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THE 8TH INTERNATIONAL BIOTECHNOLOGY SYMPOSIUM

TRANSLATIONAL BIOTECHNOLOGY : IMPACT AND WAY FORWARD

29TH - 30TH AUG 2023

SABAH INTERNATIONAL CONVENTION CENTRE, KOTA KINABALU, SABAH

PROGRAMME

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Minister of Science, Technology and Innovation (MOSTI)

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FOREWORD BY
YB CHANG LIH KANG
Minister of Science, Technology and Innovation (MOSTI)

Congratulations to the Biotechnology Research Institute, Universiti Malaysia Sabah, for convening the 8th International Biotechnology Symposium, which serves as a pivotal platform to foster biotechnology promotion and attract industry players, as well as local, and foreign investors to Malaysia. The symposium's theme, "Translational Biotechnology: Impact and Way Forward," perfectly aligns with Malaysia's National Biotechnology Policy (DBN). Acknowledging biotechnology as a crucial driver of the nation's social and economic progress, the Malaysian Government has placed it at the forefront of the journey towards becoming a developed nation. The DBN policy leverages biotechnology in agriculture, food security, healthcare, well-being, as well as industrial and circular economy initiatives. Malaysia's vision of becoming a high-tech nation by 2030 hinges on translating scientific discoveries into practical applications.

Traditionally, research has focused on fundamental discoveries, but the emergence of translational biotechnology paves the way for tangible economic contributions. By driving innovation, job creation, attracting investments, boosting exports, reducing healthcare costs, and propelling technological advancements, translational biotechnology plays a crucial role in elevating a country's economy and enhancing societal well-being. The importance of translational biotechnology has been profoundly demonstrated during the COVID-19 pandemic. It has been instrumental in the discovery and development of tests, therapies, and vaccines for COVID-19, thus showcasing its vital role in global public health preparedness and improving overall global health. As countries invest in and prioritize the biotechnology sector, they can reap substantial economic benefits while advancing humanity's well-being.

Biotechnology holds the key to the sustainable transformation of our societies. This transformation requires collaborative efforts between legislators and the industry, aligning with Sustainable Development Goals (SDGs) and the principles of IR4.0. Businesses and governments must share ambitious goals and work hand in hand to craft optimal solutions for our shared future. In this pursuit, the collaboration of science, technology, business, and government becomes our strength, propelling us towards success with greater speed and effectiveness. Together, we have the power to unleash the full potential of biotechnology and drive progress for a brighter and more sustainable future.

In this 8th Biotechnology Symposium, let us celebrate the spirit of collaboration, innovation, and determination to make a positive impact on our society and the world.

Thank you.

FOREWORD BY
PROFESSOR DATUK DR. KASIM HJ. MANSOR
Vice Chancellor of Universiti Malaysia Sabah

Assalamualaikum w.b.t and Salam Sejahtera.

Alhamdulillah. First and foremost, I would like to congratulate the Biotechnology Research Institute (BRI) for organizing the 8th International Biotechnology Symposium. Sabah is a state blessed with incredible biodiversity and resources. We are convinced that the research presented at this symposium on the theme "Translational Biotechnology: Impact and Way Forward" will have a significant impact on our community.

Secondly, I would like to advocate that symposiums such as this one serve as the ideal platform for knowledge exchange providing researchers with the perfect opportunity to share findings, insights, and discoveries.

During the course of this event, we will explore nine main themes: namely genomics, molecular microbiology, bioprocesses, transcriptomics, plant biotechnology, bioinformatics, natural product chemistry, animal biotechnology, and synthetic biology. In view of the considerable range of these themes, I sincerely wish that this symposium will grant academicians fresh perspectives on a whole host of topics, both within and outside their immediate fields of study.

Finally, on behalf of Universiti Malaysia Sabah, I would like to extend my deepest gratitude to all participants, speakers, sponsors, and supporters for their invaluable contributions to this event. I would also like to say a special 'Thank You' to the diligent organizing committee, for their unwavering commitment to ensuring the success of this symposium.

May this occasion be the most fulfilling one for all of you!

MESSAGE FROM
PROF. DR. LEE PING CHIN
Director of Biotechnology Research Institute, UMS

A warm welcome to the delegates of the 8th International Biotechnology Symposium.

Through this symposium, let us explore the transformative potential of biotechnology for a brighter and sustainable future. The theme of the symposium, "Translational Biotechnology: Impact and Way Forward," highlights the significance of translational science in addressing global challenges like renewable energy adoption, sustainable practices, waste management, biodiversity conservation, and environmentally conscious policies.

Biotechnology has reformed healthcare with precise diagnostics, personalized treatments, and groundbreaking therapies, offering hope for eradicating chronic illnesses and extending life expectancy. In agriculture, it enhances productivity with sustainable practices, reducing pesticides, and cultivating resilient crops, addressing food security challenges and poverty. Biotechnology aids environmental conservation through bioremediation, biodegradable materials, and sustainable production, fostering a greener planet while advancing human progress. In the industrial sector, biocatalysis and bioprocessing yield bio-based chemicals, reducing reliance on fossil fuels and emissions. Its impact on drug discovery improves pharmaceuticals for human health. Overall, biotechnology holds transformative potential across diverse sectors, shaping a sustainable and prosperous future.

Biotechnology's interdisciplinary nature encourages collaboration among scientists, researchers, and experts from various fields. This meeting serves as the platform for them to accelerate scientific discoveries and stimulate innovation and research across diverse domains that benefit society as a whole.

The symposium is made possible by the generous support of our sponsors and the tireless commitment of the organizing committee. I would like to extend my gratitude and appreciation to the organising committee for their exceptional efforts in successfully organizing the symposium.

Let us seize the opportunities and work collectively to pave the way for a better tomorrow. Together, we can shape a world where biotechnology serves as the bedrock of progress and the key to overcoming the most pressing challenges of our time.

Wishing all the delegates a pleasant and scientifically rewarding symposium.

MESSAGE FROM
ASSOC. PROF. DR. MD. SHAFIQUZZAMAN SIDDIQUEE

Chairman of the Organising Committee of
the 8th International Biotechnology Symposium

I take this opportunity to welcome the delegates to the 8th International Biotechnology Symposium. I am honoured and privileged to represent this symposium's organising committee at this symposium.

Biotechnology plays a significant role in contributing to several Sustainable Development Goals (SDGs) outlined by the United Nations. In SDG 2 (Zero Hunger), biotechnology can address food security challenges and sustainably increase agricultural productivity. In SDG 3 (Good Health and Well-being), the advancements in biotechnology have been crucial in addressing infectious diseases, developing personalized medicine, and improving global healthcare access and affordability. Moreover, in SDG 6 (Clean Water and Sanitation), biotechnology is used to treat water and wastewater through processes like bioremediation, which employs microorganisms to break down pollutants and contaminants. Besides that, in SDG 7 (Affordable and Clean Energy), biotechnology contributes to the production of biofuels and bioenergy, which helps in reducing greenhouse gas emissions and promoting sustainable energy sources. In SDG 13 (Climate Action), biotechnology is used in climate change mitigation and adaptation strategies. In SDG 14 (Life Below Water) and SDG 15 (Life on Land), biotechnology contributes to conservation efforts by facilitating the development of new methods to protect marine and terrestrial biodiversity.

The theme of the symposium 'Translational Biotechnology: Impact and Way Forward' highlights the importance of translational science which drives this important gathering. We can use biotechnology to mitigate these impacts including transitioning to renewable energy sources, adopting sustainable practices, implementing effective waste management strategies, conserving biodiversity, and promoting environmentally conscious policies and behaviours.

I wish to thank the international and national delegates who have made an effort to participate in this event. We have a total of 215 participants, with participants also coming from Japan, South Korea, India, Pakistan and Indonesia. I also thank our sponsors for their generous support in making this event possible. To the members of the organizing committee, thank you for your unreserved support to this event.

Wishing all the delegates a pleasant and scientifically rewarding symposium.

OPENING CEREMONY OF THE 8TH INTERNATIONAL BIOTECHNOLOGY SYMPOSIUM (SB8) 2023

Date : **29th August 2023 (Tuesday)**
Time : **8:00 am**
Venue : **Sabah International Convention Centre, Kota Kinabalu, Sabah**

8:00 am	:	Arrival of delegates and participants
8:30 am	:	Arrival of Principal Officers and Head of Departments of Universiti Malaysia Sabah
8:40 am	:	Arrival of **YBhg. Professor Datuk Dr. Kasim Hj. Mansor,** Vice-Chancellor, Universiti Malaysia Sabah
8.45 am	:	Arrival of **YBhg. Datuk Ts. Dr. Mohd Nor Azman bin Hassan** Deputy Secretary General (Technology Development), Ministry of Science, Technology & Innovation (MOSTI) Arrival of **YBhg. Datuk Ts. Dr. Aminuddin Hassim** Secretary General, Ministry of Science, Technology & Innovation (MOSTI) Arrival of **YB Datuk Arthur Joseph Kurup,** Deputy Minister of Science, Technology, and Innovation (MOSTI)
8:50 am	:	Arrival of **YB Tuan Chang Lih Kang,** Minister of Science, Technology, and Innovation (MOSTI)
9:00 am	:	Event Begins • National Anthem & State Anthem • Do'a Recital • Speech by **YBhg. Professor Datuk Dr. Kasim Hj. Mansor,** Vice Chancellor, Universiti Malaysia Sabah • Opening Speech by **YB Tuan Chang Lih Kang,** Minister of Science, Technology, and Innovation (MOSTI)
10:00 am	:	Refreshment

Dress code: Formal

SCIENTIFIC PROGRAMME
DAY 1 | 29TH AUGUST 2023 (TUESDAY)

10:00 – 10:45	**KEYNOTE** **Speaker: YBhg. Datuk Ts. Dr. Mohd Nor Azman Bin Hassan** Deputy Secretary General (Technology Development) Ministry of Science, Technology and Innovation (MOSTI) **Moderator: Prof. Dr. Lee Ping Chin** Room: Sipadan Hall 1, Level 4
PLENARY SESSION A **Chairperson: Prof. Dr. Vijay Kumar** Room: Sipadan Hall 1, Level 4	
10:45 – 11:15	**Plenary 1** **Speaker: Prof. Datuk Wira Dr. Raha Abdul Rahim** (Chief Executive Officer at the National Institutes of Biotechnology Malaysia)
11:15 – 11:45	**Plenary 2** **Speaker: Prof. Dr. K Sudesh Kumar A/L C Kanapathi Pillai** (School of Biological Sciences, Universiti Sains Malaysia)
PLENARY SESSION B **Chairperson: Prof. Dr. Jualang Azlan Gansau** Room: Sipadan Hall 1, Level 4	
11:45 – 12:15	**Plenary 3** **Speaker: Dr. Manish Biyani** (Advanced Institute of Science and Technology, Japan)
12:15 – 12:45	**Plenary 4** **Speaker: Professor Dr. Kang Dae-Kyung** (Department of Animal Resources Science in Dankook University)
12:45 – 13:00	**SPONSOR TALK** Room: Sipadan Hall 1, Level 4
13:00 – 14:00	**Lunch and Poster Session 1**

ORAL PRESENTATIONS

DAY 1 | 29TH AUGUST 2023 (TUESDAY)

	Session A Sipadan Hall 1, Level 4	**Session B** Kapalai Room, Level 2	**Session C** Dinawan Room, Level 5
	Chairperson: **Assoc. Prof. Dr. Kenneth F. Rodrigues**	**Chairperson:** **Assoc. Prof. Dr. Zaleha Abd. Aziz**	**Chairperson:** **Dr. Clarence M Ongkudon**
14:00 –14:12	OP A-1	OP B-1	OP C-1
14:12 –14:24	OP A-2	OP B-2	OP C-2
14:24 –14:36	OP A-3	OP B-3	OP C-3
14:36 –14:48	OP A-4	OP B-4	OP C-4
14:48 –15:00	OP A-5	OP B-5	OP C-5
15:00 –15:12	OP A-6	OP B-6	OP C-6

	Session D Sipadan Hall 1, Level 4	**Session E** Kapalai Room, Level 2	**Session F** Dinawan Room, Level 5
	Chairperson: **Dr. Nur Athirah Yusuf**	**Chairperson:** **Dr. Suryani Saallah**	**Chairperson:** **Assoc. Prof. Dr. Teoh Peik Lin**
15:12 –15:24	OP D-1	OP E-1	OP F-1
15:24 –15:36	OP D-2	OP E-2	OP F-2
15:36 –15:48	OP D-3	OP E-3	OP F-3
15:48 –16:00	OP D-4	OP E-4	OP F-4
16:00 –16:12	OP D-5	OP E-5	OP F-5
16:12 –16:24	OP D-6	OP E-6	OP F-6
16:24–18:00	**Refreshment and Poster Session 2**		

SCIENTIFIC PROGRAMME

DAY 2 | 30TH AUGUST 2023 (WEDNESDAY)

	PLENARY SESSION C **Chairperson: Prof. Dr. Clemente Michael Wong Vui Ling** Room: Sipadan Hall 1, Level 4
09:00 – 09:30	**Plenary 5** **Speaker: Assoc. Prof. Dr. Ruslinda A Rahim** (Director, National Nanotechnology Centre (NNC), Ministry of Science, Technology and Innovation (MOSTI))
09:30 – 10:00	**Plenary 6** **Speaker: Prof. Dr. Habibah A. Wahab** (School of Pharmaceutical Sciences, Universiti Sains Malaysia)
10:00 – 10:30	**Refreshment**

ORAL PRESENTATIONS

DAY 2 | 30TH AUGUST 2023 (WEDNESDAY)

	Session G Sipadan Hall 1, Level 4	**Session H** Kapalai Room, Level 2	**Session I** Dinawan Room, Level 5
	Chairperson: **Assoc. Prof. Dr. Mailin Misson**	**Chairperson:** **Dr. Mardani Abdul Halim**	**Chairperson:** **Dr. Cheong Bo Eng**
10:30 – 10:42	OP G-1	OP H-1	OP I-1
10:42 – 10:54	OP G-2	OP H-2	OP I-2
10:54 – 11:06	OP G-3	OP H-3	OP I-3
11:06 – 11:18	OP G-4	OP H-4	OP I-4
11:18 – 11:30	OP G-5	OP H-5	OP I-5
11:30 – 11:42	OP G-6	OP H-6	OP I-6

	Session J Sipadan Hall 1, Level 4	**Session K** Kapalai Room, Level 2	**Session L** Dinawan Room, Level 5
	Chairperson: **Dr. Mohd Khalizan Sabullah**	**Chairperson:** **Dr. Rahmath Abdulla**	**Chairperson:** **Dr. Ruzaidi Azli Mohd Mokhtar**
11:42 – 11:54	OP J-1	OP K-1	OP L-1
11:54 –12:06	OP J-2	OP K-2	OP L-2
12:06 –12:18	OP J-3	OP K-3	OP L-3
12:18 –12:30	OP J-4	OP K-4	OP L-4
12:30 –12:42	OP J-5	OP K-5	OP L-5
12:42 –12:54	OP J-6	OP K-6	OP L-6
12:54 –14:00	**Lunch and Poster Session 3**		

	Session M Sipadan Hall 1, Level 4	**Session N** Kapalai Room, Level 2	**Session O** Dinawan Room, Level 5
	Chairperson: **Dr. Khairul Azfar Kamaruzaman**	**Chairperson:** **Assoc. Prof. Dr. Wilson Yong Thau Lym**	**Chairperson:** **Assoc. Prof. Dr. Cahyo Budiman**
14:00 – 14:12	OP M-1	OP N-1	OP O-1
14:12 – 14:24	OP M-2	OP N-2	OP O-2
14:24 – 14:36	OP M-3	OP N-3	OP O-3
14:36 – 14:48	OP M-4	OP N-4	OP O-4
14:48 – 15:00	OP M-5	OP N-5	OP O-5
15:00 – 15:15	**Refreshment**		

15:15 – 16:30	**RESEARCH-INDUSTRY FORUM** **"Translational Biotechnology: Impact and Way Forward"** **Moderator: Assoc. Prof. Dr. Ts. Zarina Amin** **Speakers:** **Dr. Wan Raihana Wan Aasim** (Malaysian Technology Development Cooperation) **Goh Mung Chwee** (Sabah Tea Resort) **Robest Yong** (Innovation Ambassador by Agency Innovation Malaysia) Room: Sipadan Hall 1, Level 4

CLOSING CEREMONY OF THE 8TH INTERNATIONAL BIOTECHNOLOGY SYMPOSIUM (SB8) 2023

Date : **30 August 2023 (Wednesday)**
Time : **4:30 pm**
Venue : **Sabah International Convention Centre, Kota Kinabalu, Sabah**

4:30 pm : Arrival of **YB Datuk Dr. Haji Mohd Arifin Bin Datuk Haji Mohd Arif**
Minister of Science, Technology and Innovation Sabah (KSTI)

4:40 pm : Event Begins

- Appreciation Speech by:
  Assoc. Professor Dr. Shafiquzzaman Siddiquee,
  Chairman, The 8th Biotechnology Symposium (SB8) 2023,
  Biotechnology Research Institute, Universiti Malaysia Sabah

- Closing Remarks by:
  YB Datuk Dr. Haji Mohd Arifin Bin Datuk Haji Mohd Arif,
  Minister of Science, Technology and Innovation Sabah (KSTI)

- Presentation of Award
  - Travel Grant Award
  - Best Oral Presenter Award
  - Best Poster Presenter Award

- Coffee Break

5:30 pm : Ends

Dress code: Formal

SPEAKERS

KEYNOTE SPEAKER

YBhg. Datuk Ts. Dr. Mohd Nor Azman Bin Hassan

**DEPUTY SECRETARY GENERAL (TECHNOLOGY DEVELOPMENT),
MINISTRY OF SCIENCE, TECHNOLOGY AND INNOVATION (MOSTI)**

Expertise: Datuk Ts. Dr. Mohd Nor Azman oversees the policies and development of science, technology and innovation ecosystem to support the socio-economic development of the country.

PLENARY SPEAKER

Professor Datuk Wira Dr. Raha Abdul Rahim

**CHIEF EXECUTIVE OFFICER (CEO),
NATIONAL INSTITUTES OF BIOTECHNOLOGY MALAYSIA (NIBM)**

Expertise: Microbiology, Microbial Genetics, Molecular Biology.

PLENARY SPEAKER

Professor Dr. Habibah A. Wahab

**DEPUTY-VICE CHANCELLOR,
(RESEARCH AND INNOVATION, UNIVERSITI SAINS MALAYSIA (USM))**

Expertise: Biopharmaceutic studies, design and development of Novel Drug Delivery Systems.

PLENARY SPEAKER

Prof. Madya Dr. Ruslinda A. Rahim

**DIRECTOR, NATIONAL NANOTECHNOLOGY CENTER (NNC),
MINISTRY OF SCIENCE, TECHNOLOGY AND INNOVATION (MOSTI)**

Expertise: Nano Structure Fabrication & Carbon Nanotubes.

PLENARY SPEAKER

Professor Dr. K Sudesh Kumar A/L C Kanapathi Pillai

**SCHOOL OF BIOLOGICAL SCIENCES,
UNIVERSITI SAINS MALAYSIA (USM)**

Expertise: Environmental Microbiology, Industrial Microbiology, Environmentally-Friendly Products and Technologies, Biopolymers.

PLENARY SPEAKER

Professor Dr. Kang Dae-Kyung

**SCHOOL OF BIO-RESOURCES SCIENCE,
DANKOOK UNIVERSITY, REP. OF KOREA**

Expertise: Industrial microbiology and biotechnology.

PLENARY SPEAKER

Dr. Manish Biyani

**RESEARCH PROFESSOR,
JAPAN ADVANCED INSTITUTE OF SCIENCE AND TECHNOLOGY**

Expertise: Molecular Evolutionary Engineering, Low-cost molecular diagnostics, Bio-drug discovery, DNA-based nano architecture, Functional Proteomics and Biosensors.

ORAL PRESENTER LIST

Presentation code	Abstract code	Authors and Title Presentation	Presenter Affiliation
Oral Sessions: OP A			
OP A-1	**SO-65**	Nur Fatihah Ahmad, Muhammad Nor Syamim Mohd Sanusi, Muhammad Hamizan Zawawi, Wan Rosli Wan Ishak, Sabreena Safuan **Effect of Polyphenolic-Rich Fraction of Cornsilk (*Stigma maydis*) in Streptozotocin-Induced Type 2 Diabetic Rats**	Biomedicine Programme, School of Health Sciences, Universiti Sains Malaysia
OP A-2	**SO-81**	Azmina Hassan, Zuraidah Abdullah, Tan Niu Jin, Sabreena Safuan **Effect of *Plukenetia volubilis* L. (Sacha Inchi) Oil on Hypercholesterolemia Diet-Induced Sprague Dawley Rat**	School of Health Sciences, Health Campus Universiti Sains Malaysia
OP A-3	**SO-16**	Ahmad Asnawi Bin Mus, Hartinie Marbawi and Jualang Azlan Gansau **Establishment *Strobilanthes crispus in vitro* Culture and Assessment of Taraxerol Content from Field and *in vitro* Grown Plants**	Faculty of Science and Natural Resources, Universiti Malaysia Sabah
OP A-4	**SO-25**	Ismail Ware, Katrin Franke, Andrej Frolov, Kseniia Bureiko, Elana Kysil, Maizatulakmal Yahayu, Hesham Ali El Enshasy, Ludger A. Wessjohann **Comparative Metabolite Analysis Approach for *Piper sarmentosum* Organs Classification Based on LC-MS**	Institute of Bioproduct Development, Universiti Teknologi Malaysia
OP A-5	**SO-63**	Rizasella Jamili, Jualang Gansau, Zaleha A. Aziz **Micropropagation of the Medicinal Plant *Kaempferia parviflora* using Thin Cell Layer**	Faculty of Science and Natural Resources, Universiti Malaysia Sabah
OP A-6	**SO-78**	Izah Adlina Mohamad Shukri, Ahmad Ramli Mohd Yahya, Masratul Hawa Mohd, Nur Asshifa Md Noh 0 **Morphological and Molecular Identification of *Pyricularia oryzae* Causing Blast Disease on Rice (*Oryza sativa*)**	Bioprocess Laboratory, School of Biological Sciences, Universiti Sains Malaysia

Presentation code	Abstract code	Authors and Title Presentation	Presenter Affiliation
Oral Sessions: OP B			
OP B-1	**SO-38**	Vernon Vest Mangun, Rajeena Sugumaran, Wilson Yong Thau Lym, Nur Athirah Yusof **Genomic Analysis of Endophytic *Bacillus altitudinis* VUMS1 Isolated from Sabah's Red Algae, *Kappaphycus alvarezii***	Biotechnology Research Institute, Universiti Malaysia Sabah
OP B-2	**SO-44**	Yu Lean Huat **Digital PCR- An Emerging Technology with Broad Applications in Biotechnology**	Interscience Sdn. Bhd.
OP B-3	**SO-48**	Syahidiah Syed Abu Thahir, Sakshaleni Rajendiran, Yuvaneswary Veloo, Maslina Mohd Ali, Noor Asyikin binti Abu, Hassuzana Khalil, Vickneshwaran Muthu, Rafiza Shaharudin **Genetic Comparison of ESBL *Escherichia coli* Isolated in Dairy Farms**	Environmental Research Centre, Institute for Medical Research, National Institutes of Health
OP B-4	**SO-57**	Asha Devi Pallujam, Aiswarya Prasad, Lee Wai Leng, Tan Hock Siew, Philipp Engel, Yek Sze Huei **Revisit Apis (Honey bees) Phylogeny with Two Molecular Markers**	School of Science, Monash University Malaysia
OP B-5	**SO-55**	Bao Chi Wong, Hock Siew Tan **Dual RNA Sequencing as a Method to Elucidate the Differences in *Shigella sonnei* and *Shigella flexneri* During Infection of *Caenorhabditis elegans***	School of Science, Monash University Malaysia
OP B-6	**SO-42**	Suhaila Rusni, Mieko Sassa, Toshiyuki Takagi, Masato Kinoshita, Yusuke Takehana, Koji Inoue **Targeted Mutagenesis of *cyp1a* Gene Alters Pollutant Catabolism in Javanese Medaka, *Oryzias javanicus***	Atmosphere and Ocean Research Institute, The University of Tokyo

Presentation code	Abstract code	Authors and Title Presentation	Presenter Affiliation
Oral Sessions: OP C			
OP C-1	**SO-32**	Normaiza Nordin, Sazmal Effendi Arshad, Zarina Amin **Bioelectricity Generation using Banana Peel as Substrate in Dual-Chamber *Pseudomonas aeruginosa*-Based Microbial Fuel Cell**	Faculty of Science and Natural Resources, Universiti Malaysia Sabah.
OP C-2	**SO-72**	Nurul Atiqah Shamsuddin, Muhammad Najib Ikmal Mohd Sabri, Nur Atiqah Abdul Rasik, Kavita Pusphanathan, Muaz Mohd Zaini Makhtar **Effect of Different Pre-Treatment Methods on Dewatered Sludge Prior Usage in Membrane-Less Microbial Fuel Cell for Simultaneous Bioremediation and Energy Recovery**	School of Industrial Technology, Bioprocess Technology Division, Universiti Sains Malaysia
OP C-3	**SO-86**	Muaz Mohd Zaini Makhtar, Kavita Pusphanathan, Hafiza Shukor, Muhammad Najib Ikmal Mohd Sabri, Nur Atiqah Abdul Rasik, Nurul Atiqah Shamsuddin **Kinetic Growth Model for *Bacillus subtilis* in Dual Chamber Microbial Fuel Cell (MFC) with Sulfonated Polysulfone as Proton Exchange Membrane (PEM)**	Bioprocess Technology Division, School of Industrial Technology, Universiti Sains Malaysia
OP C-4	**SO-90**	Kavita Pusphanathan, Muaz Mohd Zaini Makhtar, Hafiza Shukor, Muhammad Najib Ikmal Mohd Sabri, Nur Atiqah Abdul Rasik, Nurul Atiqah Shamsuddin **Effectiveness of Direct Sulfonated Polysulfone in Dual Chamber Microbial Fuel Cells Based Dewatered Sludge for Power Generation**	School of Industrial Technology, Bioprocess Technology Division, Universiti Sains Malaysia
OP C-5	**SO-91**	Nur Atiqah Abdul Rasik, Muaz Mohd Zaini Makhtar, Muhammad Najib Ikmal Mohd Sabri, Nurul Atiqah Shamsuddin, Kavita Pushpanathan **Effect of Anode Acclimation Method on Biofilm Formation and Electrogenic Bacterial Population in Membrane-less Microbial Fuel Cell for Simultaneous Bioremediation and Energy Recovery**	School of Industrial Technology, Universiti Sains Malaysia
OP C-6	**SO-92**	Muhammad Najib Ikmal Mohd Sabri, Nur Atiqah Abdul Rasik, Nurul Atiqah Shamsuddin, Kavita Pusphanathan, Husnul Azan Tajarudin, Muaz Mohd Zaini Makhtar **Effect of Different Incubation Period on *Bacillus subtilis* and *Pseudomonas aerugenosa* in Membrane – less Microbial Fuel Cell for Simultaneous Chicken Manure Bioremediation and Electricity Generation**	School of Industrial Technology, Bioprocess Technology Division, Universiti Sains Malaysia

Presentation code	Abstract code	Authors and Title Presentation	Presenter Affiliation
Oral Sessions: OP D			
OP D-1	**SO-06**	Nurhikmah Abu Aziz, Annie Christianus, Wan Mohd Syazwan Wan Solahudin, Intan Safinar Ismail, Low Chen Fei **Comparative Proteomic Analysis Uncover Potential Biomarkers for the Detection of Vibrio-resistant Phenotype in Hybrid Grouper (*Epinephelus fuscoguttatus* ♀ x *Epinephelus lanceolatus* ♂) and Their Underlying Immune Mechanism**	Department of Chemistry, Faculty of Science, Universiti Putra Malaysia
OP D-2	**SO-51**	Amirah Syafiqah Zamri, Zarirah Zulperi, Fatin Nabilah Mohamad Sahadan, Yuzine Esa, Fadhil Syukri **Molecular Characterisation of Gonadotropin-Releasing Hormone (GnRH) Genes in Tropical Catfishes; *Pangasius nasutus*, *Pangasianodon hypophthalmus* and *Hemibagrus nemurus***	Department of Aquaculture, Faculty of Agriculture, Universiti Putra Malaysia
OP D-3	**SO-66**	Hoe-Han Goh **Omics Studies of Nepenthes Pitcher Plants to Elucidate Botanical Carnivory for Translational Applications**	Institute of Systems Biology, Universiti Kebangsaan Malaysia
OP D-4	**SO-14**	Noor Haliza Mohamed Ibrahim, Zurina Zainudin, Amilia Afzan Mohd Jamil, Norshariza Nordin, Habibah Abdul Hamid, Karuppiah Thilakavathy **Identifying Genetic Variants for Spontaneous Preterm Labor (sPTL) in Malay Preterm Infants through Whole-Exome Sequencing**	Department of Biomedical Science, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia
OP D-5	**SO-79**	Nursyuhaida Mohd Hanafi, Tan Chun Keat, Amalia Mohd Hashim, Nur Elina Abdul Mutalib, Minhalina Badrul Hisham **Grain Corn Silage: Physico-chemical Analysis and Amplicon Metagenomic Analysis in Tropical Region**	Agro-Biotechnology Malaysia Institutes (ABI), National Institutes of Biotechnology Malaysia
OP D-6	**SO-88**	Putri Krishna Kumara Dewi, Syarifah Dewi, Bimo A. Tejo, Novi Silvia Hardiany **Coriander (*Coriandrum sativum L.*) Seeds Extract Alleviates Brain Oxidative Stress in Obese Rats**	Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia

Presentation code	Abstract code	Authors and Title Presentation	Presenter Affiliation
Oral Sessions: OP E			
OP E-1	**SO-64**	Alif Nordin, Mohammad Tasyriq Che Omar **Deep Mutational Scanning and Energy Decomposition Analysis onto Modified-Heated MD-Screened Molecular Docking of CXCR2 and HY29-1 Improves Antibody-Antigen Binding**	School of Distance Education, Universiti Sains Malaysia
OP E-2	**SO-89**	Fatin Filzah Nur Abd Kadir, Muhamad Alif Che Nordin, Rabiatul Basria S.M.N. Mydin, Choong Yew Siew, Mohammad Tasyriq Che Omar **Molecular Interaction Analysis of Anti-IL8 scFv-10F8-6His against IL8 Monomer through Molecular Docking and Molecular Dynamic Simulation**	School of Distance Education, Universiti Sains Malaysia
OP E-3	**SO-05**	Makdi Masnoddin, Clemente Michael Wong Vui Ling, Nur Athirah Yusof **Functional Analysis of Conserved Hypothetical proteins from the Antarctic Yeast, *Glaciozyma antarctica***	Preparatory Centre for Science and Technology (PPST), Universiti Malaysia Sabah
OP E-4	**SO-49**	Rupany Selvam, Ian Han Yan Lim, Jovita Catherine Lewis, Chern Hong Lim, Michelle Khai Khun Yap, Hock Siew Tan **Identification and Characterisation of Antibacterial Aptamers against *Pseudomonas aeruginosa***	School of Science, Monash University Malaysia
OP E-5	**SO-74**	Syahriel Abdullah, Arnnyitte Alexander, Kwak Min Kyu, Chong Khim Phin ***In vitro* and i*n silico* Modelling of Sterol and Norlanostane Derivatives Isolated from the *Ganoderma boninense***	Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah
OP E-6	**SO-33**	Nur Iliyana Illang, Rafida Razali, Nurbella Sofiana Altu, Lee Ping Chin, Cahyo Budiman, Habibah A Wahab ***In silico* Screening and *in vitro* Inhibition Properties of NADI-based Plant Compounds against FKBP35 from *Plasmodium knowlesi***	Biotechnology Research Institute, Universiti Malaysia Sabah

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OP F-1	**SO-20**	Reyhaneh Farghadani, Rakesh Naidu **Curcumin as a Golden Spice in Targeting Key Cellular Signaling Pathways in Triple Negative Breast Cancer**	Faculty of Medicine, Monash University Malaysia
OP F-2	**SO-56**	Melonney Patrick, Wan Najwa Wan Mohd Zohdi, Suhaila Abd.Muid, Effat Omar **Alpha(α)-mangostin Promotes Diabetic Wound Healing: An *in vitro* Study with Mechanistic Elucidation**	Department of Biochemistry & Molecular Medicine, Faculty of Medicine, Universiti Teknologi MARA Sungai Buloh, Selangor, Malaysia
OP F-3	**SO-67**	Lusia Barek Moses, Mohd. Fadzelly Abu Bakar, Hasmadi Mamat, Zaleha Abd Aziz **Cytotoxicity and Apoptosis Induced by Unfermented Freeze-Dried Leaf Extract of Tongkat Ali (*Eurycoma longifolia* Jack.) in MCF-7 Human Breast Cancer Cell Line**	Preparatory Center for Science and Technology, Universiti Malaysia Sabah
OP F-4	**SO-80**	Bibi Nur Bazlini Baharun, Ng Phei Ying, Sabreena Safuan **Anti-Cancer Effects of *Clinacanthus nutans* and *Annona muricata* on the Initial Invasion of Breast Carcinoma**	School of Health Sciences, Health Campus, Universiti Sains Malaysia
OP F-5	**SO-68**	Martina Irwan Khoo, Nur Arnida Mohd Safuwan, Nur Asyilla Che Jalil, Aidy Irman Yajid, Nor Hayati Othman **Potential miRNA Regulation and Roles of Curcumin and Tualang Honey in a Breast Cancer Animal Model**	Department of Chemical Pathology, School of Medical Sciences, Universiti Sains Malaysia
OP F-6	**SO-60**	Deasyka Yastani, Radiana D. Antarianto, Syarifah Dewi, Sri Widia A. Jusman **Study of MTT Assay and Flow Cytometry in the Evaluation of Cytotoxicity of *Uncaria gambir* on HepG2 Cells**	Master's Programme in Biomedical Sciences, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia

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OP G-2	**SO-46**	Fatin Nabilah Sahadan, Amirah Syafiqah Zamri, Annie Christianus, Md Yasin Ina-Salwany, Fadhil-Syukri Ismail, Roshani Othman, Zarirah Zulperi **Development of GnRHa-EVAc Delivery System for Induced Spawning in Catfish sp**	Aquatic Animal Health and Therapeutics Laboratory, Institute of Bioscience, Universiti Putra Malaysia
OP G-3	**SO-62**	Muhammad Luqman Nordin, Abdin Shakirin Mohamad Norpi, Ng Pei Yuen, Khatijah Yusoff, Nadiah Abu, Kue Peng Lim, Fazren Azmi **Multi-Epitope HER2/neu-Derived Immunogen Encapsulated in Cancer Cell Membrane-Coated Nanoparticles as an Effective Vaccine against Breast Cancer**	Centre for Drug Delivery Technology, Faculty of Pharmacy, National Universiti Kebangsaan Malaysia
OP G-4	**SO-31**	Nik Nur Syafiqah Zaini Safayi, Siti Aisyah Razali, Aziz Ahmad, Muhamad Fairus Noor Hassim **Molecular Simulation of Silica Nanoparticle Transportation via LSI2 Transporter Proteins in Rice Plant, *Oryza sativa***	Faculty of Science and Marine Environment, University Malaysia Terengganu
OP G-5	**SO-40**	Shevin Rizal Feroz **Innovations in Albumin-Based Drug Delivery Systems**	Faculty of Science and Technology, Universiti Kebangsaan Malaysia
OP G-6	**SO-69**	Nor Adillah Hasbullah, Abdul Hafiz Abdul Malik, C.S. Rama, Sabreena Safuan ***In vitro* Pre-Clinical Efficacy Establishment of Multi-Targeting Small Molecules to Combat Breast Cancer**	School of Health Sciences, Health Campus, Universiti Sains Malaysia

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OP H-2	**SO-37**	Sakshaleni Rajendiran, Syahidiah Syed Abu Thahir, Yuvaneswary Veloo, Salina Abdul Rahman, Rohaida Ismail, Maslina Mohd Ali, Noor Asyikin binti Abu, Hassuzana Khalil, Vickneshwaran Muthu, Rafiza Shaharudin **One Health Concept: Antimicrobial Resistance in Dairy Farms**	Environmental Health Research Centre, Institute for Medical Research, National Institute of Health, Malaysia
OP H-3	**SO-47**	Kurnia Maidarmi Handayani, Diah Handayani, Ardiana Kusumaningrum, Febriana Catur Iswanti, Mohamad Sadikin **Macrophage Function in Close Contacts of Drug-Resistant Tuberculosis: Phagocytosis and Oxygen Burst Assay**	Department of Biochemistry and Molecular Biology, Faculty of Medicine, Universitas Indonesia
OP H-4	**SO-17**	Azura Mohd Noor, David W Rice, Claudine Bisson, Izayu Nurfarha Ruzan, Ahmad Farid Adnan **LysM Containing-Proteins for a Future Anti-Tuberculosis Drug Development**	Infectious Disease Research Center, Institute for Medical Research, NIH
OP H-5	**SO-11**	Nur Farhana Mustafa, Kian Kai Cheng, Siti Aisyah Razali, Iffah Ipuszzati Zakaria, Nurul Hanim Salin, Habibah Wahab, Muhammad Helmi Nadri **Evaluation of 5-hydroxy-3',4',7-trimethoxyflavone as Dengue NS2B-NS3 Protease Inhibitor: An *in silico* and *in vitro* Study**	Faculty of Chemical and Energy Engineering, Universiti Teknologi Malaysia
OP H-6	**SO-26**	Lim Chie Min, Sunil Kumar Lal, Nurulfiza Mat Isa, Abdul Rahman Omar, Wee Sim Choo **Anti-Influenza A Virus Effect of Betacyanins from Red Pitahaya (*Hylocereus polyrhizus*)**	School of Science, Monash University Malaysia

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OP I-2	**SO-12**	Gilbert Ringgit, Shafiquzzaman Siddiquee, Bo Eng Cheong, Muhammad Dawood Shah **Phytochemical and Antioxidant Studies of *Solanum lasiocarpum*, Sour Eggplant of Sarawak, East of Malaysia**	Biotechnology Research Institute, Universiti Malaysia Sabah
OP I-3	**SO-18**	Bellericter Binjamin, Mohd Iftar Johwan, Suzan Benedick **Physicochemical Properties, VOC, DHA and MGO Content of *Heterotrigona itama* (Hymenoptera; Meliponini) Samples from Different Geographical Areas in Sabah, Borneo**	Faculty of Sustainable Agriculture, Universiti Malaysia Sabah
OP I-4	**SO-23**	Mohd Iftar Johwan, Bellericter Binjamin, Suzan Benedick **Dihydroxyacetone (DHA) and Methylglyoxal (MGO) in *Apis cerana* Honey Samples from Different Botanical Sources and Geographical Origin in Sabah, Borneo**	Faculty of Sustainable Agriculture, Universiti Malaysia Sabah
OP I-5	**SO-58**	Thyviaah Ananthan, Venmathi Maran Balu Alagar, Nurzafirah binti Mazlan, Chuan Chee Hoe **Extraction and Characterisation of Collagen from Tomato Jellyfish (*Crambione mastigophora*)**	Borneo Marine Research Institute, Universiti Malaysia Sabah
OP I-6	**SO-71**	Nurul Ashikin Md Hazmi, Norsharina Md. Saad, Siti Rokhiyah Ahmad Usuldin, Nur Atiqah Khirul Anuar, Nazrien Kaman, Seetha Jaganathan King **Effects of Drying Methods on the Physicochemical Properties of Bioactive Compounds Derived from *Plecranthus amboinicus* and Its Derivatives**	Agro-Biotechnology Institute, National Institutes of Biotechnology Malaysia

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OP J-2	**SO-28**	Muhammad Dawood Shah, Chong Wei Sheng, Balu Alagar Venmathi Maran **Sword Fern: A Promising Biocontrol Agent against Marine Parasitic Leech Infestations in Aquaculture**	Borneo Marine Research Institute, University Malaysia Sabah
OP J-3	**SO-50**	Aslam Nor'ashikin Zuhairi, Fikri Akmal Khodzori, Hariz Khairul Hisham, Kiu Yee Tong **Coral Disease Prevalence in Kota Kinabalu Coastal Waters: The Potential of Causative Microbial Agents**	Borneo Marine Research Institute, UMS
OP J-4	**SO-73**	Jasper E James, Jacinta Santhanam, Richard D Cannon, Erwin Lamping **Unravelling Multifaceted Mechanisms of Azole Antifungal Resistance in *Fusarium keratoplasticum***	Department of Biological Sciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia
OP J-5	**SO-93**	Cahyo Budiman, Jovi Silvester, Nur Iliyana Illang, Adam Thean Chor Leow, Bimo Ario Tejo, Lee Ping Chin, Chojiro Kojima, Toshimichi Fujiwara **Dimerization and Functional Relationship of FKBP35 from *Plasmodium knowlesi***	Biotechnology Research Institute, Universiti Malaysia Sabah
OP J-6	**SO-54**	Nik Amirah Auni Nik Mohd Asri , Zarina Amin, Yew Chee Wei **Determining an Optimal DNA Extraction Method and Detecting Pathogenic Leptospira in Rodent Fecal Samples from Kota Kinabalu, Sabah**	Biotechnology Research Institute, Universiti Malaysia Sabah

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OP K-2	**SO-09**	Shafiquzzaman Siddiquee, Noor Aini Bohari , Suryani Saallah, Mailin Misson, Sazmal Effendi Arshad **Determination of Mercury in Cosmetic Products Based on the Modified Electrochemical Sensor (PANI/MWCNTS/AUNPS/ITO)**	Universiti Malaysia Sabah
OP K-3	**SO-30**	Nathaniel Leong Jenn Kwang, Mohd. Adzir bin Mahdi, Mohd. Hanif bin Yaacob, Ahmad Rifqi Md Zain, Tengku Hasnan Tengku Abdul Aziz **Surface-Enhanced Raman Spectroscopic Study of Grouper Mucus: Towards Label-Free and Non-Invasive Diagnosis of Fish Health Status in Aquaculture**	Faculty of Engineering, Universiti Putra Malaysia
OP K-4	**SO-75**	Sujjat Al Azad, Mohammad Tamrin Bin Mohamad Lal **Potential of UMS Hatchery Wastewater as Substrate for the Growth Characteristics of Purple Non-sulfur Bacterium *Afifella marina* strain ME**	Borneo Marine Research Institute. Universiti Malaysia Sabah
OP K-5	**SO-04**	Wei Sheng Chong, Muhammad Dawood Shah **Harnessing Remote Sensing to Enhance Understanding and Management of Aquatic Invasive Species**	Borneo Marine Research Institute, University Malaysia Sabah
OP K-6	**SO-21**	Ellia Kartini Mujar, Saleema Matusin, Muhammad Safwan Ahamad Bustamam, Annie Christianus, Tan Jen Kit, Intan Safinar Ismail **Physiological Response to Acute and Chronic Temperature Changes of Resilient and Susceptible Sera Hybrid Grouper (*Epinephelus fuscoguttatus* x *Epinephelus lanceolatus*) Revealed by LCMS/MS Metabolomics**	Faculty of Science, Universiti Putra Malaysia

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OP L-2	**SO-45**	Danesh Thangeswaran, Shaharum Shamsuddin, Venugopal Balakrishnan **The Protective Effect of THICAPA on APP Processing Pathway in Familial Alzheimer's Disease Patient-Derived Fibroblast Cell Line**	Institute for Research in Molecular Medicine (INFORMM), Universiti Sains Malaysia
OP L-3	**SO-13**	Kenneth Tan JunKai, Ghows Azzam and Azalina Zainuddin **Effects of Tocotrienol Rich Fraction (TRF) on *Drosophila melanogaster* Alzheimer's Disease models**	Department of Chemical Pathology, USM
OP L-4	**SO-70**	Rhubaniya Mahendran, Soo Kun Lim, Kien Chai Ong, Kek Heng Chua, Hwa Chia Chai **Elucidation of the Mechanisms of 15,16-dihydrotanshinone I (DHTS) as an Anti-proliferative Agent for Autosomal Dominant Polycystic Kidney Disease (ADPKD)**	Department of Biomedical Science, Faculty of Medicine, University of Malaya
OP L-5	**SO-85**	Nurul Elyani Mohamad, Swee Keong Yeap, Boon-Kee Beh, Huynh Ky, Kian Lam Lim, Wan Yong Ho, Shaiful Adzni Sharifuddin, Kamariah Long, Noorjahan Banu Alitheen **Coconut Water Vinegar Ameliorates Recovery of Acetaminophen Induced Liver Damage in Mice**	Biotechnology Research Institute, Universiti Malaysia Sabah
OP L-6	**SO-39**	Senty Vun-Sang, Teoh Peik-Lin, Kenneth Francis Rodriques, Mohammad Iqbal **Hepatoprotective Activity of *Ficus lepicarpa* (Moraceae) on Carbon Tetrachloride (CCl4)-Intoxicated Rats**	Biotechnology Research Institute, Universiti Malaysia Sabah

