INTERNATIONAL BIOLOGY SYMPOSIUM 2020

16 DECEMBER 2020

Towards Sustainable Research, Global Responses, Beyond Boundaries

VIRTUAL COLLOQUIUM SERIES

FACULTY OF APPLIED SCIENCES – VCS 2020/2021

UNIVERSITI TEKNOLOGI MARA

Fakulti Sains Gunaan

School of Biology

Faculty of Applied Sciences

UiTM Shah Alam

Welcoming Address

Chairperson

Virtual Colloquium Series - VCS@FSG 2020,
Faculty of Applied Sciences, UITM

Prof. Dr. Hadariah Bahron

Dear honorable speakers, colleagues, ladies, and gentlemen,

I would like to welcome all of you to the International Biology Symposium (InBioSymp) 2020. Year 2020 will be remembered as a very challenging volatile year. The coronavirus COVID-19 is affecting 218 countries and territories around the world. It has been a tough year, but as researchers, it is called upon us to be very creative and innovative, adapting to the new norms. To begin with, the Office of Industry, Community and Alumni Network (ICAN) of the Faculty of Applied Sciences (Fakulti Sains Gunaan – FSG) has taken an excellent initiative to register Virtual Symposium@FSG as part of the Virtual Colloquium Series (VCS@FSG) 2020 under the University Transformation Division (BTU) programme. This VCS@FSG 2020 is a conference series using virtual platform comprising of four different symposia in the area of Biology, Environment & Green Chemistry, Physics & Materials and Industrial Science & Technology.

So today, we begin our very first virtual symposium, InBioSymp 2020, organized by the School of Biology, Faculty of Applied Sciences, UiTM Shah Alam. Allow me to warmly applaud the organizers of this important event especially the Chairperson, Associate Professor Dr Sharifah Aminah, and her committee members, for giving me the privilege of addressing and welcoming all of you. It is a great honour and pleasure to be here today. On behalf of the InBioSymp 2020 committee, I take great pride in welcoming our honourable keynote and plenary speakers as well as all the participants of InBioSymp 2020. The committee members have done an outstanding job for organizing this event. All the speakers and participants from various institutions, which include universities, research institutes and industries inside and outside Malaysia, can exchange a broad spectrum of ideas throughout this event.

InBioSymp 2020 offers opportunities and new experiences to all scientists to present, discuss and share breakthrough ideas related to biology, virtually. The ultimate goal is to bring together biology scientists within multi-disciplinary groups. Hopefully with the best presenter award, it would encourage the appearance of high-quality research, thus making discussions, writing techniques and presentations more competitive and focusing on the recent outstanding achievements in the field of biology, and future trends and needs. I am very happy to be a part of InBiosymp2020 and would like to heartily congratulate all of you on your commitment and active participation. I hope everyone will benefit from this InBioSymp 2020 for years to come. Thank you for all that you have contributed to make this symposium possible and I wish all of you the very best.

Thank you.

Opening Remarks

Dean

Faculty of Applied Sciences, UiTM

Prof. Dr. Hajah Farida Zuraina Mohd Yusof

Assalamualaikum,

On behalf of all the academic staff of the Faculty of Applied Sciences, Universiti Teknologi MARA Shah Alam (FSG), I would like to extend our warmest welcome to distinguished guests, speakers, colleagues, friends, and all the participants to the International Biology Symposium 2020 (InBioSpmp 2020). Alhamdulillah, I am so proud to see so many participations from different countries including Malaysia, our neighboring country (Indonesia), Iran as well as England, all in one platform despite the current circumstances of Covid19 pandemic that hits us all over the world.

The InBioSymp Organizing Committee members have contributed tremendous amount of effort for the last couple of months to make this symposium possible this year. For the very first time, FSG conference is completely online. We have successfully managed the whole conference with a comprehensive online process for conference promotion, abstract and paper submission, conference registration, and other services. As a result, we have organized this symposium to discuss the truth and beauty of science, technology advancement and research update, while celebrating our global friendships around the theme *'Towards Sustainable Research, Global Responses and Beyond Boundaries'.*

Making progress with implementing sustainability is vital to securing a safe future. Failure to address our current unsustainable norms is a threat to the continuation of civilization. We are here to make a difference in the world, through our own research findings. The research community are encouraged to embrace an active role which is above and beyond neutral observer, to become a catalyst for change.

Ladies and gentlemen, your strong support and active participation has made InBioSymp 2020 possible today. We have received exceeded target number of papers presented and total number of people registered. The quality of technical programs is world-class, and the spectrum of topics is very current and broad. Hence, I hope this event could provide you a unique opportunity to meet colleagues from your own specialty area, I wish you a most fruitful experience with interesting and stimulating discussions and exchange of knowledge so that we can together, envisage the future of an innovative biological sciences.

Enjoy your participation in InBioSymp 2020. We hope you will return next year with even more colleagues for FSG conference in 2021.

Thank you.

Forward Message

Chairperson

International Biology Symposium 2020

Faculty of Applied Sciences, UITM

Assoc. Prof. Dr Sharifah Aminah

It is with great pleasure to warmly welcome you to the International Biology Symposium (InBioSymp 2020). InBioSymp 2020 is aimed to give the opportunity for researchers to get together and share experiences and knowledge encompasses recent research advances in various fields of biology. Our conference is rich and diverse with 2 international keynote speakers, 4 plenary speakers, almost 100 participants and more than 80 research papers that will be presented; therefore, this symposium promotes an international platform as an interactive research forum in the area of biological sciences via virtual oral presentations.

With a wide range of participants, this symposium is devoted to creating informal networking opportunities, sharing a wide variety of ideas, solving similar biological sciences problems, fruitful discussions and research collaboration among researchers, and all related parties from private and public sector. The richness of ideas is well-suited with the symposium tracks that were chosen during the early planning of organizing InBioSymp 2020.

The InBioSymp 2020 theme, *"Towards Sustainable Research ~ Global Responses, Beyond Boundaries"* signifies our biological systems that remain diverse and productive over the years. It also demonstrates the potential for a lasting maintenance of well-being, which in turn depends on the maintenance of the natural world and natural resources. Sustainability has become a wide-ranging term that can be applied to almost every facet of life on Earth, from local to a global scale and over a long span of time.

