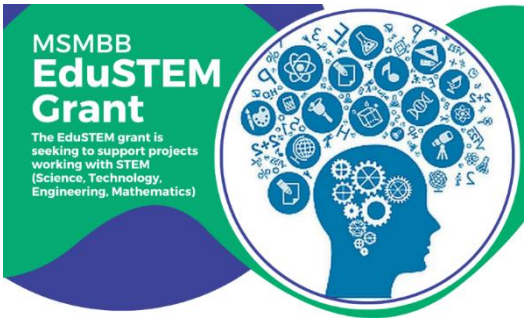
To create public interest in Science, Technology, Engineering and Mathematics (STEM) through social media platforms.

Prizes

There will be four winners for this challenge:

🏆 The top two videos with the most likes (public judges) on the Instagram account during the competition will receive RM250 each.
🏆 The top two with the most likes for content (appointed judges) will receive RM500 each.

MSMBB EduSTEM Grant



The Malaysian Society for Molecular Biology and Biotechnology (MSMBB) EduSTEM grant fund activities aligned with several UNESCO Sustainable Development Goals (SDGs) to improve the quality of education, life, health and well-being. A grant of up to RM5,000 is available to be applied for by MSMBB members.

The EduSTEM grant seeks to support projects on STEM (Science, Technology, Engineering and Mathematics) education. Preference is given to projects demonstrating innovative approaches and techniques to solve community issues and build individual, neighbourhood and/or community capacity. In addition, the project must bring direct benefits to the community.

This grant is open to all MSMBB members with the following criteria:

- Malaysian citizens ≥ 18 years old
- Project duration ≤ 1 year
- Amount ≤ RM5000 per project

How to apply?

Apply through the downloadable form at the MSMBB website. There is no specific format for the proposal. However, the applicants should provide the details stated in the form.

When to apply?

The call for submission will be announced to all members. Please email your proposal to the.msmbb.office@gmail.com.

What happens after I apply?

Your application will be shortlisted if it fits the MSMBB Community Fund priority areas.

What happens after the grant is awarded?

All successful applicants must present their progress once a year. An oral presentation at the MSMBB annual conference OR submission of a paper to a reputable journal, such as APJMBB, acknowledging the funder is mandatory.

MSMBB Best Scientist Awards 2023

The Malaysian Society for Molecular Biology and Biotechnology (MSMBB) established the Best Scientist Awards to recognise outstanding scientists who have made significant contributions to the field of molecular biology and biotechnology.

There are two categories of Awards, namely: Young Scientist Award (for members who are at the age of 40 or below) and Distinguished Scientist Award (for members who are above 40 years old)

Assessment Criteria

The following criteria will be used to evaluate Best Scientist Award nominees:

(1) Academic achievements: Scientific leadership and engagement with academic and university research; quality of high impact peer-reviewed publications; significant mentoring of graduate students, postdocs, staff members, visiting scientists, peers, industry training, etc.
(2) Professional appointments: Service to the research community through agency, professional society, or advisory work.
(3) Honours and awards: Merits received.
(4) Contributions: Service to the community and impact of research to Society.

Prizes

Only one winner will be selected for each category. Each of the winners will receive a cash prize of RM1,000.00 and a certificate of commendation.

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With effect from 1st January 2020, all accepted manuscripts (submitted on 1st January 2020 onwards) will incur an article processing charge (APC) of RM250 or USD70 prior to publication. The authors are advised to make the payment and send the proof of payment to us at apjmbb@upm.edu.my. We will proceed with the typesetting process immediately and send the Galley Proof of your manuscript within two weeks.

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New Life Membership + Registration Fee	RM420.00 (once)
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