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OP M-1	**SO-94**	Mailin Misson, Max Michael Samson, Cahyo Budiman, Suryani Saallah, Haslan Roslie, Shafiquzzaman Siddiquee, Khairul Azfar Kamaruzaman, Azian Dakulah, Adam Maia, Siti Farhany Radin, Rahinah Abdul **Characterization of Fermented Palm Kernel Cake using Locally Isolated Cellulolytic Fungi and Bacteria as Potential Animal Feed**	Biotechnology Research Institute, Universiti Malaysia Sabah
OP M-2	**SO-87**	Nor Asyikin Binti Che Husain, Haryati Jamaluddin, Mohd Anuar Jonet **Purification, Preliminary Crystallization and Modelling of Novel 4-Hydroxyphenylacetate-3-Monooxygenase from Extreme Thermophilic *Geobacillus mahadii* Geo-05 for Structural Studies**	Microbiology, Malaysia Genome and Vaccine Institute
OP M-3	**SO-10**	Nurhanani Arifshah, M.K Adriana, Ashraf Zulnizam, A.A. Amirul **Utilization of Thermally-Degraded Plastic Wastes as a Carbon Source for Polyhydroxyalkanoate Production from Microorganisms Isolated from plastic-Contaminated Sites**	School of Biological Sciences, University of Science Malaysia
OP M-4	**SO-24**	Intan Nabihah Ahmad Fadzil, Ahmad Nazri Saidin, Nurul Julia Akmar Mohd Nawi, Nurhanani Arifshah, Amirul Ashraf Abdullah **Isolation and Screening of Effective Microbes (EM) from Transformer Oil Contaminated Soil for Remediation of Polychlorinated Biphenyls (PCB) in Waste Transformer Oil**	School of Biological Sciences, Universiti Sains Malaysia, Penang & TNB Research Sdn Bhd, Kajang, Selangor
OP M-5	**SO-43**	Wan Zafira Ezza Wan Zakaria, Noor Aziah Serri, Khairunisa Yusof **Optimization of Enzymatic Saccharification of Watermelon (*Citrullus lanatus*) Rind by R Analysis**	Bioprocess Technology Division, Universiti Sains Malaysia

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OP N-1	**SO-59**	Farah Nadia Omar, Halimatun Saadiah Hafid, Azhari Samsu Baharuddin, Mohd Afandi P. Mohammed, Jaafar Abadullah **Biodegradation of Oil Palm Empty Fruit Bunches by Laccase from *Pycnoporus sanguineus* and Its Structural Changes**	Preparatory Center for Science and Technology, University Malaysia Sabah
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OP N-3	**SO-77**	Siti Nahdatul Isnaini Binti Said Hussin, Nor Izwan Hakimi Bin Nor Azmi, Ahmad Nor Hafzan Bin Mat Roni, Aziaton Afzan Binti Ibrahim **Performance Evaluation of Edible Seaweed Bioplastics Produced Through Green Processing Technology**	Agro-Biotechnology Institute, National Institutes of Biotechnology Malaysia
OP N-4	**SO-84**	Asri Widyasanti, S.TP., M.Eng**,** Iceu Agustinisari S.TP., MSi, Nada Fauziyah, Dian Ayu Eka Pitaloka and Puspita Nurlialsari **Optimization Strategy of Oleoresin Rendement for zero-Waste Ginger Product by Microwave-Assisted Extraction with Response Surface Method**	Faculty of Agroindustrial Technology, Universitas Padjadjaran, Jatinangor, Indonesia.
OP N-5	**SO-22**	Georgia Mori Aggo, Nur Asshifa Md Noh, Ahmad Ramli Mohd Yahya **Characterization and identification of rhamnolipid congeners produced by *Pseudomonas aeruginosa* USM-AR2**	School of Biological Sciences, Universiti Sains Malaysia

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OP O-1	**SO-35**	Raheel Nazakat, Siti Aishah Rashid, Khayri Azizi Kamel, Mohd Ishtiaq Anasir, Sakshaleni Rajendiran, Yuvaneswary Veloo, Syahidiah Syed Abu Thahir, Nurul Amalina Khairul Hasni, Noor Haza Fazlin Hashim, Khor Bee Chin, Nor Zahrin Hasran, Rosnawati Muhamad Robat, Mohamad Iqbal Mazeli, Wan Rozita Wan Mahiyuddin, Rafiza Shaharudin **Optimization of Sample Processing Strategies for SARS-CoV-2 Quantification in Wastewater using Digital-Droplet Polymerase Chain Reaction (ddPCR)**	Environmental Health Research Centre, Institute for Medical Research, National Institute of Health
OP O-2	**SO-41**	Siti Aishah Rashid, Khayri Azizi Kamel, Raheel Nazakat, Sakshaleni Rajendiran, Yuvaneswary Veloo, Syahidiah Syed Abu Thahir, Nurul Amalina Khairul Hasni, Mohd Ishtiaq Anasir, Noor Haza Fazlin Hashim, Rosnawati Muhamad Robat, Mohamad Iqbal Mazeli, Wan Rozita Wan Mahiyuddin, Rafiza Shaharudin **Can Sewage be a Lens to Uncover Early, SARS-CoV-2 Variant Circulation?**	Health Risk Assessment Unit, Environmental Health Research Center, Institute for Medical Research, National Institutes of Health Malaysia
OP O-3	**SO-07**	Sylvia Daim **Accelerating COVID-19 Diagnostics: Harnessing the Utility of Automated Nucleic Extractors in the Pandemic Era**	Faculty of Medicine and Health Sciences
OP O-4	**SO-34**	Rafida Razali, Vijay Kumar, Andrey Kovalevsky, Cahyo Budiman **Insights into the Dimerization Dynamics and Regulation of the Main Protease of SARS-CoV-2**	Biotechnology Research Institute, Universiti Malaysia Sabah
OP O-5	**SO-52**	Maizatul H. Omar, As'malia Md Lasim, Mohd Ridzuan M.Abdul Razak ***In vitro* Anti-SARS-CoV-2 Activities of Xanthones and *Garcinia mangostana* extracts**	Herbal Medicine Research Centre, Institute for Medical Research, National Institutes for Health

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SP-03	Max Michael Samson	Max Michael Samson, Mailin Misson, Suryani Saalah, Wilson Yong Thau Lym **Hydrogel-Biochar Composite for Control Release Fertilizer: A Preliminary Study**	Biotechnology Research Institute
SP-04	Dr. Jayanthi Nagappan	Jayanthi Nagappan, Shamala Sundram, Leslie Low Eng Ti ***De novo* genome assembly of *Ganoderma zonatum* using high-fidelity long reads**	Malaysian Palm Oil Board
SP-05	Ms Nadia Sufi Suraya Binti Ahmad Fizal	Nadia Sufi Suraya Binti Ahmad Fizal, Mailin Misson, Grace Joy Chin Wei Lei, Wilson Thau Lym Yong **Isolation and Characterization of Microalgae from Seawater for Potential Biofuel Production**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-06	Dr. Md. Safiul Alam Bhuiyan	Md. Safiul Alam Bhuiyan, Zarina Amin, Gilbert Ringgit, Ag Muhammad Sagaf Abu Bakar, Suryani Saallah, Sharifudin Md. Shaarani, Shafiquzzaman Siddiquee **An Optimization Assay for Universal Detection of Avian Infectious Bronchitis Virus (Gammacoronavirus) Using an Electro-Chemical DNA Biosensor**	Biotechnology Research Institute, University Malaysia Sabah
SP-08	Prof Madya Dr. Siti Aisyah Abd Ghafar	Siti Aisyah Abd Ghafar, Muhammad Fahmi Bin Yakop, Yong Yoke Keong, Lim Vuanghao, Rohazila Mohamad Hanafiah **Characterization of Silver Nanoparticle-β-Sitosterols and Its Cytotoxicity against Various Cancer Cell Lines**	Faculty of Dentistry, Universiti Sains Islam Malaysia
SP-09	Ms Samsidar Anwar	Samsidar Anwar, Md Shafiquzzaman Siddiquee **Development of Acetylcholinesterase Biosensor for Determination of Carbaryl Pesticide in *Brassica oleracea* Var. *capitata* L. (cabbage) and *Brassica oleracea* Var. *italica* L. (broccoli)**	Biotechnology Research Institute, University Malaysia Sabah

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SP-11	Dr. Rabiatul Adawiah binti Zainal Abidin	Rabiatul Adawiah Zainal Abidin, Hani Suraya Tajudin, Zeti Azura Mohamed Hussein **Meta-analysis of RNA sequencing (RNA-seq) studies identifies candidates gene related to abiotic stress and quality traits in *Carica papaya***	Biotechnology & Nanotechnology Research Centre, Malaysian Agricultural Research and Development Institute (MARDI)
SP-12	Roslina Binti Mohd Shah	Roslina Mohd Shah, Lea Johnsiul, Norasekin Tamchek, Ishak Zubir, Mohd Zulhilmi Abdul Rahman **Potential Use of Kokoselect as A Bio-Diagnostic Kits For Screening Of Cocoa Seedlings With Agronomic Traits**	Bahagian Bioteknologi, Lembaga Koko Malaysia
SP-13	Miss Aissvarya Shankar	Shankar Aissvarya, Ling King Hwa, Manohar Arumugam, Karuppiah Thilakavathy **Genetic Variants of Dupuytren's Contracture**	Department of Biomedical Science, Faculty of Medicine and Health Sciences, UPM
SP-14	Ms Anna Robreth @ Robert	Anna Robreth @ Robert, Cahyo Budiman, Lee Ping Chin, Khairul Azfar Kamaruzzaman, Azyyati Mohd Padzil **Heterologous Expression and Purification of Calmodulin from *Plasmodium knowlesi* using Codon-Optimized Synthetic Gene**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-15	Mr Azlan Azizi Bin Muhamad Nor	Azlan Azizi Muhamad Nor, Jeffrey Lim Seng Heng, Ahmad Arif Ismail, Muhammad Nawal Ramli, Zafrul Arif Radhi **Utilization of Soil Beneficial Microorganisms Towards Sustainable and Eco-Friendly Plant Disease Management**	MARDI Cameron Highlands
SP-16	Ms. Lea Johnsiul	Lea Johnsiul, Norasekin Tamchek, Roslina Mohd Shah, Ishak Zubir, Anisah Savanti, Mohd Zulhilmi Abdul Rahman **Assessing the Genotype Accuracy of Grafted Cocoa (*Theobroma cacao* L.) Seedlings Nurseries' Outputs using Ten Cocoa Single Nucleotide Polymorphism (SNPs) Markers for the Malaysian Cocoa Commercial Clones**	Biotechnology Division, Malaysian Cocoa Board

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SP-18	Dr. Mohd Redzwan Sabran	Mohd-Redzwan Sabran, Syarminie Subramaniam, Winnie-Pui-Pui Liew **Metagenomic Approach in Elucidating the Role of Gut Microbiota in AFB1-Induced Neurotoxicity and Depressive-like Behaviour**	Department of Nutrition, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia
SP-19	Ts. Norasekin Tamchek	Norasekin Tamchek, Lea Johnsiul **Evaluation of the Agro-Morphological Characteristics, Field Performance, and Clonal Fidelity of a Tissue Culture-Generated Cocoa Clone**	Biotechnology Division, Malaysian Cocoa Board
SP-20	Miss Nur Aliyah Binti Mohd Azrin	Nur Aliyah Mohd Azrin, Noor Dina Muhd Noor **An In-Silico Study on the Effect of Cysteine Substitution at the High Affinity Ca^{2+} Coordinating Residues of Rand Protease**	Enzyme and Microbial Technology Research Centre, Universiti Putra Malaysia
SP-21	Mrs Nurul Huda Binti Musa	Nurul Huda Musa, Abdul Hanif Khan Yusof Khan, Marina L. Kennerson, Karuppiah Thilakavathy **Comparative Evaluation of Sample Preparation and RNA Isolation Techniques for Gene Expression Analysis in Neuromuscular Diseases**	Faculty of Medicine and Health Sciences, Universiti Putra Malaysia
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SP-23	Ms Sazlinawatie Binti Aladin	Sazlinawatie Aladin, Cahyo Budiman, Khairul Azfar Kamaruzzaman and Mardani Abdul Halim **Docking and Molecular Dynamic Simulation of Calmodulin and CBM segment of FKBP35 from *Plasmodium knowlesi***	Biotechnology Research Institute, Universiti Malaysia Sabah

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SP-24	Ms Helyatul Rasmah Mahali	Helyatul Rasmah Mahali, Zarina Amin, Nur Athirah Yusof **Development of Low-Cost, One-Step Multiplex SYBR Green-based RT-qPCR Assay for Detecting SARS-CoV-2 in a Malaysian Setting using Optimized Primers**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-25	Ms Wan Nur Shuhaida Binti Wan Mahadi	Wan Nur Shuhaida Binti Wan Mahadi, Nur Athirah Binti Yusof, Clemente Michael Wong Vui Ling ***In silico* Characterization of HSP70 from *Glaciozyma antarctica* PI12 as a Model System to Understand Adaptation Strategies of Antarctica Organisms Amid Adverse Climate**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-26	Dr Siti Fathiah Masre	Siti Fathiah Masre, Raihan Nurhayati Mohamed Sohor, Zariyantey Abdul Hamid **The Effect of Oleuropein in DNA Damage of Mouse Skin Carcinogenesis Model**	Faculty of Health Sciences, Universiti Kebangsaan Malaysia
SP-27	Prof. Madya Dr. Zariyantey Abd Hamid	Zariyantey Abd Hamid, Nur Afizah Yusoff, Farah Ezleen Aqilah Abu Bakar, Siti Balkis Budin, Izatus Shima Taib **In Utero Effects of Hydroquinone on Maternal and Fetal Hematopoietic Stem/Progenitor Cells and Roles of Cell Lineages.**	Center for Diagnostic, Therapeutic and Investigative Studies (CODTIS), Faculty of Health Sciences, Universiti Kebangsaan Malaysia
SP-28	Dr Zaiton Ahmad	Zaiton Ahmad, Shakinah Salleh, Mustapha Akil, Affrida Abu Hassan, Mohamed Hasyraf Mat Nawi, Mohammad Fitri Rimi Hamidan, Nurulhayati Abu Bakar **Mutagenesis of Napier Grass (*Pennisetum purpureum*) for Improvement of Biomass Yield and Protein content**	Agrotechnology and Biosciences Division, Malaysian Nuclear Agency
SP-29	Mr Mustapha Akil	Mustapha Akil, Joseph Ndebeh, Luther Zogbo, Muniroh Md Saad, Zaiton Ahmad, Shakinah Salleh, Muhammad Izzat Rossdeen **Mutagenesis and Observation of Agronomic Characters of Commercial Grain Corn Seed (GWG888) After Acute Gamma Irradiation**	Agrotechnology and Bioscience Division, Malaysian Nuclear Agency

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-30	Norazlina Noordin	Norazlina Noordin, Shakinah Salleh, Mustapha Akil, Affrida Abu Hassan, Zaiton Ahmad, Nashimatul Adadiah Yahya, Nurhayati Irwan, Shuhaimi Shamsuddin, Norhafiz Talib, Ahmad Zaki Hussain, Isaac Kofi Bimpong, Shoba Sivasankar ***In Vitro* Mutagenesis of Cassava var. Ubi Putih Using Acute and Chronic Gamma Irradiation**	Agrotechnology and Biosciences Division, Malaysian Nuclear Agency
SP-31	Mr. Muhammad Syahir Hakimi Mohd Hazli	Muhammad Syahir Hakimi Mohd Hazli, Azalina Zainuddin, Shaharum Shamsuddin **Elucidating the Effect of Danshen on SH-SY5Y-TauMutant Cellular Model of Alzheimer's Disease**	Chemical Pathology Department, School of Medical Sciences, Universiti Sains Malaysia
SP-32	Dr. Izatus Shima Taib	Izatus Shima Taib, Asma' 'Afifah Shamhari, Nur Erysha Sabrina Jefferi, Siti Balkis Budin, Adam Muhammad Zackry Zulkifly, Fatin Norisha Roslan, Zariyantey Abd Hamid **Tocotrienol Rich Fraction Reduced the Estrogen-Like Effects Induced by Bisphenol F**	Centre of Diagnostic, Therapeutics and Investigative Studies (CODTIS), Faculty of Health Sciences, Universiti Kebangsaan Malaysia
SP-33	Dr. Zuraida Ab Rahman	Zuraida Ab Rahman, Zulkifli Ahmad Seman, Ayu Nazreena Othman, Noor Shahira Md Yusof, Fatin Athirah Mustaffa **Optimizing Parameters for CRISPR-Cas9 Mediated Genome Editing of TFIIAγ5 Gene in somatic embryos of Malaysian MR219**	Biotechnology and Nanotechnology Research Central
SP-34	Jennifer Kui Ling Chee	Jennifer Kui Ling Chee, Eric Tzyy Jiann Chong, Ping-Chin Lee **Genetic Analysis of *kelch13* Gene of *Plasmodium knowlesi* in Sabah, Malaysia**	Faculty of Science and Natural Resources
SP-35	Dr. Lau Han Yih	Han Yih Lau **Electrochemical Biosensor for the Rapid Detection of *Pseudomonas syringae* using Colloidal Gold Nanoparticles**	Malaysian Agricultural Research and Development Institute

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-37	Dr. Novi Silvia Hardiany	Novi Silvia Hardiany, Karima Yudhistina, Syarifah Dewi, Erfi Prafiantini, Ranita Astikya Carolina, Aulia Afifa Aghnat **Role of Intermittent Fasting on Aging Molecular Process in Obesity**	Dept. Biochemistry & Molecular Biology, Faculty of Medicine Universitas Indonesia
SP-38	Dr. Mardani Abdul Halim	Sharvin Manickam, Shallinie Thangadurai, Azali Azlan, Zarina Amin, Ghows Azzam, Mardani Abdul Halim **Transcriptomic Analysis of *Drosophila melanogaster* Adult Testes Overexpressing MicroRNA-2b-1**	Biotechnology Research Institute, University Malaysia Sabah
SP-39	Dr. Cheong Bo Eng	Bo Eng Cheong, Zainah Binti Abdul Sattar, Nurul Ashikin Binti Nasir, Gina B. Barbosa, Peik Lin Teoh **Fatty Acid Profiling of Oils Isolated from the Seeds of Artocarpus Fruit Species Derived from Sabah**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-40	Dr. Syarifah Dewi	Syarifah Dewi, Adiba Nur Ashri Ramadhani, Khoiriyyah Amalia Az-zahra, Wardaya **Specific Activity of Lactate Dehydrogenase in Rat Liver and Muscle Tissues Induced by Intermittent Hypobaric Hypoxia**	Department of Biochemistry & Molecular Biology, Faculty of Medicine Universitas Indonesia
SP-41	Prof. Dr. Sri Widia A Jusman	Susi Rahmiyati, Syarifah Dewi, Sri Widia A Jusman **Preparation of heme-depleted serum using ascorbic acid for the purpose of heme biosynthesis inhibition studies**	Department of Biochemistry and Molecular Biology, Faculty of Medicine, Universitas Indonesia
SP-42	Dr. Ani Retno Prijanti	Ani Retno Prijanti, Endrico Xavierres Tungka, Febriana Catur Iswanti, Reni Paramita **Autophagy in Early Onset Preeclampsia Placenta through p62 and LCA Expression was Higher than Normal Term**	Faculty of Medicine, Universitas Indonesia
SP-43	Miss Joanna Ling Siaw Jing	Joanna Ling Siaw Jing, Azwan Awang, Cahyo Budiman **Ruminants and Rabbits as Potential Hosts for SARS-CoV-2: Insights from Pull-down Assay**	Faculty of Sustainable Agriculture, Universiti Malaysia Sabah

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-44	Dr. Ahmad Mohiddin Bin Mohd Ngesom	Asmalia Md Lasim, Sheila Nathan, Fatimah Abdul Razak, Ahmad Mohiddin Mohd Ngesom, Mardani Abd Halim, Wardah Mohd Saleh, Farah Shafawati Mohd-Taib **Variation in Soil Bacterial Communities' Composition in Different Recreational Park at Hulu Langat Selangor**	Institute For Public Health, MOH
SP-45	Asmalia Md Lasim	Asmalia Md Lasim, Noor Artika Saadon, Nor Syaidatul Akmal Mohd Yousuf, Norazlan Mohmad Misnan, Mohd Ridzuan M.Abdul Razak, Nur Hana Md Jelas, Maizatul Hasyima Omar **A Comprehensive Phytochemical analysis and its Antidengue Potential of Wild and Cultivated *Schizophyllum commune***	Institute for Medical Research
SP-46	Prof. Madya Dr. Rohazila Mohamad Hanafiah	Rohazila Mohamad Hanafiah, Nur Farah Atiqah Mohd Pazli, Siti Aisyah Abd Ghafar **Transcriptomic analysis of Methicillin Resistant *Staphylococcus aureus* treated with silver nanoparticles-Kaempferol (AgNPs-K)**	Faculty of Dentistry, Universiti Sains Islam Malaysia
SP-47	Dr. Febriana Catur Iswanti	Mahdaleny, Arleni, Febriana Catur Iswanti **In Silico Docking Reveals Amygdalin as a Potential Active Herbal Compound for Binding to Multiple CXCL4 Macrophage Receptors**	Department of Biochemistry and Molecular Biology Faculty of Medicine, Universitas Indonesia
SP-49	Ms Anis Syazwani Kamarudin	Anis Syazwani Kamarudin, Nur Syahirah Azmi, Alny Marlynni Abd Majid, Rahiniza Kamaruzaman, Rabiatul Adawiah Zainal Abidin, Norliza Abu Bakar, Sew Yun Shin[1], Shahril Ab Razak **Assessment of selected rice accession for salinity tolerant using molecular and morphological approaches**	Malaysian Agricultural Research and Development Institute
SP-50	Jacqueline Wong Tze Chin	Jacqueline Wong Tze Chin, Cahyo Budiman, Teoh Peik Lin **Optimization of SARS-CoV-2 Pseudotyped Lentivirus Production**	Biotechnology Research Institute, Universiti Malaysia Sabah

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-51	Dr. Khairun Hisam Nasir	Khairun Hisam Nasir, Mohd Norfaizal Ghazali, Rabiatul Adawiah, Mohd Shahril Firdaus Abd Razak, Siti Nadrah Binti Abd Hisham, Siti Norsaidah binti Ibrahim **Development of *Mitragyna speciosa* (ketum) Simple Sequence Repeat markers**	Program Agriomik dan Bioinformatik. Pusat Penyelidikan Bioteknologi dan Nanoteknologi
SP-52	Alny Marlynni Abd Majid	Alny Marlynni Abd Majid, Shahril Ab Razak, Rahiniza Kamaruzaman, Siti Norsuha Misman, Rabiatul Adawiah Zainal Abidin **Development of functional marker targeting Pita2 gene, a blast resistant gene in rice**	Malaysian Agricultural Research and Development Institute
SP-53	Asmaiyah Kamarzaman	Asmaiyah Kamarzaman, Salumiah Mijin, Jupikely James Silip **Physicochemical Quality of *Musa acuminata* × *balbisiana* Fruit Affected by Hydro-cooling and Storage Temperature**	Faculty Of Sustainable Agriculture, University Malaysia Sabah
SP-54	Mr Fong Zhijack	Wai-Leng Lee, Zhijack Fong **Study of Chemoresistance Mechanisms and Potential Alternate Therapy in Colorectal Cancers**	School of Science, Monash University Malaysia
SP-55	Intan Zulaikha Binti Md Zainin	Intan Zulaikha binti Md Zainin, Julenah Ag Nuddin, Ruzaidi Azli bin Mohd Mokhtar **Antihyperglycemic Effect of *Bruguiera gymnorrhiza* Root Extracts in Streptozocin-induced Diabetic Mice**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-56	Nur Isam Bin Mohd Ranzi	Isam, R., Salumiah, M., Suzan, B., Duane E., Sheng, L. K., Shez, L. K. **Physical Characteristics of Saba Avocado Cv. QAV 1 Fruit at Different Maturity Stages in Relation to Oil Content**	Faculty of Sustainable Agriculture, University Malaysia Sabah
SP-57	Vellarry Maydelina Yong	Vellarry Maydelina Yong, Shafiquzzaman Siddiquee, Christine Binti Gustin **Phytochemical Composition and Toxicological Evaluation of Bosom Oil: Exploring its Therapeutic Potential for Pain Relief and Wound Healing**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-58	Lim Pei Tee	Pei Tee Lim, Wai Leng Lee **Potential Role of TGM2 in Cancers and Its Association with Resistant Oral Cancer-Derived Extracellular Vesicles**	School of Science, Monash University Malaysia

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-59	Mohammad Rahmat Bin Derise	Mohammad Rahmat Derise, Anis Adilah Mustafa, Wilson Yong Thau Lym, Kenneth Francis Rodrigues **RNA Sequencing and Analysis of *Gigantochloa levis* Tissues**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-60	Mr Mohd Shahril Firdaus Bin Ab Razak	Shahril Ab Razak, Alny Marlynni Abd Majid, Siti Norhayati Ismail, Norliza Abu Bakar, Rabiatul Adawiah Zainal Abidin, Dilipkumar Masilamany **Phylogenomic Analysis Reveal Close Relationship between Weedy Rice Variants with Commercial Rice Varieties**	Biotechnology & Nanotechnology Research Centre, MARDI
SP-61	Nanda Ariane Iskandar	Nanda Ariane Iskandar, Fitriana Nur Rahmawati, Febriana Catur Iswanti, Mohamad Sadikin **Comparison of Glutamate and γ-Aminobutyric Acid (GABA) Effect on Peripheral Blood Mononuclear Cells (PBMC) Proliferation**	Biomedical Sciences, Faculty of Medicine, Universitas Indonesia, Jakarta
SP-64	Dr. Zulfahmi Said	Zulfahmi Said, Helen Colley, Craig Murdoch **Evaluation of Tissue Engineered Oral Mucosa Model (TEOM) for Oral Mucosal Drug Delivery**	Faculty of Dentistry, Universiti Sains Islam Malaysia
SP-65	Miss Nur Umairah Atiqah Binti Sabri	Nur Umairah Atiqah Sabri, Normaliza Ab Malik, Siti Noor Adnalizawati Adnan **Antifungal Properties of *Alpinia conchigera* against Oral Candida**	Faculty Of Dentistry, Universiti Sains Islam Malaysia
SP-66	Muhammad Huzaifilyasir Bin Kamal Bashah	Muhammad Huzaifilyasir Kamal Bashah, Mohamad Asyraf Amin, Nurul Farahhana Ain Abdul Meus, Deny Susanti Darnis, Suhaila Mohd Omar, Wan Hafizuddin Wan Yussof **Chitin Extraction from Black Soldier Fly (*Hermetia Illucens*) pupal exuviae using Natural Deep Eutectic Solvent: An Eco-Friendly Approach**	Biotechnology Department, Kulliyyah of Science, International Islamic University Malaysia
SP-67	Miss Noor Izzati Mokhzani	Noor Izzati Mokhzani, Mohd Razif Mohd Idris, Normaliza Ab Malik, Zulfahmi Said **Evaluation of Wound Healing Properties of *Tualang* Honey Against Primary Oral Fibroblast Cells**	Faculty of Dentistry, Universiti Sains Islam Malaysia

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-68	Nor Amirah Binti Shamsudin	Nor Amirah Shamsudin, Jualang Azlan Gansau, Jaya Seelan Sathiya Seelan, Nor Azizun Rusdi **Isolation and Morphological identification of mycorrhizal fungi from epiphytic orchids, *Aerides odorata* Lour.**	Institute for Tropical Biology and Conservation
SP-70	Nur Nashyiroh Izayati Binti Mastor	Nur Nashyiroh Izayati Mastor, Vijay Kumar Subbiah, Wan Nazirah Wan Abu Bakar, Khurshida Begum,M. Jahangir Alam, Mohammad Zahirul Hoque **Species Distribution, Antibiotic Susceptibility Profiles, and *Van* Gene Frequencies among Enterococci Isolated from Patients at Queen Elizabeth Hospital in Kota Kinabalu, Sabah**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-71	Miss Azniza Mahyudin	Azniza Mahyudin, Ag Shazmeer Ag Safree, Daphne Adrian, Nurul 'Aqilah Farihah Abdul Lajid, Petrina Ponusamy, Malborn Solynsem, Mohamad Zahirul Hoque and Vijay Kumar Subbiah **Detection of Selected Pathogenic Bacteria from Non-Conventional Types of Bat Tissues**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-72	Dr. Dewi Sukmawati	Dewi Sukmawati, Asti Nurhidayati, Rahimi Syaidah **Mesenchymal Stem Cells Respond against Inflammatory Microenvironment Through NLRP Inflammasome Expression**	Department of Histology, Faculty of Medicine, Universitas Indonesia
SP-73	Dr. Dwirini Retno Gunarti	Dwirini Retno Gunarti, Muhamad Sadikin, Witono Basuki **Thiamine Binding Protein from Peanuts *(Arachis hypogaea L*), Bogor Groundnuts *(Vigna subterranea {L.) Verdc. syn. Voandzeia subterranea (L.) Thouars)*, and Red Beans *(Vigna angularis var. Nipponensis)***	Department of Biochemistry and Molecular Biology, University of Indonesia
SP-74	Jacqueline Vincent	Jacqueline Vincent, Ruzaidi Azli bin Mohd Mokhtar, Mohd. Azrie bin Awang, Nor Azizun Rusdi **Chemical Profiling and Bioactivity Assessment of *Etlingera coccinea* (Blume) S. Sakai & Nagam**	Institute for Tropical Biology and Conservation
SP-75	Dr. Ainaa Abdul Kahar	Ainaa Abdul Kahar, Shaiful Adzni Sharifudin, Najwa Fatihah Mohd Shafie, Mohamad Izwan Dzulkifly, Noor Azlina Masdor **Effective Encapsulation for Improved Survival of *Lactobacillus plantarum* in Simulated Gastrointestinal Tract Conditions**	Biotechnology and Nanotechnology Research Center, MARDI

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-76	Azlinda Erny Yunus	Azlinda Erny Yunus, Siti Akhtar Mohsim, Rohaiza Ahmad Redzuan, Lina Rozano, Mohd. Zulfadli Sohaime, Nor Hidayu Che Asari, Wee Chien Yeong, Siti Aisyah Jamil, Noriha Mat Amin **Antagonistic Potential of Rice Bacterial Endophytes Against Sheath Blight and Brown Spot Pathogens, *Rhizoctonia solani* and *Bipolaris oryzae***	Malaysian Agricultural Research and Development Institute
SP-77	Ms Siti Akhtar Mohshim	Siti Akhtar Mohshim, Mohd. Zulfadli Sohaime, Nor Hidayu Che Asari, Wee Chien Yeong, Lina Rozano, Azlinda Erny Yunus, Rohaiza Ahmad Redzuan, Noriha Mat Amin **Unveiling the Rich Diversity of Culturable Bacteria within the Endorhizosphere of Lowland Rice in Peninsular Malaysia**	Malaysian Agricultural Research and Development Institute
SP-78	Ms Siti Nor Najihah Binti Yasin	Siti Nor Najihah Yasin, Zulaiha A Rahman, Nadia Halib, Zulfahmi Said **Formulation and Characterization of Novel Mucoadhesive *Tualang* Honey Patches for Oral Mucosal Drug Delivery**	Faculty of Dentistry, Universiti Sains Islam Malaysia
SP-79	Ms Azriah Binti Asis	Azriah Asis, Md Shafiquzzaman Siddiquee, Prof. Dr. Vijay Kumar **Isolation of Phosphate-Solubilizing Fungi from Agricultural Soils in Sabah**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-80	Ms Nurbella Sofiana Binti Altu	Nurbella Sofiana Altu, Cahyo Budiman, Rafida Razali, Khairul Azfar Kamaruzaman, Ruzaidi Azli Mohd Mokhtar, Habibah A Wahab **Virtual Screening and Inhibition Activity of NADI-based Malaysian Plant Compounds against Receptor-Binding Domain of Spike Glycoprotein of SARS-CoV-2**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-81	Dr. Allia Najmie Binti Muhammad Yusuf	Allia Najmie binti Muhammad Yusuf, Azizah Ugusman, Mohd Helmy Mokhtar **Effects of Hyperandrogenism on Levels of Sex Steroid Hormones during Endometrial Receptivity in Rats**	Faculty of Medicine, National University of Malaysia

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-82	Dr. Istiqomah Agusta	Istiqomah Agusta, Rahimi Syaidah, Rita Maliza **Effect of Sunflower Oil on Human Keratinocytes Cell Line (HaCaT) Viability**	Department of Biochemistry and Molecular Biology, Faculty of Medicine, Universitas Indonesia
SP-83	Dr. Khairul Azfar Kamaruzaman	Khairul Azfar Kamaruzaman, Gloria Yi Wei Tseu **Current Trends for an Alternative Breast Cancer Treatment: Liposomes as a Delivery System for a Gene Therapy Strategy**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-84	Prof. Madya Dr. Kenneth Francis Rodrigues	Anis Adilah Mustafa, Kenneth Francis Rodrigues, Wilson Thau Lym Yong **Species Identification of Economically Important Bamboo Varieties and Assessment of Genetic Stability of in vitro cultured *Dendrocalamus asper* using ISSR markers**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-85	Ms Wizilla Janti Joshua	Wizilla Janti Joshua, Mohd Salleh Kamarudin, Natrah Ikhsan, Fatimah Md Yusoff and Zarirah Zulperi **Growth Performance and Expressions of Immune Response Genes of *Tor tambroides* L. (Bleeker, 1854) fed with *Chlorella vulgaris* enriched *Artemia* sp.**	Aquatic Animal Health and Therapeutics Laboratory, Institute of Bioscience, Universiti Putra Malaysia
SP-86	Ms Nadia Iryani Najri	Nadia Iryani Najri, Vijay Kumar Subbiah, Noor Hydayaty Mohd Yusuff, Mohammad Zahirul Hoque **Preliminary and Discovery the Expression of miRNA in Dengue Serotype 1 and 3 from Patients Infected Dengue in Sabah**	Faculty of Medical and Health Science, Universiti Malaysia Sabah
SP-87	Ms Eryati Binti Derman	Eryati Derman, Clarence M. Ongkudon, Rahmath Abdulla **New Technology Platform for Biodiesel Production in Malaysia**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-88	Prof. Dr. Vijay Kumar	Ahmad Mukhlis Abdul Rahman, Julian Ransangan, Vijay Kumar **Loop-Mediated Isothermal Amplification of the tox-R gene coupled with Lateral Flow Dipstick (LAMP-LFD) for the novel rapid and specific visual detection of *Vibrio harveyi***	Biotechnology Research Institute, Universiti Malaysia Sabah

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-89	Ms Sohana Binti Romeli	Lau Han Yih, Sohana Romeli, Mohd Afendy Abd Talib, Siti Norsuha Misman **Rapid and On-Site Diagnostic Method for the Detection of Blast by using DNA Isothermal Amplification and Magnetic Beads Flocculation**	Biotechnology and Nanotechnology Centre, Malaysian Agricultural Research and Development Institute
SP-90	Ms Nor Suzaida Mohd Nor	Nur Sabrina Wahid, Noriha Mat Amin, Rashid Mat Rani, Rohaiza Ahmad Redzuan, Hazalina Zulkifli, Ainaa Abdul Kahar, Nor Suzaida Mohd Nor, Kogeethavani Ramachandran, Noor Azlina Masdor and Badril Abu Bakar **Effect of Alginate Percentage on the Encapsulation Efficiency of *Bacillus pumilus* in Alginate Beads**	Biotechnology and Nanotechnology Centre, Malaysian Agricultural Research and Development Institute
SP-91	Ms Nur Shadrina Mohd Shahrel	Nur Shadrina Mohd Shahrel, Vijay Kumar, Noor Hydayaty Md Yusuf **Identification of MicroRNA-directed Cleavage of Targets in Pineapple (*Ananas comosus*) Fruit Development using Degradome Sequencing**	Biotechnology Research Institute, University Malaysia Sabah
SP-92	Ms Scholastica Lanting	Scholatica L, Nor Azizun Rusdi, Christ Wiart **Medicinal Plants and Their Traditional Uses by Dusun Tindal Community at Kampung Kiau Nuluh Kota Belud**	Institute for Tropical Biology and Conservation, University Malaysia Sabah
SP-93	Dr. Ruzaidi Azli Mohd Mokhtar	Mayrlidzatul Farhain Misrah, Nur Athirah Yusof, Zarina Amin, Cahyo Budiman, Ruzaidi Azli Mohd Mokhtar **Comparative Screening of Anti-Dengue Activity in Aqueous and Ethanol Extracts of Mangrove Plants from Sabah**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-94	Dr. Suryani Saallah	Syafiqah Syazwani Jaffar, Malai Roziah Syafiqah Malai Rozlan, Suryani Saallah, Mailin Misson, Md Shafiquzzaman Siddiquee, Jumardi Roslan, Wuled Lenggoro **Carrageenan-Mediated Green Synthesis of Silver Nanoparticles: Characterization and Antibacterial Activity**	Biotechnology Research Institute, Universiti Malaysia Sabah

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-95	Ms Nur Syafiqah Binti Mohamad Zul	Nur Syafiqah Binti Mohamad Zul, Raimi Mohamed Redwan, Pushpalatha Palaniappan, Kennedy Aaron Aguol, Mohammad Zahirul Hoque, Cahyo Budiman, Vijay Kumar **Genetic Diversity of the Tri-spine Horseshoe Crab (*Tachypleus tridentatus*) based on Twenty Microsatellite Markers**	Biotechnology Research Institute, University Malaysia Sabah
SP-96	Dr. Mohd Syahlan Mohd Syukri	Puteri Natasyah Azman, Nur Umairah Ladi, Jeanstain Patrick, Mohd Syahlan Mohd Syukri **Degradation of Naphthalene using Immobilised Laccase on Polyethyene Terepthalate grafted Maleic Anhydride Nanofiber Mat Aided with Mediators**	Faculty of Engineering, Universiti Malaysia Sabah
SP-98	Mr. Mohd Afendy Bin Abdul Talib	Mohd Afendy Abdul Talib, Son Radu, Cheah Yoke Queen, Farinazleen Ghazali **A High-Throughput and Semi-Quantitative Detection System by PCR-ELISA for Foodborne Pathogen Using Salmonella Enteritidis as a Study Model**	Biodiagnostic & Biosensor Program, Biotechnology & Nanotechnology Research Centre, Mardi
SP-99	Dr. Noriha Mat Amin	Noriha Mat Amin, Nur Azmina Shihabuddin, Azlinda Erny Yunus, Siti Akhtar Mohshim, Rohaiza Ahmad Redzuan, Lina Rozano, Wee Chien Yeong ***In Vitro* Screening of Plant Growth-Promoting (PGP) Abilities of Bacteria Isolated from the Endorhizosphere of Healthy Rice Plants**	Biotechnology and Nanotechnology Research Centre, Malaysian Agriculture Research and Development Institute
SP-100	Nur Atikah Asman	Nur Atikah binti Asman, Mohd Firdaus bin Abd Wahab, Khairul Azfar bin Kamaruzaman **Conserved Sequence from Multiple Coronavirus Strains Aiming at MHC Class II as a possible Human Coronavirus (HCoV) Vaccine Developed by Utilising an Immunoinformatic Approach**	Biotechnology Research Institute, University Malaysia Sabah
SP-101	Prof. Madya Dr. Wilson Thau Lym Yong	Mohammad Rahmat Derise, Anis Adilah Mustafa, Wilson Thau Lym Yong, Kenneth Francis Rodrigues **Establishment of Tissue Culture Platforms for Decoding the Bamboo Transcriptome in Response to Environmental Stress**	Biotechnology Research Institute, Universiti Malaysia Sabah

Abstract code	Presenter	Authors and Title Presentation	Presenter Affiliation
SP-102	Mr. Mohamad Asyraf Bin Mohd Amin	Aina Munirah Mohd Asri, Mohamad Fayyadh Mohd Hayati, Muhammad Huzaifilyasir Kamal Bashah, Mohamad Asyraf Mohd Amin, Deny Susanti Darnis, Siti Fairuz Che Othman, Suhaila Mohd Omar **Black Soldier Fly: Versatile Source of Feed and Biopolymers**	Kulliyah of Science International Islamic University Malaysia
SP-103	Ho Wan Yong	Zhi Xiong Chong, Wan Yong Ho, Swee Keong Yeap, Chee Mun Fang, Noorjahan Banu Alitheen **Modulation of miR-94 in Breast Cancer Metastasis**	Faculty of Science and Engineering, University of Nottingham Malaysia
SP-104	Dr. Eric Chong Tzyy Jiann	Eric Tzyy Jiann Chong, Mohd Ariff Zulfadhli Mohd Rahimie, Lee Ping Chin **Meta-Analysis on the Prevalence of Herpes Simplex Virus 1: From Malaysia to Asia**	Biotechnology Research Institute, Universiti Malaysia Sabah
SP-105	Dr. Yew Chee Wei	Chee-Wei Yew, Rojilin Donol, Nur Asfariena Tupah, Mohd. Zahirul Hoque, Vijay Kumar **Inferring Matrilineal Genetic Components of the Sea Nomad Population Residing Offshore of Sabah, Malaysia**	Biotechnology Research Institute, Universiti Malaysia Sabah

Plenary 1

Biotechnology Transcending Borders

Raha Abdul Rahim, Seetha King, Halimah Alias, Siti Zuraidah Mohamad Zobir, Marilyn Jaoi @ Edward, Shahlizah Sahul Hamid

National Institutes of Biotechnology Malaysia (NIBM), Agro-Biotechnology Institute Complex, Jalan Bioteknologi, 43400 Serdang, Selangor.

This paper will discuss the many facets of Biotechnology such as the health, agriculture and industrial biotechnology and how they support the SDG and 10-10 STIE. A new wave of bio-innovation propelled by the dawn of the Industrial Revolution 4.0 has seen the convergence of multidisciplinary fields in the biological sciences to the physical and digital dimensions in the areas of IR4.0, such as automation and artificial intelligence. It is important that Biotechnology players continue to build collaborations and alliances beyond borders with innovation as their focus and core strength. The role of NIBM in supporting the National Biotechnology Policy 2.0 (2021 – 2030) and the National Vaccine Development Roadmap (NVDR) will be highlighted. Focus research areas and example of current research efforts will be presented.

Plenary 2

From Data to Meaning: Structural Bioinformatics in a Complex World

Habibah A. Wahab
Research and Innovation, Universiti Sains Malaysia (USM)

The COVID-19 pandemic underscored the indispensable role of biotechnology in addressing global challenges. Central to the rapid response was structural bioinformatics, a discipline at the crossroads of molecular biology and computational analysis. In this talk, we will highlight the significance of structural bioinformatics in the era of Translational Biotechnology, emphasizing its transformative impact during the pandemic and the broader implications for our future.

Understanding molecular structures is foundational to life's functions. Structural bioinformatics, by decoding these intricacies, became a beacon in the storm of COVID-19. Through real-time analysis of the SARS-CoV-2 viral protein structures, researchers rapidly identified potential drug targets and vaccine candidates. Highlighting these achievements, we'll examine how these structural insights expedited drug repurposing efforts, vaccine development, and therapeutic interventions – a testament to the discipline's agility and relevance in times of crisis. We will also share in this talk of our ongoing efforts related to potential anti-influenza drug discovery.

Beyond immediate threats, the role of structural bioinformatics in biotechnological advancements, from enzyme fine-tuning to novel drug discoveries, cannot be overstated. The age of data abundance brings both opportunities and complexities. Emerging tools like artificial intelligence and quantum computation hint at future breakthroughs, even as they remind us of the continued learning curve. However, translating these promises into tangible biotechnological solutions requires a concerted effort. Interdisciplinary collaborations, bridging the communication gap between academia, industry, policymakers, and the public, and instilling a passion for structural bioinformatics in the next generation are essential for harnessing the full impact of structural bioinformatics.

Plenary 3

Nanotechnology for Biotechnology: Translating Innovation into Impact

Ruslinda A. Rahim
National Nanotechnology Center (NNC), Ministry of Science, Technology and Innovation (MOSTI)

Nanotechnology is a fast-emerging field of research and development since the last few decades, focusing on the creative exploitation of nano-sized materials to achieve novel applications in diverse fields including biotechnology. These applications range from molecular medicine to agriculture to climate change mitigation via biotechnological innovation. The development of nanotechnology for biotechnological applications is aimed at improving or enhancing conventional biotechnological approaches and to overcome any known limitations. In this keynote, the importance of nanotechnology in numerous biotechnology domains as outlined in the National Nanotechnology Policy and Strategy 2021-2030 as well as the National Nanotechnology and Products Roadmap 2021-2025 will be discussed, and the collaborative way forward will be outlined.

Plenary 4

Polyhydroxyalkanoate Biodegradable Plastics - A Promising New Bio-industry for Malaysia

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Plastics are essential material in our modern lifestyle, however, they are produced from petroleum, which is a non-renewable resource. The disposal of plastics materials is a major problem and this issue is made worst by the generation of microplastics particles and fibers which are persistent in the environment and bioaccumulate in living organisms. Therefore, there is an urgent need to develop and use bio-based and biodegradable plastics. Among the many types of bioplastics, polyhydroxyalkanoates (PHA) is attractive because of its thermoplastics properties and complete biodegradability in land and sea. The efficient production of PHA from sugars and oils from the agricultural residues promotes bioeconomy, circular economy and green economy. An industrial symbiosis approach to recover and purify PHA from bacterial cells is proposed to minimize waste and reduce the cost of producing PHA. The use of mealworms in the purification of PHA can benefit both the production of insect protein and PHA. Recent progress in the commercialization of PHA bioplastics in Malaysia will be presented.

Plenary 5

Probiotic Functionality of Lactic Acid Bacteria : Application of Omics Technologies for Characterization

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Probiotics are defined by WHO as “live microorganisms that when administered in adequate amounts confer a beneficial health effect on the host”, and now widely applied from humans to animals. Due to their beneficial effect on host’s health, probiotics are consumed in a variety of foods, medicine, etc. However, their probiotic effects often show inconsistency in vitro and vivo trials. To overcome this inconsistency, more elaborated and systematic characterization of probiotic properties is needed. Recent development of high-throughput platforms and various omics tools help us to understand the mechanism of probiotic properties. Here, probiotic strains of lactic acid bacteria were used to as models to characterize their probiotic properties using multi-omics tools, such as genomics, proteomics, and microbiomics. The application of omics tools for the characterization of probiotic traits will provide us insights into the comprehensive understanding of the probiotic mechanisms.