As the chairperson of InBioSymp 2020, I would like to express my utmost gratitude to the committee members for their unwavering commitment to ensure the success of this symposium. This conference would also not be possible without the generous help from the management of the Faculty of Applied Sciences, symposium moderators, track chairs, and the volunteers from our postgraduate students, who selflessly contributed to this symposium.

Most of all, I thank you, the participants, for enriching this symposium by your presence. I hope you will enjoy the content, develop new friendships, generate new ideas, and above all, have a good time.

We hope that the experiences in InBioSymp 2020 will be engraved in your memory.

Committees

Chairperson	▪ **Assoc. Prof. Dr Sharifah Aminah**
Vice Chairperson	▪ **Dr Norfatimah Mohamed Yunus**
Secretary	▪ **Dr Lyena Watty Zuraine Ahmad**
Treasurer	▪ **Dr Farizan Aris**
Registration	▪ **Assoc. Prof. Dr Asmida Ismail** ▪ **Dr Faezah Pardi**
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Publicity and Promotion	▪ **Dr Siti Khairiyah Mohd Hatta** ▪ **Dr Nurul Aili Zakaria**
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Logistic and Technical	▪ **En Shamsul Bahrin Gulam Ali** ▪ **En Azizul Zahariman** ▪ **En Khairul Azman Othman** ▪ **En Mohd Khairul Amri Ismail** ▪ **En Zamri Yaacob** ▪ **En Azlan Zul Aman Shah**

International Biology Symposium 2020

International Biology Symposium 2020 (InBioSymp 2020) is organized by the School of Biology, Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam, Selangor, Malaysia which is part of Virtual Colloquium Series@FSG 2020.

In accordance with InBioSymp 2020 theme, *Towards Sustainable Research - Global Responses, Beyond Boundaries*; we are honored to host this symposium to promote an international platform as an interactive research forum and networking in the area of biological sciences via virtual oral presentations. The lineup for our speakers inclusive of prominent scientists and researchers from different fields of biology, who would share their thoughts and findings with the participants.

Theme

Towards Sustainable Research, Global Responses, Beyond Boundaries

Symposium Tracks

- Microbiology & Biochemistry
- Molecular Biology & Bioinformatics
- Environmental Sciences & Biodiversity
- Biomedical & Health Sciences

Keynote Speakers

Prof Dr Farshad H. Shirazi
Pharmaceutical Sciences Research Centre, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

'Corona Pandemic Experience and Lessons for The Human Being'

Dr Stephen Gilbert Compton
University of Leeds & Rhodes University

'The Unusual Biology of a Malaysian Epiphytic Fig Tree and Its Pollinator'

Plenary Speakers

ENVIRONMENTAL SCIENCES & BIODIVERSITY
Ms Kumari Geetha Muniandy
Star Feedmills (M) Sdn. Bhd.

'Molecular Diagnostic Approach Toward Sustainable Shrimp Farming Industry'

MICROBIOLOGY & BIOCHEMISTRY
Dr Mohd Azinuddin bin Ahmad Mokhtar
Head of Genomics Department FGV R&D Sdn Bhd

'Combating Basal Stem Rot Disease Using Molecular Tools'

MOLECULAR BIOLOGY & BIOINFORMATICS
Mr Mohd Noor Mat Isa
Malaysia Genome Institute

'The Covid-19 Pandemic: What the SARS-COV-2 Genome Reveals'

BIOMEDICAL AND HEALTH SCIENCES
Dr Norwahidah Abdul Karim
Universiti Kebangsaan Malaysia

'Oxidative Stress and Mitochondrial Dysregulation in Autism Spectrum Disorder'

Programme Schedule

Emcee: Ms Ernie Eileen Rizlan Ross
Doa Recital: Mr Muhammad Fazrul Azim

TIME	PROGRAMME
08:00 – 09:00	**Registration of Participants (on-line)**
09:00 – 09:30	**National Anthem** **Doa Recitation**
09:30 – 10:0	**Opening Remarks** Prof. Dr. Hjh. Farida Zuraina Md Yusof Dean, Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam, Selangor. **Welcoming Address** Prof. Dr. Hadariah Bahron Chairperson, Virtual Colloquium Series @ FSG 2020
10:00 – 11:00	**KEYNOTE LECTURE** Prof Dr Farshad H. Shirazi Pharmaceutical Sciences Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran. (Title: Corona Pandemic Experience and Lessons for the Human Being)
11:00 – 12:00	Dr Stephen Gilbert Compton Faculty of Biological Sciences, University of Leeds, United Kingdom. (Title: The Unusual Biology of a Malaysian Epiphytic Fig Tree and Its Pollinator)
12:00 – 14:00	**LUNCH BREAK**
14.00 – 18.00	**PLENARY TALK AND PARALLEL SESSIONS**