Plenary 6

RICCA:
Rebirth of PCR technology for Translational Biotechnology

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On the emergence of new pandemic world, a silent question is everywhere: Are we ready to predict the next pandemic and navigate an uncertain future? To answer this, diagnostic testing plays a critical role. PCR (polymerase chain reaction) has become the most popular molecular diagnostic test for COVID-19. Since the Nobel laureate Kary Mullis invented PCR in 1983, the PCR market size worth has already surpassed USD 4.5 billion in 2019. However, it could not be happen without the discovery of *Taq* polymerase enzyme, which has become the backbone of PCR. Albeit successful, PCR is not commonly used as a clinical diagnostic at point-of-care (POC) settings for two main reasons: the difficulty of storage of PCR enzymes and the less affordability of expensive PCR thermal cycler. To address these issues, we engaged in developing a robust RT-PCR-similar approach, termed the RICCA (RNA Isothermal Co-assisted and Coupled Amplification) assay, that consists of a simple one-pot format of 'sample-in and result-out' with a primary focus on the detection of low copy numbers of RNA virus directly from saliva without the need for laboratory settings. The optimization and freeze-drying of engineered enzyme cocktail and a simple reaction with a total assay time of 15 min at a constant temperature 41°C enables the RICCA kits can be room-temperature-storable and applicable for detecting virus RNA target sequences for the on-site (low resource settings) molecular diagnosis of COVID-19 and other infectious diseases. Our next attempt of developing quantitative RICCA with automation will facilitate our preparedness for the next pandemic.

SO-01

Scaling up the Production of Myco-coagulant for Water Treatment

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A fungal strain was used to investigate the production of myco-coagulant in solid-state fermentation. A scale-up was performed using the tray method to produce myco-coagulant using the solid-state method. The influence of substrate thickness (varied from 2 to 30 mm) on myco-coagulant production was investigated. The results revealed that the turbidity removal efficiency of myco-coagulant in kaolin suspension was found to be increasing with the increase of the thickness of the coco peat substrate. Three different subculturing methods for mycelium inoculation were evaluated, which are surface inoculation, mixed inoculation, and layer inoculation. The surface inoculation approach achieved a maximum turbidity removal of 96 %. The effect of initial turbidimetry values on turbidity removal was also studied. According to the findings, the bio-coagulant developed is better suitable for use in high turbidity water than in low turbidity water. Subculturing of fungus strain from solid-state (substrate) to solid-state was also studied. These findings demonstrated that the subculturing strategy was just as effective as an inoculum-based subculture.

Keywords: Bio-coagulant; Fungus; Solid-state fermentation; Turbidity Removal

Funding Information: MYS1009 (SPI20-001-0001)

SO-02

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

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The long-established evidence of Parkinson's Disease (PD) being more prevalent and severe among men than women implied the protective role of female endogenous sex hormones. Despite reports of the neuroprotective effect of 17β-estradiol in different models of brain injury, the harmful side effects associated with its prolonged exposure prompted the search for safer alternatives in structurally similar phytoestrogens that are non-steroidal and plant-derived. In the search for disease-modifying drug candidates for PD, this study aimed to explore the neuroprotective potential of the phytoestrogens, Genistein and Resveratrol along with the endogenous hormone, 17β-estradiol against MPP+ (1-methyl-4-phenyl pyridinium) neurotoxin-induced cell death in SH-SY5Y neuroblastoma cells. MPP+-induced apoptosis was characterized by a statistically significant increase in the number of apoptotic nuclei and time-dependent ROS production while no significant increase in caspase-3 activity was detected. In the neuroprotection study, pretreatment with all three individual estrogenic compounds did not exert any significant neuroprotective effect against MPP+-induced cell death. However, considering the neuroprotective literature of these estrogenic compounds in other neurodegenerative disease models, further investigation is warranted in alternative *in vitro* and *in vivo* PD models. Additionally, deciphering the complex estrogen receptor (ER) signalling associated with these estrogenic compounds may also provide further insights into their potential protective mechanisms and bring us closer to developing effective therapeutic interventions for PD.

Keywords: neuroprotection; Parkinson's disease; estrogenic compounds; phytoestrogen; apoptosis

SO-03

Towards Sustainable Seaweed Aquaculture in Malaysia: Development of Biocontrol Formulation against *Vibrio* Infections in *Kappaphycus alvarezii* using Endophytic *Bacillus altitudinis* Strains

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Sabah is the main seaweed producer in Malaysia. Sabah Agriculture Blueprint (2021-2030) has placed seaweed as the second-highest income generator for the aquaculture sector with expected revenue of RM1.8 billion by 2030. According to FAO and the UN 2018 report, disease and low-quality seed problems are affecting Malaysian seaweed production particularly *Kappaphycus alvarezii* in Sabah. Furthermore, the FAO Food Security 2022 report stated that the ice-ice disease caused by *Vibrio* sp. infection is still a major problem responsible for the threatening diseases of seaweed cultivation, causing economic loss worldwide. Recent studies have shown that endophytic *Bacillus altitudinis* have high antagonistic activity against a broad spectrum of pathogens. Yet until now, there is no research has been done on evaluating the effects of *Bacillus altitudinis* as a biological control agent in Asia. The present study aimed to develop a biocontrol formulation using several *Bacillus altitudinis s*trains isolated from *K. alvarezii* in Sabah. Analysis done to evaluate the effects of single and multiple pools of *Bacillus altitudinis s*trains on *K. alvarezii* showed resistance towards *Vibrio* spp. infections. The result indicates that a single *B. altitudinis* strain is capable to slow down the growth of *Vibrio* spp. while multiple *B. altitudinis* strains have strong antagonistic potential to kill the *Vibrio* spp. Interestingly, the treated *K. alvarezii* with *Bacillus altitudinis s*trains prevented the formation of ice-ice diseases for both in seawater and artificial seawater with low nutrients. Based on the overall performance, the *Bacillus altitudinis s*trains could be formulated as biocontrol agents against ice-ice disease caused by Vibrio spp. tested in this study.

Keywords: *Bacillus altitudinis*; biocontrol; ice-ice disease; *Kappaphycus alvarezii*; plant pathogens

SO-04

Harnessing Remote Sensing to Enhance Understanding and Management of Aquatic Invasive Species

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Invasive species pose significant environmental and socioeconomic challenges, necessitating a paradigm shift in invasion science to better predict and mitigate their impact. Remote sensing techniques provide distinct advantages in monitoring and mapping the presence and distribution of aquatic invasive species. High-resolution spatial and temporal data can be collected using satellite imagery, aerial photography, and other remote sensing platforms, allowing for the efficient detection and monitoring of invasive species in coastal areas. These remote sensing techniques can provide critical insights into invasive species' spread, establishment, and impacts, allowing for evidence-based decision-making. This study highlights the untapped potential of remote sensing in invasion science and emphasises the need for ongoing innovation, knowledge sharing, and interdisciplinary collaboration to effectively address the challenges posed by aquatic invasive species. This study proposed a synergistic approach that uses remote sensing to study and identify invasive species by integrating knowledge from the aquaculture and maritime industries, invasive species detection techniques, limitations of aquatic remote sensing, invasion metrics, and change detection. By leveraging the power of remote sensing, we can pave the way for proactive, ecosystem-focused management strategies to protect our coastal environments.

Keywords: Invasion science, GIS, machine learning, artificial intelligence

SO-05

Functional analysis of conserved hypothetical proteins from the Antarctic Yeast, *Glaciozyma antarctica*

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Recent discoveries have revealed that *Glaciozyma antarctica* PI12 survives and adapts to the extreme Antarctic climate by producing a wide range of proteins associated with the thermal stress response. However, approximately 37% of the protein-coding genes in *G. antarctica* were classified as hypothetical proteins (HPs), so there is no detailed description of their stress response mechanisms. In the current study, three conserved HPs of *G. antarctica*, designated GaHP2, GaHP3, and GaHP4, were cloned, expressed purified, and their proteins' function and structure were evaluated. Real-time quantitative PCR analysis revealed that these genes were stress-induced, indicating their roles in heat stress regulation. Functional analysis showed that these proteins maintained their activities at a lower rate at low temperatures below 25 °C. Meanwhile, a lower citrate synthase aggregation at 43°C in the presence of GaHP2 and GaHP3 suggested the characteristics of non-ATP-binding chaperone activity. Furthermore, our comparative structural analysis demonstrated that the HPs exhibited cold-adapted traits, most notably increased flexibility in their 3D structures compared to their counterparts. For GaHP2, the aromatic clusters can be linked to its heat stability. Meanwhile, GaHP4's cold shock domain hinted at the protein's role in regulating gene transcription and translation during temperature fluctuations. Thus, this demonstrated that the HPs examined in this study adopted strategies to maintain a balance between molecular stability and structural flexibility. Conclusively, this study has established the structure-function relationships of the *G. antarctica* HPs and provided fundamental experimental data highlighting their importance in thermal stress response.

Keywords: conserved hypothetical protein, quantitative PCR, Antarctic yeast, cold adaptation

Funding Information: FRGS0463-2017

SO-06

Comparative Proteomic Analysis Uncover Potential Biomarkers for the Detection of *Vibrio*-resistant Phenotype in Hybrid Grouper (*Epinephelus fuscoguttatus* ♀ x *Epinephelus lanceolatus* ♂) and Their Underlying Immune Mechanism

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Vibrio alginolyticus is the causative agent of vibriosis, leading to the development of ulcers and hemorrhagic spots in fish. However, the response of grouper to this infection varies, with some individuals gaining resistance or susceptibility, and the underlying immunological mechanisms remain unclear. To mimic natural infection, hybrid groupers were exposed to *V. alginolyticus* through an immersion challenge. Comparative proteome analysis using high throughput LC-MS/MS was performed on mucus and serum samples from *vibrio*-resistant and -susceptible grouper, resulting in the identification of 1488 and 528 proteins, respectively. The mucus data revealed seven significant immune-related proteins in the resistant group that include allograft inflammatory factor 1, deleted in malignant brain tumors protein, cystatin B, complement component C6, complement factor 1, MHC class 1, and annexin A1. The serum data identified five significant immune-related proteins: cystatin-B, apolipoprotein(a), complement component C8, neuroblast differentiation-associated protein AHNAK isoform X34, and protein S-100G. Interestingly, potential biomarkers for disease onset and therapeutic intervention associated with the resistance phenotype were also found in mucus and serum samples. This data provides insight into the dynamic changes of protein in response to *V. alginolyticus* infection and offers a foundation for further related studies.

Keywords: Biomarker, Hybrid grouper, Immune expression, Protein profiling, Animal health

Funding Information: TRGS/1/2020/UPM/02/1/3

SO-07

Accelerating COVID-19 Diagnostics: Harnessing the Utility of Automated Nucleic Extractors in the Pandemic Era

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Automated nucleic acid extractors have revolutionized molecular biology and diagnostics by providing efficient and standardized methods for isolating nucleic acids from various sample types. These instruments have demonstrated a multitude of advantages over manual extraction techniques. Notably, they streamline and standardize the nucleic acid extraction process, while yielding high levels of purity and amplification. Consequently, diagnostic accuracy and research productivity have significantly improved. The utility of automated nucleic acid extractors has become increasingly evident in recent years and under various laboratory settings. But none has highlighted the immense advantages of automated nucleic acid extractors as clearly as the recent COVID-19 pandemic. The critical role played by these instruments in scaling up and expediting COVID-19 testing globally underscored their significance in managing widespread health crises. Their ability to process a large number of samples rapidly either fully or semi-automated, while maintaining consistency and reproducibility, proved indispensable in managing the pandemic. As technology advances, automated nucleic acid extractors are expected to play a more significant role, advancing fields like genomics, personalized medicine, and infectious disease surveillance. They hold promise especially in disease outbreak control and management, enabling swift responses to emerging health threats. In conclusion, automated nucleic acid extractors have transformed research and diagnostics, with vast potential for further advancement and applications in diverse fields of Life Science.

Keywords: automated nucleic acid extractor; COVID-19; diagnostic; pandemic

Funding Information: The establishment of the UMS COVID-19 Diagnostic Laboratory and its services at the Department of Pathology and Microbiology, Faculty of Medicine and Health Sciences in June 2020 were through the Special Emergency Funds from the Office of the Chief Minister of Sabah State.

SO-08

Antioxidant Activity and Bioactive Compounds of Black Turmeric (*Curcuma caesia*) Rhizome Extracts

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Black turmeric (*Curcuma caesia*) is a medical herb belonging to the Zingiberaceae family and is claimed to have health benefits. Determination of the bioactive compound and antioxidant activity of the rhizome part of this plant is important because it has been widely used as a folk medicine for the treatment of allergies, fever, wounds, toothache, and asthma. Their potential as natural sources that can treat diseases related to inflammation caused by long-term oxidative stress can be determined through electron transfer (ET)-based assay which includes DPPH, ABTS, and Ferric-reducing power assay (FRAP). Antioxidant assay of black turmeric rhizome methanol extract by these three assays showed the inhibition percentage at 24.0±0.023%, 62.30±0.013%, and 48.7±0.005% with IC50 14.190±0.003 mg/mL, 2.42±0.013 mg/mL, and 16.3±0.013 mg/mL respectively. LCMS coupled to Agilent 6520 Accurate-Mass Q-TOF mass spectrometer with dual ESI source had been used where 26 compounds had been detected where some of these bioactive compounds have the potential as an anti-inflammatory agent. Therefore, black turmeric has the potential for the development of food ingredients, pharmaceuticals, and nutraceuticals focused toward disease caused by inflammation.

Keywords: Black Turmeric, Antioxidant activity, Bioactive compounds, Inflammation

Funding Information: SDK0315-2020

SO-09

Determination of Mercury in Cosmetic Products Based on the Modified Electrochemical Sensor (PANI/MWCNTs/AuNPs/ITO)

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Mercury is a common ingredient found in skin lightening soaps, creams, and makeupcleansing products. It may cause skin rashes, skin discolouration, and scarring, as well as a reduction in the skin's resistance to bacterial and fungal infections. Nonetheless, in consumer cosmetic products, undisclosed amounts of Hg are manufactured. For that reason, a fast and sensitive electrochemical method was developed to determine mercury in cosmetic products with the composition of polyaniline/multiwalled carbon nanotubes/gold nanoparticles/indium tin oxide sheet using methylene blue as a redox indicator. The significantly enhanced electrochemical performance was observed using cyclic voltammetry (CV) and differential pulse voltammetry (DPV). In order to detect mercury qualitatively and quantitatively, deposition potential and deposition time were respectively optimised to be 0.10 V and 70 s. The modified sensor was revealed a wide detection range of mercury from 0.01 to 10.00 ppm with a limit of detection of 0.08 ppm. The modified sensor recoveries rate were found from 96.6–97.5% of Hg detection with an acceptable relative standard deviation (RSD) less than 1%. Therefore, it is suggested that the PANI/MWCNTs/AuNPs/ITO electrode could be a promising material for developing on-site Hg detection tools for applications in diagnostics, environmental and safety security controls, or other industries.

Keywords: mercury sensor; mercury; cosmetic; cyclic voltammetry (CV); differential pulse voltammetry (DPV); electrochemical sensor

SO-10

Utilization of Thermally-Degraded Plastic Wastes as a Carbon Source for Polyhydroxyalkanoate Production from Microorganisms Isolated from Plastic-Contaminated Sites

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With the current global population's rise, the demand for plastics in our daily lives increased sharply. The surge in demand for plastics caused several problems for the environment, especially in plastic waste management. Malaysia became one of the largest plastic waste importers in the Asia region after China changed its plastic waste import policy. Thermal degradation of plastics, known as pyrolysis, is an alternative method to traditional plastic waste management, such as landfills and incineration. Using thermally degraded waste plastic (low-density polyethylene and high-density polyethylene), the utilization of thermal degraded plastic waste products as a carbon feedstock to produce polyhydroxyalkanoate (PHA) on new microorganisms from the plastic-contaminated environment will be discussed in this research. PHA is a type of lipid granule produced by microorganisms under stress conditions that can be used as an alternative to conventional non-biodegradable plastics. *Cupriavidus* sp. USM2A2 was isolated and found to be capable of producing poly(3-hydroxybutyrate-co-3-hydroxyvalerate) P(3HB-*co*-3HV) when supplemented with waste LDPE and HDPE pyrolysis oil. The findings of this study opened the potential for innovations in plastic waste management, by thermal degradation, which is yet to be explored in Malaysia, and recycling it into biodegradable plastics which will not pose global environmental problems.

Keywords: Pyrolysis, Plastic wastes, Thermal degradation, Bioconversion, Bioplastics, Polyhydroxyalkanoate, P(3HB-*co*-3HV)

Funding Information: Tenaga Nasional Berhad Research Centre.

SO-11

Evaluation of 5-hydroxy-3',4',7-trimethoxyflavone as dengue NS2B-NS3 protease inhibitor: an *in silico* and *in vitro* study

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Dengue is one of the most prevalent viruses transmitted by the *Aedes aegypti* mosquito. Currently, no specific medication is available to treat dengue infection. This study aims to evaluate anti-dengue activity of 5-hydroxy-3',4',7-trimethoxyflavone against dengue NS2B-NS3 protease. Molecular docking analysis using CB-Dock and AutoDock Vina showed strong binding interaction of the compound against NS2B-NS3 protease. The compound exhibited comparable binding energy with values of -8.4 kcal/mol as the reference compound, quercetin (-8.2 kcal/mol). Molecular dynamics simulation using GROMACS revealed the stability of the complex throughout 100 ns. Besides, ADMET analyses of the compound demonstrated good pharmacokinetics profiles without violating Lipinski's Rule of Five. *In vitro* inhibition assay on 5-hydroxy-3',4',7-trimethoxyflavone showed IC_{50} values of 104 µg/ml. Overall, computational analyses of the compound suggested significant binding interaction with NS2B-NS3 protease. The enzyme inhibition assay further supported their potential to inhibit the enzyme activity, which could possibly hinder dengue replication. These findings hold promise for potential dengue treatment, highlighting the need for further investigation.

Keywords: 5-hydroxy-3',4',7-trimethoxyflavone; dengue NS2B-NS3 protease; *in silico*; *in vitro*

SO-12

Phytochemical and Antioxidant Studies of *Solanum lasiocarpum*, Sour Eggplant of Sarawak, East of Malaysia

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Solanum sp. is traditionally important as ethnomedicinal and dietary uses due to rich of phytochemicals that posses with antidiabetic, anti-inflammatory, antioxidant and antiulcer proven by pharmacological studies. Antioxidant activity by Solanum sp. have come into attention due to the rise issue by high accumulation of free radicals (H2O2, O–2 , and OH–) in body cause cancer, aging, atherosclerosis, diabetic complications, cataracts, autism, atherosclerosis, arthritis, cirrhosis, obesity, cardiovascular, neurodegenerative and degenerative diseases. Conventionally, these radicals could be reduce by synthetic antioxidants by butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), propyl gallate (PG), and tert-butylhydroquinone but it left sides effect such liver damage and carcinogenesis. In this study, alternative approach performed using phytochemicals in *Solanum lasiocarpum* as an antioxidant agent to encounter radicals with more natural as well as less side effects. Phytochemicals screening revealed about 145 chemical constituents identified using LCMS QTOF mass spectrometer. Phytochemical profiles' results varied from methanol, acetone and hexane but dry extract (DE) showed highest amount of phenolic, flavonoid and anthocyanins compounds than dry weight (DW). The antioxidant results of *Solanum lasiocarpum* showed the high stability by methanol extract with IC50 values of DPPH, ABTS and FRAP were 12.10, 6.36 and 17.81 mg/ml, respectively. The fruit of *Solanum lasiocarpum* has antioxidant activity exhibited by methanol solvent which it important to explore for potential natural free radicals' inhibitor.

Keywords: *Solanum lasiocarpum*, LCMS Q-TOF, bioactive constitutions, phytochemicals profiling, antioxidant activity, free radicals' inhibitor

SO-13

Effects of Tocotrienol Rich Fraction (TRF) on *Drosophila melanogaster* Alzheimer's Disease Models

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Alzheimer's disease (AD) is a worldwide neurodegenerative disease and is the main cause of dementia. The pathophysiology of AD was believed to begin with the deposition of aggregated amyloid-beta within the neurons that would lead to several damages such as, oxidative stress and neuronal signalling disruption. Tocotrienols that are famous for their antioxidant activity, were found to decrease the aggregation of amyloid beta *in vitro* as well as ameliorating cognitive impairment in amyloid-beta expressing mice. In this project, we aim to conduct a preliminary screening using *Drosophila melanogaster* to assess the effect of Tocotrienol Rich Fraction (TRF) in behavioural aspect. The assessments include rough eyes phenotype (REP) assay to assess neurotoxicity, longevity analysis for lifespan and negative geotaxis test for motor function in *Drosophila*. The result of REP assay shows no significant improvement of the rough eyes after feeding with TRF, longevity analysis and negative geotaxis assay shows no significant difference in the lifespan and motor function over the control group. Further investigations are warranted to gain deeper insights into the potential benefits of TRF in amyloid beta toxicity.

Keywords: Amyloid beta; protein toxicity; Tocotrienol Rich Fraction; Antioxidant

SO-14

Identifying Genetic Variants for Spontaneous Preterm Labor (sPTL) in Malay Preterm Infants through Whole-Exome Sequencing

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Spontaneous preterm labor (sPTL) is a complex multifactorial condition, with uncertain genetic influence. Previous studies have indicated a stronger involvement of the infant's genome compared to the mother's in sPTL. To further explore this, we conducted whole exome sequencing on arterial umbilical cord blood samples from eight Malay preterm infants. Our analysis revealed the presence of four heterozygous variants related to infection and inflammation, which is one of the common contributors of sPTL. Among these variants, a rare loss-of-function variant (NM_001130917.3:c.525G>A) was identified in *LILRA2*, with minor allele frequency (MAF) <1 % . This variant potentially disrupts a protein domain involved in immune response modulation and was found in all eight infants. Additionally, all the infants carried a rare frameshift variant (NM_005961.3:c.5303_5305del) in *MUC6* (MAF<1%), impacting cervical mucus composition. Furthermore, six infants exhibited two low-frequency missense variants (NM_004368.4:c.787G>A and NM_004368.4:c.797G>A) in *CNN2* (MAF<5%), associated with innate immune response and inflammation. Both *MUC6* and *CNN2* variants were classified as pathogenic, while the *LILRA2* variant, despite being loss-of-function, was categorized as a variant of uncertain significance per ACMG classification. These findings shed light on potential genetic variants involved in inflammation modulation, offering insights into the underlying mechanisms of sPTL. However, further research is warranted to fully comprehend their specific roles and clinical implications in the context of preterm labor.

Keywords: spontaneous preterm labor; whole exome sequencing; *LILRA2*; *MUC6*; *CNN2*

Funding Information: FRGS/1/2020/SKK08/UPM/02/1

SO-16

Establishment *Strobilanthes crispus in vitro* Culture and Assessment of Taraxerol Content from Field and *in vitro* Grown Plants

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Taraxerol is a pentacyclic triterpenoid that exhibited various medicinal properties such as antioxidative, anti-fungal and cytotoxic properties. *Strobilanthes crispus* or also known as Pecah Beling, is a local Malaysian herb that accumulate this valuable compound, albeit in low yield. Plant tissue culture provides alternative to continuous, consistent, and higher yield of taraxerol production. Therefore, this study aims to establish *in vitro* culture from auxillary shoot and nodal explant and assess the taraxerol content from *in vitro* culture and intact plant. Results showed that 78.0 ± 2.74% plantlets were successfully established from axillary shoots explant when sterilised with Chlorox™ solution (20% v/v) under nine minutes exposure, while no nodal explants managed to survive and induce explants despite all treatments used. Micropropagation of *S. crispus* using *in vitro* nodal explant in combined cytokinin (0.5mg/L KN + 0.1mg/L TDZ) induced highest number of shoots (9.4 ± 2.8 shoots per explant) with 86.4 ± 17.24% regeneration frequency observed after 30 days of culture. For shoot elongation, MS control medium promoted better shoot elongation (6.60 ± 1.90cm) compared to treatment with cytokinins. Taraxerol content analysis showed leaf part of field grown *S. crispus* accumulated higher taraxerol content (48.83 ± 0.18 mg/g dw), followed by leaf from plantlet (45.17 ± 1.25 mg/g dw) and field grown axillary shoots (26.39 ± 1.14 mg/g dw). This finding provide bases for further manipulation of taraxerol accumulation using *in vitro* culture for large-scale production.

Keywords: Taraxerol, *Strobilanthes crispus*, plant tissue culture, triterpenoid, accumulation.

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SO-17

LysM Containing-Proteins for a Future Anti-Tuberculosis Drug Development

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LysM containing-protein is a binding domain found in bacterial cell wall, noncovalently link with numerous catalytic enzymes which responsible for cell-wall management exclusively peptidoglycan can be a promising target for anti-tuberculosis drugs. *KEG15107* from *M. avium* and *Rv1288* of *M. tuberculosis* are LysM homologs and their biological properties were explored in this study. Gene cloning and protein expression for *KEG15107* with size of 25 kDa were initially performed at optimized conditions. The over-expressed protein was purified and crystallized at various crystalline conditions and co-crystallized with polyNAG molecules. Diffracted data sets of the grown crystals were analysed and structure determination was performed by using molecular replacement. Analysis of the three-dimensional structure of the *KEG15107* revealed that the protein contains four LysM domains. Three-dimensional structure of the native protein was identified as a tetramer while its complex was a dimer and the complexes bound to polyNAG. *Rv1288 was* successfully cloned and expressed in BL21 *DE3* cells and the expressed protein was purified using liquid chromatography method. *Rv1288* was detected as a hexamer shown by the calculated apparent molecular weight of the protein. Determination of a three-dimensional structure of *Rv1288* and biological functions of the proteins are on progress.

Keywords: anti-TB; LysM; *Mycobacterium*; protein-expression; protein-purification

Funding Information: NMRR-20-533-53776 (20-021) (Malaysian Research Grant)

SO-18

Physicochemical Properties, VOC, MGO and DHA Content of *Heterotrigona itama* (Hymenoptera; Meliponini) Samples from Different Geographical Areas in Sabah, Borneo

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So far, very few studies have been conducted on the stingless bee honey from Sabah despite its therapeutic properties. Therefore, the aim of this study was to determine the physicochemical properties, Dihydroxyacetone (DHA) and Methylglyoxal (MGO) content and volatile organic compounds (VOC) of *Heterotrigona itama* honey from three different geographical areas in Sabah; highland (10 samples), lowland (10 samples) and coastal (10 samples). Physicochemical parameters were assessed using established standard methods, DHA and MGO content were determined using high performance liquid chromatography (HPLC) and volatile organic compounds were identified using gas chromatography-mass spectrometry (GC-MS). The average values of physicochemical parameters were compared with the standard values set by the Malaysian standards (MS) for stingless bee honey, the Codex Alimentarius (CODEX) and the United States Department of Agriculture (USDA) standards for bee honey. Significant differences were found in the physicochemical parameters (except for moisture content, brix, DHA), MGO between highland, lowland, and coastal areas ($p < 0.05$). The highlands had the highest number of unique VOC ($n = 41$), followed by coastal areas ($n = 32$) and the lowlands ($n = 29$). The results suggest that physicochemical properties, MGO content and VOC can be used to distinguish honey of stingless bees from different geographical areas in Sabah.

Keywords: Sabah *H. itama* honey; Geographical areas; Physicochemical properties; DHA and MGO; VOC

Funding Information: This study was funded by the Malaysia Ministry of Higher Education with grant code: FRGS/1/2019/WAB01/UMS/02/3 (FRG0519-1/2019) and UMS internal funding (GUG0462-1/2020).

SO-20

Curcumin as a Golden Spice in Targeting Key Cellular Signaling Pathways in Triple Negative Breast Cancer

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Breast cancer is the most prevalent cancer globally, and it has the highest incidence and mortality rates among women. Triple-negative breast cancer (TNBC) is a subtype that lacks the expression of hormone receptors (ER and PR) and the human epidermal growth factor receptor 2 (HER2). TNBC is highly aggressive, prone to early relapse, and commonly metastasizes to the brain and lungs. It is resistant to hormonal and HER2-targeted therapies, resulting in poorer survival rates. Due to its aggressive nature, limited treatment options, and chemotherapy resistance, there is an urgent need for more effective and safer therapeutic agents. Curcumin, a bioactive compound found in turmeric, shows promise in TNBC treatment due to its pharmacological safety and multitargeting effects. In this study, curcumin's anti-breast cancer activity is explored by targeting various molecules and interfering with key signaling pathways involved in cell survival, proliferation, metastasis, angiogenesis, cancer stem cells, and apoptosis. Understanding curcumin's multifunctional anticancer action can guide future research and enhance its efficacy in clinical practice.

Keywords: drug discovery, curcumin, breast cancer, multitarget

SO-21

Physiological Response to Acute and Chronic Temperature Changes in the Serum of Resilient and Susceptible Hybrid Grouper (*Epinephelus fuscoguttatus* x *Epinephelus lanceolatus)* Revealed by LCMS/MS metabolomics

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Current acceleration of climate change has been regarded as one of the most significant threats to global biodiversity and ecological stability. Hybrid grouper, a marine carnivorous fish that has a high economic value particularly in Asian region, are particularly susceptible to temperature variations and became a major concern in aquaculture industry. In this study, LCMS/MS serum metabolomic was utilized to investigate the physiology response of hybrid grouper that are more resilient or susceptible toward chronic and acute temperature changes. The result showed a total of 65 significant metabolites (VIP > 1) from 17 Class were identified among the control, resilient chronic (TCR), susceptible chronic (TCS), resilient acute (TAR), and acute susceptible (TAS) fish. Acute temperature change showed no significant differences in metabolites between resilient and susceptible hybrid grouper. Meanwhile, hypoxanthine, guanosine, guanine, and inosine were acknowledged as biomarkers to classify hybrid grouper that are susceptible to chronic temperature change. Further pathway enrichment of these metabolites revealed that chronic temperature changes mainly affected the purine metabolism in susceptible hybrid grouper as all the potential biomarkers revealed were from the same pathway. Overall, the findings of this study gave insights into the physiological regulation of hybrid grouper that are susceptible to temperature changes, as well as a framework for future research.

Keywords: Hybrid grouper, Metabolomic, Serum, Temperature stress, Biomarker

Funding Information: TRGS/1/2020/UPM/02/1/3

SO-22

Characterization and Identification of Rhamnolipid Congeners Produced by *Pseudomonas aeruginosa* USM-AR2

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Pseudomonas aeruginosa USM-AR2, a locally isolated strain has been shown to produce copious amounts of rhamnolipid when grown in mineral salt medium supplemented with waste cooking oil as the sole carbon source. Rhamnolipid, a class of glycolipid biosurfactant is one of the most extensively studied biosurfactants due to their exceptional physicochemical and biological properties. Rhamnolipid can either be mono- or di-rhamnolipid, with each congener and homologue, having constituent fatty acids with varying chains and degrees of saturation. The congener composition of rhamnolipid mixtures produced in *P. aeruginosa* USM-AR2 fermentation process was characterized by liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis. LC-MS/MS analysis revealed 14 rhamnolipid congeners, with Rha-C_{10}-C_{10} as the main congener and mono-rhamnolipid congeners accounting to 76.5% of the total rhamnolipid mixture. The rhamnolipid resulted in a surface tension reduction of water to 30 mN/m at a critical micelle concentration of 5.0 mg/L. This information will assist in refining cultivation protocols and provide insights into the potential applications of rhamnolipid, which is anticipated, to be composition dependent.

Keywords: *Pseudomonas aeruginosa* USM-AR2, rhamnolipid, congener, LC-MS/MS, critical micelle concentration

Funding information: Fundamental Research Grant Scheme (203.PBIOLOGI.6711906)

SO-23

Dihydroxyacetone (DHA) and Methylglyoxal (MGO) in *Apis cerana* Honey Samples from Different Botanical Sources and Geographical Origin in Sabah, Borneo

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Honey contains Dihydroxyacetone (DHA) and methylglyoxal (MGO) that have varying concentrations depending on the botanical and geographical origin of honey, but still relatively unexplored in Sabah. This study aimed to determine the levels of DHA and MGO in *Apis cerana* honey samples with a total of 3 replicates of each honey sample in the form of unprocessed or raw honey collected from six study sites in Sabah including Ulu Kiulu, Tuaran (Lowland Rainforest Park), Nadau, Tamparuli (Highland Forest Park), Membatu Laut, Kudat (coconut farm), BHBC, Kudat (*Acacia* forest), Gana, Kota Marudu (rubber and orchard) and FSA, Sandakan (oil palm and orchard). The contents of DHA and MGO in honey of *Apis cerana* were investigated by high performance liquid chromatography (HPLC). The findings revealed variations in the levels of DHA and MGO depending on the botanical sources and geographical origin. Gana's honey sample exhibited the highest DHA concentration (mg/kg), followed by Membatu Laut, FSA, Ulu Kiulu, BHBC and Nadau. The honey sample from BHBC had the highest MGO concentration among the study sites, followed by Membatu Laut, Ulu Kiulu, FSA, Gana and Nadau. This study provides the first data on DHA and MGO levels in honey from honey bees in Sabah.

Keywords: *Apis cerana*; botanical sources; DHA; geographical origin; MGO

Funding Information: FRG0519-1/2019 and GUG0443-1/2020

SO-24

Isolation and Screening of Effective Microbes (EM) From Transformer Oil Contaminated Soil for Remediation of Polychlorinated Biphenyls (PCB) in Waste Transformer Oil

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Known for its recalcitrant nature, health and environmental hazards, polychlorinated biphenyls (PCB) still pose a threat even after its long history of massive commercialization and nationwide ban. Polychlorinated biphenyls were commonly used as coolant or dielectric in electrical appliances such as capacitors, lighting ballasts and transformers and due to its stable nature, it is still detectable in transformer oil from transformers that were manufactured prior to its ban. To degrade the PCBs, bioremediation through usage of telluric bacteria from soil affected with transformer oil spill has been explored. A total of eleven bacterial strains have been successfully screened for the ability to degrade polychlorinated biphenyls in selective liquid medium. The eleven isolates were identified and designated as *Acinetobacter baumannii* 1A-3, *Comamonas testosteroni* 1A-5, *Cupriavidus taiwanensis* 2A-1, *Cupriavidus oxalaticus* 2A-2, *Acinetobacter junii* 2A-10, *Diaphorobacter nitroreducens* 3A-1, *Bacillus cereus* 3A-3, *Acidovorax delafieldii* 3A-6, *Stenotrophomonas acidaminiphila* 3A-9, *Acinetobacter baumannii* 3A-10 and *Stenotrophomonas nitroreducens* 4A-6 based on 16S rRNA sequencing with PCBs degradation rate of 25.65%, 43.60%, 60.00%, 58.31%, 7.23%, 43.26%, 52.98%, 55.00%, 47.04%, 2.17% and 57.36% respectively after 20 days of incubation. The three most efficient isolates in degrading PCBs were *Cupriavidus taiwanensis* 2A-1 (60.06%), *Cupriavidus oxalaticus* 2A-2 (58.31%) and *Stenotrophomonas nitroreducens* (57.36%).

Keywords: Polychlorinated biphenyls, PCB, Bioremediation, Transformer Oil-contaminated Soil, PCB in Transformer Oil

Funding: Tenaga Nasional Berhad Research Sdn Bhd

SO-25

Comparative Metabolite Analysis Approach for *Piper sarmentosum* Organs Classification Based on LC-MS

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Piper sarmentosum Roxb. (Piperaceae) is a traditional food and medicinal plant that is widely distributed throughout the tropical and subtropical regions of Asia, offering both culinary and health benefits. In this study, the secondary metabolites of *P. sarmentosum* organs were identified and their relative abundances were characterized. The metabolic profiles of leaves, roots, stems, and fruits were extensively investigated using liquid chromatography high-resolution mass spectrometry (LC-HRMS), and the resulted data were processed by multivariate statistics. Manual interpretation of tandem mass spectrometric (MS/MS) fragmentation patterns indicated the presence of 154 tentatively identified metabolites, the majority of which were alkaloids and flavonoids. Analysis of principal components and hierarchical clustering revealed that flavonoids, lignans, and phenyl propanoids are most prevalent in leaves, aporphines in stems, piperamides in fruits, and lignanamides in roots. Overall, this study provides extensive data on the metabolite composition of *P. sarmentosum*, supplying useful information for bioactive compounds discovery and patterns of their preferential biosynthesis or storage in specific organs.

Keywords: *Piper sarmentosum*; LC-MS; multivariate analysis; metabolite profiling; alkaloids

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SO-26

Anti-Influenza A Virus Effect of Betacyanins from Red Pitahaya (*Hylocereus polyrhizus*)

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Influenza affects 5 to 10% of adults and 20 to 30% of children worldwide, with influenza A virus (IAV) responsible for pandemics and annual epidemics, causing the most severe illnesses resulting in patient hospitalizations or death. With IAV threatening the next global influenza pandemic, it is a race against time to search for antiviral drugs. Betacyanins are unique nitrogen-containing and water-soluble reddish-violet pigments that have been reported to possess antiviral properties against dengue virus. The objective of this study was to examine the antiviral effect of betacyanins from red pitahaya (*Hylocereus polyrhizus*) on IAV-infected lung epithelial A549 cells. IAV propagated from embryonated chicken eggs were used to infect A549 cells at a multiplicity of infection of one. HPLC analysis of extracted betacyanin showed four betacyanins in the betacyanin fraction, namely phyllocactin, hylocerenin, betanin, and isobetanin. Cytotoxicity assay showed that betacyanin fractions were not cytotoxic to A549 cells at concentrations below 100 µg/mL. Betacyanin fraction concentrations of 12.5, 25.0, and 50.0 µg/mL prevented the formation of viral cytopathic effect and reduced virus titer in IAV-infected cells, protecting host cells from virus-induced injuries and preventing future virus production. A downregulation of protein and mRNA nucleoprotein expression levels, a key viral factor essential in virus survival and replication, was observed after treatment with 25.0 and 50.0 µg/mL of betacyanin fraction. These results provide evidence for anti-viral activity exhibited by betacyanin from red pitahaya.

Keywords: Antiviral; Betacyanin; Influenza A virus; Red pitahaya

Funding Information: FRGS/1/2020/SKK0/MUSM/02/1

SO-28

Sword Fern: A Promising Biocontrol Agent against Marine Parasitic Leech Infestations in Aquaculture

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Zeylanicobdella arugamensis, a marine parasitic leech, poses a significant threat to cultured groupers and other fish species in Southeast Asian countries. This study explores the efficacy of Sword Fern (*Nephrolepis biserrata*), a medicinal plant commonly found in Sabah, Malaysia, as a natural solution for combating *Z. arugamensis* infestations. Solvent extracts of Sword Fern were experimentally tested at various concentrations to evaluate their antiparasitic properties against *Z. arugamensis* and their ability to disinfest hybrid groupers, the leech's primary host. Liquid chromatography quadrupole time-of-flight mass spectrometry (LC-Q-TOF-MS) analysis determined the composition of Sword Fern extract, revealing the presence of metabolites, including terpenoids, flavonoids, phenolics, and aromatic compounds. Remarkably, the methanol extracts of Sword Fern exhibited significant anti-parasitic activity, resulting in 100% mortality of the leeches. The average time required to eradicate the leeches at 100 mg/ml concentrations was less than 5 minutes. Furthermore, hybrid groupers were successfully disinfested in less than 30 minutes at a 10 mg/ml concentration. The findings highlight the potential of Sword Fern as a promising biocontrol agent against *Z. arugamensis* infestations, offering an effective and environmentally friendly approach to address the economic challenges faced by fish farmers in Southeast Asia.

Keywords: Sword Fern, metabolites, marine leech, *Zeylanicobdella arugamensis*, cultured fish

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SO-29

The Efficacy of Fungal-Derived Chitosan Coatings as Antimicrobial Agents: Dual Microbial and Agricultural Approach

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Chitosan is a renewable biopolymer, which has gained increase attention as a potential antimicrobial agent. Alternatively, mushrooms can be utilized as a non-animal source for chitosan production. This study examines the coating of mushroom-derived chitosan in the context of antimicrobial properties by implementing dual microbial and agricultural approach. Chitosan was derived from seven edible mushroom species (*Pleutorotus ostreatus, Hericium erinaceus, Lentinula edodes, Aurcularia auricula-judae, Tremella fuciformis, Ganoderma lucidum* and *Schizophyllum commune*) was compared to commercial chitosan. In microbial approach, the minimum inhibitory concentration (MIC) against Gram-positive and Gram-negative bacteria was tested. The zone of inhibition ranged from 2 to 6 mm for all vegetal chitosan, while the commercial was only at maximum 5 mm and the acetic acid solution at 0 mm. In agricultural approach, the fungal-derived chitosan coatings for cherry tomatoes and okra stored at room and chill temperatures were investigated. All samples had up to 90% total bacteria concentration reduction compared to the control sample (no coating). The vegetal chitosan coatings not only minimize the fungal and bacterial growth, yet also maintain okra and cherry tomato quality after 30 days. Hence, these findings help develop sustainable and environmentally friendly methods for microbial contamination control and fresh produce safety.

Keywords: Chitosan; Mushrooms; Active packaging; Postharvest treatments; Shelf-life extension

Funding Information: GUG0557-1/2022

SO-30

Surface-enhanced Raman Spectroscopic Study of Grouper Mucus: Towards Label-free and Non-Invasive Diagnosis of Fish Health Status in Aquaculture

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Fish epidermal mucus serves as a crucial reservoir of antipathogenic compounds and the first line of the immune defence system. Despite its significant role in the physiology and health of fish, detailed profiling of fish epidermal mucus has yet to be explored, mainly through Surface enhanced Raman Spectroscopy (SERS). Realising the need to develop an effective label-free and non-invasive diagnosis of fish health in aquaculture, this study investigated grouper mucus using SERS in a colloidal system instead of SERS substrates. The gold nanoparticles were first synthesised using the standard citrate reduction method and characterised using UV-visible spectroscopy, Transmission Electron Microscope (TEM), and Dynamic Light Scattering (DLS) analysis. The influence of acidified sodium sulphate (Na2SO4) at pH 3 as the aggregating agent on the enhancement of the SERS spectrum of different analyte samples, including lysozyme solution, rhodamine 6G (R6G) dye, and hybrid grouper (*Epinephelus fuscoguttatus* x *Epinephelus lanceolatus*) mucus, was then evaluated at various concentrations. Based on the results, an optimal Na2SO4 concentration of 1 M was recorded to achieve the highest enhancement of the SERS signal for R6G and grouper mucus, while the optimal concentration for lysozyme was 0.1 M. The results indicate a higher degree of aggregation induced by lysozyme than R6G and grouper mucus. Similarly, an optimal Na2SO4 concentration of 1 M was recorded to achieve the best enhanced SERS signal for the grouper mucus. Still, the signals were inconsistent across all peaks, with only the peaks corresponding to proteins showing the highest enhancement. Remarkably, the few overlapping peaks of the SERS spectra of lysozyme and grouper mucus made it possible to confirm the presence of lysozyme. Overall, the rapid and straightforward SERS protocol proposed in this work offers great potential for rapid and cost-efficient analysis of fish epidermal mucus.

Keywords: Fish epidermal mucus; Surface-enhanced Raman Spectroscopy; Aggregating agent; Lysozyme; Gold nanoparticles; Grouper fish

Funding Information: TRGS-5536101

SO-31

Molecular Simulation of Silica Nanoparticle Transportation via LSI2 Transporter Proteins in Rice Plant, *Oryza sativa*

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Silica nanoparticles (SiNPs) from agricultural waste is considered as beneficial element needed by certain plant.It helps in mediating the biotic and abiotic stress. In rice, *Oryza sativa,* a protein known as LSI2, regulate silica transportation throughout the plant. In this study, computational approach is used to elucidate SiNP interaction with a specific efflux LSI2 transporter proteins via molecular docking and molecular dynamic simulation. FTsite and ClustalX were used to determine the active binding site of the protein. Molecular docking were done using Autodockvina and molecular dynamics simulation of LSI2-$SiOH_4$, complexes was applied using GROMACS version 2021.4 with CHARMM 27 force field. Docking analysis revealed the interaction between $Si(OH)_4$ and several amino acid at active site of LSI2 via hydrogen bond and hydrophobic interaction. Despite having a weak binding affinity, the analysis on molecular dynamic simulation shows good stability of LSI2-$SiOH_4$ interaction. Therefore, it suggested that $Si(OH)_4$ have a transient interaction with LSIs and the flow of $Si(OH)_4$ absorption in rice plants from root to the node I via plasmodesmata is happen at a similar rate. This analysis also can improve the understanding on the effect of SiNPs on rice plant under molecular and atomic level.

Keywords: Binding affinity; *Oryza sativa*; Silica nanoparticles; Silicon transporter protein; Simulation

Funding Information: Long-Term Research Grant Scheme (LRGS) from the Ministry of Higher Education Malaysia for the research program “Development of Climate Ready Rice for Sustaining Food Security in Malaysia” under grant No: LRGS/1/2019/UPM/01/2

SO-32

Bioelectricity Generation using Banana Peel as Substrate in Dual-Chamber *Pseudomonas aeruginosa*-Based Microbial Fuel Cell

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Banana peel (BP) waste are still underutilized in Malaysia, which can be used as source of renewable energy. The CHNS result shows that the C:N ratio of BP is 27:1 which is within the optimum C:N ratio for the microbial food requirement. Microbial fuel cell (MFC) is a device that utilizes biomass to convert chemical energy into electrical energy with help of the microbial catalysis. The present study evaluates the current reading of MFC supplemented with BP waste as substrate for *pseudomonas aeruginosa* ATCC 27853. Fluctuation of current increases as concentration of banana peel extract (BPE) decreases from 1:10, 1:20, 1:40 and 1:80, thus making 1:10 BPE optimum. Current fluctuation is related to microbial activity due to the sufficiency of nutrients which subsequently affect the performance of MFC. BPE and banana peel slurry (BPS) comparison shows that BPS is optimum. BPE reaches a maximum current of 3.91 uA in ascending phase which is higher compared to BPS (3.65 uA). In descending phase, BPE current, drops to 2.31 uA compared to 2.99 uA of BPS. In stationary phase, BPS able the maintain a higher current compared to BPE. MFC maximum current was doubled to 6.52 uA when PEM was treated priorly.

Keywords: Microbial fuel cell, Banana peel, Electricity generation, Current reading, *P. aeruginosa* ATCC 27853

SO-33

In silico Screening and *in vitro* Inhibition Properties of NADI-based Plant Compounds against FKBP35 from *Plasmodium knowlesi*

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The emergence of the zoonotic malaria parasite, *Plasmodium knowlesi* in Malaysia has posed a major threat to public health. Deactivation of FK506-binding protein 35 of *P. knowlesi* (Pk-FKBP35), a member of peptidyl-prolyl cis-trans isomerase (PPIase), is assumed to lead to a lethal effect on the parasite without resistance effect. Nevertheless, the discovery of safe and efficient inhibitors against Pk-FKBP35 remains challenging. Meanwhile, 4000 compounds of Malaysian plants in the Natural Product Discovery database (NADI) might serve as promising antimalarial drug candidates. This study aims to screen the NADI-based plant compounds and investigate their inhibition activity against the Pk-FKBP35. To address this, 4092 compounds were retrieved from the database and docked into a 3D model of the catalytic domain (CD) of Pk-FKBP35 using the EasyDock vina 2.2 platform. The screening resulted in oleanolic acid exhibiting the best docking affinity towards CD of Pk-FKBP35 with a binding energy of -8.8 kcal/mol. The interaction map indicated that oleanolic acid interacts with the vital residues for catalysis of the protein, including Asp55, Ile74, Trp77, Tyr100, Phe117, Cys105, and Ser108. When catalytic PPIase activity of this enzyme was measured in the presence of oleanolic acid, a remarkable reduction in the inhibitory activity was observed, with an IC50 value of 51.45µM± 1.10. This suggested that oleanolic acid is promising to be further developed as an antimalarial drug targeting FKBP35.

Keywords: *Plasmodium knowlesi;* FKBP35; Zoonotic malaria; *In silico* screening; Peptidyl-prolyl cis/trans isomerase

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SO-34

Insights into the Dimerization Dynamics and Regulation of the Main Protease of SARS-CoV-2

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The 3-chymotrypsin-like protease (3CLpro) is a potential target for inhibiting the replication of the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). Interestingly, 3CLpro is known to be catalytically active in its dimeric form, possibly targeting the dimeric interface as a druggable spot. Accordingly, understanding the dimerization properties of this protein may be useful towards the development of a viable drug target. This study, therefore, aims to investigate the oligomerization profile of 3CLpro of SARS-CoV-2 (3CLpro-CoV-2) and identify the important residues for dimerization. The 3CLpro-CoV-2 was first expressed in *Escherichia coli* BL21(DE3) and purified under Ni-NTA chromatography. Oligomerization analysis under size exclusion chromatography revealed that the dimeric state of 3CLpro-CoV-2 is concentration-independent but changes under different pH conditions (pH 5.0 and pH 10.0). This indicates that non-ionic interactions play a key role in its dimerization. Structurally, an alanine-valine zipper was identified at the dimeric interface, possibly providing a strong non-ionic dimerization interaction. Further mutational analysis of this zipper revealed that the mutant tends to form a monomeric structure with much lower activity than its wild type. Accordingly, the zipper is considered a viable target for novel drugs aiming to disrupt dimerization for the deactivation of 3CLpro-CoV-2.

Keywords: SARS-CoV-2; 3CLpro; oligomerization; gel filtration; zipper mutant

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SO-35

Optimization of Sample Processing Strategies for SARS-CoV-2 Quantification in Wastewater using Digital-Droplet Polymerase Chain Reaction (ddPCR)

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Quantification of SARS-CoV-2 in wastewater has gained significant attention. However, there are no standardized sample processing strategies available. An effective sample processing method will increase the recovery of SARS-CoV-2, thus enhancing the sensitivity of subsequent detection. This study aimed to compare two sample processing methods for SARS-CoV-2 quantification in wastewater. Grab and 24-hour composite samples were collected from a hospital's sewage treatment plant treating Covid-19 patients in Klang Valley. All samples were processed using two protocols, P1 and P2. P1 involved direct isolation using Maxwell® RSC-Enviro-TNA kit. While, P2 involved in-house optimization, wherein the samples were subjected to sonication, ultracentrifugation, and Tween-20 treatment before being processed similarly as P1. SARS-CoV-2 N2 and E genes were quantified using digital-droplet PCR. Grab sample concentrations using P1 ranged from 2.07-3.64 copies/µl (N2) and 1.31-1.82 copies/µl (E), compared to 0.38-1.04 copies/µl (N2) and 0.20-0.40 copies/µl (E) with P2. Composite sample concentrations ranged from 3.27-3.40 copies/µl (N2) and 0.87-1.31 copies/µl (E) using P1, compared to 0.73-0.81 copies/µl (N2) and 0.20-0.26 copies/µl (E) with P2. Both protocols were suitable as the sample processing methods to quantify SARS-CoV-2 in wastewater with P1 yielded higher concentration than P2.

Keywords: Wastewater sample processing, SARS-CoV-2, Covid-19, Digital-droplet PCR

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SO-37

One Health Concept: Antimicrobial Resistance in Dairy Farms

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Antibiotic resistance (AR) is a global public health concern. Since animal husbandry plays a major role in contributing to AR, this study embraced the One Health concept in determining the distribution of AR among enterococcal isolates and to identify the genes involved. Eight dairy farms were randomly selected in Selangor State, Malaysia. Samples were collected from workers, milk tanks and environment which includes soil, effluent water and cow dung. Bacterial identification and antimicrobial susceptibility testing were performed via VITEK-2 system. Whole genome sequencing was performed among selected isolates. A total of 89 isolates were recovered from human (n=35), milk (n= 31) and environment (n=23) samples with 32% were multidrug resistance (MDR) which were predominantly from human. Highest resistance among enterococcal isolates were observed towards tetracycline (51%) and quinupristin/dalfopristin (49%). Resistance genes towards nine types of antibiotics from seven selected isolates were encoded. Quinupristin/dalfopristin is among the treatment of choice for vancomycin resistant enterococcal infections. Its resistance will leave clinician with very limited options in treating patients. Therefore, stricter use of antibiotics in animal husbandry should be regulated. More innovative approaches should be explored by the emailities in tackling this issue.

Keywords: Antibiotic Resistance; Enterococcus; Dairy farms; Whole Genome Sequencing

Funding Information: This study was funded by Ministry of Health, Malaysia under P42 00500 117 1004

SO-38

Genomic Analysis of Endophytic *Bacillus altitudinis* VUMS1 Isolated from Sabah's Red Algae, *Kappaphycus alvarezii*

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Sabah's red algae, *Kappaphycus alvarezii* is facing a problem whereby the production of seaweed is declining over the years due to a disease called ice-ice disease caused by *Vibrio* spp. Antimicrobial chemicals are used to overcome this problem but this method is costly and may harm the environment and aquatic organisms. Many studies have reported *Bacillus* sp. as antagonistic microorganisms used as biological agents alternatives to synthetic fungicides to control plant pathogens. *Bacillus altitudinis* VUMS1 is an endophytic bacteria isolated from *Kappaphycus alvarezii* obtained from Semporna, Sabah. Our results showed that VUMS1 has biocontrol potential against *Vibrio* spp. The current study was driven to identify the genes involved in antimicrobial activity. The whole genome sequence showed that the VUMS1 genome size is 3,754,982 bp with 3,854 protein-coding where 2,535 are genes with assigned functions. The analysis revealed the presence of genes that are involved in an antimicrobial and antifungal activity such as fengycin, bacillibactin and bacilysin. The biocontrol potential of VUMS1 was evaluated against *Vibrio parahaemolyticus* and *Vibrio alginolyiticus,* isolated from diseased *K. alvarezii*. Results showed that the growth of *V. alginolyticus and V. parahaemolyticus* treated with VUMS1 decreased by 98% and 72%, respectively on day-5 of treatment. The results of this work indicate that *B. altitudinis* VUMS1 may contribute to the biocontrol activity against *Vibrio* infection in *K. alvarezii*. This is the first report of endophytic *B. altitudinis* from *K. alvarezii* with biocontrol properties. Future studies will determine the potential application of the *B. altitudinis* VUMS1 in biological control and growth promotion for sustainable seaweed farming.

Keywords: *Kappaphycus alvarezii*; *Bacillus altitudinis;* endophytic bacteria; Whole genome sequencing; Genomic analysis; Biocontrol potential

SO-39

Hepatoprotective Activity of *Ficus lepicarpa* (Moraceae) on Carbon Tetrachloride (CCl_4)-Intoxicated Rats

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Ficus lepicarpa B. (Moraceae) is a medicinal plant that is used by the local tribes of Malaysia as a vegetable dish, a tonic, and to treat illnesses such as fever, jaundice and ringworm. The purpose of this study was to look into the possible therapeutic effects of crude methanolic extract *F. lepicarpa* leaf extract against carbon tetrachloride (CCl_4)-induced liver damage in rats. Adult Sprague Dawley rats were given *F. lepicarpa* extract orally once daily for 14 days (100, 200, and 400 mg/kg body weight) before receiving CCl_4 oral therapy (1.0 mL/kg body weight) on the 13th and 14th days. The levels of serum alanine aminotransferase (ALT), aspartate aminotransferase (AST), hepatic antioxidant enzymes, and malondialdehyde (MDA) were measured. Immunohistochemistry was used to detect oxidative stress indicators (4-hydroxynonenal [HNE] and 8-hydroxydeoxyguanosine [8-OHdG]) as well as proinflammatory markers (tumour necrosis factor-α [TNF-α], interleukin-6 [IL-6], and prostaglandin E2 [PGE_2]). Biochemical, histological and immunohistochemical findings were in agreement to support the hepatoprotective effect of *F. lepicarpa* against CCl_4-mediated oxidative hepatic damage. The presence of phenolic antioxidants and their ability to scavenge free radicals may be responsible for its hepatoprotective properties.

Keywords: *F. lepicarpa*; carbon tetrachloride; antioxidant enzymes, immunohistochemistry

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SO-40

Innovations in Albumin-Based Drug Delivery Systems

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Presence at the target site at a sufficient concentration and for an adequate duration of time are the two main determinants for effective pharmacological action of a drug. To fulfill these criteria, various strategies of drug delivery have been developed to address different challenges regarding drug pharmacokinetics, each offering distinct advantages albeit with certain drawbacks. In recent years, several albumin-based drug delivery systems have been developed to exploit the advantageous properties of albumin related to its natural function as a drug carrier. Primarily, these include the availability of multiple drug binding sites, a remarkably long in vivo half-life in plasma, and its intrinsic ability to recognize a multitude of cellular receptor which facilitate the uptake of drugs. Currently available albumin-based drug delivery systems can be generally categorized according to their mode of drug incorporation such as non-covalent as-sociation, covalent conjugation, albumin fusions, and albumin nanosystems. These systems have demonstrated favorable results in both preclinical and clinical settings with significant improvements over conventional methods of drug delivery and possess great potential for development as the delivery platform of choice for future therapeutics.

Keywords: Serum albumin, Drug delivery, Pharmacokinetics

Funding Information: FRGS/1/2019/STG04/UKM/02/6

SO-41

Can Sewage be a Lens to Uncover Early, SARS-Cov-2 Variant Circulation?

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Surveillance is an important epidemiological tool in management of COVID-19 outbreak and its variants. Clinical testing to infer lineage prevalence is challenging at scale, especially in locations with limited resources, participation, or testing/sequencing capacity, which can also induce biases. This study aimed to demonstrates wastewater surveillance (WS) as an efficient tool both for SARS-CoV-2 detection and early warning for its variant circulation by using 2 sampling strategies. Samples were collected from hospital in the Klang Valley in January 2023. To increase the possibility of detection and quantification (N1 and N2) of SARS-CoV-2 RNA digital polymerase chain reaction (dPCR), was used. We implemented a nanopore RNA sequencing monitoring system for variant detection.The virus was found in all influent wastewater samples, with varying concentrations in grab (N1:2.56– 18.81 copy/µl, and N2: 0.53–15.78 copy/µl) and 24-hour composite (N1:8.40– 13.16 copy/µl, and N2:4.53–4.70 copy/µl) samples. The study identified Omicron-descendent sublineage XBB.1.5, XBB1.3 and XBB1.15 variant which were not yet reported by clinical genomic surveillance at the time of detection. This work demonstrates how WS may support clinical surveillance by offering a practical alternative for both SARS-CoV-2 detection and circulation of new emerging variants in a community, enabling more proactive public health responses.

Keywords: Wastewater; SARS-CoV-2 RNA; COVID-19; Surveillance; Variant

Funding Information: This work was funded by the Malaysian Ministry of Health with the grant number 22-023.

SO-42

Targeted Mutagenesis of *cyp1a* Gene Alters Pollutant Catabolism in Javanese Medaka, *Oryzias javanicus*

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Marine pollution caused by persistent organic pollutants (POPs) attracts global attention due to its harmful effects on living organisms and the environment. This study proposes a monitoring system for POPs using Javanese medaka, *Oryzias javanicus*; and demonstrates the successful application of a genome editing technique through the knockout of *cytochrome P450 family 1A* (*cyp1a*), a gene controlling organic pollutant metabolism. The aims are (1) to reveal the response of *O. javanicus* on polyaromatic hydrocarbons (PAHs) and (2) to determine the *cyp1a* gene function in pollutant metabolism. Firstly, an acute toxicity test on the wild-type fish was performed and detected an increment in mortality rate and *cyp1a* mRNA expression induction in a concentration-dependent manner. Subsequently, a knockout attempt by CRISPR/Cas 9 system generated a strain with a four-base deletion on the *cyp1a* gene. For the screening of knockout mutations, two novel methods were developed, (1) construction of specific primer sets and (2) environmental DNA (eDNA) extraction technique. Pollutant exposure on the two strains revealed the *cyp1a* role in controlling the modes of toxicity. Finally, RNA sequencing (RNA-seq) and transcriptomic analysis are in progress to compare the changes in their gene expression profile.

Keywords: environmental DNA; gene knock-out; marine pollution; PAHs; transcriptome

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SO-43

Optimization of Enzymatic Saccharification of WATERMELON (*Citrullus lanatus*) Rind by R Analysis

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Watermelon waste was chosen as the primary material due to its abundant discarded rinds, which make up a significant portion of the waste, and its widespread consumption in Malaysia. The cellulose, hemicellulose, and pectin present in watermelon rinds, which are lignocellulosic materials, were subjected to hydrolysis. This process involved the utilization of cellulase and auxiliary enzymes to convert polysaccharides into monosaccharides (simple sugars), resulting in the production of valuable end products. Therefore, in this study, R software was used to optimize the saccharification yield from enzymatic hydrolysis of watermelon rind. Four parameters were investigated, including substrate loading (1-5 g), enzyme loading (5-85 U/mg), temperature (35-55 °C), and hydrolysis time (6-30 hours). The preliminary screening results indicated that all parameters had a significant effect on saccharification yield. A mathematical model was developed using Response Surface Methodology (RSM) to predict the optimal conditions of enzymatic hydrolysis. The model demonstrated a strong correlation between actual and predicted values, with a predicted R^2 value of 0.9635%. The optimization conditions determined for substrate loading, enzyme loading, temperature, and hydrolysis time were 1.15 g, 24.85 U/mg, 44.79 °C, and 11.47 hours, respectively. Under these conditions, the actual saccharification yield of watermelon rind was measured at 70.72%.

Keywords: Saccharification; Enzymatic Analysis; Watermelon rinds; Optimization; Response Surface Methodology

Funding Information: FRGS/1/2022/STG02/USM/02/6 (Fundamentals research grant scheme (FRGS))

SO-44

Digital PCR- An Emerging Technology with Broad Applications in Biotechnology

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Digital polymerase chain reaction (dPCR) remains a “hot topic” in the last two decades due to its potential applications in many scientific fields including biotechnology, cell biology and medical diagnostics. The driving innovation behind the dPCR is through the random distribution of nucleic acid molecules into many partitions using the microfluidic chips, channels, or droplets. The generated droplets were then going through similar workflow including thermal cycling and imaging like any other PCR methods. Each partition serves as an individual PCR reaction, delivering remarkable sensitivity and quantification of target nucleic acids. Furthermore, the proportion of PCR-positive partitions suffices to determine the concentration of the target sequence without a need for calibration. Although Real-Time PCR (qPCR) has become the gold standard technique to measure target molecules but the resulting data can be often highly variable and non-reproducible. Digital PCR is able to overcome the limitations of qPCR by providing superior accuracy precision and confidence, which enables applications that require robust multiplexing, absolute quantification, rare disease detection and etc. Here we highlight the importance, technical principles, and potential opportunity of dPCR. We also review the current progress and advancements of dPCR that had implementing in the biotechnology fields.

Keywords: Digital PCR; Absolute Quantification; Partitioning; Multiplexing

SO-45

The Protective Effect of THICAPA on APP Processing Pathway in Familial Alzheimer's Disease Patient-Derived Fibroblast Cell Line

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Familial Alzheimer's disease (FAD) is hereditary and developed at an unusually early age. The toxic amyloid-beta (Aβ) deposition is one of the hallmarks of FAD. The prevalence of FAD is alarming and there are no drugs available to cure this neurological disorder. THICAPA, a novel compound belongs to the Tetrahydroisoquinoline group of amines. These amines are naturally found in the brain and foods which exert wide medicinal properties including anti-inflammatory properties, and affine ligands for CNS receptors. In this study, we have shown THICAPA modulated amyloid precursor protein (APP) processing pathway in FAD patient-derived fibroblast cell line (AG06840). Cytotoxicity assay revealed a non-significant effect of THICAPA towards AG06840 and healthy fibroblast (GM05879) cell lines. The reactive oxidative species (ROS) assay has shown a half-fold reduction in the THICAPA-treated AG06840 cell line. Besides, APP processing pathway secreted proteins quantifications using sandwich ELISA shows a significant reduction of Aβ40, Aβ42, sAPPα, sAPPβ and CTFβ in the amyloidogenic pathway. Meanwhile, a slight increase in sAPPα secretion was observed in the non-amyloidogenic pathway. These findings indicate THICAPA could ameliorate the production of ROS and toxic Aβ species in AD pathogenesis. Together, our data reveal that THICAPA possesses the potential to further develop as a targeted therapy for AD.

Keywords: Alzheimer's disease; Amyloid beta; APP pathway; Fibroblast; THICAPA

Funding Information: TRGS/1/2020/USM/02/3/3

SO-46

Development of GnRHa-EVAc Delivery System for Induced Spawning in Catfish sp.

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Catfish species is a well-known aquaculture product that has a high demand, especially in Asia. However, they have few dysfunctions in their reproductive system; failure in the final oocyte maturation (FOM) and low quality of sperms. Gonadotropin-releasing hormone agonists (GnRHa) have been used to stimulate the release of pituitary luteinizing hormone, required to induce maturation. In this study, we developed a sustained-release delivery systems of GnRHa through ethylene-vinyl acetate copolymer, EVAc, which slowly releases the GnRHa within 2-5 weeks. The products, 2 mm in diameter and 6 mm in length, each containing 100 µg GnRHa with 2.5 mg domperidone, were stored at -30 °C until use. Previously, the GnRH-EVAc implant has been effectively in inducing FOM, ovulation, and spawning in female of more than 40 cultured species. Meanwhile in male, the impant has been tested in more than 20 species, producing significant increases in milt production for up to 5 weeks. Future research should focus on the optimization of GnRH-EVAc implant to determine the optimum doses, stability and productivity. This will enhance the efficiency and efficacy of the implant to improve the reproduction of cultured catfish sp. for sustainable aquaculture production.

Keywords: EVAc; Catfish; Delivery system; GnRH; Molecular characterization

Funding Information: FRGS/1/2020/WAB04/UPM/02/6

SO-47

Macrophage Function in Close Contacts of Drug-Resistant Tuberculosis: Phagocytosis and Oxygen Burst Assay

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The immune response approach in the host of M. tuberculosis is one of the choices for treating tuberculosis, especially in drug-resistant cases. Therefore, research is needed to determine the function of macrophages in individuals diagnosed with drug-resistant TB compared to close contact cases diagnosed with latent TB or proven healthy. This study aimed to examine the function of macrophages in these groups. PMBC was isolated and then cultured, and the phagocytosis was determined when at least one SRBC was attached to the macrophage membrane. The macrophages' ability to oxidize foreign bodies was measured using the WST-1 Assay Kit, and a myeloperoxidase assay was performed using H_2O_2 as a substrate. This study enrolled six drug-resistant tuberculosis patients and 18 close contact individuals (8 LTBI; 10 healthy) at Universitas Indonesia Hospital. We found that phagocytosis activities were higher in the LTBI group than healthy and drug-resistant tuberculosis group ($p<0,001$), and the WST-1 assay in a drug-resistant group lower than in other groups ($p<0,001$). These variables had strong positive correlations ($r=0,64$, $p<0,005$). Myeloperoxidase activities in the drug-resistant tuberculosis group were higher than others ($p=0,017$). Differences in macrophage function in close contact groups are expected to provide baseline data for future treatment and prevention.

Keywords: drug-resistant tuberculosis; latent tuberculosis; macrophages; phagocytosis; oxygen burst

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SO-48

Genetic Comparison of ESBL *Escherichia coli* Isolated in Dairy Farms

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Extended-Spectrum Beta-Lactamases (ESBL) *Escherichia coli (E. coli)* is a growing concern globally, and addressing its presence in farms is crucial due to potential farm-to-fork transmission. Thus, a preliminary investigation was conducted to determine the antimicrobial resistance level and genetic profile of *E. coli* isolates in dairy farms. Thirteen *E. coli* isolates obtained from eight dairy farms, from humans, milk, and cow dung were subjected to next-generation sequencing based on resistance patterns. SPAdes and Prokka were used to assemble and annotate the raw read. PubMLST and Resfinder were used to determine the sequence types and resistance genes respectively. According to the resistance pattern analysis, 15.4% of *E. coli* was multidrug resistant, with ampicillin being the most resistant at 38.5% followed by cefuroxime, cefotaxime, and ceftriaxone, each at 15.4%. This isolated sequence type was mostly ST 58, with 23% having novel ST. ESBL were found in 38.5% of the isolates that carried the *bla*$_{\text{CTX-M}}$, *bla*$_{\text{TEM}}$, and *bla*$_{\text{OXA}}$ genes. Presence of ESBL *E. coli* genes were evident from this study. Monitoring antimicrobial resistance patterns in dairy farms is an important way to combat the misuse of antibiotics and aid related bodies in tackling the spread from source to consumer.

Keywords: Antibiotic Resistance; Escherichia Coli; Next generation sequencing; Extended-Spectrum Beta-Lactamases (ESBL)

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SO-49

Identification and characterisation of antibacterial aptamers against *Pseudomonas aeruginosa*

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Antibiotic resistance is a global health crisis, resulting in an increasing number of people suffering from severe illnesses and dying due to infections that were once easily curable with antibiotics. *Pseudomonas aeruginosa* is a major pathogen that has rapidly developed antibiotic resistance. Interestingly recent reports suggest that DNA aptamers may act as potential candidates for novel antimicrobial agents. In this study, we demonstrated that an existing aptamer can affect the growth of *P. aeruginosa*. A computational screen for aptamers that could bind to a well-conserved and essential outer membrane protein, BamA, in Gram-negative bacteria was conducted. Molecular docking of about 100 functional DNA aptamers with BamA protein was performed via both local and global docking approaches. Genetic algorithm analysis was also carried out to rank the aptamers based on their binding affinity. The top hits of aptamers with good binding to BamA protein were synthesised to investigate their in vitro antibacterial activity. Among all aptamers, Apt31, known to bind to an antitumor, Daunomycin, exhibited the highest HADDOCK score and resulted in a significant ($p < 0.05$) reduction in *P. aeruginosa* growth. Apt31 also induced membrane disruption that resulted in DNA leakage.

Keywords: Aptamers, *Pseudomonas aeruginosa*, Machine Learning, Antimicrobial

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SO-50

Coral Disease Prevalence in Kota Kinabalu Coastal Waters: The Potential of Causative Microbial Agents

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The Indo-Pacific coral populations are under increasing threats from bleaching events and coral disease outbreaks. However, there is a significant lack of data and information on coral disease research conducted in Malaysian waters, despite the reefs being exposed to various human activities. In light of this, this study aims to determine the prevalence of coral disease and signs of compromised health at 27 reef sites in the Kota Kinabalu coastal waters. Coral surveys were conducted using the Coral Video Transect (CVT) method, and prevalence was measured with the Coral Point Count with Excel Extension (CPCe) software. The findings indicated that the majority of surveyed reefs were healthy (82.9% ± 1.8) compared to diseased (5.0% ± 0.6) and compromised (12.1% ± 1.5) coral colonies. Reef sites with the highest exposure towards human activities exhibited a high prevalence of coral diseases (e.g., skeletal eroding band, ulcerative white spot and white syndromes) and signs of compromised health (e.g., sediment necrosis, skeletal damage and algae overgrowth). Preliminary examination using 16S rRNA gene sequencing revealed six *Vibrio* spp. (*V. coralliilyticus*, *V. hepatarius*, *V. brasiliensis*, *V. tubiashi*, *V. campbellii* and *V. ishigakensis*) on infected corals, with *V. coralliilyticus* had the highest prevalence and potentially causing the occurrence of coral diseases.

Keywords: Coral Disease; Coral Compromised Health; CVT Method; *Vibrio* spp.; Tunku Abdul Rahman Park.

Funding Information: Fundamental Research Grant Scheme (FRGS/1/2022/WAB05/UMS/02/4; FRG0574–1/2022) – Ministry of Higher Education Malaysia.

SO-51

Molecular Characterisation of Gonadotropin-Releasing Hormone (GnRH) Genes in Tropical Catfishes; *Pangasius nasutus*, *Pangasianodon hypophthalmus* and *Hemibagrus nemurus*

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Pangasius nasutus (patin buah), *Pangasianodon hypophthalmus* (striped catfish), and *Hemibagrus nemurus* (river catfish) are among the most popular tropical catfish species due to their sweet taste and nutritional values. *Pangasius nasutus*, a slow-growing fish whose supply still depends on wild-caught fish, the population is diminishing in natural streams, as shown by a decline in the number of yearly specimens landed from 2002 to 2021. *Pangasianodon hypophthalmus* is having issues with late maturation and time-consuming production, which requires a minimum of three years for broodstock to produce eggs in captivity, while *H. nemurus* has been constrained by the failure of female broodstock to complete final oocyte maturation, and synchronising broodstock maturity in captivity has limited its production. Therefore, study of gonadotropin-releasing hormone (GnRH) is essential to understanding its molecular properties in the hormonal regulation of gonadal development and gametogenesis in catfish. This study involved identifying the GnRH isoforms that are present in catfish, cloning and characterising a complete open reading frame (ORF) of GnRH genes, comparing sequence alignments, and analysing a phylogenetic tree to gain a better understanding of the GnRH genes in catfishes. The findings of this study can be used as a baseline for developing recombinant GnRH that enables a better reproductive strategy in catfish species to increase their production in the aquaculture industry.

Keywords: Gonadotropin-releasing hormone; *Pangasius nasutus*; *Pangasianodon hypophthalmus*; *Hemibagrus nemurus*; phylogenetic tree

Funding information: LRGS/1/2019/UPM/01/1

SO-52

In vitro anti-SARS-CoV-2 Activities of Xanthones and *Garcinia mangostana* Extracts

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The high prevalence of COVID-19 with non-specific treatment and challenges associated with vaccine development and its side effects continue to pose threat to the economy and society of affected populations. Xanthones the main constituents in *Garcinia mangostana* have been reported to have anti-SARS-CoV-2 efficacies in silico with the scarcity of data in vitro. For the present study, the efficacy of xanthones and *G. mangostana* extracts against SARS-CoV-2 were tested in vitro. Methanol and acetone extracts of *G. mangostana* pericarp and xanthones were tested against SARS-CoV-2 using cytopathic effect (CPE) inhibition assay. The cytotoxic effects of the tested extracts and compounds were evaluated via MTT assay. Our findings revealed that xanthones (α-mangostin; EC_{50} 3.29 µM, SI:3.96, 3-isomangostin ; EC_{50} 8.30 µM, SI:2.43) and extracts (Methanol extract; EC_{50} 6.97 µg/mL, SI: 2.78, acetone extract; EC_{50} 3.46 µg/mL, SI: 4.11) demonstrated inhibitory activity against SARS-CoV-2 at concentrations that tolerance to cell viability. These findings are evidence of the anti-SARS-CoV-2 potential of *xanthones and G. mangostana extracts* as tested in vitro. Results obtained provide the basis for further study on the target molecules and mechanism of action.

Keywords: *Xanthones*; *G. mangostana*; SARS-CoV-2; CPE reduction assay

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SO-54

Determining an Optimal DNA Extraction Method and Detecting Pathogenic Leptospira in Rodent Fecal Samples from Kota Kinabalu, Sabah

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Rodents are notorious as natural reservoirs for several zoonotic pathogens including leptospira, a causative agent for leptospirosis. Despite being an endemic disease in Sabah yet the current epidemiological data in Kota Kinabalu is lacking. It is crucial to determine optimal DNA extraction method by assessing bacterial diversity in the samples to enhance accuracy and reliability of the outcomes prior to downstream analysis. This study aimed to determine an optimal DNA extraction method for rodent fecal sample and conducting biosurveillance for pathogenic leptospira. A total of 202 fecal droppings were collected from the Kota Kinabalu District, and the species of rodents were determined through COI gene amplification. Five of the fecal samples were subjected to determination of optimal DNA extraction method by evaluating six extraction methods: QIAamp PowerFecal Pro DNA Kit (PF), QIAamp AllPrep PowerViral DNA/RNA Kit (AP), QIAamp UCP Pathogen Kit (UCP), ZymoBIOMICS DNA Miniprep Kit (ZY), and two conventional methods using different lysis buffer containing 4M guanidium thiocyanate (GTC) and 1% CTAB, respectively. Among the evaluated methods, the QIAamp PowerFecal Pro DNA kit (PF) yielded better quality of DNA and more diverse bacterial community. All fecal samples were then extracted using the PF method, and the DNA extracts were amplified by targeting lipL32 gene. Leptospira was detected in 47 (23.3%) of the samples, with molecular typing revealing that nine samples belonged to *L. interrogans*. This study highlights the importance of optimizing DNA extraction method for the sample and sheds light on the prevalence of leptospira in the rodent population in Kota Kinabalu.

Keywords: DNA extraction, biosurveillance, zoonotic, leptospira, rodents

SO-55

Dual RNA Sequencing as a Method to Elucidate the Differences in *Shigella sonnei* and *Shigella flexneri* during Infection of *Caenorhabditis elegans*

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In recent decades, *Shigella sonnei* has replaced *Shigella flexneri* as the predominant cause of shigellosis in developed countries. Unfortunately, the cause of the global expansion of *S. sonnei* is not well investigated. To elucidate the possible mechanisms, *S. sonnei* and *S. flexneri* transcriptomics were analysed for their responses during host infection. The *Caenorhabditis elegans in vivo* model was used because its intestinal cells share similar morphology with human intestinal epithelial cells. The transcriptomics of both bacteria and host were analysed through dual RNA sequencing at different time points of infection. Results showed that during *C. elegans* infection, *S. sonnei* significantly upregulates translation, ATP synthesis, protein synthesis and pyruvate metabolisms as early as one-day post-infection compared to *S. flexneri.* Additionally, after 72 hours, *S. sonnei* significantly upregulates genes involved in the electron transport chain, iron intake and glycerol metabolism, which are linked to virulence in other bacteria. Interestingly, the innate immune system genes in *C. elegans* are downregulated after 72 hours of *S. sonnei* infection, which is not seen in *S. flexneri* infection. These differences may explain the recent overtake of *S. flexneri* by *S. sonnei* as the predominant cause of shigellosis.

Keywords: *Shigella*; Dual RNA sequencing; Transcriptomics; Host-pathogen model

Funding information: FRGS/1/2020/STG03/MUSM/03/1; MUM HIRSF 2022 (STG000174)

SO-56

Alpha(α)-mangostin Promotes Diabetic Wound Healing: An *in vitro* Study with Mechanistic Elucidation

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Poor wound healing is a serious complication of diabetes mellitus, culminating in chronic, non-healing diabetic foot ulcer (DFU). Current treatments for DFU are costly. Alpha (α)-mangostin, one of the most active xanthones in the mangosteen pericarp, has been reported to promote wound healing. However, its effectiveness in expediting diabetic wound healing is unknown. The aim of this study was to investigate the effect of alpha-mangostin on cell migration and growth factor expressions in a diabetic wound healing model. Human coronary artery endothelial cells (HCAEC) and human dermal fibroblast (HDF) cells were incubated with 35 mM glucose solution for 72 hours. Alpha-mangostin of different concentrations (0.15, 2.5, and 5 µg/ml) and carboxymethyl cellulose (positive control) were then introduced to the incubation plates, negative controls were incubated with (i) glucose solution and (ii) unstimulated control (culture medium alone). A scratch assay was performed and the rate of cell migration was calculated. Growth factors released by the cells (PDGF, TGF-β, FGF, CTGF, VEGF, IL-6, TIMP & MMP-9) were measured using the ELISA method. Alpha-mangostin at 0.15 ug/ml showed the fastest rate of endothelial and fibroblast cell migration at 6, 12, 18, 24, and 48 hours compared to negative controls ($p= p<0.0001$, and $p<0.001$,). Alpha-mangostin treatment led to increased PDGF, TGF-β, FGF, TIMP, and reduced MMP-9 levels compared to glucose controls. The findings indicate that in an *in vitro* diabetic wound healing model, Alpha-mangostin stimulates endothelial and fibroblast cell migration, increased the release of growth factors, and lowered the MMP-9 secretion. This study suggested that alpha-mangostin is potentially useful for the treatment of DFU.

Keywords: Alpha(α)-mangostin; diabetic wound healing; endothelial cells; fibroblast cells; wound healing assay; protein expression assay

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SO-57

Revisit *Apis* (Honey bees) Phylogeny with Two Molecular Markers

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The phylogeny of honey bees (genus *Apis*) has been the subject of scientific debate and controversy over the decades. It is generally accepted that *Apis* consists of at least ten recognised species. Advancements in molecular techniques, particularly the analysis of DNA markers such as mitochondrial DNA (mtDNA) and nuclear DNA, have provided valuable insights into the evolutionary relationship of honey bees. In this study, two mtDNA regions - cytochrome c oxidase subunit 1 (CO1) and 16S ribosomal RNA (16S rRNA) were PCR amplified and sequenced for five different morphologically determined honey bee species (*A. mellifera, A. cerana, A. dorsata, A. florea,* and *A. andreniformis*) collected throughout Peninsular Malaysia. The DNA sequences were used to infer phylogenetic relationships within *Apis.* The phylogenetic analyses for partial 16S rRNA sequences strongly supported the basic topology of *Apis* grouping into three major clusters : dwarf bees (*A. florea* and *A. andreniformis*), giant bees (*A. dorsata*), and cavity-nesting bees (*A. mellifera* and *A. cerana*). However, the placements of giant bees and cavity-nesting bees showed differences in topology derived from partial CO1 sequences, especially *A. mellifera* clustered separately from *A. cerana* and *A. dorsata*. The phylogeny of *Apis* inferred from the mitochondrial genome sequences retrieved from NCBI GenBank is also consistent with the basic topology. These results suggest that studying the evolutionary relationship within the genus *Apis* using CO1 marker does not resolve the apparent relationships between the species despite being the most widely used molecular marker in the field of insect phylogenetics.

Keywords: Honey bees; *Apis*, phylogeny; cytochrome c oxidase 1, 16S ribosomal RNA; molecular markers.

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SO-58

Extraction and Characterisation of Collagen from Tomato Jellyfish (*Crambione mastigophora*)

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Jellyfish are known to occur in large aggregations and blooms in the ocean, posing a problem to multiple sectors of human activity such as tourism and fisheries. However, these jellyfish may prove to be a valuable source of marine collagen, which has yet to be utilized commercially. In this study, collagen was extracted from the umbrella, oral arms and the whole body of tomato jellyfish (*Crambione mastigophora*) using the ultrasound-assisted acid solubilised collagen method and characterized using FTIR. The proximate composition obtained from three parts of jellyfish, denoted as, BELL, ORL and WHL, were compared. The ultrasound-assisted acid solubilised collagen method afforded a higher yield of collagen than that of the conventional acid extraction method. The isolated collagens had almost the same amino acid composition, while their functional groups presence was Amide A, B, I, II, and III. These results were in accordance with commercial collagen, suggesting that the use of jellyfish-derived collagen would be congruent with those already available in the commercial market. Further tests such as colour analysis using UV absorption and scanning electron microscope imaging of lyophilized jellyfish collagen will be performed to determine the viability of jellyfish-derived collagen. Nevertheless, these preliminary results show promise in the successful utilisation of jellyfish-derived collagen for commercial purposes in the future.

Keywords: Marine collagen, Jellyfish, Extraction process, Extraction yield, Proximate analysis, Physicochemical properties

SO-59

Biodegradation of Oil Palm Empty Fruit Bunches by Laccase from *Pycnoporus sanguineus* and Its Structural Changes

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Biodegradation of lignocellulosic contents from oil palm empty fruit bunch (OPEFB) fibres adapt effective pre-treatments to ensure successful bioconversion. Biological pre-treatments display distinct advantages such as low energy and capital cost, minimal dependence on chemicals, mild conditions, less harmful inhibitors or by-products formation and high substrate specificity. This work investigated performance of local isolate *Pycnoporus sanguineus* for OPEFB biodegradation process via solid-state fermentation. This research employed not only physico-chemical analysis, but also emphasized on physical element on OPEFB fibres structures. Optimization of physical parameters such as temperature, inducer concentrations and substrate loading was studied to obtain highest laccase production by *P.sanguineus*. Results showed that maximum laccase production (xx) was obtained using extractive-free OPEFB, fermentation at 30 °C, substrate loading of 10% and 4 mM of 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) as inducer. Fourier transform infrared (FTIR) spectra, thermogravimetric analysis (TGA) and scanning electron microscope (SEM) micrographs showed prominent chemical and surface structural changes of untreated OPEFB, NaOH treated, benzene treated as well as laccase treated OPEFB. X-ray microtomography (µ-CT) analysis unveiled damages on the OPEFB structures, indicating delignification process as evident from the volume reduction after biodegradation process. These observations were supported by tensile testing data, laccase and total phenolic content.

Keywords: Laccase; oil palm empty fruit bunches (OPEFB); Biodegradation; Delignification; Microtomography

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SO-60

Study of MTT ASSAY and Flow Cytometry in the Evaluation of Cytotoxicity of *Uncaria gambir* on HepG2 Cells

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Indonesia is the largest producer of gambir sap (*Uncaria gambir* (Roxb) Hunter) in the world. Gambir plant has been widely used as a traditional medicine for various diseases, including cancer. In this study, the cytotoxic effect of the ethanol extract of *Uncaria gambir* (EG) on the Hep G2 cell line was assessed by MTT assay (3-(4,5-dimethylthiazol -2-yl) -2,5-diphenyltetrazolium bromide) and by flow cytometry using 7-amino actinomycin D (7-AAD). Ethanol extract of gambir was added to the HepG2 cell cultures with various concentrations (500; 1000; and 2000 µg/mL) and incubated for 48 hours. The concentration that inhibited 50% viability compared to the control (IC50) calculated by the MTT test was 1098.39 µg/mL. Staining of cell viability using flow cytometry with 7-AAD as marker, confirmed an increase in HepG2 cell death at a concentration of EG 500; 1000; and 2000 µg/mL compared to control. The MTT cytotoxicity assay and the 7-AAD cell viability staining technique both demonstrated increased cell death associated with EG concentration in HepG2 cells. Taken together, these results suggest that 7-AAD cell viability staining is in line with the conventional MTT assay in evaluating the cytotoxicity of EG on HepG2 cell line.

Keywords: MTT assay; flow cytometry; cytotoxicity; *Uncaria gambir*; HepG2 cells

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SO-61

Study on Two Different Types of Photobioreactor for Cultivation of *Chlorella vulgaris*

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The cultivation of *Chlorella vulgaris* using two different five litre photobioreactor vessel were investigated. The process study involving difference pH, light intensity, and carbon dioxide (CO_2) concentration were conducted to evaluate the performance of each reactor. The performance of aerated vessel (tubular shape) versus fabricated vessel (oval shape) were analysed resulted in 21.05% of lipid concentration produced in aerated vessel and 20.14% lipid concentration fabricated vessel at optimum conditions. It was found the aerated vessel work best in pH 10.5, 5% CO_2 and 1000 lux light intensity, while fabricated vessel optimum conditions are pH 10.5, 15% CO_2 and using white light emitting diode (LED) system. In conclusion, both systems gave a good performance and can be considered for further study using other types of microalgae.

Keywords: *Chlorella vulgaris*, cultivation, photobioreactor, lipid

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SO-62

Multi-epitope HER2/neu-derived Immunogen Encapsulated in Cancer Cell Membrane-Coated Nanoparticles as an Effective Vaccine against Breast Cancer

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Breast cancer is the most common cancer diagnosed and causes significant mortalitiy among women worldwide. The HER2/neu oncogene, which is abnormally overexpressed in breast cancer cells is the prime target of many current breast cancer vaccination strategies. Recently, the role of B cells in fostering anti-tumor responses has been appreciated on top of the well-established T-cell immunity. Thus, in this work, we have developed a multi-epitope peptide-based immunogen comprising both cytotoxic T lymphocytes (GP2) and B cell (P4) peptide epitopes derived from HER2/neu oncoprotein, which was further conjugated to a carrier protein (KLH) as a source of T helper epitopes, named as KLH-GP2-P4. The KLH-GP2-P4 was further encapsulated into a liposomal nanoparticle camouflaged with cancer cell membrane (LPCCM-[KLH-GP2-P4]) to enhance its immunogenicity potency. Nanoparticles coated with cancer cell membrane represent a biomimetic approach as it will endow the natural entity displayed on its surface, such as tumor-specific antigens (TSAs). Our immunogenicity evaluation revealed that LPCCM-[KLH-GP2-P4] induced greater uptake by antigen presenting cells, higher HER2/neu-specific IgG antibody titers and elevation of cytokines secretion (skewed towards Th1 responses) compared to other vaccine constructs. Additionally, sera from mice immunized with LPCCM-[KLH-GP2-P4] exhibited potent cytotoxic activity against the tested cancer cells. Remarkably, LPCCM-[KLH-GP2-P4] elicited superior antitumour efficacy in comparison to other groups as characterized by the delayed tumour growth and the survival rate of mice against HER2/neu-positive tumor (TUBO cells) challenge in both prophylactic and therapeutic settings. Furthermore, the formulated vaccines were found to be safe in mice as characterized by body weight changes, histopathological examination of the major organs, serum biochemical analysis and abnormal toxicity monitoring. Collectively, our novel vaccine formulation represents a breakthrough in the development of an effective breast cancer vaccine strategies and merits further investigation for clinical translation.

Keywords: vaccination, tumor cell membrane, HER2/neu, breast cancer

SO-63

Micropropagation of the medicinal plant *Kaempferia parviflora* using Thin Cell Layer

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The lack of available and suitable source materials is one of the limiting factors in the micropropagation of *Kaempferia parviflora*. This study aimed to evaluate the potential of using Thin Cell Layers (TCL) as the explants for shoot induction and regeneration of the species. This study was performed using aerial shoots of *K. parviflora* as explants. The aerial shoot segments of 4-5 mm length were cultured on MS medium containing various concentrations of 6-benzylaminopurine (BAP), kinetin, thidiazuron, α-Naphthaleneacetic acid and 2,4-dichlorophenoxyacetic acid. The response of the explants to shoot induction and regeneration was observed weekly and recorded for eight weeks. The data were subjected to analysis of variance (ANOVA) and the means were compared using Duncan's Multiple Range Test (DMRT) at a significant value of $p<0.05$. Among the treatments, the highest percentage (44.4%±19.2) of explant produced shoots was obtained on MS media with 1mg/L BAP. Well-developed shoots were rooted on MSO and the regenerated plantlets were successfully established in the soil. This study showed that TCL can effectively be used as the source materials for micropropagation of *K. parviflora.*

Keywords: *Kaempferia parviflora*, Micropropagation, Thin Cell Layer, Aerial Shoot

SO-64

Deep Mutational Scanning and Energy Decomposition Analysis onto Modified-Heated MD-Screened Molecular Docking of CXCR2 and HY29-1 Improves Antibody-Antigen Binding

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Hundreds of antibody-based drug as targeted therapy has been approved for various diseases including cancer, autoimmune and infectious diseases. However, development of antibody as therapy requires a fine-tuning between enhancing the intended target specificities without trading the antibody-antigen binding affinity. Computer-aided simulation allowed simulation interacting biomolecules and prediction of affinity-enhancement mutagenesis without the hassle and resource-consuming laborious laboratory experimentation. Here, we reported the works entailed the enhancement of antibody-antigen binding by the means of deep mutational scanning and energy decomposition analysis. Anti-CXCR2 antibody, HY29-1, was designed with high affinity towards CXCR2 receptor and our modified-heated MD analysis has identified the best docked complex between CXCR2 and HY29-1 antibody. Long MD simulation (1 µs) analysis revealed interacting residues within variable-heavy & light chains and epitope-paratope detailing with intermolecular forces. Each of the interacting residues were exhaustively assessed and submitted for deep mutational scanning. Several key interacting residues were identified, ranked, and mutated. Mutant antibodies were clustered and rescored using long MD simulation. Mutants, HY2908-m01 and HY2908-m02 showed improvement in binding affinity based on Molecular mechanics with generalised Born and surface area solvation (MM/GBSA) estimation (between -97 and -77 kcal/mol compared to -50 kcal/mol parent antibody). Further experiments will be done in a laboratory setting to validate the computational data.