PARALLEL SESSION 1

Virtual Room 1: Environmental Sciences & Biodiversity

PLENARY TALK **Moderator: Assoc Prof Dr Norrizah Jaafar Sidik**		
Ms Kumari Geetha Muniandy **Star Feedmills (M) Sdn. Bhd.** ***Molecular Diagnostic Approach Toward Sustainable Shrimp Farming Industry***		
Virtual Room 1: **Environmental Sciences & Biodiversity** **Track Chair:** **Assoc Prof Dr Norrizah Jaafar Sidik** **Panels:** **Dr Nur Nadiah Md Yusof** **Dr Faezah Pardi** **PIC:** **Dr Faezah Pardi**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Saiyidah Raffhanah Basri (EBS16-Saiyidah)	Floristic Variation and Distribution of Tree Communities at Pulau Dayang Bunting Forest Reserve, Langkawi
15:00 – 15:15	Hasya Hannani binti Ruziman (EBS17-HananniRuziman)	Edaphic Influences on Tree Species Composition and Community Structure in a Secondary-Lowland Dipterocarp Forest of Kota Damansara Forest Reserve, Selangor
15:15 – 15:30	Nurul Zawani binti Zolkfilee (EBS19-NurulZawani)	Edaphic Influences on Tree Species Composition, Biomass Distribution and Community Structure at Bukit Lagong Forest Reserve, Selangor
15:30 – 15:45	Nur Nazifah Binti Mohamad (EBS20-Nazifah)	Physico-Chemical Water Analysis of Sg. Sinai and Sg. Simpang Endap, in Mambong, Serian, Sarawak
15:45 – 16:00	Syed Abdul Jabar (EBS21-Jabar)	Modification of Prey-Predator Model to reveal the relationship between small-clawed otter (*Aonyx cinereus*) visitation and diet composition in a rice field landscape
16:00 – 16:15	Nur Alya Nabilah binti Azis (EBS22-NurAlyaNabilah)	The Effects of Acute Gamma Irradiation on Morphology of *Vigna radiata*
16:15 – 16:30	Shamsiah Abdullah (EBS23-Shamsiah)	Morphological Changes in gamma irradiated *Capsicum annuum* L. *var.* Kulai
16:30 – 16:45	Siti Noor Hajjar Md Latip (EBS24-NoorHajjar)	Pesticidal effect of Cypermethrin, *Bacillus thurigiensis* and Flubendiamide on oil palm pollinator weevil, *Elaidobius karamenicus*
CLOSING SESSION		

PARALLEL SESSION 1b

Virtual Room 1b: Environmental Sciences & Biodiversity

PLENARY TALK [Virtual Room 1] **Moderator: Assoc Prof Dr Norrizah Jaafar Sidik**		
Ms Kumari Geetha Muniandy **Star Feedmills (M) Sdn. Bhd.** ***Molecular Diagnostic Approach Toward Sustainable Shrimp Farming Industry***		
Virtual Room 1b: **Environmental Sciences & Biodiversity** **Track Chair:** **Dr Azani Saleh** **Panels:** **Dr Azani Saleh** **Assoc Prof Dr Asmida Ismail** **PIC:** **Assoc Prof Dr Asmida Ismail**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Zainab Sholehah binti Abdul Rashid (EBS26-AbdulRashid)	Leaf Anatomy of the Medicinal Plant *Sphagneticola trilobata* (L.) Pruski
15:00 – 15:15	Nurul Syahirah Mansur (EBS27-NurulSyahirah)	Leaf anatomical study of three medicinal *Psychotria* species (Rubiaceae)
15:15 – 15:30	Roshani Othman (EBS28-Roshani)	Distribution and Phylogenetic Relationships of local Malaysian Snakehead Fish *Channa* sp. using Mitochondrial 16S rRNA Gene in Raja Musa Peat Swamp Forest
15:30 – 15:45	Ferdi Andeska (EBS29-Andeska)	Temporal availability of otters' prey in an asynchronous rice field landscape
15:45 – 16:00	Nur Shaadah Zainuddin EBS30-Zainuddin)	^{238}U, ^{232}TH and ^{40}K Concentration for Soil at Universiti Teknologi Mara Pahang Jengka
16:00 – 16:15	Marini Ibrahim (EBS31-MariniIbrahim)	Protein Hydrolysates Extracted from Fish Sources in Selangor
16:15 – 16:30	Che Nurul Aini Binti Che Amri (EBS32-CheAmri)	Leaf Anatomy and Micromorphology of *Rhinacanthus Nasutus* (L.) Kurz (Snake Jasmine) From Peninsular Malaysia
16:30 – 16:45	Khairunnisa Binti Mohammad Hamdi (EBS33-MohdHamdi)	The Impact of Recreational Activity on Water Quality and Characterisation of Bacteria from Recreational River Water in Kuching, Malaysian Borneo
16:45 – 17:00	Noramira Nozmi (EBS34-Noramira)	Daily Activity Patterns of Three Female Orangutans (*Pongo pygmaeus*) in Captivity
CLOSING SESSION		

PARALLEL SESSION 2

Virtual Room 2: Microbiology & Biochemistry

PLENARY TALK **[Moderator: Assoc Prof Dr Noor Hana Hussain]**		
Dr Mohd Azinuddin bin Ahmad Mokhtar **FGV R&D Sdn Bhd** ***Combating Basal Stem Rot Disease Using Molecular Tools***		
Virtual Room 2: **Microbiology & Biochemistry** **Track Chair:** **Assoc Prof Dr Noor Hana Hussain** **Panels:** **Dr Wan Razarinah Wan Abdul Razak** **Dr Maslinda Musa** **PIC:** **Dr Nurul Aili Zakaria**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Siti Suhaila Harith (MB46-SitiSuhaila)	Isolation Bacteriophage of *Pseudomonas aeruginosa* and evaluation of their activity against onions
15:00 – 15:15	Jeganathan Tharshan Jeyakanesh (MB41-Jeyakanesh)	Structural Characterization of Cytotoxic Exopolysaccharides Produced by *Bifidobacterium pseudocatenulatum* ATCC 27919 Cultivated in Aloe Vera Medium
15:15 – 15:30	Toh Seng Chiew (MB42-Toh)	Preliminary antimicrobial effects of Jerangau Merah (*Boesenbergia stenophylla*) against pathogenic *Klebsiella pneumoniae, Vibrio cholerae* and *Shigella flexneri*
15:30 – 15:45	Nurul Ammar Illani binti Jaafar (MB43-Jaafar)	Diversity of Microorganisms in Stingless Bee Brood Cell
15:45 – 16:00	Kabiru Abubakar Musa (MB44-Musa)	Do Metal Ions Affect the Binding Behavior of Antimalarial Drugs to Human Serum Albumin: Fluorescence Spectroscopic Investigation
16:00 – 16:15	Olaide Olawunmi Ajibola (MB45-Ajibola)	Cell viability, Physicochemical and Sensory Characteristics of Probiotic Coconut juice During Cold Storage
16:15 – 16:30	Alya Nur Athirah Binti Kamaruzzaman (MB47-AlyaNurAthirah)	Inhibitory Action of Topical Antifungal Creams Against *Candida albicans* Biofilm