Keywords: Deep Mutational Scanning, Energy Decomposition, Modified-Heated MD, Antibody-Antigen binding, MMGBSA, Binding Affinity, CXCR2

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SO-65

Effects of Polyphenolic-Rich Fraction of Cornsilk (*Stigma maydis*) in Streptozotocin-Induced Type 2 Diabetic Rats

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Diabetes Mellitus (DM) is characterised by hyperglycemia resulting from defects in insulin secretion, insulin action or both. High blood glucose can lead to many complications such as heart disease, nerve damage, stroke and kidney disease. Current available drugs such as metformin is clinically approved to lower blood sugar have some side effects such as diarrhea, vomiting and lactic acidosis. There is growing evidence about the effectiveness of using herbal supplements in preventing and controlling DM. The aim of this study is to assess polyphenolic-rich fraction (PRF) of cornsilk in reducing fasting blood glucose level in type 2 diabetes (T2DM) induced SD rats. The induction of diabetes was carried out using high-fat diet (HFD) for 7 weeks followed by injection of 35 mg/kg of STZ. PRF of corn silk extracts showed significant reduction in fasting blood glucose level compared to the diabetic induced rats at 200mg/kg. Besides that, PRF was able to improve the histological changes in the liver, kidney, and pancreas of STZ-induced diabetic rats compared to control. In conclusion, PRF of corn silk can act as anti-hyperglycaemic agent in T2DM. Further research should focus on the mechanism and long term impact of PRF in T2DM.
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Keywords: Diabetes type 2; Corn silk; hyperglycemia

Funding Information: FRGS/6171252

SO-66

Omics Studies of *Nepenthes* Pitcher Plants to Elucidate Botanical Carnivory for Translational Applications

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Insectivorous plants are Darwin's most wonderful plants that have fascinated botanists and researchers for centuries. Tropical Nepenthes pitcher plants constitute one of the most species-rich families, especially in the Malay Archipelago. Recent advancements in omics technologies of sequencing and mass spectrometry have accelerated the field of functional genomics in botanical carnivory. Fundamental molecular understandings are crucial for bioprospecting, industrial applications, and crop improvement. Our group applied multi-omics approaches, encompassing transcriptomics, proteomics, and metabolomics aided by bioinformatics analysis for molecular profiling towards a holistic understanding of pitcher molecular physiology. Such an integrated approach on three local *Nepenthes* species allowed us to uncover the effects of plant hybridisation on the molecular expression in the pitcher tissues and fluids. We also studied the dynamic changes of pitcher fluid compositions during early pitcher opening. Functional analysis of neprosin, a novel protease with post-proline cleavage activity is currently ongoing. Through *in silico* structure-function analysis, we discovered that neprosin belongs to a new glutamic peptidase family. This talk will cover these three topics from our findings in the past decade, leading towards the potential industrial applications.

Keywords: Carnivorous plant; Metabolomics; Nepenthes; Proteomics; Transcriptomics; Systems Biology

Funding Information: FRGS/1/2019/STG05/UKM/02/10

SO-67

Cytotoxicity and Apoptosis Induced by Unfermented Freeze-Dried Leaf Extract of Tongkat Ali (*Eurycoma Longifolia* Jack.) in MCF-7 Human Breast Cancer Cell Line

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This study was conducted to determine the cytotoxicity effect of *Eurycoma longifolia* (Jack.) leaf extracts and its possible anticancer mechanism of action against MCF-7 breast cancer cell line. The leaves of *E. longifolia* were processed into unfermented and fermented batches before being dried using freeze and microwave-oven drying techniques. Crude lyophilized extract of hot water infusions was prepared and screened for their cytotoxicity effect using MTT assay against MCF-7 cell line. Apoptosis analysis and the expression of apoptotic protein were conducted using flow cytometry technique, whereas caspases and cytochrome c activities were measured using an ELISA reader. The results determined that the unfermented freeze-dried leaf extract was the most toxic towards MCF-7 cells in a dose-dependent manner, with an IC50 value of 45.0 ± 3.5 µg/ml. The number of apoptotic cells in treated MCF-7 cells occurred in a time-dependent manner for 24, 48 and 72 h, primarily attributed by the induction of G2/M cell cycle arrest. There was an activation of caspase-8 and cytochrome c, with decreases of Bcl-2 and increases of p53 and Bax activities throughout the treatment periods. These findings suggest that this extract may induce two apoptosis pathways, i.e., caspase-8-initiated pathway and/or mitochondrial-initiated caspase-9-mediated pathway.

Keywords: Cytotoxicity; mechanism; MCF-7; *Eurycoma longifolia*; hot water infusion

SO-68

Potential miRNA Regulation and Roles of Curcumin and Tualang honey in a Breast Cancer Animal Model

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Tualang honey and curcumin are known for their rich phenolic contents and anti-cancer properties, particularly in breast cancer. This study explored the potential effects of Tualang honey and curcumin combination in mammary tumorigenesis and miRNA regulation in the 1-methyl-1-nitrosourea (MNU) rat model. The study found no significant differences between the untreated (PC) and curcumin-Tualang honey (CURTH) groups in tumour incidence, multiplicity, latency, size, weight, and grade. The small-RNA sequencing results listed miR-135b-5p, miR-547-3p, miR-509-5p, miR-3585-5p, and miR-547-5p as the top significantly upregulated miRNAs, while miR-137-3p, miR-325-3p, miR-1-5p, miR-709, and miR-741-3p were the significantly downregulated. The target gene prediction via miRTarBase identified Tpm1, Zeb1, Cdkn1b, Cdkn1c, and Cyp2a3 as the top five miRNA-regulated genes. Using Panther pathway analysis for differentially expressed miRNA in the CURTH group, the five most significantly regulated pathways were p53, PI3 kinase, p53 feedback loops 2, and interleukin signaling, while genes involved in the cell cycle were among highly ranked in the Reactome Pathway analysis. In summary, Tualang honey and curcumin were shown to regulate miRNAs in rat breast cancer, even though it was not significantly observed phenotypically.

Keywords: Curcumin; Tualang honey; Breast cancer; MNU; Animal model

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SO-69

In Vitro Pre-Clinical Efficacy Establishment of Multi – Targeting Small Molecules to Combat Breast Cancer

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Breast cancer has been recorded as the highest mortality rate worldwide which 90% causes are due to metastasis. The evolution of anticancer resistance successfully defeated the effectiveness of current cancer treatments and can cause a series of new complications post – treatment. In this research, a novel dual anticancer compound (code name: PC5, PC6) were tested on normal cell (Human Umbilical Vein Endothelial Cells) and a representatives of cancer cell lines (human breast cancer, MDA-MB-231). MDA-MB-231 cell line were used as cancer inducer in C57BL/6 female mice through in vivo study. In vitro results showed that the IC50 of PC5 and PC6 were 0.29 ± 0.09 and 0.87 ± 0.04 on HUVEC and 3.34 ± 0.06 and 2.79 ± 0.04 on MDA-MB-231 respectively. PC6 showed a significant anti-migratory effect when compared to the control. The number of metastatic foci in lung histology shows a reduction in PC6 group compared to the cancer-induced group albeit no significant differences. We postulated that the duration of treatment is too short for the PC6 compound to show effective results. The potential of PC6 compound should be studied further in term of duration of treatment before a conclusive deduction is made.

Keywords: Cancer; Metastasis; small – molecule; in vitro; in vivo

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SO-70

Elucidation of The Mechanisms of 15,16-dihydrotanshinone I (DHTS) As An Anti-proliferative Agent for Autosomal Dominant Polycystic Kidney Disease (ADPKD)

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Autosomal dominant polycystic kidney disease (ADPKD) is a hereditary kidney disorder which leads to cystic expansion of the kidney. The limitations and side effects of current treatment call for the need of better treatment option for ADPKD. Dihydrotanshinone I (DHTS) has been shown to inhibit cancer cell proliferation, which is also the hallmark for ADPKD. Hence, this study aims to repurpose DHTS for ADPKD treatment. Cytotoxic assay showed that DHTS could induce time- and concentration-dependent viability reduction of WT 9-12 (ADPKD) cells across the 72-hour treatment with various DHTS concentrations. Additionally, real time cell analyzer (RTCA) demonstrated that 32µM DHTS was able to achieve IC50 in WT 9-12 cells after 24 hours of treatment. In the cell cycle analysis, 32µM DHTS induced G1 phase arrest in WT 9-12 cells at 24 hours. All analyses did not show significant effects of DHTS treatment on HK2 (normal renal tubule) cells. Preliminary iTRAQ results revealed a myriad of proteins differentially expressed in WT 9-12 cells compared to HK2 cells, and protein with expression changes after DHTS treatment of WT 9-12 cells. The functions of these differentially expressed proteins may explain the underlying mechanisms of DHTS as an anti-proliferative agent for ADPKD, serving as a promising alternative treatment for ADPKD.

Keywords: ADPKD; DHTS; cytotoxicity; proliferation; cell cycle.

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SO-71

Effects of Drying Methods on the Physicochemical Properties of Bioactive Compounds Derived from *Plecranthus amboinicus* and its Derivatives

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Plecranthus amboinicus has a long history in therapeutic uses, such as antimicrobial, antifungal and anti-inflammatory properties for treating a variety of upper respiratory tract ailments such as asthma, flu and pharyngitis. This study investigates the physicochemical properties of the secondary metabolites derived from *Plecranthus amboinicus* (locally known as Lemuju) and the optimal drying technique for preservation. Drying methods play a crucial role in traditional herbal medicine, as they influence the quality and healthcare benefits of herb-derived compounds. Various dehydration techniques were employed to retain the herb's essential compounds. The research focused on thymol, a bioactive compound present in *Plecranthus amboinicus*, comparing its total phenolic content and antioxidant activities in both crude water extract and hard lozenge forms; particularly to evaluate its moisture content, pH, hardness, and dissolution rate to assess the lozenges' overall quality, shelf stability, and consumer acceptance. Understanding the best preservation techniques and the impact on compound stability, future herbal medicine production can be optimized. The findings from this study can be used as a basis for the development of a herbal lozenge as a remedy for upper respiratory tract ailments and be used as a guiding platform for the development of other herbal remedies from local biodiversity.

Keywords: *Plecranthus amboinicus;* herbs; medicinal plants; lemuju; preservation

Funding Information: Development Funding, 12th Malaysia Plan, Economic Planning Unit, Ministry of Economy

SO-72

Effect of Different Pre-Treatment Methods on Dewatered Sludge Prior Usage in Membrane-Less Microbial Fuel Cell for simultaneous bioremediation and Energy Recovery

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Microbial Fuel Cell (MFC) technology is gaining popularity among researchers all over the world as one of the most creative energy generation alternatives. Membrane-Less MFC (ML-MFC) is a form of MFC technology configuration that has broad application in simultaneous waste bioremediation, and energy generation. The substrate used in the study was dewatered sludge and was being treated with several types of pretreatments prior used in the ML-MFC system. The different pre-treatment methods were i) thermal treatment (60, 80, 100, 120 and 140 ℃), ii) alkaline treatment (pH 8, 9, 10, 11 and 12), iii) ultrasonication treatment (10, 20, 30, 40 and 50 kHz) and were assessed it effect in term of electrogenic bacteria (EB) growth , sludge degradation rate, COD removal and power density generation. The ML-MFC system was setup with the electrode distance (3 cm), moisture content (45 %), and incubation temperature (35 ℃), incubation time (7 days), inoculum size (10 %). The experiment was optimized using the one-factor-at-a-time (OFAT) approach. The best performance of ML-MFC for generation of power density (11.27 mW/m^2), degradation rate of DS (89.48 %) and biomass (1.92 mg/L) under optimum treatment conditions of 100 ℃ (thermal treatment), pH 10 (alkaline treatment) and 30 kHz (ultrasonication treatment) has been obtained from this study.

Keywords: Membrane-less Microbial Fuel Cell; Dewatered Sludge; Biomass Conversion; Voltage; Renewable Energy

SO-73

Unravelling Multifaceted Mechanisms of Azole Antifungal Resistance in *Fusarium keratoplasticum*

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Fusaria are significant fungal pathogens causing diseases in humans (fusariosis), animals, and important crops. *Fusarium keratoplasticum*, the predominant species causing fusariosis, is resistant to most azole antifungals, which limits its treatment options. Understanding these resistance mechanisms is, therefore, critical for the development of more effective treatment options for this life-threatening disease. This study investigated the azole resistance mechanisms of *F. keratoplasticum* by studying its transcriptional response to voriconazole, and by expressing and characterizing the azole drug target orthologs, *cyp51A, cyp51B, cyp51C*, and the ABC transporter *abc1*, in *Saccharomyces cerevisiae*. Key ergosterol biosynthesis genes, most notably *erg6A* (912-fold), *cyp51A* (52-fold), and *ebp1* (20-fold) were induced upon voriconazole exposure. The dramatic upregulation of *erg6A* and *cyp51A* and the human Δ8,Δ7-sterol isomerase ortholog, *ebp1*, suggested the induction of an alternative salvage pathway upon azole inhibition of the main ergosterol biosynthesis pathway. Overexpression of *cyp51A, cyp51B* and *cyp51C* in *S. cerevisiae* did not alter the host's azole susceptibilities. Overexpression of the voriconazole-induced *abc1* (5-fold), however, conferred resistance to azoles and other xenobiotics. These findings provide important new insights into the azole resistance mechanisms of *F. keratoplasticum*. They will aid in developing more effective interventions to combat these devastating infectious diseases of plants and humans.

Keywords: efflux pump; ABC transporter; Abc1; Cyp51; Erg6; azole resistance

Funding Information: FRGS/1/2018/SKK11/UKM/02/1

SO-74

In vitro and *in silico* modelling of sterol and norlanostane derivatives isolated from the *Ganoderma boninense*

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There are few studies that link between a phytopathogenic fungus *Ganoderma boninense* and antibacterials. We previously found antibacterial activities of the sterol and norlanostane derivatives isolated from *G. boninense* mycelia. However, biophysical evidence for antibacterial mechanisms of both compounds is lacking. Herein, we demonstrate that *in vitro* and *in silico* modeling experiments using these metabolites are performed. The minimum inhibitory concentration of both compounds suggested significant antibacterial activities against Gram-positive/Gram-negative bacteria at 30 and 50 µg/mL, respectively. *In vitro* antibacterial activities of both compounds were active against bacterial cells through metabolic cessation, as evidenced by a reduction in the ATP luminescence activity by down to <1%. Antibacterial effects through cell wall/membrane disruption were solely observed in Gram-negative bacteria. These mechanisms implied that the action is exerted internally rather than through the disruption of the bacterial coat. Molecular docking prediction elucidated that these compounds exhibited their antibacterial mechanisms of actions through the inhibition of TopoIV by the initiation of interaction at the amino acid residues SER-79, PRO-112, ALA-115, and MET-116. This study is the first to demonstrate two isolated antibacterial compounds from *G. boninense*, providing evidence that show great potential for their use as antibacterial agents in the treatment of bacterial infections.

Keywords: antibacterial activity; ergosterol; ganoboninketal; *Ganoderma boninense*; minimum inhibitory concentration; molecular docking

Funding Information: FRGS0384-SG-2/2014

SO-75

Potential of UMS Hatchery Wastewater as Substrate for the Growth Characteristics of Purple Non-sulfur Bacterium *Afifella marina* strain ME.

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Fish rearing tank generate waste both organic and inorganic, the sources are primarily from uneaten food and fish feces and rich in nutrients. Phototrophic bacterium *Afifella marina* strain ME as isolated from shaded and exposed microhabitats of a mangrove ecosystem in Kota Kinabalu, Sabah, Malaysia. The pure bacterium was grown in finfish rearing wastewater. The aim of this study to monitor the growth characteristics in term of dry cell weight (g/L) and total carotenoids (mg/g dry cell weight) production in bacterium *Afifella marina* strain ME. The wastewater was characterized and observed nitrogen (mg/L) and phosphorus (mg/L) are the major nutrients in waste components of the fish hatchery, which are capable to support the growth characteristics of *Afifella marina*. The bacterium grew well in undiluted, non-sterilized wastewater. The highest dry cell weight of 3.20±0.18 (g/L) with the production of 1.001± 0.123 (mg/g dry cell weight) were determined with 40% of inoculum levels (v/v) from 120-h culture. On the other hand, production of dry cell weight and total carotenoids were observed lower with the 30% and 50% inoculum levels. Although no significant differences were observed while compared dry cell weight and total carotenoids production among 40% and 50% of inoculum levels. Bacterium *Afifella marina* strain ME is capable to grow in finfish rearing wastewater but depend on inoculum level.

Keywords: *Afifella marina*, growth, finfish wastewater, inoculum levels

SO-77

Performance Evaluation of Edible Seaweed Bioplastics Produced Through Green Processing Technology

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In recent years, there has been a significant increase in public awareness of environmental protection and the use of bioplastics. Seaweed offers various advantages over other feedstocks, making it a suitable biomaterial for bioplastics. However, present production involves intricate procedures, uses a lot of energy and chemicals, and generates a lot of trash. A potential option is the environmentally friendly synthesis of seaweed bioplastics with minimal waste creation and no extra chemical use; nevertheless, this area is still immature and further research is required. Therefore, the aim of the study is to examine the physical and nutritional properties of seaweed bioplastics created using green technology. This study also discusses its decomposition performance in air and soil in comparison with commercial petroleum-based and oxo-biodegradable plastics from the market. The findings of this study suggested that properties of seaweed bioplastics produced by green technology are highly relevant and suited for edible food packaging application such as seasoning sachet, tea and coffee sachet, tablet capsule, food wrap and many more. Its properties could be adjusted to its functionality by adding appropriate compounds. Moving forward, the greenness and simplicity of the technology could be further explored in order to assess its economic feasibility and practicality for a bigger-scale production.

Keywords: Seaweed; Edible bioplastics; Green technology; Degradable

Funding Information: NIBM/SF/2022-4

SO-78

Morphological and Molecular Identification of *Pyricularia oryzae* Causing Blast Disease on Rice (*Oryza sativa*)

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Rice (*Oryza sativa*) is one of Malaysia's most significant crops, with a high demand in Malaysian cuisine. Rice blast, caused by the fungus *Pyricularia oryzae*, is one of the most serious rice diseases, causing enormous damage to the Malaysian rice population. This study was conducted to isolate and characterize fungal isolates associated with rice blast collected in a paddy field in Alor Setar, Kedah. A total of seven fungal isolates were isolated and morphologically identified as *Pyricularia* sp. Morphological characterization of all isolates showed thin grayish green mycelia and the reverse colony was light brown. The fungal isolates produced two-septate pyriform (pear-shaped) conidia with solitary, unbranched, and light brown conidiophores. All isolates showed similar morphological characteristics, thus a representative isolate was further identified through DNA sequencing and phylogenetic analysis of the internal transcribed spacer (ITS) region for species confirmation. Based on DNA sequences of ITS and phylogenetic analysis, the representative isolate was confirmed as *P. oryzae*. Pathogenicity tests of all isolates on rice leaves revealed diamond-shaped symptoms with a grayish center and brown edge.

Keywords: *Oryza sativa*; *Pyricularia oryzae;* Morphological and molecular identification; Phylogenetic analysis

SO-79

Grain Corn Silage: Physico-chemical Analysis and Amplicon Metagenomic Analysis in Tropical Region

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Physico-chemical analysis and bacterial communities in grain corn silage were studied in a tropical region. The effects of three treatments (deionized water, *Lactobacillus fermentum*, *Lactobacillus buchneri*) on silage quality and bacterial communities were assessed. Silage samples were analysed for dry matter, pH, water-soluble carbohydrates, lactic acid, acetic acid, propionic acid, and butyric acid concentrations. Genomic DNA was extracted, and 16S rRNA gene sequencing was performed. Bioinformatics analyses were conducted to examine bacterial community composition and diversity. Results showed that after 21 days of ensiling, dry matter was not significantly affected by the treatments. However, pH and water-soluble carbohydrates were significantly reduced in all treatment groups. Lactic acid concentrations were higher in the *Lactobacillus fermentum* treatment compared to the control. Propionic acid concentrations were generally low in all treatments. Bacterial community analysis revealed an increase in *Lactobacillus sp*. population after ensiling. Indices of bacterial diversity also increased. Beta diversity analysis indicated significant changes in bacterial community composition. The results suggest that bacterial additives can improve silage quality in tropical regions by influencing pH, water-soluble carbohydrates, lactic acid, and the presence of certain organic acids. Implementing bacterial additives in silage production practices can enhance efficiency and overall silage quality.

Keyword: Amplicon metagenomics; Bacterial additive; Silage quality; Tropical region.

Funding Information: FRGS/1/2018/STG05/MOSTI/02/1

SO-80

Anti-Cancer Effects of *Clinacanthus nutans* and *Annona muricata* on the Initial Invasion of Breast Carcinoma

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Globally, the cause of cancer-related deaths is mainly by metastases rather than the primary tumour growth. Recent advances in the available treatment of breast cancer had caused significant adverse effects and cancer recurrence thus, the need of alternative effective treatment The aim of this study is to determine the anti-cancer effects of *Clinacanthus nutans* (CN) and *Annona muricata* (AM) aqueous extracts using in vitro anti-proliferative and anti-migratory assay. Methylene blue and trypan blue exclusion assays were used to study the anti-proliferative effect, meanwhile scratch wound migration assays with MCF-7 and MDA-MB-231 were used to study the anti-migratory effect. Cell morphological changes were observed in control and treated group with different concentration of plant extract. Aqueous CN extract showed poor antiproliferative effect with IC50 >200µg/ml for MCF-7 cells and 31.15µg/ml towards MDA-MB-231 cells. Aqueous AM extract showed the IC50 of 13.05µg/ml for MCF-7 cells and 39.00µg/ml towards MDA-MB-231 cells. However, both extracts showed no significant changes in the scratch wound migration assay. In conclusion, both extracts showed promising anti-proliferative effect especially towards the triple negative breast cancer cell. Further study should be carried out to determine the anti-proliferative affects both extracts before a conclusive interpretation could be made.

Keywords: Breast cancer; *Clinacanthus nutans* (CN); *Annona muricata* (AM); metastasis; natural product

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SO-81

Effect of *Plukenetia volubilis L.* (Sacha Inchi) Oil on Hypercholesterolemia Diet-Induced Sprague Dawley Rat

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Plukenetia volubilis L. or Sacha Inchi has gotten a lot of interest in recent years because of its unique nutritional composition, resulting in the introduction of differently marketed products based on Sacha Inchi. This study is conducted to investigate the effects of Sacha Inchi oil on diet-induced hypercholesterolemia in Sprague Dawley rat models. After 4 weeks of the induction phase and 4 weeks of treatment, blood samples were collected from each rat for analysis. Upon euthanasia, the liver, kidney, aorta, lung, and brain were processed and stained with haematoxylin and eosin (H&E) for histopathological examination. Treatment with Sacha Inchi shows a positive effect on hypercholesterolemia diet-induced SD rats. The level of TC, non-HDL, and LDL shows significant decrease in all treatment groups compared to the normal and hypercholesterolemia groups. No significant changes can be observed in the liver and renal function tests compared to the normal group. Histology of the liver in the hypercholesterolemia group under H&E staining shows mild degenerative changes. Atherogenic and coronary risk index shows a significant reduction in the treatment group compared to the hypercholesterolemia group. Results show that Sacha Inchi can act as anti-hypercholesterolaemic agent while having protective effect on the liver and renal function.

Keywords: Sacha Inchi, hypercholesterol, LDL.

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SO-83

Structural Variants and Obesity in Asia - A review

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Obesity has a been public health concern globally affecting countries economically and health. It could lead to further health complications contributing to chronic diseases including cancers and type 2 diabetes. Numerous strategies have been implemented to fight obesity including studying obesity aetiology and genetics association. Recent advances in Genome Wide Association Studies (GWAS) and fine mapping reveal novel findings of susceptible loci for obesity risks. Structural variations on chromosomes 11q11, 1p21.1, 10q11.22, 10q26.3, 16q12.2, 16p12.3, and 4q25 prove to have connections with obesity risks. However, studies conducted are commonly focused on European populations which proves to be insufficient to reveal obesity's missing heritability. Studies in non-European population are still limited and needed to provide extra insights on genetics and obesity association. Our review aims to summarize the current connections between structural variants and obesity aetiology in Asian cohort. We proposed the possible mechanism of putative variants affecting weight gain, hormonal changes, and appetite preferences. Thus, not only contributing to a better understanding of obesity aetiology, but ethnic specific obesity loci could also be identified developing a better approach of personalized medicine.

Keyword: Obesity, Structural Variant, BMI, Asians

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SO-84

Optimization Strategy of Oleoresin Rendement for zero-Waste Ginger Product by Microwave-Assisted Extraction with Response Surface Method

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Ginger residue is one of the waste products of essential oil distillation that has not been used optimally. Ginger residues still contain Bioactive compounds which can be used as by-products with added-value such as oleoresins. The study aimed to find optimal conditions for the solvent ratio, extraction power level, and extraction time to obtain optimum yield of ginger residue oleoresin by using response surface method. The oleoresin extraction was carried out in several stages using microwave assisted extraction with 96% ethanol and n-hexane as polar and non-polar solvent. The total oleoresin yield was analyzed by using response surface model for second order function, namely Box-Behnken Design (BBD) type. The optimum yield of 5,65% oleoresin was successfully obtained in the optimum for n-hexane solvent were the ratio of solid-solvent 1:10, power level of 40%, and an exraction time of 2 minutes. Whereas, it can be scaled-up upto 4 times from the control sample with the optimum yield of 9,45% oleoresin was successfully obtained in the optimum for ethanol solvent were a ratio of 1:8, power level of 50% and extraction time 4 minutes. The high probability oleoresin rendement was obtained by microwave-assisted extraction with response surface method was promising for zero-waste ginger product.

Keywords: oleoresin; ginger residue; microwave-assisted extraction; *response surface method;* zero-waste.

SO-85

Coconut Water Vinegar Ameliorates Recovery of Acetaminophen Induced Liver Damage in Mice

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Vinegar has long been used in food preparation and traditional Chinese medicine for its multiple health benefits. The present study investigates the potential of coconut water vinegar in promoting recovery on acetaminophen induced liver damage. Mice were injected with 250 mg/kg body weight acetaminophen for 7 days to induced liver inflammation and were treated with distilled water (untreated), Silybin (positive control) and coconut water vinegar (0.08 mL/kg and 2 mL/kg body weight) for the subsequent 14 days. Level of oxidation stress and inflammation among treated and untreated mice were compared. The untreated group exhibited significant increment of serum liver profiles, morphological changes in liver, higher level of cytochrome P450 2E1, lower level of liver antioxidant and increased level of inflammatory related markers indicating the occurrence of liver inflammation. On the other hand, acetaminophen challenged mice treated with 14 days of coconut water vinegar were recorded with reduction of serum liver profiles, improved liver histology, restored liver antioxidant, reduction of liver inflammation and decreased level of liver cytochrome P450 2E1 in dosage dependent level. The findings suggest that coconut water vinegar can help mitigate liver damage caused by acetaminophen by restoring antioxidant activity and suppressing inflammation.

Keywords: Coconut water vinegar; liver inflammation; acetaminophen; *in vivo*

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SO-86

Kinetic Growth Model for *Bacillus subtilis* in Dual Chamber Microbial Fuel Cell (MFC) with Sulfonated Polysulfone as Proton Exchange Membrane (PEM)

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The study presents the generation of electricity in a microbial fuel cell (MFC) utilizing a sulfonated polysulfone (SPSf) membrane. The SPSf membrane was synthesized using dimethylacetamide (DMAC) as a solvent and the non-solvent-induced phase separation process. The objective of incorporating the SPSf membrane was to improve proton ion transport efficiency, as evaluated through ion exchange capacity (IEC) testing. Dewatered sludge containing a mixed culture of electrogenic bacteria (EB) served as the fuel source in the ML-MFC. Scanning electron microscope (SEM) observations confirmed the formation of a biofilm at the anode surface of the ML-MFC. Phylogenetic analysis identified the presence of *Bacillus subtilis* within the biofilm, indicating their active role in facilitating electron transfer processes. The EB acted as a biocatalyst, enhancing the degradation of chemical oxygen demand (COD) and the overall performance of the ML-MFC. The performance of MFC could be seen on day 5th under resistor of 470 ohm which contributed to a current density and power density of 0.81 mW/m^2 and 11.635 mA/m^2, respectively. To model the growth of EB, unstructured kinetic models, namely the Logistic model, were proposed and validated. Statistical analysis revealed that the logistic models exhibited high R^2 values (>0.89) and low root-mean-square error (RMSE) values (0.03), indicating their suitability for describing EB growth in the MFC. The logistic model was identified as the most suitable for describing EB growth in the ML-MFC based on the experimental data. These findings contribute to the advancement of microbial fuel cell technology and its potential application in sustainable energy generation.

Keywords: Microbial fuel cells, dewatered sludge, bioremediation, proton exchange membrane, sulfonated polysulfone

SO-87

Purification, Preliminary Crystallization and Modelling of Novel 4-Hydroxyphenylacetate-3-Monooxygenase from Extreme Thermophilic *Geobacillus mahadii* Geo-05 for Structural Studies

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4-hydroxyphenylaceteate-3-monooxygenase (GMHpaB) enzyme catalyzes the hydroxylation of 4-hydroxyphenylacetate (4HPA) to 3,4-dihydroxyphenylacetate (3,4-DHPA) in the first phase of 4HPA degradation pathway. Analysis of GMHpaB amino acid sequence and its conserved domains were carried out using Expasy and InterproScan servers, respectively. Homology model of GMHpaB was generated using SWISS MODEL which has 38% sequence identity as the template. Gene encoding for GMHpaB from extreme thermophile, *Geobacillus mahadii* Geo-05 was cloned and expressed in *E. coli* BL21(DE3). The protein was purified to homogeneity in three steps purification; (i) Immobilized Metal Affinity Chromatography, (ii) Ion Exchange Chromatography, and (iii) Gel Filtration Chromatography Subsequently, the purified enzyme was crystallized under two different temperatures. Sequence analysis revealed that the enzyme possessed a low sequence similarity of 38% with other reported equivalent enzymes, which points to its novelty in terms of functional and structural characterization. GMHpaC is an enzyme consisting of 492 amino acids with a predicted molecular mass of 56kDa. Purified GMHpaB produced protein crystals in a variety of forms under few crystallization conditions. Model analysis demonstrated that GMHpaB is a homotetramer, with each monomer consisting of three domains. The middle domain, which is a beta barrel domain, is folded with the N and C-terminal domains to create a groove for substrate binding sites. The Ramachandran Plot showed that the GMHpaB model generated using SWISS MODEL was structurally accurate with 90% of the residues belonging in the most favoured regions. In conclusion, the experimental results may contribute to future experimental structural studies of GMHpaB, in parallel with *in silico* analysis that can offer helpful insights in enzyme-substrate interactions.

Keywords: HpaB, Monooxygenase, Purification, Crystallization, Modelling *G. mahadii* Geo-05

SO-88

Coriander (*Coriandrum sativum L.*) Seeds Extract Alleviates Brain Oxidative Stress in Obese Rats

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Obesity causes prolonged oxidative stress in various organs. The brain is among the most susceptible organs to oxidative stress, a condition linked to various neurodegenerative and neurophysiologic disorders. Natural agents with antioxidant activities are extensively studied as therapeutic modalities for obesity and its various adverse effects. This study explored the effect of coriander seeds ethanolic extract/CSSE on brain oxidative stress of obese rats. Rats were given high fat diet for 12 weeks to induce obesity and then given 100 mg/kg body weight/day of CSSE for 12 weeks. Malondialdehyde/MDA was measured as an oxidant marker, glutathione/GSH and catalase specific activity were measured as endogenous antioxidant markers. MDA levels were significantly lower ($p<0.001$) in the obese group given CSSE (0.213nmol/mg tissue) than the obese control group (0.250nmol/mg tissue). A significant increase in GSH concentration ($p<0.05$) was also found in the obese group given CSSE (0.758µg/mg protein) than the obese group (0.539µg/mg protein). There was no significant change in specific activity of catalase among the groups. In conclusion, 100 mg/kg body weight of CSSE intake for 12 weeks could significantly alleviate oxidative stress in the rat brain. Thus, CSSE acts as a potential natural agent for reducing obesity's adverse effects on the brain.

Keywords: Obesity; High-fat diet; Brain; Oxidative stress, *Coriandrum sativum* L.

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SO-89

Molecular Interaction Analysis of Anti-IL8 scFv-10F8-6His against IL8 Monomer through Molecular Docking and Molecular Dynamic Simulation

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High levels of IL-8 expression are associated with poor prognosis in various type of inflammatory diseases, including rheumatoid arthritis, psoriasis, and cancer. Targeting IL-8 signalling by antibodies emerged as a potential therapeutic strategy for these diseases. The human monoclonal antibody (HuMab) 10F8 and the hybridoma 35B11-B bind to an epitope on human IL-8, respectively. 10F8 inhibited the interaction between IL-8 and neutrophil in eczema and pustulosis palmoplantaris patient while 35B11-B decreased size lesion in rat model. The binding interaction of monoclonal antibodies and IL-8, especially how CDR loops could bind the N-terminal of IL-8, has not been fully deliberated from the molecular-level. Here we used a combination of molecular docking, heated and long coarse-grained molecular dynamics simulations to identify the key residues of established interaction. Based on heated MD simulation, the pose of complexes generated by ClusPro showed good stability of binding throughout of 70 ns simulation. Based on long molecular dynamic simulations, a couple of key residues for the binding were identified throughout of 1000 ns simulation. TYR-53, ASP-99, and ARG-100 of heavy chain CDR together with TYR-33 of light chain CDR contributed mostly to the binding interaction. Meanwhile, TYR13 and LYS15 of IL-8 were important for the better values of MMGBSA. Furthermore, the results of decomposition residues analysis in good agreement with the interaction analysis data. This study provided a reference list of residues that important between antibody and IL-8 and will provide guidance for future development and design of new and more stable recombinant antibody against IL-8.

Keywords: IL-8; antibody against IL-8; Heated Molecular Dynamic (MD) Simulation; Long simulation; MMBGSA

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SO-90

Effectiveness of Direct Sulfonated Polysulfone in Dual Chamber Microbial Fuel Cells Based Dewatered Sludge for Power Generation

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In this era of bioprocess technology, microbial fuel cells (MFCs) are one of the key players of innovative technology that has the ability to recover renewable energy by spontaneously treating the wastewater; therefore, they can be viewed as sustainable dual-utility devices. The MFC basically involves electrogenic bacteria (EB) act as biocatalysts in degrading the carbon constituents in dewatered sludge and converting the chemical energy into electrical energy. This bioremediation will lead to the movement of protons generally hydrogen ion from anode electrode to the cathode electrode in which the protons emitted by the EB. An MFC often comprises a polymeric proton exchange membrane (PEM) as an employed electrolyte. The study began with synthesized of sulfonated polysulfone (SPSf) from polysulfone (PSf) via direct sulfonation with concentrated sulphuric acid as a sulfonating agent. SPSf blend proton exchange membranes (PEMs) acted as novel alternative membrane were created using three different solvents such as N-methyl pyrrolidone (NMP), dimethylacetamide (DMAC), dimethylformamide (DMF) by utilising the non-solvent induced phase separation process. The purpose of PEMs improved the efficiency of membrane to transport the protons ions which can be identified through ion exchange capacity (IEC) testing The IEC for SPSf/NMP, SPSf/DMAc and SPSf/DMF were 1.8 meq/g, 1.47 meg/g and 1.33 meq/g respectively. The incorporation of sulfonation groups to PSf enhanced its conductivity significantly due to the existence of additional protonated sites (SO_3H) and water-mediated routes for proton conduction. FTIR spectroscopy, contact angle, water uptake, and IEC were used to characterise the synthesised PEMs. The maximum generated voltage 0.544V at a power density of 0.1911mW/m^2 for the constructed membranes, while pure PSf yielded 0.170 V at a power density of 0.06 mW/m^2 under similar experimental conditions. The observed good IEC, high power production (0.9 mW), and high COD removal (85%) features showed that the SPSf membrane has the potential to significantly boost the productivity of dual chamber MFCs.

Keywords: Microbial fuel cells, dewatered sludge, bioremediation, proton exchange membrane, sulfonated polysulfone

SO-91

Effect of Anode Acclimation Method on Biofilm Formation and Electrogenic Bacterial Population in Membrane-less Microbial Fuel Cell for Simultaneous Bioremediation and Energy Recovery

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The growing demand for sustainable waste treatment and renewable energy sources has led to the exploration of innovative technologies such as microbial fuel cells. Biofilm formation plays a crucial role in the performance of a membrane-less microbial fuel cell (ML-MFC) as it facilitates efficient electron transfer from the bacteria to the electrode. Biofilm serves as a conductive matrix, allowing the electrogenic bacteria (EB) to establish direct contact with the electrode surface as revealed by scanning electron microscopy (SEM) analysis. Through direct contact, electrons generated by microbial metabolism can be transferred, improving the MFC's overall electrical performance. The impact of anode acclimation method to enhance the biofilm formation in ML-MFC was investigated in this study. Electrodes were immersed in a broth mixture with 30% v/v inoculum size and the effect of immersion period (1, 2, 3, and 4 days) was investigated in this study. Acclimation procedures were shown to improve power generation of ML-MFC. The maximum power density yield with the acclimated anode recorded was 123.7mW/m^2, an increment of about 5 folds compared to the controlled MFC (25.6 mW/m^2). The outcomes emphasise the significance of anode acclimation to accelerate the formation of biofilm and electrogenic bacterial population on the electrode surface, thus facilitating electron transfer and ultimately influencing the overall performance of ML-MFC to generate power and bioremediation of organic matter. This will ensure the potential for environmentally friendly waste management and the generation of renewable energy, providing opportunities for ML-MFC implementation in the agricultural and livestock waste management industries

Keywords: membrane-less microbial fuel cell; biofilm anode acclimation; renewable energy from biomass; electricity; electrogenic bacteria

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SO-92

Effect of Different Incubation Period on *Bacillus subtilis* and *Pseudomonas aerugenosa* in Membrane – less Microbial Fuel Cell for Simultaneous Chicken Manure Bioremediation and Electricity Generation

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The need for energy resources had been emerging worldwide then has raised questions about the low environmentally friendly and high-cost processes for energy production nowadays. Membrane-less microbial fuel cell (ML-MFC) has been emerging as one of the popular also as one of the potential solutions to the issues of electricity generation. MFC are bio-electrical devices that harness the natural metabolism of electrogenic bacteria (EB) to produce electrical energy. In this study *Bacillus subtilis* (BS) and *Pseudomonas aerugenosa* (PA) were used to catalyst the transformation of carbon source in chicken manure as source of renewable energy. The study was carried out by setting the experimental conditions with the ambient temperature (34± 1℃) pH (12), electrode distance (3cm), initial moisture content (40 % vol/wt) were set as constant. The result focused on the performance of BS and PA in ML-MFC system for 7 days to14 days of incubation periods. The specific growthrecorded0.0262 g(l/h) (BS strain) and 0.0141 g(l/h) (PA strain) for 7 days, meanwhile the specific growth0.0057 g(l/h); BS strain and0.00163 g(l/h); PA strain recorded after 14 days incubation. The ML-MFCs were carried out for 14 days incubation period and the BS and PA growth reflected significantly on the voltage and power generated. The highest voltage (BS; 0.06V, PA 0.043 V) and power density (BS; $3.9x10^{-3}mW/m^2$, PA; $6x10^{-4}mW/m^2$) were recorded after 14 days of incubation. Series of ML – MFC contributed a promising performance for BS which was0.05V and $9.05x10^{-4}mW/m^2$ compared to PA was 0.022V and $9.05x10^{-4}mW/m^2$. Moreover, the reduction macro-micronutrients were analyzed through ICP-OES, COD removal and FTIR analysis. The study concluded that BS showed better performance in terms of EB growth (21.7 %; 14days), cod removal (2.1 %; 14 days), and power density generation (54.7 %; 14 days) compared to the PA strain.

Keywords: Biomass conversion; Membrane-less Microbial fuel cell; Chicken manure; Renewable energy; Green technology

SO-93

Dimerization and Functional Relationship of FKBP35 from *Plasmodium knowlesi*

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Plasmodium knowlesi expresses a 35-kDa FK506-binding protein (Pk-FKBP35) that is a promising target for developing antimalarial drugs resistant to resistance. Full-length Pk-FKBP35 (FL-FKBP35) comprises a catalytic FK506-binding domain (FKBD) and a tetratricopeptide repeat domain (TPRD) with a calmodulin binding motif (CBM) at the C-terminal. The FL-FKBP35 is a dimeric protein, where its dimerization is suspected to be crucial for proper folding and optimal function, yet never been confirmed. This study investigates the role of dimeric structure in Pk-FKBP35 function. To address, the FL-FKBP35, isolated domains (FKBD and TPRD), a ΔCBM (FL-FKBP35 without CBM), and a TPRD* (TPRD without CBM) were over-expressed in *Escherichia coli* BL21(DE3) and purified. Biochemical assays revealed that only full-length Pk-FKBP35 optimally catalyzed the slow folding of cis-prolyl bond-containing protein (RNase T1). Both full-length Pk-FKBP35 and TPRD existed as fully dimeric forms, while FKBD and ΔCBM remained stable monomers, with TPRD* showed aggregation in solution. This confirmed TPRD role in facilitating Pk-FKBP35 dimerization, with CBM being crucial for dimerization. Furthermore, the far-UV circular dichroism spectrum of ΔCBM resembled FKBD, suggesting proper folding only in the FKBD domain. These highlighted the necessity of dimerization for the proper folding of TPRD and optimal functioning of Pk-FKBP35.

Keywords: Malaria; *Plasmodium knowlesi;* FKBP35; Calmodulin; Peptidyl-prolyl cis-trans isomerase

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SO-94

Characterization of Fermented Palm Kernel Cake Using Locally Isolated Cellulolytic Fungi and Bacteria as Potential Animal Feed

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This study investigated the potential of locally isolated cellulolytic fungi and bacteria for fermenting palm kernel cake (PKC) as animal feed. The characterization includes physical observations, proximate analysis, reducing sugar, hemicellulose and cellulose content, and cellulase activity of the fermented PKC. Bacterial fermentation lasted for 7 days (day 0, 3, and 7), while fungal fermentation extended to 14 days (day 0, 7, and 14). The findings show comparable pH stability (around pH 5) and slight temperature variations (around 22-25°C) in bacterial and fungal-fermented PKC. Both bacterial and fungal fermentations exhibit increased crude fat and protein levels, while crude fiber shows slight differences. Significantly higher reducing sugar levels were observed in fungal fermentation (149%) compared to bacterial fermentation (98%) on day 7 fermentation. The cellulase activity in both fermentations leads to efficient saccharification, resulting in a decrease in hemicellulose (bacteria: 21%, fungi: 52%) and cellulose content (bacteria: 30%, fungi: 68%) over time. The findings suggest that fungal fermentation exhibits superior performance in terms of reducing sugar levels, cellulase activity, hemicellulose and cellulose degradation compared to bacterial fermentation. This study provides valuable insights on optimizing fermentation conditions to enhance the nutritional value and digestibility of PKC as sustainable feed production.

Keywords: Palm kernel cake (PKC), fermentation, cellulolytic, bacteria, fungi, animal feed

Funding Information: DIS0014-2020 and SBK0514-2022

SP-02

Nutritional Value and Antioxidant Properties of *Kappaphycus alvarezii* Residue for Potential Use as Biofertilizer

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The search for sustainable and environmentally friendly alternatives to chemical fertilizers has led to increased interest in seaweed biofertilizers, which are rich in nutrients, phytohormones, and bioactive compounds. In this study, the nutritional values and antioxidant properties of seaweed *Kappaphycus alvarezii* solid residues was evaluated as a potential biofertilizer. The residues were generated from carrageenan processing through biological, physical, and chemical extraction methods. The results showed that the biological extraction method produced the highest seaweed residue (68.9%) compared to other extraction methods. The residues from all extraction methods had a moisture content of approximately 98% and a fat content of around 3%. All seaweed residues contained nitrogen, phosphorus, potassium, and other minerals at certain levels. Among the nutrients, sodium was found to be the most abundant in all residues, ranging from 525 mg/kg to 745 mg/kg. The antioxidant properties of the seaweed residues (49% - 52%) were almost comparable than those of raw seaweed (56%) across all tested concentrations. These preliminary findings suggest that seaweed waste biofertilizer can be utilized for sustainable agriculture and green waste management. Further research is needed to optimize the extraction methods and evaluate its effectiveness on crop yields and soil health.

Keywords: *Kappaphycus alvarezii*; carrageenan extraction; seaweed waste; nutritional content, biofertilizer

Funding Information: SBK0514-2022

SP-03

Hydrogel-Biochar Composite for Control Release Fertilizer: A Preliminary Study

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Control-released fertilizers (CRFs) have gained attention due to their ability to retain water and nutrients. In addition, CRFs can gradually release the nutrients over an extended period, thereby improving crop nutrient uptake and reducing environmental impact. Natural polymers and waste materials offer an eco-friendly, economical, and sustainable approach to the development of CRFs. This study aimed to develop controlled-release hydrogel-biochar composites using alginate-chitosan biopolymer and oil palm empty fruit bunch biochar. In the present study, different hydrogel formulations were prepared with varying ratios of ALG-CHI and $CaCl_2$ crosslinker (1:1:1, 2:2:2, and 3:3:3). The physicochemical properties of the hydrogels were investigated, including swelling, and water retention. The 1:1:1 ratio hydrogel had an irregular spherical surface, possibly due to ruptured beads during fabrication. In contrast, the hydrogel beads of 2:2:2 and 3:3:3 ratios were regularly spherical, with the 2:2:2 ratio being more transparent. Both showed comparable mechanical strength using fingertip force testing. All tested ratios showed water retention ability above 95%. The hydrogel composite with a 1:1:1 ratio had the highest swelling ability (32.22 times). The hydrogel formulations with ratios of 2:2:2 and 3:3:3 also demonstrated good swelling, with the former having a higher yield. These preliminary findings suggest that the developed ALG-CHI hydrogel composites have promising properties for use as controlled-release materials. Further studies are needed to optimize the formulation with nutrients and investigate their nutrient release ability in soil and water.

Keywords: Control Release Fertilizer Composite, Biopolymer, Biowaste, Empty Fruit Bunch Biochar.