16:30 – 16:45	Masnita Fatihah Md Zahir (MB48-MdZahir)	Antimicrobial and Antifungal Activity of Chitosan Prepared from Cuttlebone Against Pathogens Causing Skin Infection
16:45 – 17:00	Nur Anisah Binti Johari (MB50-Nuranisah)	Efficiency of Commercial Disinfectants Against *Salmonella typhimurium* Biofilm
17:00 – 17:15	Puteri Nur Aliah Wan Faizal (MB51-WanFaizal)	Inhibition Properties of *Actinobacteria* Extracts Towards β–lactamase
17:15 – 17:30	Nur Ilida Mohamad (MB84-NurIlida)	Antibacterial Activity and Organic Acid Formation by *Lactobacillus* sp. Originated from Pickled Guava and Papaya
17:30 – 17:45	Sylviana Sinawat (MB85-Sinawat)	Identification and Characterization of *Lactobacillus* spp. from Animal Milk as Potential Probiotic Bacteria
17:45 – 18:00	Nur Liyana Mohammad Mohaidin (MB40-Nurliyana)	Antibiofilm and Cytotoxicity Properties of Green Synthesized Iron Oxide Nanoparticles
CLOSING SESSION		

PARALLEL SESSION 2b

Virtual Room 2b: Microbiology & Biochemistry

PLENARY TALK **[Moderator: Assoc Prof Dr Noor Hana Hussain]** **Virtual Room 2**		
Dr Mohd Azinuddin bin Ahmad Mokhtar **FGV R&D Sdn Bhd** ***Combating Basal Stem Rot Disease Using Molecular Tools***		
Virtual Room 2b: **Microbiology & Biochemistry** **Track Chair:** **Assoc Prof Dr Tg Elida Tg Zainal Mulok** **Panels:** **Dr Aziyah Abdul Aziz** **Dr Wan Rozianoor Mohd Hassan** **PIC:** **Dr Norashirene Mohamad Jamil**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Noor Nadia Syahira Binti Mohd Kamal (MB52-Syahira)	Probiotic Properties of Lactic Acid Bacteria from Three Species of Stingless Bees in Malaysia
15:00 – 15:15	Maimunah Mustakim (MB53-Mustakim)	Isolation and Identification of Amylase Producing *Bacillus* sp. from Local House Waste Contaminated Soil
15:15 – 15:30	Norshahida Binti Mat Jaya (MB54-Norshahida)	Screening of Schiff Base Ligands Derived from Phenylenediamine And Its Metal Complexes as A Potential Efflux Pump Inhibitor Against *Klebsiella pneumoniae*
15:30 – 15:45	Nurhaida (MB55-Nurhaida)	Anti-*Staphylococcus aureus* Activity of Butanol Extract Isolated from Endophytic Fungus *Aspergillus flavus* IBRL-C8
15:45 – 16:00	Siti Fatimah binti Suboh (MB56-Siti Fatimah)	Antimicrobial Activity of *Strobilanthes crispus* Leaves Aqueous Extract Against Tested Human Pathogens
16:00 – 16:15	Nurul Iman Binti Mohamad (MB57-Mohamad2)	Surveillance of *Burkholderia* sp. in Bukit Merah Orang Utan Island (BMOUI), Perak
16:15 – 16:30	Nurul Asyiqin Binti Rihzam (MB58-NurulAsyiqin)	Comparative Evaluation of Antiseptic Wipes and Chlorohexidine Gluconate Bathing

		Solution against Bacteria Causing Nosocomial Infections
16:30 – 16:45	Rohana Mat Nor (MB59-RohanaMatNor)	Cellulolytic bacterial fermented Moringa leaf potential as a protein source in non-ruminant animal feed
16:45 – 17:00	Seri Amelie binti Muliyadi (MB60-SeriAmelie)	Bioremediation of Textile Wastewater Using *Pleurotus pulmonarius*
17:00 – 17:15	Syaida Anati Binti Abd Rashid (MB61-SyaidaAnati)	Inhibition of *Corynebacterium pseudotuberculosis* Biofilm by DNA Synthesis and Protein Synthesis Inhibitors
17:15 – 17:30	Siti Solihah Khaidir (MB83-Solihah)	Microwave-Assisted Synthesis, Characterization and Anticancer Activity of Tetranuclear Schiff Base Complexes
17:30 – 18:00	Nursuria Bt Md Setamam (MBB72-Nursuria)	Detection of Non-Polar Chemical Compositions of *In-vitro* Culture Products of *Pogostemon cablin* via GC/MS
CLOSING SESSION		

PARALLEL SESSION 3

Virtual Room 3: Biomedical & Health Sciences

PLENARY TALK **[Moderator: Assoc Prof Dr Zaidah Zainal Ariffin]**		
Dr Norwahidah Abdul Karim **Universiti Kebangsaan Malaysia** ***Oxidative Stress and Mitochondrial Dysregulation in Autism Spectrum Disorder***		
Virtual Room 3: **Biomedical & Health Sciences** **Track Chair:** **Dr Khairul Adzfa Radzun** **Panels:** **Dr Amaliawati Ahmad Latiffi** **Dr Khairul Adzfa Radzun** **PIC:** **Dr Lyena Watty Zuraine Ahmad**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Mashani Mohamad (BHS04-Mohamad)	Liver Ultrastructural Changes in Rat Model of Insulin Resistance
15:00 – 15:15	Wan Alif Afiq Wan Nor Ruddin (BHS05-Wan)	Optimization of Plasma RNA Extraction for Nanostring nCounter miRNA Panel
15:15 – 15:30	Ahmad Tamim Ghafari (BHS06-Ghafari)	Phytochemical Screening and Quantification of Phenolic Content in *Vitex trifolia's* Leaves Hydro-alcoholic Extract
15:30 – 15:45	Muhammad Zulfiqah Bin Sadikan (BHS08-Zulfiqah)	Open Field Mirror Test as a Tool for the Assessment of Visual Impairment in Rats with Streptozotocin-Induced Diabetic Retinopathy
15:45 – 16:00	Raja Nur Firzanah Syaza Binti Raja Sharin (BHS09-Raja Sharin)	Development of an *In vitro* Caco-2 Intestinal Model to Study Lapatinib-Induced Changes in Gut Permeability
16:00 – 16:15	Khuriah Abdul Hamid (BHS10-Khuriah)	The Effects of Oil Components and Homogenisation Conditions on The Physical Characteristics and Stability of Oil-in-Water Emulsion Formulations
16:15 – 16:30	Mariyam Mala (BHS11-Mala)	Elicitation of Total Phenolics and Flavonoids in *Trigonella foenum-graecum* Using Yeast Extract Elicitor