Funding: SGI0159-2023

SP-04

De novo genome assembly of *Ganoderma zonatum* using high-fidelity long reads

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Basal and upper stem rot diseases of oil palm are caused by the pathogenic white rot fungi, Ganoderma *boninense* and *Ganoderma zonatum*. There are limited studies on the biology of *G. zonatum*'s infection in oil palm, and no good quality genome data has been made available thus far. HiFi assembly leverages long-reads that span the entire length of the genomic regions, aiding in resolving repetitive and complex regions. Therefore, the objective of this study is to sequence and *de novo* assemble the studied genome using HiFi data and assemblers. Here, single-molecular real-time (SMRT) sequencing (PacBio) was performed and high-accuracy long-reads of 640x sequencing coverage were obtained for *G. zonatum*. The HiFi reads were assembled with default parameters via HiCanu, Hifiasm, Peregrine-2021, wtdbg2, Raven and Flye assemblers. The assemblies were evaluated on the number of contigs, N50, assembly completeness (BUSCOV5) and assembly quality (QV). The HiFi dataset produced 235 [genome size (GS): 57.39 Mbp], 110 (GS: 52.14 Mbp), 94 (GS: 47.99 Mbp), 70 (GS: 51.33 Mbp), 40 (GS: 52.49 Mbp) and 28 (GS: 50.05 Mbp) contigs with HiCanu, Hifiasm, wtdbg2, Raven, Peregrine-2021 and Flye, respectively. The assessment of genomes with BUSCOV5 and QV scores were 95.7% (44.59), 93.2% (38.22), 95.0% (35.19), 95.65% (39.67), 95.9% (34.11) and 96.1% (62.66), respectively. Thus, based on the genome statistics and assessment, Flye is the assembler of choice for the *G. zonatum* genome.

Keywords: *Ganoderma*; Basal Stem Rot (BSR); Upper Stem Rot (USR); Genome assembly; *E. guineensis*

Funding Information: MPOB

SP-05

Isolation and Characterization of Microalgae from Seawater for Potential Biofuel Production

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The growing pursuit of sustainable and renewable energy has sparked a remarkable interest in microalgae as a highly promising resource for biofuel production. The vast marine environment is home to an extensive range of microalgae species, each exhibiting distinctive metabolic capabilities and growth traits. Understanding the diversity and characteristics of microalgae from seawater is essential for harnessing their biofuel production potential and establishing a sustainable and environmentally friendly energy source. This study focuses on the isolation and characterization of microalgae species obtained from seawater with the aim of identifying potential candidates for biofuel production. The water samples were collected from Likas coastal waters and the isolation and cultivation were carried out under sterile conditions. The isolated microalgae strains were then characterized through morphological observations using the light microscope to assess the cellular structure, size, and shape of the microalgae. These characteristics are crucial in assessing the potential for biofuel production. The results of this study provide valuable insights into the diversity of microalgae species present in seawater and their potential for biofuel production. Several promising strains with desirable characteristics for biofuel production were identified and further research is needed to increase the lipid production by the microalgae.

Keywords: Microalgae; seawater, isolation; characterization; biofuel production

Funding Information: SGI0159-2023

SP-06

An Optimization Assay for Universal Detection of Avian Infectious Bronchitis Virus (Gammacoronavirus) Using an Electro-Chemical DNA Biosensor

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Avian infectious bronchitis is a highly contagious and acute disease of chicken coronavirus caused by infectious bronchitis virus (IBV), which is characterized by respiratory infections, nephropathy and permanent damage to the oviduct, resulting in high mortality. IBV leads to severe economic losses due to the increased number of serotypes and inadequate controlling facilities for farm-based diagnosis, therefore it is becoming a major challenge for the prevention and controlling. Electrochemical DNA biosensor was employed for the detection of the specific-target orf genes (Universal) of IBV. The process of immobilization and hybridization were conducted onto the gold electrode (AuE) with covalently binding of NH2-ssDNA probe (single stranded DNA), followed with the target DNA as well as mismatched DNA. The optimization parameters were conducted such as buffer, pH, scan rate, incubation time, redox indicators and effects of temperature using cyclic voltammetry (CV). The optimum parameters were found in the range of 0.0 to +1.6 V in a 50 mM Tris–HCl (pH 7.0), Methylene Blue (MB), a scan rate of 100 mV/s and accumulation time of 5 s, respectively. The probe DNA was formed with strong hybridization efficiency with the target DNA of IBV. Under the optimum parameters, electrochemical DNA biosensor was clearly differentiated between the probe DNA, non-complementary DNA and mismatched DNA. A cross reactivity study has been conducted to differentiate other non IBV viruses which are related to respiratory pathogens of poultry disease based on the different levels of current signal. The optimal results will be supported to apply in modification of AuE for developing a portable device to identify the IBV in the farm.

Keywords: Avian infectious bronchitis virus; electrochemical biosensor; cyclic voltammetry; Immobilization; Hybridization

SP-08

Characterization of Silver Nanoparticle-β-Sitosterols and Its Cytotoxicity against Various Cancer Cell Lines

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β-sitosterols are known to possess anticancer activity. However, its efficacy is limited by low water solubility. Therefore, the objective of this study was to characterize silver nanoparticles-β-sitosterol (AgNP-βs) and cytotoxicity evaluation against various cancer cell lines. Methods used were UV-Vis spectroscopy, DLS, TEM, SEM-EDX, FTIR, and MTT assay. Average size of AgNP-βs is 76.62 ± 41.19 nm with pdi value of 0.275. Zeta potential of AgNP-βs produced is -40.2 mV. TEM showed AgNP-βs was mostly hexagonal shape in aggregated form. AgNP-βs showed a rough surface by SEM and an intense peak at 3.0 keV in EDX suggesting Ag is the main element in AgNP-βs. FTIR showed the existence of O-H bonds (phenols) and C-H stretch bonds proving β-sitosterols bind with AgNPs as capping agents. Cytotoxic activity of AgNP-βs was tested against several cancer cell lines such as MCF-7, A375, and A549. Results shown IC_{50} ranged from 25 µg/mL to 80 µg/mL with the lowest IC_{50} against A375 (25.0 ± 0.1 µg/mL) and the highest IC_{50} against MCF-7 (77.0 ± 1.02 µg/mL). No toxicity was found when AgNP-βs were tested on normal cell lines even at the highest concentration (100 µg/mL). β-sitosterols showed great potential as an anticancer agent.

Keywords: Silver nanoparticles, β-sitosterol, cancer cell lines

Funding Information: FRGS/1/2021/STG05/USIM/02/2

SP-09

Development of Acetylcholinesterase Biosensor for Determination of Carbaryl Pesticide in *Brassica oleracea* Var. *capitata* L. (cabbage) and *Brassica oleracea* Var. *italica* L. (broccoli)

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Carbaryl pesticide is widely applied to protect crops against pests in agriculture. Overuses of carbaryl are hazardous as it interrupts human central nervous system by causing signal transmission to be impaired. Because of the hazardous effects resulted by the prolonged exposure to the pesticide, rapid detection is highly concerned. In this study, a new electrochemical method was developed based on immobilization of acetylcholinesterase (AChE) enzyme via glutaraldehyde (GA) as a crosslinking agent onto glassy carbon electrode (GCE) modified by the homogenously dispersed of multiwalled carbon nanotubes (MWCNTs) and gold nanoparticles (AuNPs) in chitosan for detection of carbaryl pesticide. The combination of all these nanomaterials observed using SEM, EDX and TEM. After the careful optimization of sensing conditions (pH 7 for 0.1M Tris-HCl buffer, 20s for reaction time, 0.1V/s for scan rate, 6 min for inhibition time), low detection limit for carbaryl was found of 4.95 x 10^{-3} mg/L with good repeatability, reproducibility and storage stability. The developed AChE biosensor showed rapid and high sensitive tool for determination of carbaryl in vegetable samples.

Keywords: Acetylcholinesterase; Carbaryl; Biosensor; Pesticide; Nanomaterials

SP-10

Neutrophil Phenotype Changes in Periodontitis

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Chronic periodontitis is a dental disease characterized by non-resolving inflammation which leads to host-mediated tissue damage and bone loss around the teeth. The human oral tissues are always exposed to potential and harmful microorganisms and to combat the infections in this area, neutrophils as the most abundant leucocyte arrive at the site of infections to eliminate pathogens. They contain the antioxidant glutathione to maintain homeostasis. A clinical study was set up to investigate the role of periodontitis on alterations to peripheral blood neutrophils: four periodontitis patients were compared to healthy controls and two patients before and after periodontal therapy. In this study, neutrophils were isolated from whole blood to assess glutathione, chemotaxis, and glutathionylated proteins. Tandem mass tags as quantitative proteomics was used for peptide identification and quantification in neutrophils. In periodontitis patients, there was less glutathione in neutrophils in comparison to healthy donors, but it increased after non-surgical treatment. A similar pattern was observed for neutrophil chemotaxis. Therefore, changes in glutathione antioxidants could be associated with chemotactic ability. Proteomic analysis of extracts from patients and control neutrophils demonstrated modulation of glutathione regulation in periodontitis patients.

Keywords: Periodontitis; Neutrophils; Glutathione

Funding Information: Ministry of Higher Education Malaysia

SP-11

Meta-analysis of RNA sequencing (RNA-seq) studies identifies candidates gene related to abiotic stress and quality traits in *Carica papaya*

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A meta-analysis was performed on publicly available RNA-seq datasets to investigate the molecular mechanisms underlying abiotic stress response and quality traits in *Carica papaya*. A comprehensive RNA-seq pipeline was employed to process raw sequencing data, identifying 7043 expressed genes across drought, ripening, and flavor traits. Furthermore, 6198 differentially expressed genes (DEGs) were found in association with drought, ripening, and flavor. Functional annotation of these DEGs revealed their involvement in essential biological processes such as metabolism, cellular processes, signaling, and information storage and processing. Additionally, a gene co-expression network analysis and clustering analysis based on the Markov clustering method were performed to explore the gene-gene interactions, providing insights into the organization of co-expressed genes. The findings of this meta-analysis utilizing public RNA-seq data provide valuable resources for selecting potential targets for genome editing and offer the potential for uncovering novel plant stress tolerance mechanisms and pathways. This study contributes to understanding Carica papaya's response to abiotic stress factors and quality traits, enabling more informed approaches to improve crop yield and quality in this species.

Keywords: meta-analysis, RNA-seq, gene co-epxression network, *Carica papaya*

SP-12

Potential Use of Kokoselect as a Bio-Diagnostic Kits for Screening of Cocoa Seedlings with Agronomic Traits

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Cocoa plants usually need three to five years to reach full maturity. As a result, selecting a cocoa clone tree that produces fruit with the desired traits will be time-consuming and costly, requiring frequent attention for at least five years before any objective physical assessment can be performed. Growing cocoa is expensive in terms of land, agricultural resources, labour, and other things. As a result, cocoa growers will unavoidably face the issue of cocoa seedling operators selling subpar clones. Cacao growers may not be aware of an issue until the farmed cocoa plants have matured and the quality of the chocolate produced has been determined. The global cocoa genome sequencing project's completion has greatly aided the genetic advancement of the cocoa tree. Identification and correlation of SNPs with favourable agronomic features in any crop, notably cocoa, is important. SNPs-related traits identified in KokoSelect include high cocoa butter content, higher production, and resistance to pests and diseases such as Cocoa Pod Borer, Black Pod disease, and Vascular Streak Dieback disease. Instead of wasting time and resources screening large numbers of cocoa seedling plants, cacao growers will be able to select rare recombinants.

Keywords: SNPs, cocoa, traits

SP-13

Genetic Variants of Dupuytren's Contracture

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Dupuytren's contracture (DC) causes flexion contractures in the digits, primarily affecting Northern European descendants. Despite extensive genetic research on DC, there is a lack of compiled information and functional validation on previously identified variants. Furthermore, the studies primarily focused on Europeans/Caucasians, with no reports on other populations. Thus, this review aims to compile previously identified variants to facilitate future functional validation studies and serve as a reference for variant studies in other populations. Relevant studies were screened across ScienceDirect, PubMed databases, and Google Scholar search engine using the keywords 'Dupuytren's contracture,' 'Dupuytren's disease,' 'variant,' 'genes,' and 'genetics.' Eighteen genome-wide association studies (GWAS) and cohort studies from 2003 to 2021 were selected. The lack of exome studies is due to the exclusion of non-coding mutations, limiting their suitability for studying complex diseases like DC. In these studies, intron variants were the most identified as they have a stronger causative effect on DC. Notably, the intronic variant (NM_017549.5:c.478+445C>T) in *EPDR1* was identified in two GWAS studies and was found disrupting WNT signalling, contributing to the fibrotic phenotype. Additionally, one study reported three missense variants from *ITGA11* (NM_001004439.2:c.1297G>A), *PJA2* (NM_014819.5:c.2113G>A) and *MMP14* (NM_004995.4:c.817G>A) spanning the integrin, TGF-ß and WNT signalling pathways respectively. In conclusion, the reported variants can be functionally validated and studied in other populations to identify causative variants, potentially serving as biomarkers or therapeutic targets.

Keywords: Dupuytren's contracture; WNT signalling; *EPDR1*; variants

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SP-14

Heterologous Expression and Purification of Calmodulin from *Plasmodium knowlesi* using Codon-Optimized Synthetic Gene

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Calmodulin (CaM) is a vital protein for the survival of *Plasmodium knowlesi*, a simian malaria parasite infecting macaques and humans in Southeast Asia. Therefore, a comprehensive understanding of this protein is required to discover appropriate druggable spots for antimalarial drug development. This, however, requires the availability of proteins in sufficient amounts and purity for further studies. This study is therefore aimed to develop the strategy for heterologous expression and purification of CaM of *P. knowlesi* (Pk-CaM). To address this, the gene sequence of Pk-CaM was firstly retrieved from PlasmoDB (accession code: PKNH_0420800.1) which was further optimized for expression under *Escherichia coli* host cell, chemically synthesized and cloned onto pET28a plasmid. The expression of Pk-CaM was performed at 37°C by induction with 1 mM IPTG, which yielded a fully soluble form of Pk-CaM. Further purification of this protein using Ni2+-NTA affinity chromatography resulted in an acceptably pure Pk-CaM as indicated by a 20-kDa single band under SDS-PAGE. The yield of pure Pk-CaM was 15 mg from 1 L culture. We report here the confirmed protocols for expressing and purification of the Pk-CaM protein.

Keywords: Calmodulin; *Plasmodium knowlesi*; Calmodulin-binding motif; Antimalarial drug

Funding Information: FRG 0566-1/2022

SP-15

Utilization of Soil Beneficial Microorganisms Towards Sustainable and Eco-Friendly Plant Disease Management

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In the current agricultural practices, applications of various synthetic chemicals such as pesticides and fertilizers have been used extensively and excessively. Although these chemicals benefited to agricultural industries, improper use of pesticides will give adverse effects to human health and environment. *Streptomyces* spp. are well known as most worthwhile microorganisms and have been widely used as secondary metabolites for various medical purposes. Not only for pharmaceutical industries, *Streptomyces* spp. also play the vital role in agriculture and has been reported as good decomposer, inhabit rhizosphere and becoming plant growth promoting rhizobacteria (PGPR) and also act as biocontrol agent. Due to its advantages, the importance of Streptomyces species has been explored as biological control agent for controlling various plant diseases. In this study, Streptomyces have shown its potential as biological control for fusarium wilt disease of banana and grey leaf spot disease of coconut. Therefore, MARDI is in the effort to produce suitable and effective formulation of these Streptomyces as bio-based fungicide towards eco-friendly approach for controlling important agriculture diseases for the future. This effort is in support to reduce the usage of agriculture pesticide inputs to our food to become safer food for future.

Keywords: Streptomyces; Biological control; Disease

Funding Information: MARDI

SP-16

Assessing the Genotype Accuracy of Grafted Cocoa (*Theobroma cacao* L.) Seedlings Nurseries' Outputs using Ten Cocoa Single Nucleotide Polymorphism (SNPs) Markers for the Malaysian Cocoa Commercial Clones

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The Malaysian cocoa commercial clones are improved cocoa planting materials with desirable agronomic traits, specially selected for planting in Malaysia's agro-climatic conditions and usually propagated through grafting. Cocoa has high occurrence of self-incompatibility thus the use of accurate planting materials is crucial especially at the early stage of planting to reduce inferior cocoa planting material contamination, improve yields potentials, and better pest and diseases management, which will bring positive economic impact on the individual cocoa farmer and the cocoa industry. However, due to the lack of distinguishable morphology differences, it is challenging to evaluate the genotype accuracy of the grafted cocoa seedlings produced by the cocoa nurseries. The assessment of seven hundred and twenty seven grafted cocoa seedlings from cocoa nurseries in Ranau, Sabah and sixty adult trees from a cocoa seedlings producer scions source garden in Kota Marudu, Sabah was conducted using a set of ten Single Polymorphism Nucleotides (SNPs). The occurrence of off-types or mislabeled planting materials produced by the cocoa nurseries and cocoa nursery scions source garden were assessed and authenticated. Cross-checking on the samples from cocoa nurseries and scions source garden has established that mislabeling and genotype errors occurred during the planting materials propagation process.

Keywords: cocoa; SNP markers; cocoa seedlings; genotype accuracy; KASP genotyping.

Funding Information: 12th Malaysian Plan Development Fund (P20001001210005); MCB Internal Research Fund (02-03-TRF0011)

SP-17

Heterologous expression of FL-Chit and CD-Chit Gene from *Arthrobacter* sp. 6A1 using an *Escherichia coli* System

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A cold-adapted bacterium from the Antarctic region, *Arthrobacter* sp. 6A1, was previously found to produce chitinase, a group of enzymes of N-acetyl-β-D-glucosaminide-β-linkages in chitin. Accordingly, this enzyme is promising for bioremediation or bioconversion of chitinous waste to other valuable products. The full-length of chitinase from the 6A1 strain (FL-Chit) is organized into a catalytic domain (CD) and another accessory domain. Nevertheless, the feasibility of recombinant production of this protein for further studies and applications has never been studied. This study aims to establish a method to express and purify FL-Chit and its catalytic domain (CD-Chit) using *E. coli* host cells. To address this, FL-Chit or CD-Chit gene was firstly cloned into pET22b+ and transformed into several strains of *E. coli* BL21, including CodonPlus (DE3), Rosetta (DE3), and DE3. The gene's expression was induced using 0.2 mM IPTG at 37 °C, 180 rpm when the OD_{600} reached 0.8, followed by incubation at 18 °C for 16 h. The result showed that all the *E. coli* expressed FL-Chit and CD-Chit and were fully soluble. The proteins were then purified using Ni-NTA chromatography, showing that CD-Chit expression is higher than FL-Chit for every 1 L of culture, which are 8.208 mg and 0.458 mg, respectively. The findings provide a guide for optimizing the production of *Arthrobacter* sp. 6A1 chitinase of *E. coli* host cells.

Keywords: *Arthrobacter* sp. 6A1, Chitinase, Antarctic bacteria, heterologous expression, protein purification

Funding Information: SDK0335-2020

SP-18

Metagenomic Approach in Elucidating the Role of Gut Microbiota in AFB_1-Induced Neurotoxicity and Depressive-like Behaviour

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Aflatoxin B_1 (AFB_1) poses significant risks to food safety and public health. Previous study showed AFB_1 caused depressive-like behaviour in rats, similar with chronic unpredictable mild stress (CUMS), a rodent model of depression. While the toxic effects of AFB_1 on the nervous system have been reported, its neurotoxicity effects via gut microbiota modulations remains unexplored. This study aims to investigate the alterations in gut microbiota composition toward AFB_1 exposure and its role in mediating the neurotoxicity effects. Rats were exposed with different doses of AFB_1 and CUMS treatments. Faecal DNA was extracted and subjected to 16S rDNA identification technology and bioinformatics analyses. AFB_1 and CUMS altered the relative abundance and bacterial diversity of the rats' gut microbiota. Besides, the gut microbial composition of high-dose AFB_1 and CUMS groups deviated from the norm and Prevotella/Prevotellaceae, a depression marker, was abundance in both groups. It can be postulated that gut microbiota dysbiosis and dysregulation of gut-brain axis due to AFB_1 neurotoxicity leading to the progression of depressive-like behaviour. This study shows the complex interactions between AFB_1, gut microbiota, and disease progression, paving the way for novel strategies targeting the gut microbiota through probiotic intervention in mitigating the toxicity effects of AFB_1.

Keywords: Aflatoxin B_1; Neurotoxicity; Depressive-like behaviour; Gut Microbiota; Gut Dysbiosis

Funding Information: Fundamental Research Grant Scheme (FRGS/1/2018/SKK06/UPM/02/2)

SP-19

Evaluation of the Agro-Morphological Characteristics, Field Performance, and Clonal Fidelity of a Tissue Culture-Generated Cocoa Clone

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The development of plant tissue culture techniques such as protoplast culture and somatic embryogenesis, has facilitated the *in vitro* regeneration of *Theobroma cacao* L. Genetic uniformity is essential for clonal propagation and preservation of elite genotypes with superior characteristics. This study assessed the agro-morphological characteristics and field performances of a mature cocoa tree produced through tissue culture and conventional propagation methods. The clonal fidelity of tissue culture-generated cocoa plants and conventionally propagated cocoa clones were evaluated using the MCB cocoa SNP panel for DNA fingerprinting. Even though it was not the mother plant, DNA fingerprinting showed that the tissue-cultured cocoa tree was a true-to-type clonal tree. Agro-morphological characteristics of cocoa plants showed significant differences in phenotypic and field performance between tissue culture and conventional grafting methods. Tissue-cultured cocoa trees exhibit jorquette branches, a typical characteristic in seed-propagated, making them taller than cocoa clones generated through conventional methods. Tissue-cultured cocoa trees have a smaller girth circumference than conventionally propagated cocoa trees. Early flowering was observed in tissue culture cocoa trees, which started approximately 12 months post-planting, while conventionally propagated cocoa trees require 18 to 36 months to display the same characteristic.

Keywords: *Theobroma cacao* L.; cocoa tissue culture; agro-morphological traits; DNA fingerprinting; clone verification.

Funding Information: MCB Internal Research Fund (02-03-TRF0008; 02-03-TRF0011)

SP-20

An In-Silico Study on the Effect of Cysteine Substitution at the High Affinity Ca^{2+} Coordinating Residues of Rand Protease

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Rand protease is a serine protease that shared common characteristics with members of the MEROPS S8 subtilisin family. It is thermostable, highly stable in organic solvent and broad in specificity. Many structures of homologous protein solved by X-ray crystallography and NMR have been deposited to Protein Data Bank (PDB) allowing this study to rely on structure prediction by deep learning to build three-dimensional (3D) structure of full length and mature Rand protease (flRP and mRP). Hydrophobicity is known to be an important element in the stability of thermophilic proteins. Cysteine which displays strong hydrophobic nature by itself is known to stabilize the three-dimensional structure of proteins, which is of great importance for extracellular proteins that might be exposed to extreme environments. In silico cysteine mutation to seven predicted high affinity Ca^{2+} coordinating residues were introduced, and the mutants were subjected to molecular dynamic simulation to study its effect on the structural hydrophobicity of flRP and mRP. Results indicated that high affinity Ca^{2+} coordinating surface loop could influence the hydrophobicity of both flRP and mRP.

Keywords: Rand protease; subtilisin; cysteine; hydrophobicity; Ca^{2+}

Funding information: FRGS/1/2020/STG02/UPM/02/12

SP-21

Comparative Evaluation of Sample Preparation and RNA Isolation Techniques for Gene Expression Analysis in Neuromuscular Diseases

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Muscle biopsy is crucial for molecular profiling of neuromuscular diseases including myotonia congenita and requires high-yield RNA from muscle tissue. This study addresses two key objectives aimed at improving gene expression analysis: optimizing tissue sample preparation and RNA isolation techniques to maximize RNA yield, and determining the optimal sample type for tissue-based disease by comparing muscle tissue and blood samples. The investigations were done using two different tissue sample preparations (liquid nitrogen and disposable homogenizer pestle), and two different isolation techniques i.e., spin-column and salt-precipitation using commercially available kits. Isolated RNA from muscle tissue and blood were converted to cDNA and subjected to RT-PCR using gene-specific primers and gel electrophoresis. Tissue processed with liquid nitrogen and homogenizer pestles yielded RNA concentrations of 12.9 and 8.5 ng/µl using spin-column kit, while the salt-precipitation kit resulted in higher concentrations of 28.0 and 128.7 ng/µl, respectively. The findings revealed that the combination of homogenizer pestles and the salt-precipitation kit produced the most concentrated RNA. Gene expression analysis demonstrated specific PCR product amplification from muscle tissue RNA, whereas blood sample RNA resulted in multiple non-specific binding products, highlighting tissue's superiority over blood samples for tissue-based disease investigation. These findings enhance our understanding of sample preparation and RNA isolation techniques, thereby optimizing gene expression analysis in the study of neuromuscular diseases.

Keywords: neuromuscular diseases; myotonia congenita; RNA extraction; muscle tissue; gene expression

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SP-22

Acute Oral Toxicity of Iron Oxide-Chitosan Encapsulated Tea Polyphenols Nanoparticles in Sprague-Dawley Rats

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Nano-encapsulation is an emerging technique for the encapsulation of tea polyphenols to improve its bioactive stability and bioavailability. This study aimed to investigate the acute oral toxicity effect of iron oxide-chitosan encapsulating tea polyphenols nanoparticles (IO-Chit-NanoTP) in Sprague-Dawley rats. A total of twelve 8-week-old male rats were divided into Group A (control) and Group B (2000 mg/kg bw) for the acute toxicity study. A single dose of 2000 mg/kg IO-Chit-NanoTP were administered to Group B through oval gavage and were monitored for 14 days. The rats were sacrificed, and samples were collected for hematological and histopathological analysis. No mortality and sign of toxicity were observed during the treatment period. There were no statistically significant differences between group in the haematological and biochemical parameters of the rats treated with IO-Chit-NanoTP after 14 days of treatment. Histopathological scorings of liver and kidney also showed no remarkable lesions that could be attributed to the effect of 2000 mg/kg bw of IO-Chit-NanoTP administration. The results indicate that oral administration of IO-Chit-NanoTP did not cause significant adverse effects and suggest its tolerability up to 2000 mg/kg in rats.

Keywords: Tea polyphenols; nanoparticles; iron oxide nanoparticles; acute toxicity

Funding Information: FRGS/1/2018/SKK10/UPM/02/5

SP-23

Docking and Molecular Dynamic Simulation of Calmodulin and CBM Segment of FKBP35 from *Plasmodium knowlesi*

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The possible interaction between a 35-kDa FK506-binding protein and calmodulin of *Plasmodium knowlesi,* designated as *Pk-FKBP35* and *Pk-CaM*, respectively, is a viable antimalarial drug target to address the rise in *P. knowlesi* infection cases in Borneo. The network of both proteins is possibly due to the presence of a calmodulin-binding motif (*Pk-CBM*) at the C-terminal of *Pk-FKBP35*. Nevertheless, no study to date has investigated the interaction between *Pk-FKBP35* and *Pk-CaM*, limiting our understanding of this interaction. This study aims to decipher the structural properties of the interaction between *Pk-CBM* and *Pk-CaM* through molecular docking analysis. Accordingly, 3D models of *Pk-CaM* were first constructed using SWISS-MODEL, while the 3D model of *Pk-CBM* is extracted from the validated *Pk-FKBP35* model. Both models were then used for molecular docking simulation using HADDOCK software, coupled with molecular dynamic simulation under the YASARA platform. As a result, the docking revealed the best complex with a favourable HADDOCK score (-70.2 ± 5.9). The complex was also found to be stable during simulation for 100 ns, as indicated by RMSD and gyration changes. The docking results also revealed that the N-terminal segment of *Pk-CBM*, where the IR motif is localized, serves as a binding site for *Pk-CaM*. It is worth noting that the interaction between *Pk-CaM* and the N-terminal region of *Pk-CBM*, particularly the IR motif, was revealed. The interaction map obtained from LigPlot revealed that the *Pk-CBM* residues involved in the interaction were Ile 262, Arg 263, Asn 264, Ser 265, Tyr 266, Asp 267, Leu 270, Leu 273, Lys 274, Arg 277, and Lys 281. Overall, the study confirms the possible interaction of *Pk-CaM* and *Pk-CBM*, highlighting the potential of disrupting this interaction for the development of new antimalarial drugs targeting *P. knowlesi*.

Keywords: Malaria, *Plasmodium knowlesi*, FKPB35, Calmodulin, Molecular docking, Molecular dynamic simulation

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SP-24

Development of Low-Cost, One-Step Multiplex SYBR Green-based RT-qPCR Assay for Detecting SARS-CoV-2 in a Malaysian Setting using Optimized Primers

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The COVID-19 outbreak has swiftly become a global concern by early 2020, spreading at an unprecedented rate with seemingly endless mutations. For laboratory diagnosis, low-cost detection of SARS-CoV-2 is urgently needed, particularly in developing countries with limited resources. Probe- or TaqMan-based RT-qPCR is currently the gold standard for diagnosing infected individuals, as recommended by the World Health Organization (WHO). However, this assay is expensive, making it difficult to use for diagnosis on a large scale. Therefore, in this study, we develop an alternative approach for RT-qPCR diagnosis by employing the DNA intercalating dye SYBR Green. We designed and evaluated high-performance primer sets for four respective genes (RdRp, Spike[S], Envelope[E] and Nucleocapsid[N]) based on the Malaysian SARS-CoV-2 genome sequences retrieved from the GISAID database. In this study, all primers are designed to detect the conserved regions specified only for SARS-CoV-2 via sequence alignment analysis. We optimized the RT-PCR reaction of the COVID-19 genes based on singleplex melting curve analysis at the initial stage. After several rounds of optimization on multiplex assays of different primer combinations, the optimized method finally targeted at least 2 genes in a single reaction tube. With each set of primers producing different amplicon sizes, the E-value varied from 90.7 to 105.4%, R^2-value from 0.914 to 0.996, and the slope value from -3.146 to -3.566. The best primer for RdRp, S, E and N gene detections had an efficiency of 107.9%, 105.4%, 104.4%, and 101.9%, respectively. The cost of each sample for an RT-PCR run is expected to be below RM10. Overall, this one-step and one-tube designed SYBR green-based method can revolutionize the COVID-19 diagnosis to be applied on a broad scale for an effective containment approach, especially in low-income countries.

Keywords: RT-qPCR, SYBR Green, Multiplex, SARS-CoV-2, COVID-19 conserved regions, COVID-19

SP-25

In silico Characterization of HSP70 from *Glaciozyma antarctica* PI12 as a Model System to Understand Adaptation Strategies of Antarctica Organisms Amid Adverse Climate

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The 70-kDa heat-shock proteins (HSP70) are integral components of the cell's molecular chaperones and folding catalysts. *Glaciozyma antarctica PI12* (GaPI12) is an obligate psychrophilic yeast isolated from the Casey Research Station and possesses at least six HSP70 genes in its genome. Two HSPP70 genes were significantly inducible by thermal stress while the other four are still uncharacterised. The functions of these HSP70s in GaPI12 in terms of similarities and differences are yet to be discovered. This study aimed to determine the structure and function of HSP70 from GaPI12 which will lead to the understanding of the adaptation strategies in this organism through structural and functional annotation. HSP70 genes derived from genome data of GaPI12 were extensively analysed computationally via physicochemical analysis, phylogenetic study, homology modelling and structure validation, and comparative analysis of the generated models. Results showed that reliable 3D models of HSP70 were successfully generated using SWISS-MODEL and AlphaFold2 homology modelling. Highly reliable models were identified via PROCHECK's Ramachandran plot, ERRAT, PROVE, Verify 3D, ProQ and ProSA analyses. Among the new findings are the molecular signatures such as ionic, aromatic-aromatic, aromatic-sulphur and cation-pi interactions that may reflect the yeast response and adaptation strategies during the adverse climate. This proves HSP70's structural adaptation and evolution in terms of its thermal resistance to global warming.

Keywords: HSP70; *Glaciozyma Antartica* PI12, Homology Modelling; Structural Adaptation

SP-26

The Effect of Oleuropein in DNA Damage of Mouse Skin Carcinogenesis Model

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Oleuropein (OL) is a phenolic compound normally found in olive trees such as leaves and fruits. OL has shown various biological effects such as antioxidant, antimicrobial and anti-proliferation effects. Research on olive extracts has been well known and actively carried out due to its antitumor properties. Previous studies have shown that OL can prevent and lower the rate of DNA damage in human breast cancer cells and human colon cancer cells. However, the effect of OL on DNA damage at a specific stage in skin cancer remains to be investigated. Therefore, the aim of this study is to determine the effect of OL on DNA damage using the two-stage mouse skin carcinogenesis model that is induced by DMBA and TPA carcinogens. Total of 24 ICR mice were used in this study and were divided into four groups (n=6 per group) consisting of vehicle control group (70% acetone), carcinogen control group (DMBA/TPA), pre-initiation treatment group (OL/DMBA/TPA), and post-initiation treatment group (DMBA/OL/TPA). After 16 weeks, the immunohistochemistry analysis revealed that both p53 and p21 were highly expressed in the pre-initiation treatment group. In addition, the rates of DNA damage significantly reduced in the pre-initiation group ($p<0.05$) as compared to the carcinogen control group via comet assay analysis. This study suggests that OL that was given before the initiation stage was capable of reducing the DNA damage in mouse skin carcinogenesis model.

Keywords: Oleuropein; DNA damage, Skin cancer; Mouse model

SP-27

In Utero Effects of Hydroquinone on Maternal and Fetal Hematopoietic Stem/Progenitor Cells and Roles of Cell Lineages

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Previous research reported that prolonged benzene exposure during in utero fetal development increases the risk for hematological malignancies at fetal stage. However, the in-utero effects and role of cell lineage-mediated benzene toxicity targeting fetal and maternal hematopoietic stem / progenitor cells (HSPCs) remains unexplored and to be investigated. Briefly, pregnant mice (n=24) were divided into 3 groups comprised of control and Hydroquinone (HQ) -treated groups. HQ, a benzene metabolite was administered at 25 (HQ25) and 50 (HQ50) mg/kg body on gestational day (GD) 12,14 and 16 followed by fetal and maternal bone marrow (BM) harvest on GD18. Then, Colony-forming Unit (CFU) assays were carried out for 14 days to obtain myeloid and 7 days to obtain erythroid and pre-B lymphoid progenitors. The colony counts for fetal myeloid, erythroid and pre-B lymphoid progenitors in HQ50 group were significantly inhibited ($p<0.05$) as compared to control. However, in HQ25 group only colony counts for pre-B lymphoid progenitor was significantly inhibited ($p<0.05$) in comparison to control. Meanwhile, both maternal groups (HQ50 and HQ25) showed significant reduction ($p<0.05$) in colony counts for all progenitors as compared to control. In conclusion, in utero exposure to HQ able to alter the maternal and fetal HSPCs niche.

Keywords: benzene, toxicity, in utero, hematopoietic stem / progenitor cells, cell lineage.

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SP-31

Elucidating the Effect of Danshen on SH-SY5Y-TauMutant Cellular Model of Alzheimer's Disease

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Alzheimer's disease (AD) is one of the most important medical problems in older population. It is known that the molecular mechanism of AD is complex. The production and accumulation of amyloid-β at the beginning of the disease does not completely explain the underlying mechanism of AD. Tau protein arises as a second important factor that is responsible for the subsequent underlying mechanism of AD. Tau protein is part of the family of microtubule associated protein (MAP) that is normally enriched in axons. Tau have been reported to be present in a hyperphosphorylated state in AD patients, producing accumulation of neurofibrillary tangles (NFT) which one of the hallmarks of AD. In recent years, scientific literatures reported that *Salvia miltiorrhiza* or Danshen potentially acts as a natural therapeutic agent in AD. Danshen have abundance of neuroprotective effects such as antioxidant, anti-inflammation, anti-apoptosis and high potential to enhance cholinergic signalling. Therefore, this study aims to elucidate the toxicity effect of Danshen on Alzheimer's disease cellular model using SH-SY5Y-TauMutant cell line. The SH-SY5Y-TauMutant cell line was differentiated into matured neuron and treated with Danshen extract for 24 hours with range of concentrations (0-100 µg/mL). After 24 hours of treatment with Danshen, cell viability was performed using MTS assay. Results showed the treatment with Danshen extract for 24 hours increased viability of SH-SY5Y-TauMutant cells compared to untreated cells. The optimum concentration was obtained at 40ug/ml. In conclusion, Danshen was potential increase the viability of SH-SY5Y-TauMutant cells and might act as a significant therapeutic agent for targeting tau protein in cellular Alzheimer's disease model.

Keywords: Alzheimer's disease, Danshen, tau protein, SH-SY5Y cell line.

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SP-32

Tocotrienol Rich Fraction Reduced the Estrogen-Like Effects Induced by Bisphenol F

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Bishenol F (BPF) acts as endocrine-disrupting chemical causing male reproductive hormone disturbance. Tocotrienol Rich Fraction (TRF) is a well-known antioxidant, however its effect on the levels of male reproductive hormones is remain unclear. Therefore, this study was carried out to evaluate the effect of TRF on the male reproductive hormones and testicular morphology in Sprague Dawley rats induced by BPF. Male Sprague Dawley rats (n=40) were divided into 5 groups: control, TRF (EVNol SuprabioTM: 100 mg/kg group), BPF (BPF: 10 mg/kg), BE50 (BPF+TRF:50 mg/kg) and BE100 (BPF+TRF:100 mg/kg). All the substances were be given orally via force-feed needle for 28 days. At the end of experimental periods, blood was taken for determination of luteinizing hormone (LH), testosterone (T) and estradiol (E2) levels and testes for histological observation. The results showed TRF at the dose of 100 mg/kg had significantly increased the T levels as compared to the BPF group ($p<0.05$). The testicular histology observation showed TRF had the potential in reducing the estrogen-like effects induced by BPF. In conclusion, TRF able to reduce the estrogen-like effects induced by BPF via its ability to control the testosterone levels in male Sprague-Dawley rats.

Keywords: Endocrine disrupting chemical; bisphenol; steroidogenesis; testis

Funding Information: FRGS/1/2021/STG03/UKM/02/3

SP-33

Optimizing Parameters for CRISPR-Cas9 Mediated Genome Editing of TFIIAγ5 Gene in Somatic Embryos of Malaysian MR219

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Bacterial blight, caused by the pathogen Xanthomonas oryzae pv. oryzae (Xoo), poses a significant threat to rice production in Malaysia. Genetic improvement through targeted genome editing holds great potential for developing resistant rice varieties. In this study, we aimed to confer resistance against bacterial blight in a Malaysian rice variety through precise genome editing by targeting TFIIAγ5 gene using the CRISPR-Cas9 system. Upon transformation with the gRNA-TFIIAγ5 DNA construct, serial optimization process of transformed callus has been carried out involved examinations of several key parameters. These parameters included the size of the callus, the density of the Agrobacterium culture cells, the duration of the drying time, and the co-cultivation period. Through meticulous experimentation and analysis, it was observed that the development of hygromycin-resistant somatic embryos occurred after a period of 8 months post-transformation. Significantly improved transformation rates were achieved by incubating calli within the range of 0.5-2 mm in size with an Agrobacterium suspension having a culture density of OD600 0.2 for a duration of 30 minutes, followed by a drying time of 2.5 hours, and a subsequent co-cultivation period of 2-3 days. These findings highlight the critical role of these optimized parameters in enhancing the efficiency and success of the CRISPR-Cas9 mediated genome editing process, ultimately contributing to the development of bacterial blight-resistant rice varieties with improved transformation rates.

Keywords: rice MR219, Genome Editing of TFIIAγ5, somatic embryos

SP-34

Genetic Analysis of *kelch13* Gene of *Plasmodium knowlesi* in Sabah, Malaysia

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Malaria is caused by the infection of *Plasmodium* parasites, which threatens more than half of the world's population. The *P. falciparum kelch13* gene mutations are associated with delayed parasite clearance after artemisinin-based combination therapy (ACT). However, whether these mutations are present in *P. knowlesi*, which is dominantly reported in Sabah, Malaysia, is unclear. Therefore, this study aims to analyze the diversity of the *kelch13* gene of *P. knowlesi* in the five divisions of Sabah. Ninety-five *P. knowlesi* DNA samples were obtained from the five divisions in Sabah, and the *kelch13* gene was amplified using a nested PCR approach. The amplicons were cloned into a plasmid and subjected to direct sequencing. The sequencing data were aligned and analyzed using MEGA 11 and DnaSP v6 software. The phylogenetic tree constructed based on a neighbour-joining approach using the *kelch13* sequences showed a diverse clade of *P. knowlesi*, with a nucleotide diversity (π) of 0.451 and a haplotype diversity of 0.947. The deduced amino acid sequences were classified into 14 haplotypes, providing evidence of distinct *P. knowlesi* types or lineages in Sabah. Compared to *P. falciparum*, the *kelch13* sequences from this study exhibited a greater π of 0.490 and haplotype diversity of 1.000, indicating the presence of genetic variants of the *kelch13* gene between these two species. Further analysis of the kelch 13 variations at the protein level, including F446I, N458Y, C469Y, and F495L, in *P. falciparum* that were previously reported to be associated with ACT resistance was not observed in *P. knowlesi* isolates in this study. In conclusion, the *kelch13* gene of *P. knowlesi* isolates in Sabah is diverse, with high nucleotide and haplotype diversities. Mutations that confer malarial drug resistance in *P. falciparum* are not observed in *P. knowlesi*.

Keywords: Artemisinin-based combination therapy; Genetic diversity; *kelch13*; *Plasmodium knowlesi*; Sabah

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SP-35

Electrochemical Biosensor for the Rapid Detection of *Pseudomonas syringae* using Colloidal Gold Nanoparticles

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It is challenging to develop molecular diagnostics with rapid and sensitive features. Herein, an electrochemical biosensor using gold nanoparticles was developed for the highly specific detection of plant pathogen DNA (*Pseudomonas syringae*). Firstly, magnetic beads were used to enhance the target DNA after PCR-amplification. The assay detects the PCR-amplified target DNA with the specific DNA probes. The amplified targets were captured using gold nanoparticles labeled with DNA probes, which were subsequently detected using differential pulse voltammetry (DPV). High specificity allowed for the detection of PCR products with as low as 1500 copies. The sensitivity of the assay was greatly improved by 100x to 15 copies of RPA product when PCR was replaced with Recombinase Polymerase Amplification (RPA). Finally, high specificity was also attained in the pathogen DNA detection on the affected plant, showing that the assay has a lot of potential for practical field use.

Keywords: Electrochemical biosensor, colloidal gold nanoparticles, plant pathogen detection

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SP-37

Role of Intermittent Fasting on Aging Molecular Process in Obesity

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Increasing of metabolic imbalance in obesity causes reduced lifespan and speeds up the cellular and biomolecular process of aging. This study aimed to explore the effect of intermittent fasting on FOXO3 expression, proteasome activity and oxidative stress in obesity as parameters that play a role in the aging molecular process. It was randomized clinical trial study conducted on 50 obese males in Jakarta which consist of 25 subjects for the control and 25 subjects for the intervention group. The intervention group did the 5:2 intermittent fasting/IF (2 days fasting in a week, every Monday and Thursday) for 8 weeks. Subject's whole blood was taken before and after intervention for analysis of FOXO3 expression, proteasome activity and oxidative stress by measuring carbonyl, glutathione/GSH, total antioxidant capacity. The increased of FOXO3 expression was significantly higher in IF group compared to control. Proteasome activity increased significantly after following IF for 8 weeks in the intervention group. Carbonyl was significantly lower, GSH and total antioxidant capacity were significantly higher in IF group than the control. Therefore, IF 5:2 for 8 weeks increase FOXO3 expression and proteasome activity as well as decreasing oxidative stress which has a potential benefit for delaying aging process in obesity.

Keywords: Intermittent fasting, FOXO3, proteasome, oxidative stress, obesity

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SP-38

Transcriptomic Analysis of *Drosophila melanogaster* Adult Testes Overexpressing MicroRNA-2b-1

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MicroRNAs (miRNAs) are short RNA molecules, typically about 22 nucleotides in length, that do not code for proteins. Their primary function is to regulate gene expression by binding to messenger RNA (mRNA) and inhibiting its translation into protein. MiR-2b-1 is a member of the miR-2 family, the largest family of miRNAs found in *Drosophila melanogaster*, with a total of eight members. This miRNA family is conserved across invertebrates, highlighting its evolutionary importance. In *D. melanogaster* gonads, miRNAs have been found to be crucial for maintaining the stem cell niche. Specifically, overexpression of miR-2b-1 in adult flies aged 3-5 days leads to the development of testicular bulging, resembling a tumor-like phenotype. This observation suggests that miR-2b-1 has a significant impact on testicular physiology in *D. melanogaster*. An analysis of the effects of miR-2b-1 overexpression revealed that it influences several biological processes. Specifically, it enriches gene ontology categories related to DNA repair, nucleus-related components, and RNA binding activities. These findings provide valuable insights into the molecular mechanisms and pathways affected by miR-2b-1 overexpression in *D. melanogaster*.

Keywords: *Drosophila melanogaster*, miRNAs, mir-2b-1, Testes, Transcriptomics

Funding Information: Fundamental Research Grant Scheme (FRGS) (203/PBIOLOGI/6711778)

SP-39

Fatty Acid Profiling of Oils Isolated from the Seeds of Artocarpus Fruit Species Derived from Sabah

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Edible plant seed oils contain high percentage of unsaturated fatty acids, which have been reported to possess health-promoting effects in human. The high demand of plant seed oils has prompted the search for promising oil crops derived from Sabah. The seeds from Artocarpus species from Sabah such as the Tarap (*Artocarpus odoratissimus*), Cempedak (*Artocarpus chempeden*) and Nangka (*Artocarpus heterophyllus*) have been reported to contain fatty acids, but there is no report on the extensive characterization of the fatty acids of the seeds until today. Therefore, this study is proposed to extensively characterize 37 fatty acids in the seeds of the three Artocarpus species using gas chromatography coupled with flame ionization detector (GC-FID). Of all the three Artocarpus species, Tarap seeds were found to contain the highest unsaturated fatty acids (57.47±5.35%), followed by Nangka seeds (50.04±23.03%) and Cempedak seeds (36.01±15.82%). Tarap seeds were also found to contain a high percentage of a very long chain monounsaturated fatty acid, i.e. nervonic acid (16.68±2.82%), with 24 carbons and reported to enhance the brain functions. The fatty acid profiles obtained from this project will provide insights on the suitability of these seeds to be further developed into health-promoting edible oil, which may benefit the socio-economy of Sabah in the future.