16:30 – 16:45	Musliana Binti Mustaffa (BHS13-Mustaffa)	GuttaFlow Bioseal as Monocone Obturation Technique in Curved Root Canals. A Scanning Electron Microscopy Study
16:45 – 17:00	Helmizar H. (BHS82-Helmzar)	The Effect of Additional *Dadih* on Lactic Acid Bacteria and Nutritional Value of Pudding as a Food Supplementation for Pregnant Women
17:15 – 17:30	Rhanye Mac Guad (BHS15-Rhanye)	Association of Tumor Necrosis Factor-α (TNF-α) Gene Polymorphism and Dengue in Sabah, East Malaysia Population
17:30 – 17:45	Suzana Yusof (BHS85-Suzana)	Knowledge, Attitude and Practice towards Tobacco Smoking Among Secondary School Students
17:30 – 17:45	Kazi Hasan Jamil (BHS86-Jamil)	Exploring Extraction and Purification of Tannic Acid from *Camellia Sinensis* (Tea Leaves) for Potential Haemostatic Application in Dental Surgery
CLOSING SESSION		

PARALLEL SESSION 4

Virtual Room 4: Molecular Biology & Bioinformatics

PLENARY TALK **[Moderator: Prof Dr Hj Mohd Faiz Foong Abdullah]**		
Mr Mohd Noor Mat Isa **Malaysia Genome Institute** ***The COVID-19 Pandemic: What the SARS-COV-2 Genome Reveals***		
Virtual Room 3: **Molecular Biology & Bioinformatics** **Track Chair:** **Prof Dr Hj Mohd Faiz Foong Abdullah** **Panels:** **Dr Wan Nurhayati Wan Hanafi** **Dr Fakharul Zaman Raja Yahya** **PIC:** **Dr Roziah Kambol**		
Time	**Presenter**	**Paper Title**
14.45 – 15.00	Hazwani Mohd Yusof (MBB68-Hazwani)	Extracellular Metabolites Profile of Different Stages Colorectal Cancer Cell Lines
15:00 – 15:15	Assoc Prof Ts Dr Asmah Awal (MBB69-Asmah)	Somatic Embryogenesis of *Hevea brasiliensis* Muell. Arg. RRIM 600
15:15 – 15:30	Muhamad Zai Mirza Bin Zaini (MBB70-Zaini)	Transcriptomic Analysis Reveals to The Role of Cell Division During Mango Fruit Development.
15:30 – 15:45	Nor Raihan Mohammad Shabani (MBB71-NorRaihan)	Identification of MHC Class II-Bound Peptides of *Shigella flexneri* 2a-Infected Macrophages for Immunopeptidomics
15:45 – 16:00	Nur Shukriyah Mohamad Hazir (MBB73-Shukriyah)	Mitochondrial Substrate Profiling of Polyethylene-Induced Osteoclasts Differentiation Supplemented With Tocotrienol-Rich Fraction.
16:00 – 16:15	Mohd Syahril Bin Mohd Zan (MBB74-MohdSyahril)	Isolation and Identification of Pathogenic Bacteria in Satay at Kuala Pilah, Negeri Sembilan by Using MPN-PCR.
16:15 – 16:30	Nawal Binti Zulkiply (MBB75-Nawal)	*In silico* Identification of Antigenic Proteins Expressed in *Staphylococcus aureus*

16:30 – 16:45	Nurul Najwa Ahmad Nasim (MBB76-NurulNajwa)	Assessment of FTA Card Method in Detecting EgSHP Gene of Oil Palm Leaves
16:45 – 17:00	Che Muhammad Khairul Hisyam Bin Ismail (MBB77-CheMuhammad)	Elucidating the Expression Profile and *In-Silico* Analysis of Iron-Binding Proteins of *S. flexneri* Clinical Isolates as Vaccine Construct
17:00 – 17:15	Amir Asyraf Bin Zainudin (MBB78-AmirAsyraf)	Population Structure Revealed by 16S rRNA of *Penaeus monodon* (Fabricius, 1798) Broodstocks in the Indo Pacific Region
17:15 – 17:30	Zainab Aliyu Muhammad (MBB79-Zainab)	Investigation on DNA Content of Oil Palm Leaves Tissues Stored onto FTA Card
CLOSING SESSION		

Floristic Variation and Distribution of Tree Communities at Pulau Dayang Bunting Forest Reserve, Langkawi

Saiyidah Raffhanah Basri[1,2*], Mohd Nizam Mohd Said[2]

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Abstract: Island populations are considered as less diverse and more differentiated compared to adjacent mainland. It is essential to know the status of our forest biodiversity to be aware about the percentage of habitat loss. The study was carried out to determine floristic variation and distribution patterns of tree communities at Pulau Dayang Bunting Forest Reserve, Langkawi. Ten study plots of 20 m × 25 m each were selected and all trees with diameter at breast height (DBH) of 5 cm and above were enumerated and identified. The data from the study were analyzed for species diversity, species richness and evenness. The species diversity was determined by using Shannon Diversity Index and species richness were computed by using Margalef Index. A total of 521 trees which comprised of 71 species, 57 genera and 27 families were recorded. Euphorbiaceae was the most speciose family represented with 12 species, while *Diospyros transistoria* (Ebenaceae) was identified as the most frequent species of which out of 10 study plots, this species occurred in nine plots (90%). Density wise, Euphorbiaceae recorded the highest density of 238 individuals/ha, while at species level, *Diospyros transistoria* had the highest density of 128 individuals/ha. The diversity results show that Shannon Diversity Index (H') and Margalef's Index was low at (3.64) and (11.19), respectively and the evenness index however was high (0.85). The information from this forest documentation will be useful for the purpose of better management and conservation.