Keywords: Fatty acid methyl ester (FAME); Tarap; Cempedak; Nangka; GC-FID

Funding Information: SBK0455-2021

SP-40

Specific Activity of Lactate Dehydrogenase in Rat Liver and Muscle Tissues Induced by Intermittent Hypobaric Hypoxia

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As the altitude increases, the partial pressure of oxygen will decrease and causes hypobaric hypoxia condition. During hypoxia, the lactate dehydrogenase (LDH) enzyme will be activated. This study analysed rat liver and muscle tissue LDH-specific activity and lactate and glucose levels in blood plasma after intermittent hypobaric hypoxia exposure. Twenty-five Wistar rats were divided into five groups, one control group and four hypobaric hypoxia (HH) exposure groups consisting of group 1 (1x HH), group 2 (2x HH), group 3 (3x HH) and group 4 (4x HH) with a range seven days between exposure. This study found no increase in the specific activity of LDH in liver tissues at 1x HH exposure; LDH is increased at 2x HH exposures and is parallel to the glucose plasma level. Increased LDH-specific activity was found in muscle tissues at 1x HH exposure, which decreased in the intermittent group. This result is parallel to the lactate plasma level. The specific activity of LDH in liver tissue contributes to maintaining glucose plasma levels. However, the specific activity of LDH in muscle tissue contributes to lactate plasma levels after intermittent hypobaric hypoxia exposures.

Keywords: Lactate dehydrogenase; Hypobaric hypoxia; Liver; Muscle

SP-41

Preparation of Heme-Depleted Serum using Ascorbic Acid for the Purpose of Heme Biosynthesis Inhibition Studies

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ABSTRACT NOT AVAILABLE.

SP-42

Autophagy in Early Onset Preeclampsia Placenta through p62 and LC3A Expression was Higher than Normal Term

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Autophagy is associated with the pathogenesis of preeclampsia. Cell in case of lack of nutrition, autophagy is an important factor that is considered in preeclampsia. This study aims to reveal the differences in autophagy protein markers p62 and LC3 in the preeclampsia and normal placenta. Cross sectional design and consecutive sampling methods chose 53 midportion placental tissues from 26 placentas of preeclampsia (PE) from Cipto Mangunkusumo National Hospital and 27 normal placentas (C) were obtained from Budi Kemuliaan Hospital. Relative expression mRNA measured using RT-PCR, SYBR No ROX and Livak method, while LC3 and p62 protein level meassured by ELISA kit. Data resut was not normally distributed, though non parametric Mann-Whitney statistical test was used. LC3 protein concentration of PE was significantly higher than C, p=0,001*. Relative expression of LC3 mRNA of preeclampsia was not significantly higher than C, p=0,5. The p62 protein concentration of PE was not significantly lower than C, p = 0,408. Relative expression of PE p62 mRNA was significantly lower than C, p = 0,006*. Positive correlation between LC3 and p62 mRNA in placenta group of preeclampsia was moderate, r = 0,491, p = 0,0055*. Autophagy (LC3A, p62) in preeclampsia is higher than normal placenta.

Keywords: Autophagy, LC3A, p62, placenta, early onset preeclampsia,

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SP-43

Ruminants and Rabbits as Potential Hosts for SARS-CoV-2: Insights from Pull-down Assay

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The susceptibility of livestock to SARS-CoV-2, the virus responsible for COVID-19, has received little attention despite its importance as a human food source. In this study, we used proteomics to investigate the interaction between the virus's spike glycoprotein (S protein) and the protein extracts from ruminants and monogastric animals. Proteins were extracted from different swine, rabbits, cattle, and goat tissues and subjected to protein quantification and angiotensin-converting enzyme (ACE) activity assay. Our results showed that protein content varied among tissues and livestock species and that ACE activity was present in all tissues, although in varying degrees. The pull-down assay showed that interacting proteins were present in the small intestine, heart, lungs, and small intestine from rabbits, heart tissues from cattle, and small intestine of goats, indicating greater susceptibility to SARS-CoV-2 compared with swine. Further protein identification by LC-MS / MS showed that possible interacting proteins included beta-actin protein, keratin 10, enzyme sucrase-isomaltase, hemoglobin (alpha and beta subunit), angiotensin-converting enzyme, and myosin-7, which is responsible for cardiac muscle contraction. In summary, SARS-CoV-2 most likely uses filament proteins as entry ports to hijack host energy for its replication, causing destructive effects on normal cellular activity and biological processes, particularly in the cardio-respiratory and immune systems. Nevertheless, further studies are needed to confirm the suspicion and to gain a comprehensive understanding of viral epidemiology.

Keywords: Coronavirus, livestock, food safety and security, protein-protein interaction, mass spectrometry

Funding Information: SDK0187-2020

SP-44

Variation in Soil Bacterial Communities' Composition in Different Recreational Park at Hulu Langat Selangor

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The isolation of soil bacteria from environments represents a major challenge, but also an opportunity to characterize the potential impact of pathogenic bacteria on the transmission of microbial disease to human. This study aimed to identify soil bacterial community from Hulu Perdik, Sungai Lopo, Sungai Congkak and Gunung Nuang recreational areas in Hulu Langat, Selangor using next generation sequencing (NGS) targeting bacterial 16S rRNA. DNA was extracted from soil samples collected from four recreational areas and analyzed using next generation sequencing (MiSeq System). Subsequent by read assembly and multivariate statistical analysis were performed to evaluate the data. A total of 39,342,839 contigs, with an average read length of 300 bp was obtained. Metagenomics analysis revealed that *Proteobacteria, Acidobacteriota, Actinobacteriota* and *Bacteroidota* accounting of 41.84%, 17.01%, 8.56 % and 8.49%% were found dominant in all four areas. At the order level, *Burkholderiales* and *Rhizobiales* emerged as dominant group in all areas. Other group such as *Flavobacteriales* (7.13%), *Vicinamibacterales* (6.70%), *Enterobacterales* (5.32%), *Bacillales* (3.33%) dan *Bacteroidales* also been found with a low number. These studies provide an information of microbial diversity associated with recreational areas and might serve as a useful baseline data to public health decision makers.

Keywords: Bacteria, NGS, Pathogenic, Soil

Funding Information: FRGS/1/2018/STG03/UKM/02/1

SP-45

A Comprehensive Phytochemical analysis and its Antidengue Potential of Wild and Cultivated *Schizophyllum commune*

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Schizophyllum commune, commonly known as Kulat Sisir or Cendawan Kukur, has been used widely in Malaysia and Indonesia. Beyond its culinary use, *S. commune* is believed to possess anti-dengue properties. Due to the limited natural resources and huge demand, people tend to cultivate *S. commune* to secure the supply chain. However, variation in quality between wild and cultivated *S. commune* remain a concern. This study aimed to compare the chemical constituents of wild and cultivated *S. commune* samples from different location in Kelantan (Wild: KW), Temerloh (Wild: TW), Kelantan (Cultivated: KC) and Negeri Sembilan (Cultivated: NC). An analytical method based on FTIR, HPTLC and LCMS was used for the simultaneous determination of selected compounds in S. commune. Ergosterol, linoleic acid, 3-methylisoquinoline was used as a chemical marker for phytochemistry analysis. Additionally, the single dose antiviral efficacy of *S. commune* was evaluated through immunofluorescence and plaque assay. The findings suggest that the wild strain of *S*. *commune* may serve as the novel bioactive compounds with effective anti-dengue properties. These findings could lead for future ethnobotanical, nutritional, and pharmaceutical research.

Keywords: Mushroom, *Schizophyllum commune*, Antidengue

Funding Information: Ministry of Health

SP-46

Transcriptomic Analysis of Methicillin Resistant *Staphylococcus aureus* Treated with Silver Nanoparticles-Kaempferol (AgNPs-K)

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a multidrug resistant strain. It 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. 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 treated that treated with AgNps-K. RNAs of non-treated MRSA acted as control. 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. Data analysis revealed that multiple mechanisms of action were involved in antibacterial activity of AgNPs-K towards MRSA.

Keywords: MRSA, Silver nanoparticles, Kaempferol

Funding Information: FRGS/1/2020/STG05/USIM/02/2

SP-47

In Silico Docking Reveals Amygdalin as a Potential Active Herbal Compound for Binding to Multiple CXCL4 Macrophage Receptors

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The effect of active herbal compounds on CXCL4 macrophage receptors remains understudied. This research aimed to determine the binding capability of three active herbal compounds, namely 6-shogaol, amygdalin, and resveratrol, to three CXCL4 receptors. The research method was employed in silico LBDD (ligand-based drug design)-QSAR molecular docking simulation. The results demonstrated that amygdalin compared to 6-shogaol dan resveratrol, exhibited the highest binding affinity among the active herbal compounds for all three CXCL4 receptors. Specifically, amygdalin displayed a binding affinity of -7.7 kcal/mol with CCR1 compared to 6-shogaol with -6.7 kcal/mol and resveratrol in -6.2 kcal/mol, with CXCR3 amygdalin shows -8.7 kcal/mol meanwhile 6-shogaol only -6.4 kcal/mol and resveratrol in -7.1 kcal/mol, and last with CSPG4 amygdalin result was -5.9 kcal/mol follow by resveratrol in -5.2 kcal/mol and 6- shogaol in -4.9 kcal/mol. The findings highlight that amygdalin is likely to bind to CXCL4 receptors, suggesting its potential influence on CXCL4 activity. This research contributes to understanding the molecular interactions between active herbal compounds and CXCL4 receptors, potentially paving the way for further investigations into the therapeutic applications of amygdalin in modulating CXCL4-mediated processes.

Keywords: receptor; CXCL4; CCR1; CXCR3

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SP-49

Assessment of Selected Rice Accession for Salinity Tolerant using Molecular and Morphological Approaches

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Salinity stress research is vital for agriculture because soil salinity significantly limits plant productivity on agricultural lands. The discovery of rice salt tolerance traits and associated molecular mechanisms could aid breeders in improving salt tolerance genetically. In this study, a set of rice accession consisted of 13 rice accessions including susceptible and tolerant checked accession were evaluated using molecular and morphologically. Nine simple sequence repeats (SSR) markers linked to *Saltol* QTL were selected to characterize based on molecular approach. The amplification of the SSR generates a total of 48 alleles. The polymorphism information content (PIC) value ranged from 0.39 to 0.76 with an average of 0.57. The dendrogram analysis based on Unweighted Pair Group Method with Arithmetic Mean (UPGMA) revealed the presence of two major clusters namely7 Cluster I and Cluster II. Cluster I consist of rice accession grouped together with susceptible checked variety meanwhile Cluster II consist of rice accession grouped together with tolerant checked variety. STRUCTURE analysis shows two populations (K=2) that grouped 13 rice cultivars into two groups. Based on pairwise genetic distance analysis based on shared allele, MR307 had the closest genetic similarity with Pokkali and Nona Bokra with 0.63 and 0.36 genetic distances. Based on molecular and morphological analysis, Chali, Guabon-H, MR297, Uban, MR303, MR307 and MR220 were identified as tolerant genotypes. This information provides some useful insight toward future breeding programs potential tolerant genotype.

Keywords: Morphological descriptor, *Oryza sativa*, Salinity tolerance; SSR marker

Funding Information: KRBNA1-1001 & PRB502

SP-50

Optimization of SARS-CoV-2 Pseudotyped Lentivirus Production

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Pseudoviruses have emerged as valuable substitutes for infectious viruses as they possess surface viral envelope proteins similar to wild-type viruses but lack the ability to replicate due to the deletion of pathogenic genes. They are widely employed in studies investigating virus binding mechanism, quantifying antibody and vaccine titers, and conducting antibody neutralization assays. However, there is still a need for an optimized pseudovirus system which includes different constructs and backbone combinations to efficiently produce pseudoviruses. Therefore, our aim was to optimize the pseudovirus conditions to produce effective pseudoviruses for drug screening. Here, we employed two different HIV backbone vectors, to construct pseudoviruses with full-length spike. The vector demonstrated higher transfection efficiency was employed to transfect various cell types, each showing different amenability during the transfection. Furthermore, we optimized the pseudovirus packaging parameters to ensure a sufficient yield of pseudovirus. The resulting SARS-CoV-2 pseudoviruses, produced using this optimized protocol, were characterized and validated for their functional infection response. In conclusion, flexibility to manipulate and modify pseudovirus constructs with variant genes will greatly accelerate drugs and vaccines development against emerging SARS-CoV-2.

Keywords: Spike protein; Pseudoviruses; SARS-COV-2

Funding Information: SDK0198-2020

SP-51

Development of *Mitragyna speciosa* (ketum) Simple Sequence Repeat Markers

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Ketum (*Mitragyna specciosa*) is narcotic tropical plant belong to Rubiaceae family that indigenous to Southeast Asian countries. In Malaysia, there are various ketum species that grown well and has potential medical properties. *Mitragyna* species is a narcotic plant and forbidden for commercialization production in Malaysia. Authentication identification of *Mitragyna* species is essential for elite *Mitragyna* species for commercial once it legalize by Malaysian government. Ketum SSR has been mined from *M. specciosa "Rifat"* genome from Medicinal plant Genomic resources (http://mpgr.uga.edu) and identified 499,985 potencial SSR from 16,534 scaffold. 3 highest scaffold with SSR distribution were scaff 336 (7282 SSR), scaff 128498 (7038 SSR) and scaff 128390 (6875 SSR). The majority motifs of SSR distribution were dinucleotide. (656,595), follow by oleh trinukleotida (81,861) and tetranukelotida (30,104). TG/AC/TC motif from dinucleotide and TTC/GAA/AAG motif fom trinucleotide showed highest motif distribution. Total of 3445 SSR were designed for primer designed and 100 SSR were selected for oligoprimer synthesis. 60 SSR primers has been succeeded to produce PCR product and used to genotype ketum accession collected from different location in Malaysia peninsular. Ketum phylogenetic tree has been generated that consists of 2 clusters.

Keywords: *Mitragyna species, Simple sequence repeat (SSR) and Phylogenetic tree*

SP-52

Development of Functional Marker Targeting Pita2 Gene, a Blast Resistant Gene in Rice

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Blast disease, which is caused by *Magnoparthae oryzae*, is one of the devastating biotic stresses in rice that results in yield losses. Cultivation of the resistant rice varieties has been proven as an environment-friendly and effective approach to address this problem. As such, this study developed a high-quality functional marker of Pita2 gene, a resistant gene that controls blast disease resistant in rice. In this study, the mapping population of MR211 X IRBLta2-Re was generated. The F2 population was used for genotyping purposes, while the F2:3 lines were employed for phenotyping purposes. Both genotyping and phenotyping data were used in association analysis to narrow down the Pita2 region. A total 36 SNP markers were developed to genotype the mapping population. Out of 36 SNPs, only 33 SNPs exhibited acceptable call rates, and followed the Mendelian ration of F2 population (1:2:1). Association analysis revealed one nonsynonymous SNP shows significant in controlling blast resistant in rice. The application of the developed SNP marker is bound to enhance both efficiency and accuracy in the selection. The linkage drag phenomenon may be minimised as well as the marker targeting only the functional polymorphism of the gene.

Keywords: Blast; *Magnoparthae oryzae*; SNP marker

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SP-53

Physicochemical Quality of *Musa acuminata* × *balbisiana* Fruit Affected by Hydro-cooling and Storage Temperature

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Saba banana or *Musa acuminata* × *balbisiana* is a well-known cultivar utilized for commercial production mostly in the Philippines. Generally, bananas will rapidly ripen and alter until fully deteriorate with the presence of high temperature and causes an acceleration of biochemical activity, which results in fruit tissue damage and spoilage. Hydro-cooling is one of the pre-cooling techniques that can minimize the heat field and slow down the ripening process. In this research, experimental works on hydrocooled Saba banana at 8℃ (T1) and 10℃ (T2), then stored at cold temperature 11±2℃ (FT) and 15±2℃ (CT) and room temperature 26±2℃ (RT) for 4 weeks duration were conducted. On day 28 an analysis of Saba banana found fruits hydrocooled at T1 and T2 then stored in CT showed lower weight loss at 39.92 g and 35.01 g. Higher visual appearance value with low defects percentage was recorded for both hydro-cooling treatments which stored in CT at 25-50% defects. Fruit firmness for both hydro-cooling treatments and stored at CT remains high at 8.53 kg/cm^2 and 8.63 kg/cm^2. Total soluble solid and titratable acidity for both hydro-cooling treatment and storage CT and FT remains low compared to banana stored at RT which shows drastically increased at days 7. pH value for both hydro-cooling treatments and cold storage temperatures remains high, ranging from around 6.56 to 7.29 as indicated the banana is still unripe. The results indicate that Saba banana fruits pre-cooled with hydro-cooling (8℃, T1 and 10℃, T2) and stored in cold storage at 15±2℃ (CT) shows better physicochemical quality in Saba banana fruits.

Keywords: Saba banana; Hydrocooling; Storage temperature; physicochemical quality

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SP-54

Study of Chemoresistance Mechanisms and Potential Alternate Therapy in Colorectal Cancers

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Chemoresistance in colorectal cancers (CRC) poses a significant challenge, with insensitivity to apoptosis induction being identified as the primary culprit. Ferroptosis, a non-apoptosis programmed cell death (PCD) pathway that operates independently of most other PCDs was suggested as a potential avenue for overcoming chemoresistance lately. Therefore, we aimed to explore the potential of ferroptosis inducers in addressing the chemoresistance of CRC in this study. Adaptive cisplatin-resistant cell lines (HCT116/I24781, HCT116/I248 and HCT116/I555) with at least 15-fold higher cisplatin resistance were developed from HCT116 cells, with HCT116/I24781 exhibiting the strongest and most stable cisplatin resistance. Synergistic interaction between ferroptosis inducer RSL3 and cisplatin was observed in both HCT116 (CI = 0.7587) and HCT116/I24781 (CI = 0.6060) cells, with resistant cells displaying a more pronounced synergistic effect. Combined treatment activated a higher level of caspase-3 activity in the resistant cells, demonstrating the potential of ferroptosis inducer RSL3 in overcoming cisplatin resistance in CRC. Intriguingly, inhibiting caspase activity using pan-caspase inhibitor zVAD-fmk or using ferroptosis inhibitor ferrostatin-1 both failed to rescue cell death induced by combined treatment in HCT116/I24781. These findings suggest that the combined treatment induced a non-ferroptosis, caspase-independent cell death specifically in resistant cells that are worth further in-depth investigation on the mode of action.

Keywords: Chemoresistance; Cell death; Colorectal cancer; Apoptosis; Ferroptosis

SP-55

Antihyperglycemic Effect of *Bruguiera gymnorrhiza* Root Extracts in Streptozocin-induced Diabetic Mice

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Mangrove plants are believed to possess a wide range of bioactive compounds due to their ability to thrive in harsh conditions such as high salinity, low air humidity and high temperature. *Bruguiera gymnorrhiza* is one of the mangrove species that is commonly found in Sabah and its root has been discovered to have antidiabetic activity. However, previous investigations focused solely on ethanolic extract of *Bruguiera gymnorrhiza* root (BGR). Thus, this study aimed to assess antihyperglycemic activity of BGR methanolic extract in various fractions (aqueous, butanol, chloroform) using streptozocin-induced diabetic mice as an experimental model. The diabetic mice were administered different fractions of BGR extract at dose of 250 mg/kg, while standard drug, Metformin (200 mg/kg), served as reference. Blood glucose levels were measured on day 0th, 7th and 14th following the oral administration of BGR fractions in a fasting state mice. After 14 days treatment period, the results showed that the aqueous fraction of BGR extract significantly reduced the blood glucose levels in diabetic mice compared to other BGR fractions. The significant antihyperglycemic effect observed in aqueous fraction of BGR extract strongly indicates the presence of major potent antidiabetic components for decreasing the elevated blood glucose levels in diabetic mice.

Keywords: *Bruguiera gymnorrhiza*; Mangrove; Diabetes; Antihyperglycemic

Funding Information: SDG0920

SP-56

Physical Characteristics of Saba Avocado Cv. QAV 1 Fruit at Different Maturity Stages in Relation to Oil Content

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In Malaysia, avocado was planted by small holder and grown as monocrop as Sabah was the sole producer state in Malaysia cultivating avocado with 134.00 Ha land producing 268.60 Mt of Avocado with 169.40 Mt located at Tenom (Department of Agriculture, 2021). With the high demand and opportunities in the global market, local cultivar of avocado has potential to be developed as a new commercial crop in Malaysia. This fruit is not easy to determine the exact maturity time for harvest leaving the critical decisions and subjective interpretation to local farmers putting profit in huge risk. Fruits were harvested at different maturity stages (18, 20, 22 and 24 weeks after fruit set). Results indicated that oil content and dry matter highly significant (P≤0.001) with 6.43% oil content and 16.98% dry matter where it has strong positive correlation (r=0.98) at different harvesting stages. The pulp firmness and colour are not significantly different at different harvesting stages. The physical characteristics are important in defining the ideal harvesting time of local avocado. For that reason, this study was conducted to determine the physical characteristics of avocado fruit at different harvesting stage as it is important for local growers to manage production meeting the industrial demand and achieving optimum profits.

Keywords: Avocado, fruit growth, oil content, physical characteristics, harvesting stages

SP-57

Phytochemical Composition and Toxicological Evaluation of Bosom Oil: Exploring its Therapeutic Potential for Pain Relief and Wound Healing

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Bosom oil, a formulation derived from Bambangan seed and other synergistic plant extracts, has gained attention for its potential therapeutic benefits, particularly in pain relief and wound healing. Despite its potential benefits, a comprehensive scientific study exploring the phytochemical profile and toxicological aspects of Bosom oil for pain relief and wound healing remains lacking. This study aims to bridge the existing knowledge gap by conducting an in-depth investigation into the properties of Bosom oil. The primary objective is to analyze its phytochemical composition to identify the bioactive compounds responsible for its therapeutic potential. The sample collection was freeze-dried, ground, and stored for future analysis. The extraction procedure included vortexing the ground samples with a solvent, followed by sonication and maceration in a thermo shaker incubator. Centrifugation was performed to separate the supernatant, which was then dried using an Eppendorf concentrator. The resulting mother stock was dissolved in methanol and stored at -20°C for further analysis. The bioactive compounds present in the extracts were analyzed using chromatography assays, enabling the identification of the phytochemical profile of the aqueous extract. The outcomes of this study are expected to shed light on the bioactive compounds responsible for the pain relief properties of Bosom oil, with the aim of exploring its potential use in alleviating other types of pain, such as menstrual pain and breast soreness. In conclusion, this investigation holds promise for the development of a natural and effective remedy for pain management and wound healing, with potential applications in healthcare and pharmaceutical industries.

Keywords: Toxicology, Bioactive compounds, Therapeutic potential

SP-58

Potential Role of TGM2 in Cancers and Its Association with Resistant Oral Cancer-Derived Extracellular Vesicles

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Transglutaminase 2 (TGM2) is a multifunctional protein implicated in various pathological conditions. Previous proteomic profiling demonstrated high levels of TGM2 in extracellular vesicles (Evs) isolated from cisplatin-resistant oral squamous cell carcinoma (OSCC) cells. Consequently, we hypothesized that upregulation of TGM2 contributes to poor prognosis in cancers and that its presence in Evs could be a potential drug responses indicator. To investigate the prognostic value of TGM2, bioinformatic analysis was conducted, revealing a significant association between elevated TGM2 expression and poorer overall survival rates in head and neck cancer. Further examination of TGM2 regulation was performed in H-series OSCC cells with varying cisplatin sensitivities. Western blot analysis demonstrated higher TGM2 levels in cisplatin-resistant H314 cells compared to cisplatin-sensitive H103 cells, indicating a positive correlation between TGM2 expression and cisplatin resistance in OSCC cells. TGM2 transamidation activity assays revealed increased cross-linking activity upon cisplatin treatment, suggesting that cisplatin exposure enhances TGM2 activity. Moreover, significantly higher TGM2 levels were observed in H314-derived Evs, suggesting the abundance of TGM2 inside Evs showed positive correlation with cisplatin resistance with OSCC. Collectively, these findings highlight the possible association of TGM2 with cisplatin resistance, and its level in EV serves potential in predicting cisplatin sensitivity in OSCC.

Keywords: oral squamous cell carcinoma; transglutaminase 2; extracellular vesicles; bioinformatics; chemoresistance

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SP-59

RNA Sequencing and Analysis of *Gigantochloa levis* Tissues

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Bamboo is one of the most important non-timber forest plants in the world. The bamboo forest in Sabah is rich in diversity, with *Gigantochloa levis* being one of the dominant species. In this study, high-throughput RNA-Seq was performed on *G. levis* tissues (leaf, shoot, and stem) using the Illumina NovaSeq platform. Total RNA was extracted from the three tissues using the *TransZol* UP Plus RNA Kit, according to the manufacturer's instructions with modifications. The total RNA was successfully extracted with concentrations were between 594.6 ng/µl and 981.4 ng/µl. The $A_{260/280}$ and $A_{260/230}$ absorbance ratios ranged from 2.17 to 2.20 and 2.20 to 2.25, respectively, while RIN were between 8.3 and 9.2. Illumina platform generated the least amount of raw reads from leaf tissues, with 234,823,160 reads, and the most from shoot tissues, with 275,274,528 reads. The percentage of clean reads was >98.0% for each sample and the Q30 values were between 90.12% and 90.63%. The clean reads were mapped to the moso bamboo reference genome using Bowtie2. The overall alignment rate ranged from 46.87% to 74.29%. The findings of this study are expected to be valuable resources for future genetic and functional genomic studies on this important bamboo species.

Keywords: RNA extraction; RNA-seq; *Gigantochloa levis*; Bowtie2

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SP-60

Phylogenomic Analysis Reveal Close Relationship between Weedy Rice Variants with Commercial Rice Varieties

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Weedy rice is taxonomically categorized as the same species as cultivated rice (Oryza sativa), but it is distinguished mainly by seed shattering and dormancy character, which appear to increase their distribution which significantly led to yield reduction. The aims of this study are to determine the genetic diversity and differentiation of weed rice accessions from Peninsular Malaysia and to explore the possible origin of these weed accession by comparing their genetic relatedness to rice cultivars (*O. sativa*) and wild rice (*O. rufipogon*) based on whole genome variation. Genomic analysis of 27 accessions which consisted of 15 commercial/cultivated cultivars, 10 weedy rice accessions and two accessions of wild rice revealed all the weedy rice accession were closely related to commercial/cultivated rice varieties especially mega varieties (MR297 and MR219) but distantly related to wild rice. The Neighbour Joining based dendrogram revealed two major clusters were formed namely Cluster 1 and Cluster 2. Cluster 1 consist of wild rice only meanwhile Cluster 2 consisted of weedy rice and rice cultivars. The result was supported by principal component analysis (PCA) based on SNP markers. This suggested the studied weedy rice accessions were evolved from commercial rice varieties rather than wild rice. The study provides an insight towards an approach need to be taken in order to solve the weedy rice problem. The rich of genetic diversity in weedy rice accession accompanied with direct seeded approach will complicate to control the weedy rice in the future and subsequently jeopardise rice production. Thus, an effective and efficient approach to control and manage weedy rice must be developed to prevent weedy rice from extensive spreading and infestation across all rice-planting areas in Malaysia.

Keywords: Genetic relationship; Phylogenomic; red rice; SNP marker

Funding Information: KRBNA1-1001

SP-61

Comparison of Glutamate and γ-Aminobutyric Acid (GABA) Effect on Peripheral Blood Mononuclear Cells (PBMC) Proliferation

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Glutamate and GABA are monoamine molecules that regulate nerve cells. These compounds also have receptors on immune cells. Glutamate and GABA regulation of immune cells include chemotaxis, differentiation, proliferation and apoptosis. Aim of this study is determining proliferation rate of PBMC stimulated with glutamate compare to GABA. The proliferation rate was assessed by trypan blue method. PBMC was collected from 10 healthy male donors. Isolated $7x10^5$ PBMCs were stimulated with Glutamate or LPS or LPS+GABA or untreated, incubated for 24 hours 5 % CO_2 37 ^oC in a complete medium of amino acids, vitamin B complex and ions. An increase in proliferation both in glutamate and GABA treated group with viability increase of 17% glutamate, 4% LPS, 10% GABA than control group. It was suggested that Glutamate and GABA has role as metabolite in mitochondria. As conclusion, these results suggest that Glutamate and GABA have positive impact on cellular proliferation supporting energy metabolism and cellular longevity in healthy human PBMC.

Keywords: Proliferation; PBMC; Glutamate; GABA

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SP-64

Evaluation of Tissue Engineered Oral Mucosa Model (TEOM) for Oral Mucosal Drug Delivery

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Fabrication of TEOM that retains the structure, differentiation status and permeability of native oral mucosa remains a significant challenge for researchers. Extensive characterization needs to be performed to ensure that the TEOM is a reliable replica of oral mucosa and suitable for downstream applications. This study aimed to characterize TEOM and assess drug toxicity and delivery of novel oral patches containing clobetasol propionate (CP). Histologically, TEOM mimicked native oral mucosa displaying a stratified epithelium, fibroblast-containing connective tissue and basement membrane. TEM confirmed the presence of desmosomes and hemidesmosomes in the epithelium. IHC revealed the expression of differentiation (cytokeratin 4,13,14), proliferation (Ki-67), and cell adhesion (e-cadherin, claudin-4) markers. The maximal viability and TEER were found on days 25 and 20, respectively. Permeability analysis showed that only small molecules (3 kDa) could pass through the epithelium. Novel electrospun patches containing CP exhibited good physicochemical characteristics and drug release profiles, and toxicity testing revealed that the compound was considered a non-irritant. CP could be detected in theissuees and receptive medium after one hour of patch exposure. In conclusion, TEOM demonstrated robust characteristics that are highly desirable for testing candidate drugs and drug delivery systems intended for administration to the oral mucosa.

Keywords: Tissue Engineered Oral Mucosa Model; Oral Mucosal Drug Delivery; Oral patches; Drug toxicity; Clobetasol propionate

SP-65

Antifungal Properties of *Alpinia conchigera* Against Oral Candida

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The concern of aspiration pneumonia in immunocompromised individuals associated with poor oral health conditions has raised worldwide attention. 1'-S-1'-Acetoxychavicol acetate (ACA) from *Alpinia conchigera* rhizome is proposed as a potential antifungal agent against opportunistic pathogenic oral *Candida* species, including *Candida albicans*, *Candida glabrata* and *Candida tropicalis*. This study aimed to determine the antifungal potential of ACA against *Candida albicans* ATCC 14053, *Candida glabrata* ATCC2001, *Candida tropicalis* ATCC 750, and 8 other species of clinically obtained *Candida* consisting of *Candida albicans*, *Candida glabrata* and *Candida tropicalis*. The antifungal activities of ACA were determined through Minimum Inhibitory Concentration (MIC), Minimum Fungicidal Concentration (MFC), time-kill assay and Scanning Electron Microscopy (SEM) tests. The study revealed that ACA exhibited both inhibition and killing activity on the growth of all tested pathogens with MIC and MFC values ranging from 1.5 to 25.0 mg/mL. In time-kill assay, ACA showed complete eradication at MIC values in most of the tested species within 2 to 8 hours. Changes in the external morphology of *Candida* after being treated with ACA were studied through observation under SEM. The morphology of selected *Candida albicans* was deformed by ACA. In conclusion, ACA has a great potential as an antifungal agent against the tested *Candida* species by disrupting the external structure.

Keywords: Aspiration pneumonia; Acetoxychavicol acetate; Antifungal; Oral *Candida*

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SP-66

Chitin Extraction from Black Soldier Fly (*Hermetia Illucens)* Pupal Exuviae using Natural Deep Eutectic Solvent: An Eco-Friendly Approach

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Chitin and its deacetylated derivative, chitosan, are natural polymers commonly obtained from exoskeleton of crustaceans. They are used in numerous applications including agriculture, textile, and biomedicine. However, the current industrial extraction of chitin is based on a non-environmentally friendly chemical process, using strong acid and alkali. In this study, a greener approach using a natural deep eutectic solvent (NADES) (choline chloride-lactic acid ([Ch]Cl:LA) was used to extract chitin from pupal exuviae of black soldier fly (BSF). The extracted chitin was later deacetylated into chitosan using 40% NaOH at 80°C. The effectiveness of different dissolution times, temperatures, and the initial mass of BSF pupal exuviae to the chitin and chitosan produced were determined. The chitin and chitosan extracted were characterized using ATR-FTIR, TGA (Thermogravimetric Analysis) and SEM (Scanning Electron Microscopy). The highest chitin yield was obtained after 6 hours of dissolution time, at 80°C, and the initial BSF mass of 10 g (p-value<0.05). FTIR analysis revealed that BSF chitin was α-chitin, closely resembling commercial chitin (shrimp), with a degree of deacetylation of the resulting chitosan ranging from 73% to 82%. The result confirms the potential of NADES as a greener solvent for chitin extraction from BSF which can be deacetylated into chitosan.

Keywords: Chitin; Chitosan; Black soldier fly; Pupal exuviae; NADES

Funding Information: FRGS/1/2021/STG03/UIAM/02/3

SP-67

Evaluation of Wound Healing Properties of *Tualang* Honey Against Primary Oral Fibroblast Cells

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Honey is widely acknowledged for consisting multifaceted health benefits that are useful for wound healing regeneration and could be exploited as an alternative supplement to aid in regenerating the primary cells which have limited lifespans and propagation. This study aimed to evaluate the regenerative properties of *Tualang* honey (TH) (IT House Company, Selangor) supplemented with various concentrations against the primary oral fibroblast (POF) cells. The effect of TH against POF showed that the cellular viability was affected in a concentration- and time-dependent manner. The regenerative effect of TH was observed at low concentrations (0.09% – 1.56%) without affecting the morphology of the cells analyzed by using MTT assay and inverted microscope (Olympus CKX53). For the scratch assay, the wound regenerated rapidly at concentrations of 0.19% and 0.39% TH at 24 hours and 48 hours, respectively, compared to the control ($p < 0.05$). For the Growth Inhibition Assay using Mitomycin C, concentrations of 0.1%, 0.3%, and 3.1% TH were able to regenerate the growth of POF cells. Overall, TH has shown the potential in regenerating wounds of POF without altering the morphological properties at low concentrations. However, the inhibitory effects of TH were exhibited at high concentrations against POF cells.

Keywords: *Tualang* honey; Primary oral fibroblast cells; Wound healing properties; Regenerative properties; Inhibitory properties

Funding information: FRGS/1/2020/STG05/USIM/03/1

SP-68

Isolation and Morphological Identification of Mycorrhizal Fungi from Epiphytic Orchids, *Aerides odorata* Lour

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Most orchid species depend on a mutually beneficial partnership with endophytic mycorrhizal fungi for seed germination and seedling growth. Nevertheless, not all mycorrhizal fungi exhibit this relationship. *Aerides odorata* Lour, an epiphytic orchid, exhibits a wide range of endophytic fungi that assist the plant through nutrient supplementation and the synthesis of plant growth regulators. Thus, this study aims to isolate and identify the mycorrhizal fungi from *A. odorata* that may promote seed germination. The potential fungi are obtained by isolating them from the healthy root tips of two mature plants cultured on potato dextrose agar (PDA). These isolated fungi are then characterised based on morphological characteristics (colony texture, colony colour (above and below), radial growth rate, growth pattern, sclerotia presence, hyphal diameter and length). A total of 60 endophytic fungi, with 28 fusarium and 32 yet to be identified, have been successfully isolated. The isolated fungi will be used for symbiotic seed germination tests in the next stage of this study. The techniques developed for this orchid species will enable the isolation and precise morphological identification of mycorrhizal fungi.

Keywords: Epiphytes, Fungi, Isolation, Identification, Morphology

Funding Information: GUG0599-1/2023

SP-70

Species Distribution, Antibiotic Susceptibility Profiles, and *Van* Gene Frequencies among Enterococci Isolated from Patients at Queen Elizabeth Hospital in Kota Kinabalu, Sabah

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The rise in drug resistance to antibiotics used to treat Gram-positive bacterial infections has complicated the treatment of enterococcal infections. Resistance to vancomycin, one of the most potent antibiotics, is a major concern as enterococci exhibit both intrinsic and acquired resistance. The purpose of this study was to identify the species type, antibiotic susceptibility profiles, and *vanA*/*vanB* gene frequencies in enterococci isolated from hospitalized patients at Queen Elizabeth Hospital in Kota Kinabalu, Sabah. Various clinical body fluid specimens, including stool, urine, pus, cerebrospinal fluid, and blood samples, as well as high vaginal and tracheal swabs, were collected from 162 patients between July 2009 and June 2021 and processed for isolation and DNA extraction. VITEK 2 (bioMérieux, Inc., Durham, NC) Automated System was used for species-level confirmation and susceptibility testing, and PCR was subsequently used to determine *vanA*/*vanB* gene carriage. Species identification revealed five enterococcal species, including 91 *E. faecalis*, 64 *E. faecium*, 3 *E. gallinarum*, and 1 isolate each of *E. hirae* and *E. avium*. Resistance to antibiotics and *Van* gene frequencies was generally low. No vancomycin resistant isolates were found in the rare enterococcal species. The antibiotic resistance patterns of clinical *enterococcus* isolates suggest the emergence of low vancomycin resistance with an increased rate of multidrug-resistant enterococci in a tertiary hospital Kota Kinabalu Sabah, which can contribute to major therapeutic options being limited. Therefore, in environments with limited resources, species-level identification of enterococci is required to inform infection control and enterococcal infection treatment.

Keywords: *Enterococcus*, *Enterococcus faecium*, *Enterococcus faecalis*, Vancomycin resistant enterococci, Kota Kinabalu Sabah

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SP-71

Detection of Selected Pathogenic Bacteria from Non-Conventional Types of Bat Tissues

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Bats unavoidably pose a hazard to human health as reservoirs for more than 60 zoonotic diseases. Bat-human contact increases as a result of habitat degradation brought on by human encroachment and bats' peridomestic roosting habits in cities. Their link with pathogenic bacteria transmission is fuelled by the capability to host multiple zoonotic viruses simultaneously and transmit them to humans in several ways. Blood samples are typically regarded as the gold standard in detecting pathogens for the majority of zoonotic disease studies since the methods are practical and give reasonably accurate results. Therefore, the purpose of this study is to assess other tissues besides blood as potential genetic materials for the detection of bacterial pathogens in the bats' population of Sabah. For this purpose, samples were obtained from several protected forest areas and also from an urban settlement in Sabah. Specimens were excised for their blood (n=26), liver (n=65), muscle (n=18), lungs (n= 6), gut (n=6) spleen (n=6), kidney (n=6), heart (n=6) and intestine (n=10). DNA was isolated from these specimens and subsequently PCR-based detection of six bacterial pathogens namely, *Bartonella* spp., *Rickettsia* spp., *Brucella* spp., *Ehrlichia* spp., *Leptospira* spp., and *Coxiella* spp. were conducted. We found positive detection of *Brucella* spp. (n=6) and *Ehrlichia* spp. (n=3) from the liver samples collected from *Rhinolophus* sp. and *Kerivoulinae* sp. samples. Meanwhile *Coxiella* spp. has been detected from liver, lungs and gut samples of *Cynopterus minutus*, *C. brachyotis*, *C. sphinx* and *Myotis muricola*. The results provided a fresh perspective on genetic sample collection for bacterial studies. They present researchers with an opportunity to utilise zoological specimens from museums and repositories, which is more feasible than collecting blood samples. This is particularly advantageous when conducting research in remote areas such as Sabah's interior or insular islands, as it allows for the preservation of various tissues.

Keywords: Bats, Bacteria, Non-conventional, Pathogens, Tissue, *Brucella*, *Ehrlichia*.

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SP-72

Mesenchymal Stem Cells Respond against Inflammatory Microenvironment through NLRP3 Inflammasome Expression

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Along with the development of cell-based therapy, the survival and function of the transplanted cells in an inflammatory microenvironment have become a crucial consideration. Mesenchymal Stem Cells (MSCs) are one of the most frequently applicated cells in clinical cases. NLRP3 inflammasome is currently known as one of the culprits in many pathological conditions related to inflammation. In this study, we investigated the responses of MSCs under the inflammatory microenvironment and the possible NLRP3 pathway involvement. We used lipopolysaccharide (LPS) to induce inflammatory conditions in vitro, which was applied for 24 and 48 hours of 10 µg to MSCs. We then analyzed the cell morphology, viability, and migratory ability, followed by the expression of NLRP3 inflammasome and TLR4. The Results showed that the inflammatory environment attenuates the regenerative potential of MSCs by significantly ($p<0.05$) impairing their viability and migratory capacity, especially at 48h of LPS induction, followed by the increased expression of NLRP3 inflammasome and TLR4. Our results indicate the possible role of NLRP3 inflammasome in MSCs impairment under inflammatory conditions.

Keywords: Mesenchymal stem cells, lipopolysaccharide, microenvironment, NLRP3 inflammasome

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SP-73

Thiamine Binding Protein from Peanuts *(Arachis hypogaea L)*, Bogor Groundnuts *(Vigna subterranea {L.) Verdc. syn. Voandzeia subterranea (L.) Thouars)*, and Red Beans *(Vigna angularis var. Nipponensis)*

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Thiamine (Vitamin B1) has various functions in the body, primarily playing a crucial role in energy metabolism. Organs that are highly sensitive to thiamine deficiency are the nervous system and the heart, which can lead to symptoms of polyneuritis and cardiovascular diseases, causing various serious problems. Therefore, it is highly important to measure thiamine levels in bodily fluids using an easy and cost-effective method without compromising sensitivity and selectivity. An option for this is thiamine measurement analogous to ELISA principle, known as ELPLA (Enzyme Labelled Protein Ligand Assay), where thiamine-binding protein (TBP) acts as a substitute for antibodies. The objective of this study is to determine qualitatively and quantitatively the thiamine binding protein in red beans, peanuts, and Bogor groundnuts. The protein is isolated and purified using, sequentially, 90% salting out (w/v), dialysis, gel filtration chromatography (Sephadex G 100), ion exchange chromatography (DEAE cellulose), affinity chromatography, and Ninhidrin reaction test. The results show that all three sources, when tested with Ninhidrin, contain TBP, with the highest pure yield found in red beans at 1.116 mg/mL, followed by peanuts at 0.997 mg/mL, and Bogor groundbeans at 0.901 mg/mL. TBP from all three sources exhibits a negative charge, as demonstrated by cellulose acetate electrophoresis.

Keywords: red bean, peanut, bogor groundnut, thiamine binding protein, isolation and purification

SP-74

Chemical Profiling and Bioactivity Assessment of *Etlingera coccinea* (Blume) S. Sakai & Nagam.

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Etlingera coccinea (Blume) S. Sakai & Nagam belongs to the *Zingiberaceae* family, is widely distributed across various regions in Southeast Asia. It possesses a distinct pungent fragrance and holds a special status as a delicacy by the Kadazan Dusun people in Sabah, Malaysia. The inner stem and its florescence are consumed, and the entire plant holds significant value in traditional medicine. Due to its importance within local community, this research was undertaken to study its chemical composition and potential biological properties. Samples were collected from six distinct localities in Sabah, namely Ranau, Sandakan, Danum, Ulu Kimanis, Paitan and Long Pasia. The yield of essential oils extracted using hydrodistillation technique were in the range from 22.33% - 30.50% of its fresh weight. The extracted oils underwent chemical profiling using GC-MS analysis and were evaluated for their antimicrobial activity. Throughout the investigation, a total of 29 different volatile compounds were identified in the essential oil samples, with neral, dodecanal and citronellyl propionate as major compounds. The essential oils derived from all specimens exhibited significant inhibition against the tested microbes excluding of *Bacillus* sp., *Salmonella typhin*, *Salmonella thyphymunium* and *Listeria monocytogenes.* Nevertheless, further study is necessary to determine the specific bioactive compounds responsible for the bioactive potential in this particular species.

Keywords: Essential oil, chemical profiling, antimicrobial

SP-75

Effective Encapsulation for Improved Survival of *Lactobacillus plantarum* in Simulated Gastrointestinal Tract Conditions

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Probiotic is defined by microorganisms that survives the extreme conditions of the host as mostly described by simulated gastrointestinal tract (GIT) condition. In a way to ensure the survival of the mircoorganisms and survive at the targeted area (intestine), an encapsulation technology is applied to protect and thus guarantee the viability of the cultures. Encapsulation by extrusion method was applied to *Lactobacillus plantarum* C33C in calcium-alginate microcapsule to protect the cultures from extreme conditions of GIT. The microencapsulated L. plantarum was tested for its tolerance on different pH conditions which were pH 6.5, 2.0 and 7.2 to indicate the simulated conditions of oral, stomach and intestine conditions, respectively. Sequential protocol was also applied to evaluate the viability of the cultures after exposed to the three different conditions sequentially at respective time. Generally, the microencapsulated L. plantarum survived in all three GIT conditions with only 2 log reduction after 120 min incubation time in each GIT conditions as compared to more log reduction resulted from non-encapsulated *L. plantarum*. In addition, sequential exposure to different GIT conditions showed lower number of log reduction compared to non-encapsulated *L. plantarum* as indication of higher viability of microencapsulated than free *L. plantarum* during the simulated GIT. In conclusion, encapsulation in calcium-alginate microcapsules improved the survival of the cells from extreme GIT conditions as well as ensure its delivery to the targeted area for the host to absorb its health functions effectively.

Keywords: Encapsulation; *Lactobacillus plantarum*; Simulated Gastrointestinal Tract; Probiotic;

Funding Information: P-RB502-1001

SP-76

Antagonistic Potential of Rice Bacterial Endophytes Against Sheath Blight and Brown Spot Pathogens, *Rhizoctonia solani* and *Bipolaris oryzae*

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Microorganisms play an important role in agricultural systems where they live in close association with plants and can exert different kinds of positive effects on their health and growth. Endophytes are beneficial microbe communities that are capable of colonizing the internal tissues of the host plants. In the present study, a total of 60 bacterial endophytes were isolated from the roots, stems, and leaves of healthy rice plants using Nutrient Agar (NA), Luria Bertani (LB) and Kings B (KB) agar in which 13 and 9 of them showed antagonistic effects against *Rhizoctonia solani* and *Bipolaris oryzae*, the pathogen of sheath blight and brown spot disease in rice. The percentage inhibition of radial growth (PIRG) ranges from 65 to 85% for *R. solani* and 57 to 78% for *B. oryzae* suggesting that these isolates might have the potential to be used as biocontrol agents against the two diseases. Based on the 16S rRNA gene sequences, the isolates were identified as *Bacillus subtilis* (4 isolates), *Burkholderia anthina* (2 isolates), *Burkholderia vietnamiensis* (6 isolates), *Burkholderia cepacia* and *Chromobacterium* sp. All six isolates of *B. vietnamiensis* recorded the highest PIRG against *R. solani* i.e. from 74 to 85% and showed more than 60% inhibition against *B. oryzae*. The *Burkholderia* genus is extremely versatile in the environment and has been reported for its great potential to promote plant growth via different mechanisms. The application of these species constitutes promising candidates in agriculture not only as biocontrol but also as biofertilizers. Further work is currently in progress to determine their plant growth-promoting (PGP) abilities such as nitrogen fixation, Indole acetic acid (IAA) production as well as phosphate and potassium solubilisation.

Keywords: Endophytes; antagonistic; 16S rRNA; Sheath blight; Brown spot

Funding information: MOA

SP-77

Unveiling the Rich Diversity of Culturable Bacteria within the Endorhizosphere of Lowland Rice in Peninsular Malaysia

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The endorhizosphere, the root-associated soil region, harbours a diverse microbial community that profoundly influences plant health and growth. A total of 60 bacterial endophytes were successfully isolated from the roots and stems of lowland rice cultivated from the northern and southern of Peninsular Malaysia. The isolates underwent rigorous screening to evaluate their remarkable antagonistic potential against pathogenic fungi, leading to the identification of core endophytes with exceptional plant growth promotion (PGP) capabilities. Each morphotype was identified by 16S rRNA gene sequence-based analysis. The sequencing data resulted in the classification of the isolates into four dominant phyla: Firmicutes (57.1%), Proteobacteria (22.8%), Bacteroidota (11.2%), and Actinobacteria (8.9%). Remarkably, this revealed the prevalence of several genera, including *Bacillus*, *Burkholderia*, *Acinetobacter*, *Enterobacter*, Pseudomonas, *Pantoea*, *Chryseobacterium*, and *Microbacterium*. Additionally, less abundant genera such as *Cytobacillus*, *Curtobacterium*, *Lysinibacillus*, *Herbaspirillum*, and *Rhizobium* were also identified, highlighting the diverse microbial composition within the isolates. Understanding the composition and function of bacteria isolated from this study is vital for developing sustainable agricultural practices. Thus, the isolated bacteria will undergo extensive characterization to unveil their exceptional PGP abilities, encompassing the production of phytohormones, micro mineral solubilization, and potent antagonistic activities against key fungal pathogens that threaten rice cultivation.

Keywords: Rice; Endophytes; Plant growth; 16S rRNA; Crop management

Funding: Ministry of Agriculture and Food Security (MAFS)

SP-78

Formulation and Characterization of Novel Mucoadhesive *Tualang* Honey Patches for Oral Mucosal Drug Delivery

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The formulation of mucoadhesive patches has gained significant attention due to their therapeutic effect compared to the conventional formulation, which is considered ineffective due to its limited therapeutic efficiency. In this study, mucoadhesive patches composed of polyvinyl alcohol and starch incorporated with *Tualang* honey (TH) were formulated for oral mucosal drug delivery. The cytotoxicity assay of TH against primary oral fibroblasts (POF) cells showed the highest cell viability with 109.29±4.74% (0.19%). The average weight of patches ranged between 85.03 ± 1.15 to 166.43 ± 9.90 mg, while thickness was 0.37 ± 0.024 to 0.47 ± 0.009 mm, and pH range of 6.79±0.029 to 7.95±0.040. Folding endurance was 378±2.87 to 380±2.64, and it showed that incorporating honey into the patches could increase the strain while reducing the tensile strength. SEM images showed a smooth surface morphology and exhibited significant swelling within 30 minutes. *In-vitro* release studies indicated a sustained release of honey from the patches. Stability analysis demonstrated no significant changes in patch quality over six months under different environmental conditions. Cytotoxicity analysis of TH-loaded patches revealed no cytotoxic effects on POF cells, with cell viability exceeding 132.80±20.18% (1.5% TH). In conclusion, TH-loaded patches offer a promising formulation for oral mucosal drug delivery as the patches exhibited uniform and consistent physicochemical and good mechanical properties, sustained release and no cytotoxic effect.

Keywords: oral mucosal drug delivery; *Tualang* honey; oral patches; oral diseases; primary oral cells

Funding Information: FRGS/1/2020/STG05/USIM/03/1

SP-79

Isolation of Phosphate-Solubilizing Fungi from Agricultural Soils in Sabah

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Phosphorus is one of the major growth-limiting macronutrients required for proper plant growth, particularly in tropical areas, due to its low availability in the soil. Approximately, 95-99% of phosphorus is present in organic forms that are insoluble and poorly available for plant intake. Various organisms particularly fungi found to effectively transform insoluble phosphate into soluble forms that can easily absorb by plants. The exploitation of fungi as inoculants for bio-fertilizer is considered to some extent an alternative to chemical fertilizer in the agricultural sector due to their extensive potential in enhancing crop production and food safety. Thus, this study aimed to isolate and identify the potential phosphate-solubilizing fungi to use as bio-fertilizer. A total of ten soil samples were collected from the agricultural crops of banana and groundnut in Ranau and Kundasang. This resulted in a collection of 100 fungal isolates species from these two areas. The identity of this isolate was characterized based on its morphological characteristics including molecular analysis of ITS regions. The identified fungi were evaluated for phosphate solubilization by the Pikovskaya's medium. The isolated phosphate-solubilizing fungi belonged to two genera, *Lecanicillium* and *Aspergillus*. These species can be candidated and exploited for further evaluation as bio-fertilizers.

Keywords: Fungi; Agricultural soil; Phosphate solubilizing; Biofertilizer

Funding Information: UMSGREAT (GUG0276-2/2018)

SP-80

Virtual Screening and Inhibition Activity of NADI-based Malaysian Plant Compounds against Receptor-Binding Domain of Spike Glycoprotein of SARS-CoV-2

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The COVID-19 pandemic caused by SARS-CoV-2 continues to affect countries worldwide, including Malaysia. Despite the administration of various vaccines, the emergence of new variants raises concerns about their effectiveness. The receptor binding domain of the SARS-CoV-2 spike glycoprotein (RBD S-protein) is a critical target for therapeutic intervention. This study aims to screen and explore the inhibitory potential of NADI-based Malaysian plant compounds against RDB S-protein. Accordingly, over 4000 compounds from the database were screened using EasyDockVina 2.2 software, coupled with molecular dynamic (MD) simulation using YASARA. The screening resulted in two best compounds of taraxerone and punicalin for RBD S-protein, with binding affinities of -8.8 kcal/mol and -6.8 kcal/mol, respectively, which were better than the control drug umifenovir (-5.7 kcal/mol). Both compounds were also predicted to be non-toxic based on the ADMET (absorption, distribution, metabolism, excretion, and toxicity) properties. Further *in vitro* inhibition assay indicated that taraxerone exhibited the best inhibition activity against RBD-ACE-2 receptor complex, with an IC50 value of 6.99 µM, outperforming punicalin (IC50 value of 9.76 µM). The interaction map indicated that the interaction between taraxerone with RBD S-protein is by blocking some vital residues of Gly496, Gly502 and Tyr505 through hydrophobic bonds. Altogether, taraxerone holds potential as a drug inhibitor candidate for SARS-CoV-2. This study, therefore, may provide an insightful information on NADI-based Malaysian plant compounds with therapeutic potential against the virus.

Keywords: Virtual screening, RBD S-protein, NADI compounds, Molecular dynamic (MD) simulation

Funding Information: DKC2008

SP-81

Effects of Hyperandrogenism on Levels of Sex Steroid Hormones during Endometrial Receptivity in Rats

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Hyperandrogenism is a fundamental causal factor in the disruption of endometrial receptivity and impaired regulation of sex steroid hormones. In this study, we investigated the effects of high dose of testosterone on the levels of sex steroid hormones in pregnant Sprague-Dawley (SD) rats. A total of 30 nulliparous female SD rats were used for this study. After pregnancy was confirmed, the following treatment was administered on day 1 of pregnancy: Peanut oil (vehicle) 1mg/kg/day (control group), 1 mg/kg/day testosterone (group 2), 1 mg/kg/day testosterone with 1mg/kg/day finasteride (group 3), 1 mg/kg/day testosterone with 1mg/kg/day anastrozole (group 4) and 1 mg/kg/day testosterone with 1mg/kg/day finasteride and anastrozole (group 5) for 3 days, representing the early gestation period. Serum levels of testosterone, progesterone, and oestrogen were then determined by enzyme-linked immunosorbent assay (ELISA). The untreated pregnant rats (control group) had high progesterone and oestrogen levels and low testosterone levels. In this study, testosterone levels were significantly increased in all treated groups compared to the control group ($p < 0.05$). Progesterone and oestrogen levels were also significantly low in all treated groups compared to the control group ($p < 0.05$). In conclusion, progesterone and oestrogen levels were strongly influenced by the presence of high testosterone levels during endometrial receptivity in the rat model. These results provide a basis for the factors that influence endometrial receptivity in the presence of hyperandrogenism.

Keywords: sex steroid hormones; hyperandrogenism; progesterone; oestrogen

Funding Information: FRGS/1/2019/SKK08/UKM/02/6-81

SP-82

Effect of Sunflower Oil on Human Keratinocytes Cell Line (HaCaT) Viability

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Sunflower oil (SFO) is a vegetable-based oil which is commonly applied topically as natural remedy for soothing itch and part of wound care. However, the scientific evidence supporting its use including safe tolerated and effective concentration on skin is scarce. It is important to establish the cytotoxicity of SFO on keratinocytes as the most exposed area during topical use. In this research, a spontaneously human keratinocytes cell line (HaCaT) was used. Approximately 10^4 cells were grown in a 96-well plate in DMEM solution supplemented with 10% FBS and 5% Penicillin/Streptomycine at 37°C, 5% CO2 for 24 hours. The previous medium was discarded and cells were treated with DMEM contains various concentrations of SFO (0,5%, 1%, 2%, 4% and 8% v/v) dissolved in 1 % DMSO. Cells treated with complete DMEM served as a positive control. After 24 hours of incubation, cell viability was determined using the MTT assay and expressed as a percentage of positive control. The HaCaT viability after treated with SFO were: 128% (SFO 0,5%), 126% (SFO 1%), 86% (SFO 2%), 91% (SFO 4%) and 38 % (SFO 8%). Thus, it can be concluded that SFO is safe for topical use at concentration 1-4%.

Keywords: Sunflower oil; Keratinocytes; HaCaT; MTT Assay

Funding Information: PUTI Q2 (Universitas Indonesia)

SP-83

Current Trends for an Alternative Breast Cancer Treatment: Liposomes as a Delivery System for a Gene Therapy Strategy

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Breast cancer incidence and mortality rates have increased exponentially during the last decade, particularly among female patients. Current treatments, including surgery and chemotherapy, have significant negative physical and mental impacts on patients. As a safer alternative, gene therapy utilising a therapeutic gene with the potential to treat various ailments is being considered. Gene delivery generally utilises viral vectors. However, immunological reactions and even mortality have been recorded as side effects. Thus, non-viral vectors, such as liposomes, a nanoparticle system composed of lipid bilayers, are being considered. Liposomes have demonstrated tremendous potential due to their limitless ability to combine many functions into a system with desirable characteristics and functionality. The three major lipid groups involve cationic, anionic and neutral liposomes all have unique characteristics in terms of stability, cytotoxicity, transfection ability, cellular uptake, as well as limitations as a gene carrier. Due to the more practical approach of employing electrostatic contact with both negatively charged nucleic acid and the cell membrane, cationic liposomes appear more suited for formulation as an ideal delivery system. Since other alternatives have numerous complications, additional modifications need to be made to achieve a functional gene therapy system. Thus a closer look at the research and clinical trends will provide a deeper understanding towards development of an alternative breast cancer treatment.

Keywords: Breast cancer; Gene therapy; Liposome; Nanoparticles

Funding Information: RACER/1/2019/STG05/UMS//1/Fundamental Research Grant Scheme for Research Acculturation of Early Career Researchers, Malaysian Ministry of Higher Education, GUG0516-2/2020/University Malaysia Sabah Postgraduate Research Grant

SP-84

Species Identification of Economically Important Bamboo Varieties and Assessment of Genetic Stability of in vitro cultured *Dendrocalamus asper* using ISSR markers

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Bamboos constitute a genetically diverse pool of germplasm that are gaining increasing importance in the agroforestry industry owing to their adaptability to diverse ecological niches, their economic potential and their role in mitigating climate change. Taxonomic and systematic studies of bamboos are traditionally based on morphological features, but this can lead to misidentification and mixing up the bamboo species. To this end, DNA barcoding has shown great potential in identifying species and testing the genetic stability of germplasm in vitro. The present study attempted to assess the suitability of two DNA barcoding markers (*matK* and *rbcL*) for the identification of important species in Sabah and developing an in vitro framework for the micropropagation of selected species. The genetic stability of one variety *Dendrocalamus asper* was assessed using Inter Simple Sequence Repeats (ISSR) markers. The findings of this study led us to conclude that both, *matK* and *rbcL* sequence data could be applied to identify and resolve the taxonomy of bamboos in Sabah. The genetic stability of invitro culture plants was found to be stable over five subcultures as evidenced by the ISSR data. The findings of this study confirm that DNA barcoding using the two loci supports barcoding of Sabah native bamboos and that ISSRs can be employed successfully for the assessment of commercial clones in vitro. The applications of these markers can be extended to the selection and micropropagation of bamboos.

Keywords: Bamboo; DNA barcoding; *matK*; *rbcL*; ISSR, *Dendrocalamus asper*

Funding Information: DN20091

SP-85

Growth Performance and Expressions of Immune Response Genes of *Tor tambroides* L. (Bleeker, 1854) fed with *Chlorella vulgaris* enriched *Artemia* sp.

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The slow growing nature of *Tor tambroides* remains as an open topic due to its exquisite value and potential in aquaculture. There is little knowledge on the effects of *C. vulgaris* enriched *Artemia* sp. on the growth performance and the expressions of growth and immune response genes of this species during larval stage. The larvae were divided into three treatments; T1: control (commercial feed), T2: unenriched *Artemia*, T3: enriched *Artemia*. The larvae were weaned with the commercial feed 3 times daily and fed with the treatments (T1-T3) once a day from 14-29 DAH. T3 had resulted in the highest body weight gained, total length, specific growth rate, relative growth rate and highest survival. The expression of growth genes; growth hormone and myostatin genes at the end of the study showed that larval group fed with T3 had the highest upregulation of growth hormone gene. Meanwhile, the myostatin gene was upregulated in the larval group fed with T2 though T3 showed no statistical difference. The immune genes, MHCC1a was upregulated and had the highest fold in T3 larval group. The expression of CC3 gene in larval in both groups showed statistical difference to T1. This study showed that *C. vulgaris* enriched *Artemia* had enhanced the growth and expressions of growth and immune genes of *T. tambroides* larvae and could potentially be applied during its weaning period.

Keywords: *Artemia*, *Chlorella vulgaris*, enrichment, *Tor tambroides*, larvae

Funding Information: JPMJSA 1509

SP-86

Preliminary and Discovery the Expression of miRNA in Dengue Serotype 1 and 3 from Patients Infected Dengue in Sabah

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A combination of biomarkers is needed to detect all stereotype dengue in a single reliable biomarker but unfortunately not exists in clinical practice. Identifying early prognostic markers of severe compilations may improve dengue management and decrease mortality cases. This study is aimed to identify miRNA expression profiles in patients with severe dengue serotype 1 and 3. A total of 88 patients with serotype DENV-1 and DENV-3 infection were identified along with 30 healthy controls. Serum RNAs was isolated from these subjects and subjected to high-throughput small RNA (sRNA) sequencing. This research was approved by the Medical Research Ethics Committee (MREC), Ministry of Health, Malaysia (No. NMRR-18-2782-42195). After trimming and quality control of the reads, we shortlisted 37 respectively from DENV-1 and DENV-3 miRNAs candidates that were promising for downstream analysis. From this, 10 miRNAs as upregulated in DENV-1 while, 8 was downregulated in the sera of patients. From DENV-3 we identified 7 miRNAs that was upregulated while, 12 was downregulated in the sera of patients. Verification of the miRNA expression by stem-loop RT-qPCR is ongoing. Understanding differential expression of microRNA and functions during dengue infections would provide the development of therapeutic which could be strategized to act either as miRNA antagonist or mimic that may serve as reliable biomarkers of disease severity during early stages of dengue infection.

Keywords: Dengue, microRNA, biomarkers, DENV-1, DENV-3 expression

SP-87

New Technology Platform for Biodiesel Production in Malaysia

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In the future, conventional fossil fuels may not be able to meet the continuous demand for energy requirements such as petroleum and coal anymore. Thereby, the development and innovation of a new fuel, biodiesel which is sustainable and renewable has been explored to replace fossil fuels. However, Malaysia's biodiesel industry faces many challenges in fully implementing biodiesel in the country. This paper addresses both the new and old technology platforms in producing biodiesel. All of these technologies are compared in terms of cost, environmental friendliness, temperature and time requirement. This is to determine which technology is better for biodiesel production. Therefore, new technology can be developed to achieve zero waste and environmentally friendly biodiesel in the future.

Keywords: Biodiesel; Enzyme; Monolith; Chemical

Funding Information: FRG0583-1/2022 (FRGS/1/2022/STG05/UMS/02/4)

SP-88

Loop-Mediated Isothermal Amplification of the *tox-R* gene coupled with Lateral Flow Dipstick (LAMP-LFD) for the novel rapid and specific visual detection of *Vibrio harveyi*

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Vibrio harveyi is a serious pathogen for marine organisms particularly in hatcheries and grow-out ponds that attacking their immune system. Rapid detection method of *V. harveyi* is urgently needed to prevent the bacterial spread. Here we described a rapid and specific visual detection method based on the Loop-Mediated Isothermal Amplification in combination with Lateral Flow Dipstick (LAMP-LFD). Biotinylated LAMP amplicons were produced by the set of six novel designed primers including the biotin-labeled inner primer that recognized specifically the target sequences of *V. harveyi* followed by hybridization with the FAM-labeled probe and LFD detection. The addition of loop primers improves the reaction time of LAMP by more than half as quickly as 10-15 min. Moreover, with the application of LFD, the result can be obtained without the need for gel electrophoresis with higher specificity and selectivity since the hybridization with specific probe to the LAMP amplicons is employed. LAMP-LFD is specific as it only produces positive result for *V. harveyi* sample. The sensitivity of PCR-UV analysis was only at 10^4 copies while LAMP-LFD was able to detect low amount at 10^3 copies. This method provides for a useful tool to rapidly detect and monitor *V. harveyi* outbreaks.

Keywords: Loop-mediated isothermal amplification; Lateral Flow Dipstick; Polymerase Chain Reaction; *Vibrio harveyi*; rapid detection; *tox-R* gene; vibriosis

Funding Information: Science Fund grant, Ministry of Science, Technology and Innovation of Malaysia (project code: SCF0066).

SP-89

Rapid and On-Site Diagnostic Method for the Detection of Blast by using DNA Isothermal Amplification and Magnetic Beads Flocculation

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Agriculture losses due to crop infections is a major concern across the globe. In Malaysia itself, paddy yield losses due to fungal diseases is a threat to the crop industry. Blast causing by *Pyricularia oryzae* is one of the major diseases in rice worldwide. Rapid and accurate diagnosis of blast for on-site detection is pivotal at an early stage for effective disease control strategy. This study developed loop mediated isothermal amplification (LAMP) with specific primers targeting blast, followed by a flocculation assay for isualizing positive amplification in the LAMP assay. The assay was sensitive to picogram amounts of gDNA (0.5 pg or 5 conidia). LAMP assay on blast gDNA showed flocculation, but negative results on *Rhizoctonia solani*, *Helminthosporium oryzae* and *Sarocladium oryzae* confirming the specificity of the assays. Thus, the results confirmed that the combination of these techniques is highly specific, sensitive and robust for the early detection of blast to adopt precautionary control measures.

Keywords: Blast, *Pyricularia oryzae*, LAMP, flocculation

Funding Information: PRB-401

SP-90

Effect of Alginate Percentage on the Encapsulation Efficiency of *Bacillus pumilus* in Alginate Beads

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Bacterial Panicle Blight (BPB), caused primarily by *Bukhloderia glumae*, is highly destructive and can cause significant losses of up to 75% in severely infested fields. Antagonistic bacteria isolated from plant surface, soil and rhizosphere have been extensively used to control major crop diseases caused by various fungal and bacteria. A total of 149 bacterial isolates from Endau, Johor and 59 isolates from laboratory culture collection was screened for antagonistic activity and anti-QS activity against *B. glumae*, in which 29 and 28 of them were tested positive for each characteristic. An isolate, B1-2-4 identified as *Bacillus pumilus*, was then selected to be encapsulated in alginate beads at different alginate percentage. This approach provides an appropriate micro-environment combined with physical protection for a sustained period to avoid decline. Alginate concentration of 1.5% has the highest encapsulation efficiency of 88.5%. It was also observed that for all percentage of alginate, at pH 7.4, the bacteria were released instantly in comparison at pH 5.5 and pH 6.5, where the bacteria were released gradually over time. Encapsulation of the isolate in alginate beads has shown to be a viable option for control release of the isolate.

Keywords: *Bukhloderia glumae,* biocontrol, control release

Funding Information: P-502F

SP-91

Identification of MicroRNA-directed Cleavage of Targets in Pineapple (*Ananas comosus)* Fruit Development using Degradome Sequencing

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A large number of microRNAs (miRNA) have been previously discovered in pineapple (*Ananas comosus*), which is a model organism for tropical non-climacteric fruits. These miRNAs are believed to be involved in the regulation of many endogenous genes. *In silico* computational analysis can provide predictive identification of microRNAs (miRNAs) and their putative target genes. However, the main criterion used to distinguish between regulated and non-regulated genes in pineapple is that the targeted transcripts (mRNA) will undergo degradation. Therefore, by using degradome sequencing we aim to provide first hand empirical data to identify gene targets that are regulated by miRNA in MD2 pineapple by identifying mRNA transcripts that have been expressed and subsequently degraded by these small RNA molecules. We first performed degradome sequencing, which is likened to a modified 5'-rapid amplification of cDNA ends (RACE) with next generation sequencing (NGS) which allows the identification of over-represented 5'-ends (miRNA cleavage sites) within mRNAs. Subsequently, we discovered 144 targets which were mapped to at least 21 miRNA families and were consistently expressed in all three biological replicates. Among them, seven miRNAs associated with plant development along with eight target mRNAs (including auxin response factor, squamosa promoter-binding-like protein, transport inhibitor response 1 protein, growth-regulating factor 5 and transcription factor GAMYB) were detected in MD2 pineapple using RT-qPCR. Furthermore, to confirm and validate the cleavage sites of the target genes cleaved by miR159, miR160 and miR408, a modified 5’ RACE PCR was conducted followed by DNA sequencing. The results showed that the predominant cleavage site in the miRNA target genes were at position 11 from the 5’ end of the miRNA complementary region. The findings here provided validation of miRNA targets through clear empirical data. Our findings shows that miRNA play a key role in regulating the expression of target genes and will assist towards understanding the mechanisms of MD2 pineapple fruit development.

Keywords: Degradome sequencing; microRNAs; pineapple fruit; mRNAs; *Ananas comosus*

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SP-92

Medicinal Plants and Their Traditional Uses by Dusun Tindal Community at Kampung Kiau Nuluh Kota Belud

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The traditional use of medicinal plants has been a longstanding practiced in the rural areas worldwide. Contemporary research has placed significant importance on documenting this indigenous knowledge. Due to the lack of interest among the younger generation in its acquisition and maintenance, this knowledge is on the verge of extinction. Consequently, this study aims to document the medicinal plant knowledge of Dusun Tindal in Kampung Kiau Nuluh, Kota Belud. The research involved direct interviews with 61 informants and the use of semi-structured questionnaires covering local plant names of plants, preparation methods, part used, and the disease treated. A total 33 plant species from 23 families were identified with Poaceae family being the most dominant (representing 15.20% of the recorded species). The most commonly utilized plant part was roots (30%) and the preferred method of preparation was decoctaion (55%). The reported diseases were classified into 22 distinct ailments groups based on user reports. This study contributes valuable insights to the field of ethnomedicine by uncovering medicinal plants in an unexplored region.

Keywords: Ethnobotany; Medicinal plant; Fever; Traditional; Therapeutic

SP-93

Comparative Screening of Anti-Dengue Activity in Aqueous and Ethanol Extracts of Mangrove Plants from Sabah

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Dengue virus is a global pathogen that lacks an effective vaccine or therapy. Screening medicinal plants for anti-dengue properties provides a promising avenue to identify potent compounds. Mangroves, known for their resilience in harsh conditions, produce a diverse range of natural products with unique biochemical profiles, which hold potential for anti-dengue treatments. This study aims to evaluate the anti-dengue activity of selected mangrove plant species from Sabah against DENV2 NS2B-NS3pro, utilizing an enzymatic protease assay. Six mangrove species (*Avicennia marina*, *Bruguiera gymnorrhiza*, *Ceriops tagal*, *Rhizophora apiculata*, *Rhizophora mucronata*, and *Xylocarpus granatum*) were investigated, with various plant parts subjected to aqueous and ethanol extraction. The results demonstrated significant anti-dengue activity in both aqueous and ethanolic extracts of the mangroves against DENV2 NS2B-NS3pro, with IC_{50} values ranging from 0.95 µg/ml to 6.24 µg/ml. Notably, the ethanolic extract of *Rhizophora apiculata* leaves exhibited the highest inhibition, with an IC_{50} value of 0.95 µg/ml. These findings suggest that the ethanolic extracts from *Rhizophora apiculata* leaves hold promise as potential candidates for dengue treatment. This study underscores the importance of natural products as valuable sources for the development of novel anti-dengue treatments, highlighting the need to explore mangroves in the quest for effective therapeutic options.

Keywords: Mangrove, anti-dengue, DENV2 NS2B-NS3pro

Funding Information: This study was supported by the Universiti Malaysia Sabah under an External Collaboration Research Grant Scheme (GKP0021-2018) “Characterization of anti-tuberculosis and dengue virus antiviral activities of Mangrove plant extracts”.

SP-94

Carrageenan-Mediated Green Synthesis of Silver Nanoparticles: Characterization and Antibacterial Activity

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Silver nanoparticles (AgNPs) have garnered significant attention due to their distinctive properties, particularly their antimicrobial activity. Green synthesis methods are emerging as environmentally friendly alternatives to produce AgNPs. Herein, we report the green synthesis of AgNPs with a unique flower-like structure using carrageenan extracted from the red seaweed *Kappaphycus alvarezii*. The presence of a surface plasmon resonance (SPR) peak at 420 nm in the UV-Vis spectrum indicates the formation of AgNPs. Fourier Transform Infrared (FTIR) spectra demonstrated the crucial role of carrageenan's functional groups in both reducing and stabilizing the AgNPs. X-ray diffraction (XRD) and energy-dispersive X-ray (EDX) analysis confirmed the crystalline nature and face-centered cubic structure of the AgNPs, with 86% composition of elemental silver. Microscopic examinations revealed the flower-like AgNPs structure with intricately intertwined and irregular lamellar petals. The growth mechanism of this unique structure was elucidated by transmission electron microscopy (TEM) and atomic force microscopy (AFM) analyses. Furthermore, the AgNPs exhibited promising antibacterial properties against *E. coli* and *S. aureus*. This study highlights the potential of carrageenan as an effective and environmentally friendly reducing agent for the synthesis of AgNPs, thereby offering broad prospects for their applications in the fields of food and biomedicine**.**

Keywords: Silver nanoparticles, carrageenan, *Kappaphycus alvarezii,* antibacterial

Funding Information: GUG0550-1/2022

SP-95

Genetic Diversity of the Tri-spine Horseshoe Crab (*Tachypleus tridentatus*) based on Twenty Microsatellite Markers

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The tri-spine horseshoe crab, *Tachypleus tridentatus*, is a species under conservation pressure. Anecdotal reports indicate a decrease in the number of horseshoe crab populations worldwide and particularly in Sabah. This phenomenon may impact the loss of genetic diversity of the species. Based on this, we hypothesized that there is a reduced level of genetic diversity in the horseshoe crab populations in Sabah. If proven correct, there is an urgent need to mitigate the loss of genetic diversity in the populations. We have collected a total of 63 samples from four divisions of Sabah which were Kudat, representing the Kudat Division, Kota Belud and Kota Kinabalu, representing the West-coast Division, Bongawan, representing the Interior Division, and Sandakan, representing the Sandakan Division. Primers were subsequently designed to develop twenty novel microsatellite markers which were then used to determine the levels of genetic diversity in the populations. All loci were observed to be polymorphic with the number of alleles ranging from 2 to 6 per locus. The overall observed heterozygosity for the 20 loci ranged from 0.277 to 0.409 while the expected heterozygosity ranged from 0.277 to 0.529. The low heterozygosity values are in agreement with the high average inbreeding coefficient value of 0.0066. The results indicate that there is a low amount of genetic variability in the populations studied. In conclusion, the findings highlight a significant decrease in genetic diversity among horseshoe crab populations in Sabah, underscoring the urgent need for conservation efforts to preserve their long-term survival.

Keywords: Microsatellite; horseshoe crab; molecular markers; *Tachypleus tridentatus;* Sabah.

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SP-96

Degradation of Naphthalene using Immobilised Laccase on Polyethyene Terepthalate grafted Maleic Anhydride Nanofiber Mat Aided with Mediators

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Naphthalene, the simplest polycyclic aromatic hydrocarbon (PAH), was present in petroleum waste. Several methods had been used to degrade naphthalene, but this study focused specifically on the degradation of naphthalene via immobilised laccase. Laccase was immobilized through covalent attachment onto a highly efficient enzyme carrier made of Polyethylene Terephthalate grafted Maleic Anhydride Nanofiber Mat. The main objective of this study is to degrade the naphthalene using immobilised laccase with the aid from mediators. Natural mediators, such as syringaldehyde (SYR) and acetosyringone (ACE), as well as synthetic mediators, including 2,2′-azino-bis(3-ethylbenzothiazoline)6-sulfonate (ABTS) and 1-hydroxybenzotriazole (HBT), were utilized in this study. The results indicated that a laccase concentration of 0.3 mg/mL, combined with a 90-minute immobilization period at 22.7°C contributed the highest immobilization yield and activity recovery. Nevertheless, the immobilised laccase demonstrated optimum activity at pH 3 and 60 ^{o}C reaction temperature while for the reusability test, it can retained approximately 80% of its initial activity after 10 consecutive cycle. The immobilised laccase successfully degraded 20% of naphthalene after 24 hr of incubation and increased to ±37% degradation rate with the aid of ABTS, SYR and ACE mediators.

Keywords: Bioremediation; Immobilised; Laccase;

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SP-98

A High-Throughput and Semi-Quantitative Detection System by PCR-ELISA for Foodborne Pathogen Using *Salmonella* Enteritidis as a Study Model

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In this study, the designed ENT capture probe has successfully been applied in the PCR-ELISA and hybridized with the targeted amplicons to yield measurable signal by the 96-well microplate reader. The PCR-ELISA method has been established to detect *S.* Enteritidis in the artificially-infected raw chicken meat and chicken sausage samples as a model to elucidate the detection ability of the PCR-ELISA in selected food matrices. Two distinct characters of the samples which are non-processed matrix (raw chicken meat) and highly processed matrix (chicken sausages). The comparison conducted found that the PCR-ELISA method is superior in the sensitivity and higher specificity than the conventional PCR assay. The LOD that has been achieved by this technique, 9.4 CFU/mL for chicken meat and 2.46 CFU/mL for chicken sausage is relatively 10-fold lower than the conventional PCR. This proved that the PCR combined with ELISA increased the sensitivity than using the PCR assay alone. PCR-ELISA offers an alternative platform and improved assay than PCR and real-time PCR for detection of *S.* Enteritidis in semi-quantitative and high-throughput manner. The PCR-ELISA method established in this study, could be used as a screening tool for large-scale routine surveillance and monitoring of foodborne pathogen contamination.

Keywords: PCR-ELISA, *S*. Enteritidis, high-throughput, semi-quantitative, detection

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SP-99

In Vitro Screening of Plant Growth-Promoting (PGP) Abilities of Bacteria Isolated from the Endorhizosphere of Healthy Rice Plants

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Endophytes are harmless microbes that reside in different plant tissues. Endophytes are beneficial for the growth of the host plant and help to sustain plant growth and yield during abiotic and biotic stresses. Studying the interactions between host plants and their endophytes could be an effective strategy to enhance crop productivity in agriculture. In this study, 18 selected rice endophytes consisting of *Bacillus* sp. (6 isolates), *Burkholderia* sp. (4 isolates), Corynebacterium sp., *Curtobacterium* sp., *Enterobacter* sp., *Herbaspirillum huttiense*, *Microbacterium testaceum*, *Rhizobium larrymoorei*, *Acinetobacter baylyi*, and *Pseudomonas parafulva* were evaluated for their plant growth-promoting abilities (PGP) *in vitro*. The most widespread activities within the 18 bacterial isolates were Indole acetic acid (IAA) production (17/18 isolates), followed by Nitrogen (N) fixation (14/18 isolates) and phosphate (P^+) solubilisation (8/18 isolates). Among the isolates, *Burkholderia* sp. exhibited all three PGP properties along with *Curtobacterium* sp., *Herbaspirillum huttiense* and *Acinetobacter baylyi*. For P^+solubilisation, *Burkholderia anthina* and *Burkholderia cepacia* showed clear dissolution and largest halos with P^+solubilisation index (PSI) of 4.43 and 3.30 respectively. On the other hand, *Bacillus aryabhattai* and *Bacillus flexus* were the most excellent N fixer as they grew quickly on nitrogen-free media. The species of *Bacillus*, *Burkholderia* and *Pseudomonas* have been well-documented as plant growth-promoting rhizobacteria (PGPR) and have been identified as the predominant communities in the soil or as endophytes. These results indicated that rice endophytes have high PGP potential and may be good candidates for use as biofertilizers for rice. Future work will include inoculating the rice seedlings with selected endophytes exhibiting all the PGP features.

Keywords: Rice, Endophytes, Beneficial, Plant Growth-Promoting, Biofertilizers

Funding Information: MOA

SP-100

Conserved Sequence from Multiple Coronavirus Strains Aiming at MHC Class II as a possible Human Coronavirus (HCoV) Vaccine Developed by Utilising an Immunoinformatic Approach

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The latest coronavirus outbreak caused by SARS-CoV-2 has claimed hundreds of thousands of lives across the globe, destroying life in both social and economic sectors. Due to the massive damage caused by this outbreak, huge amount of efforts has been put by researchers in finding vaccines to control the pandemic, which the first vaccine manages to be developed in less than a year. However, the rapid mutations of the virus have created a number of viral variants, making the available vaccines less effective and even redundant. Therefore, this work aims to develop a potential vaccine that utilises the conserved region of multiple human coronavirus (HCoV) strains to tackle the current and future possible coronavirus outbreaks. This vaccine development strategy involves targeting the MHC Class II protein complex instead of the ACE2 human receptor, as it is responsible for inducing the humoral immune response that will be used against viral infections. The conserved peptides that were screened were docked with MHC Class II and then finalised by performing molecular dynamics (MD) simulations to ensure their stability within human body conditions. Peptides were used in this study due to its safety and it is quick to be translated from sequences to a vaccine. Hundreds of epitopes were predicted by NetMHCIIpan4.0, yet only the strong binding epitopes with alleles that are susceptible to the coronavirus infection were chosen for further screening of their antigenicity via the VaxiJen 2.0 server. These peptides were docked with the MHCII complex using AutoDock Vina. The docking studies show most of the peptides had a feasible binding energy, with eight of them showing the most favourable results. These peptides were then simulated using GROMACS for 50 ns, and despite showing a stable RMSD value, 4 different peptides showed the most favourable results and were shortlisted for subsequent works. Thus, these peptides were simulated further to 200 ns, and the results showed a good RMSD graph with around a 0.05 and 0.10 fluctuation value with less than 0.25nm, indicating a stable protein complex interaction. These findings may provide insight into the possibility that potential vaccine interactions with the MHC II complex will be able to activate immune response production, ultimately protecting an individual from coronavirus infection.

Keywords: Drug discovery, md simulation

SP-101

Establishment of Tissue Culture Platforms for Decoding the Bamboo Transcriptome in Response to Environmental Stress

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Bamboo, a magnificent perennial arborescent grass in the Poaceae family and Bambuseae subfamily, has enormous economic importance as a fast-growing plant. However, limited planting material, genetic variation, and pest and disease transmission make conventional propagation challenging. Bamboo tissue culture offers a solution not only for mass propagating plants under controlled conditions, but also for transcriptome studies of gene expression in specific plant parts that may respond differentially to environmental changes. This study develops an *in vitro* propagation system for the tropical bamboo species *Gigantochloa levis* using nodal segments with axillary buds as explants. The explants were surface sterilised before being cultivated on semi-solid Murashige and Skoog (MS) medium with various concentrations of plant growth regulators. Different concentrations of 6-benzylaminopurine (BAP) were used for shoot initiation and multiplication, while varying concentrations of indole-3-butyric acid (IBA) were used for root development. The highest rates of shoot bud initiation (91.67%) were observed with 2 mg/l BAP 14 days after inoculation, whereas shoot multiplication and root development are still being studied. This study is expected to improve *G. levis* propagation protocols and aid in bamboo transcriptome research in response to environmental stress, providing critical insights into stress tolerance and adaptive responses in bamboo.

Keywords: *Gigantochloa levis*; Nodal explants; Tissue culture; Transcriptome

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SP-102

Black Soldier Fly: Versatile Source of Feed and Biopolymers

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The black soldier fly (BSF; *Hermetia illucens L*.; *Diptera*: *Stratiomyidae*) larvae feed on organic waste, accumulate protein and fat in the body and convert organic waste to biofertilizer. The increasing number of large-scale BSF farms around the world also offer high availability of pupal exuviae as by-product that is high in chitin, a biomaterial with multiapplication. Here we present investigative studies on the effect of different drying methods of BSF larvae towards protein, fat and fatty acids content during processing as well as the characteristic of chitin and chitosan from BSF pupal exuviae. Larvae were washed and subjected to oven and freeze-drying before being analysed for moisture, protein, fat and fatty acids content. Meanwhile, chitin was extracted from pupal exuviae and deacetylated into chitosan using 45 % NaOH. The analysis indicated that different drying methods did not significantly influence the protein and fat content of larvae (p-value<0.05). The SEM image and FTIR analysis of chitin and chitosan from BSF pupal exuviae were comparable to commercial chitin and chitosan from shrimp. The BSF usage as organic waste biotreatment promotes a circular economy as it is a sustainable and resource-efficient system where waste is minimized, and resources are utilized in a closed-loop manner.

Keywords: BSF Larvae, protein, Chitin; Chitosan; *Hermetia illucens*

Funding Information: FRGS/1/2021/STG03/UIAM/02/3

SP-103

Modulation of cell mobility, stemness and drug response by miR-3934 in MCF-7

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MicroRNAs are small non-coding RNA molecules that modulate gene expression. MicroRNAs are implicated in the progression and development of cancer, thereby serving as potential biomarkers for cancer diagnostics and prognosis. Our previous research identified miR-3934 was enriched in cancer stem cell-like subpopulation in breast cancer cells. Thus, this study was aimed at investigating the role of miR-3934 in regulating cell mobility, stemness and drug response in MCF-7 cells. The expression of miR-3934 was manipulated through overexpression and inhibition techniques, followed by MTT, wound healing and mammosphere formation assay. Transcriptomic sequencing was performed to identify changes in gene expression influenced by miR-3934 modulation. Overexpression of miR-3934 significantly increased the drug resistance of MCF-7 to cisplatin and doxorubicin while migration rate was increased by 29% as compared to control. While there was no significant effect on mammosphere formation ability, the sizes of mammospheres were significantly higher in this group as compared to the other groups. In the transfected MCF-7 cells, 6277 and 4384 differentially expressed genes were identified in the miR-3934-overexpressed and -inhibited groups, respectively. Functional enrichment analysis revealed the dysregulation of cellular metabolism and DNA damage response pathways following miR-3934 overexpression while epithelial-to-mesenchymal transition and stemness pathways were implicated with miR3934 inhibition. Remarkably, pathways related to migration were significantly dysregulated with both modulations. The regulation of miR-3934 in MCF-7 cells underscores its potential importance in mediating metastatic pathways in luminal breast cancer.

Keywords: microRNA; breast cancer; cancer stem cell; metastasis; drug resistance; transcriptomic

Funding information: Fundamental Research Grant Scheme (FRGS/1/2018/STG05/UNIM/02/1) by Ministry of Higher Education, Malaysia

SP-104

Meta-Analysis on the Prevalence of Herpes Simplex Virus 1: From Malaysia to Asia

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The neuroinvasive capability of herpes simplex virus 1 (HSV-1) is well-known, posing an increased risk of Alzheimer's disease. Hence, it is vital to gain a comprehensive understanding of HSV-1 prevalence in humans. This study aims to determine HSV-1 prevalence in the Malaysian population, and across Asia using a meta-analysis approach. Saliva samples from 451 Malaysian volunteers were collected to detect the presence of HSV-1 in the population using a molecular approach, while an extensive literature search from the year 2013-2023 was conducted to identify relevant studies for inclusion in the meta-analysis. To assess heterogeneity in the meta-analysis, the I^2 index and Q-test were employed. Additionally, publication bias was evaluated using a Funnel plot and Egger's test. The results showed that 41.9% of the Malaysian volunteers tested positive for HSV-1. The meta-analysis involved a total of 26 studies with 31,464 subjects across Asia, and the overall pooled prevalence rate of HSV-1 was found to be 72.0%, calculated using a random-effect model based on the observed heterogeneity. Further analysis revealed that Western Asia had the highest prevalence (79.1%), followed by East Asia (71.7%), Southeast Asia (65.3%), and South Asia (25.8%). Notably, no publication bias was detected in the meta-analysis. In conclusion, these findings indicate that approximately three-quarters of the Asian population is infected with HSV-1. Given the strong association between HSV-1 and Alzheimer's disease, it is crucial to delve into the underlying mechanisms, emphasizing the need for further research and attention in this area.

Keywords: Prevalence; Meta-analysis; HSV-1; Alzheimer’s disease; Asian population

Funding Information: Universiti Malaysia Sabah (SLB2237)

SP-105

Inferring Matrilineal Genetic Components of the Sea Nomad Population Residing Offshore of Sabah, Malaysia

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The Sea Nomad population residing offshore of the eastern region of Sabah is known as Bajau Laut or Palau. They practice semi-nomadic lifestyle on boats or stilts houses around small islands. They have been isolating themselves from other populations in the mainland, leading to little genetic admixture with other ethnic groups since the historical maritime era. It is thus hypothesized that Bajau Laut people retain their matrilineal genetic components as compared to surrounding populations. A total of 89 blood samples from individuals residing in three islands offshore of Semporna, Sabah, were collected. DNA was isolated and the complete hypervariable region of the mitochondrial DNA (nt 16024-574) was amplified and sequenced. The mtDNA haplogroup was then determined using the Mitomaster webtool. Intriguingly, only seven haplogroups i.e. B4c1b2a2, M7c1a4a, D2c, F1a, F3b1a1 and M74b1 were found, and the first haplogroup constitutes 82% matrilineal genetic components of all individuals. This is in opposite to a previous study on Bajo in Kendari, another sea nomads near Sulawesi, Indonesia, who have 15 mtDNA haplogroups and B4c1b only makes up 7.4% of the sampled individuals. Furthermore, Land Bajau from Sabah, who is known to have inter-marriages with other ethnic groups, have >20 haplogroups but only 7.3% of the sampled individuals are made up of B4c1b2a2. In conclusion, these comparisons indicate that there has been no 'maritime creolization' among the Bajau Laut with other surrounding ethnic groups, which is contrasting to the previous findings in other seafaring groups in Insular Southeast Asia. In the future works, the complete mtDNA sequence at 16,569 bp of selected individuals will be sequenced to identify all variations that will provide sufficient information for inferring genetic origin and migration history of the Sea Nomads via phylogeography analyses.

Keywords: Sea Nomads, Bajau Laut, mtDNA haplogroup, genetic component.

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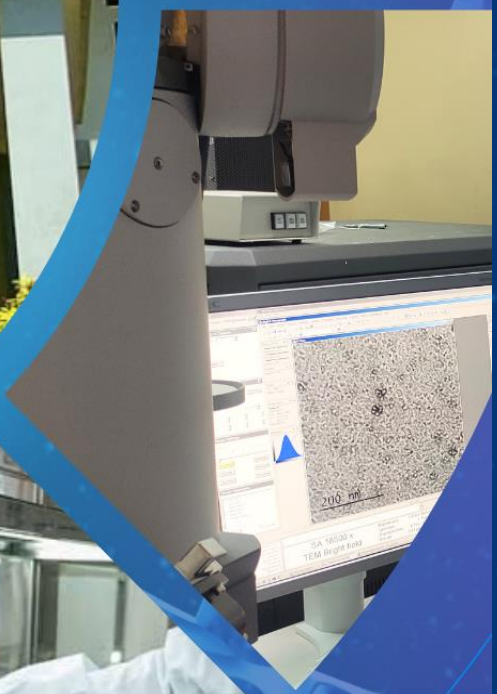

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