Keywords: Biodiversity; Diversity index; Floristic variation; Forest; Langkawi

Edaphic Influences on Tree Species Composition and Community Structure in a Secondary-Lowland Dipterocarp Forest of Kota Damansara Forest Reserve, Selangor

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Abstract: This research was conducted to determine tree species diversity and its relationship with edaphic factors at a secondary-lowland dipterocarp forest in Kota Damansara, Selangor. Ten study plots of 25 m x 20 m each were established randomly covering a total area of 0.5 ha. In each plot, all trees with diameters at breast height (DBH) of 5 cm and above were measured at 1.3 meters from the ground. Soil samples were taken from each plot, for physico-chemical analysis. A total of 205 trees from 46 species and 22 families were recorded in 0.5 ha study plots of Kota Damansara Forest Reserve (KDFR). As for species diversity, this forest showed a high Shannon-Weiner Diversity Index (H') of 3.43 (H'max = 3.83) and high evenness value of 0.89 which portrays the uniformity of tree species distribution in the study sites. KDFR recorded a total biomass estimation of 531.8 t/ha, contributed by 458.58 ha t/ha of above-ground biomass and 73.12 t/ha of below-ground biomass. Meanwhile, the soil analysis in this study demonstrated that most of the study plots were dominated by sandy clay texture. The percentage of organic matter content obtained ranged from 3.94% to 14.24%. The forest soils were acidic, as shown by a low soil pH of 3.86. Redundancy analysis indicated that several tree species such as *Cinnamomum iners, Cratoxylum arborescens, Myristica cinnamomea* and *Syzygium grandis* appeared to be closely related with soil chemical properties such as available nutrients of Ca, P, K. Data and information on tree species composition, physico–chemical characteristics of soil as well as the relationship between tree species distribution and edaphic factors from this study are important and may be used as a guideline for future ecological research in tropical forest areas.

Keywords: Kota Damansara Forest Reserve; ecology; species diversity; tree species, tropical forest

Edaphic Influences on Tree Species Composition, Biomass Distribution and Community Structure at Bukit Lagong Forest Reserve, Selangor

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Abstract: A study was conducted to determine the community structure of tree species in relation to edaphic factors at Bukit Lagong Forest Reserve, Selangor. Fourteen study plots of 25 m x 20 m were established which cover a total area of 0.7 ha. All trees with diameter at breast height of 5 cm and above were measured, identified and recorded. A total of 26 families, 47 genera and 53 species were enumerated from 448 tree individuals. The Dipterocarpaceae was the most speciose family with six recorded species. The Lauraceae recorded the highest family density of 107.14 individuals/ha while *Syzigium* spp. (Myrtaceae) had the highest species density of 85.71 individuals/ha. The total basal area (BA) was 36.02 m^2/ha in which Dipterocarpaceae contributed the highest value of 8.02 m^2/ha, whilst *Endospermum diadenum* showed the highest basal area with 4.51 m^2/ha at species level. Dipterocarpaceae and *Syzygium* spp. was the most important family and species with Important Value Index of 13.11% and 8.79% respectively. The Shannon-Weiner diversity (H') index of tree community showed a value of 3.41 (H'max = 3.97), Evenness Index of 0.57 and Margalef Richness Index (R') of 8.52. The total biomass recorded was 525.20 t/ha in which 455.24 t/ha was contributed by above ground biomass and 69.96 t/ha from below ground biomass. The soil texture was sandy loam which were dominated 64.29% of the area, whilst organic matter content ranges from 3.53% to 5.71% with pH value of 4.69±0.35. Environmental factors such as soil pH, inorganic nutrients and available nitrogen are closely associated with several tree species in the study plots as shown by ordination diagram from Redundancy Analysis (RDA). Overall, the results of this study show that the forest is rich in biodiversity and provide a justification for conservation action in this forest.

Keywords: Bukit Lagong Forest Reserve, Community Structure; Edaphic influences; Biomass; Species diversity

Physico-Chemical Water Analysis of Sg. Sinai and Sg. Simpang Endap, in Mambong, Serian, Sarawak

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Abstract: This study was performed to determine the chemical characteristic of water in Sg. Simpang Endap and Sg. Sinai, in Mambong, Serian. The samplings were conducted at Mambong, Serian on November 2016 and January 2017. *In-situ* data was collected from four stations and subjected to analyses according to Standard and Hach methods. Laboratory analyses were carried out for following parameters: nitrite, nitrate, total ammonia nitrogen, organic nitrogen, total alkalinity, soluble reactive phosphorus and chlorophyll-*a* according to Standard and Hach Method. The results showed that station 1 and 2 in Sg. Simpang Endap were significantly higher values in temperature, pH, conductivity, nitrite-N, nitrate-N, total alkalinity, total ammonia nitrogen and organic nitrogen compared to station 3 in Sg. Sinai ($P \leq 0.05$). The high values of water quality parameters in station 1 were caused by effluent from landfill and agricultural activity that increases the concentration of respective parameters by agriculture runoff. Decreased in concentration of respective water parameters in station 2 was due to dilution along Sg. Simpang Endap. Thus, overall water quality in Sg. Simpang Endap was categorized as slightly polluted. Meanwhile, station 4 in Sg. Sinai showed higher concentration of total ammonia nitrogen, organic nitrogen, total alkalinity, soluble reactive phosphorus and chlorophyll-*a* compared to station 3 ($P \leq 0.05$). Station 4 was located nearby the roadside of residential and commercialized area; hence, the water parameters were influenced by anthropogenic activity. Station 3 was undisturbed area and secondary forest which had no pollution factor. Station 3 acts as control station against all stations. In conclusion, Sg. Simpang Endap was affected by effluent from the landfill.

Keyword: Anthropogenic, water quality, Sg. Simpang Endap, Sg. Sinai

Modification of Prey-Predator Model to reveal the relationship between small-clawed otter (*Aonyx cinereus*) visitation and diet composition in a rice field landscape

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Abstract: In food webs, species compete with each other for resources. The prey-predator model could be used to analyze food webs dynamics. There are two types of predators; generalist and specialist. Generalist predators are species that are flexible on food composition and may switch resources, while specialist predators are species that only prey on particular species. An example of a generalist predator is the small-clawed otter (*Aonyx cinereus)*. The small-clawed otter not only preys on fishes, but also frogs, snails, insects, and others. This study examines mathematically a modified prey-predator model on a di-trophic food web for a generalist predator. The model then fit observational data of small-clawed otter visitation and their diet composition in a rice field landscape from which the corresponding parameter values were obtained. The results show that the otters' flexible foraging behavior affects the composition of the prey species on their diet. The modified model can be used to predict otter visitation and other cryptic animals where their population numbers are difficult to calculate. Potencies and challenges of using the model were discussed in this paper.

Keywords: Lotka-Volterra; small-clawed otter; generalist predator; latrine site; differential equation

The Effects of Acute Gamma Irradiation on Morphology of *Vigna radiata*

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Abstract: Mutation induction is a widely used method in the agricultural sector to alter the traits of plants especially for commercialisation purpose and as a mitigation measure to ensure food security in the future. Gamma radiation is one of the physical mutagens that is used in mutation breeding methods to bring out desirable traits in crops. This research was aimed to determine the morphological effects and the lethal dose (LD_{50}) of the acute gamma irradiation on mung beans (*Vigna radiata*). The seeds were exposed to different doses of acute gamma radiation; 0, 200, 400, 600, 800, 1000, 1500, 2000, 2500, 3000 and 3500 Gy. These irradiated seeds were planted for seven days and the physical appearance of the plants were observed during this period. The result showed that the germination percentage for all doses are above 80% and most seeds germinated on the first day. Generally, irradiated seeds have a higher germination rate compared to non-irradiated seeds. The seeds irradiated at 800 Gy recorded the fastest germination rate, which was 29 seeds per day compared to the non-irradiated seeds which germinated at the rate of 24 seeds per day. Besides, the plant height and root length were reduced as the dose of acute gamma radiation increased. However, no chlorophyll mutation or abnormal embryonic leaves were observed for all doses during the germination period. The lethal dose (LD_{50}) determined based on the plant height was at 752.50 Gy. As a conclusion, the acute gamma irradiation of different doses altered the germination rate, plant height and root length of mung bean plants. The results obtained from this study can be used as a reference for future studies on the mutations induced by acute gamma radiation in other plants.

Keywords: acute gamma radiation; induced mutagenesis; lethal dose; mung bean; *Vigna radiata*

Morphological Changes in gamma irradiated *Capsicum annuum* L. *var*. Kulai

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Abstract: Changes in the temperature, precipitation and sunlight affects the agricultural ecosystem, giving rise to pests and diseases and changes in biodiversity have severely affected the productivity of many crops including chilli. In Malaysia, pests and diseases are common and persistent problems that hinder chilli production which local farmers have to deal with. Development of new variety of chilli with improved characteristics is crucial to overcome this problem. In this study, *Capsicum annuum* seeds were exposed with 0, 20, 40, 60, 80, 100, 200, 300, 400, 500 and 600 Gy of gamma rays. The effects of gamma rays were assessed towards germination, survival rate and several morphological characters. The results revealed that the gamma radiation affect the germination, survival rate, fruit length, fruit weight, plant height, and most of the results were lower upon exposure to higher doses particularly 100 Gy and above. Germination rate, plant height, survival plant rate and other morphological characteristics of irradiated plant were observed to improve at lower doses (40, 60 and 80 Gy). Apparently, lower gamma ray doses, were more suitable to study the effect on seed germination as well as other morphological characters. The findings of this study provide basic information for mutation breeding in *Capsicum annuum* L. using gamma radiation which is useful for breeding program of this crop.

Key words: *Capsicum annuum*; gamma radiation; gamma ray; mutagenesis; mutation breeding

Pesticidal effect of Cypermethrin, *Bacillus thuringiensis* and Flubendiamide on oil palm pollinator weevil, *Elaeidobius kamerunicus*

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Abstract: *Elaeidobius kamerunicus* Faust (Coleoptera: Curculionidae) is widely known as the pollinating weevil of oil palm, *Elaeis guineensis* Jacq. Application of chemical control in pest and disease management especially for controlling bagworm, *Metisa plana* in oil palm showed less attention on the chemical effect to other organisms, especially the pollinator. In addition, less study of pesticide effects on pollinator weevil and oil palm yield have been conducted before. The objective of this study is to identify and to compare the effects of the Flubendiamide, *Bacillus thuringiensis* and Cypermethrin on the *Elaeidobius kamerunicus* mortality rate. *E. kamerunicus* were collected from an oil palm plantation in FELDA Serting Hilir, Negeri Sembilan. The male inflorescence of the oil palm trees was used to determine the re-emergence and mortality rate of *E. kamerunicus* with direct and indirect treatment application of the selected pesticides. All treatments were repeated for five replicates and *E. kamerunicus* mortality were observed for seven days under laboratory condition. The result showed there was a significant effect in different types of insecticide (p-value = 0.000) on the mortality of *E. kamerunicus.* Direct application the study indicated the highest mortality effect was caused by Cypermethrin and followed by *Bacillus thuringiensis*. Application of Cypermethrin showed the largest mortality effect and the least re-emergence rate of *E. kamerunicus*. In conclusion, Flubendiamide is suggested to be used for controlling pests and at same time can preserve the pollinator weevil, *E.kamerunicus*.

Keywords: *Bacillus thuringiensis;* Cypermethrin; *Elaeidobius kamerunicus*; Flubendiamide; mortality rate

Leaf Anatomy of the Medicinal Plant *Sphagneticola trilobata* (L.) Pruski

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Abstract: Leaf anatomical and micromorphological study were done on species of *Sphagneticola trilobata* (L.) Pruski under the Asteraceae family. People in the past had been using *S. trilobata* to treat diseases such as hepatitis, bug bite, or indigestion. Nowadays, modern medical research shows that *S. trilobata* has active chemicals against bacteria such as *Bacillus subtilis*. Since there is no comprehensive study has been done especially for taxonomic study of *S. trilobata* in Malaysia, therefore aim of this study is to determine and investigate the leaf anatomical and micromorphological characteristics that can be used in identification and also supportive data in classification of species studied. Methods of this study involved the transverse section for petiole, midrib, lamina and margin by using sliding microtome, epidermal peel methods and observation under light microscope. The leaf micromorphological study was observed under Scanning Electron Microscopy Zeiss Model EVO 50. The findings of these studies have demonstrated the characteristics of leaf anatomy and micromorphology for species studied that could be used in identification and classification of species such as type of vascular bundle, type of stomata, wax and trichome. In conclusion, the findings of this study have shown that the anatomical and micromorphological characteristics have taxonomic value and can be useful in identification, differentiation, and classification at species level.

Keywords: Leaf Anatomy; Leaf Micromorphology; Asteraceae, *Sphagneticola trilobata*

Leaf anatomical study of three medicinal *Psychotria* species (Rubiaceae)

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Abstract: Microscopy study is one of the tools for herbal authentication. Therefore, comparative study on leaf anatomy was conducted on three medicinal *Psychotria* species from Peninsular Malaysia, namely as *Psychotria griffithii* Hook.*f*., *P. montana* Blume and *P. sarmentosa* Blume. Previous studies have reported that indigenous people from Selangor and Pahang use *P. montana* and *P. sarmentosa* to treat fever, indigestion and as afterbirth treatment. The objective of this study is to identify leaf anatomical characteristics that significance for species identification and classification. The procedures involved cross section using sliding microtome on the petiole, lamina, midrib and leaf margin, leaf epidermal clearing and observation under light microscope and scanning electron microscope. Results have shown that all species have straight to curvy anticlinal cell walls, paracytic stomata, complete system of marginal venation and sclerenchyma cells present in midrib and lamina. *Psychotria griffithii* is different from other two species by the complex main vascular bundle in lamina (O-shaped); presence of druse and raphide in lamina; brachysclereid, arenchyma and sclerenchyma cells in petiole, and parallelocytic stomata (minor). Presence of acicular crystals and long-stalked simple unicellular trichome can be only observed in *P. montana*, whereas in *P. sarmentosa*, the diagnostic characters are presence of collenchyma cells in petiole; starch grains in midrib and lamina; prismatic crystals in lamina; long-stalked multicellular trichome, and long-stalked unicellular trichome (echinate ornamentation). In conclusion, leaf anatomical characteristics can be used to identify *Psychotria* species.

Keywords: leaf anatomy; medicinal plants; *Psychotria griffithii*; *Psychotria montana*; *Psychotria sarmentosa*

Distribution and Phylogenetic Relationships of local Malaysian Snakehead Fish *Channa* sp. using Mitochondrial 16S rRNA Gene in Raja Musa Peat Swamp Forest

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Abstract: The family *Channidae* or also known as snakeheads fish includes air breathing blackwater fishes have gained attention due to unique nature, commercial value in the aquarium trade and their biomedical properties. However, the distribution and genetic relatedness among Channa species in peat swamp forest remains insufficient and poorly understood. The objective of this study, to determine the composition of Raja Musa Peat Swamp Forest (RMFR) Channa species, and to establish their identity and phylogenetic relationship. In the present study, four species of Channa (*Channa striata, Channa micropeltes, Channa gachua and Channa lucius*) were identified. Compared to other members of Channa, *Channa striata* is widely distributed across the peatswamp where it was recorded in four different compartments (C76; 3°46.661'N; 101°34.432'E, C91; 3°26.009'N; 101°22.661'E, C99; 3°28.183'N; 101°26.634'E and C100; 3°28.181'N; 101°26.528'E) in RMFR. Further investigation on the four species was performed to distinguish among the four species and study their relationships using partial sequences of 16S rRNA of mitochondrial gene. The sequence analysis of the gene revealed two distinct groups which are *C. gachua* and *C. micropeltes* display the highest genetic distance (0.1232). Interestingly, the topology of the constructed tree (Neighbor Joining and Maximum Parsimony) using MEGA software justifies that all the species sampled are closely related. Based on this analysis, the 16S rRNA gene is sufficient for identification of Channa species in Malaysia. Based on the phylogenetic tree, the five major clades were separated by different species with bootstrap values in the range of 40–100%. These findings will establish the genetic relationship between the species of Channa for future use, particularly in designing selective breeding programme. The information could be used to produce successful hybrids with superior quality which can be utilized in both pharmaceutical and food industry.

Keywords: Phylogenetic, peat swamp forest, snakehead fish, 16S rRNA gene

Temporal availability of otters' prey in an asynchronous rice field landscape

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Abstract: Otters are the top predator in wetland habitat as well as in the rice field landscape. As the top predator, otters have important ecological functions in maintaining species diversity of its food web. Prey selection of otters is influenced by the availability of prey species in the habitat. Rice fields in the tropical region have unique temporal seasonality because of the cultivation stage. Therefore, information on the temporal availability of the otters' prey species in rice field landscapes is valuable to design wildlife-friendly farming practices. We examined whether otters' prey availability is influenced by cultivation stages. We surveyed various otters' prey species including fishes, snails, frogs, and water insects in four different cultivation stages: preparation, vegetative stage, generative stage, and post-harvest. The prey species were collected in rice fields adjacent to latrine sites of small-clawed otter (*Aonyx cinereus*). we performed the analysis of variance to examine the relationship between cultivation-stage and availability of prey of otter. ANOVA revealed the abundance of mollusc influenced by the cultivation-stage (P-value < 0,05), whereas the other 3 prey categories were not affected by the cultivation stage. Based on our results, we emphasize the implementation of wildlife-friendly rice farming to maintain species diversity.

Keywords: diversity; abundance; latrine site; top predator

^{238}U,^{232}TH and ^{40}K Concentration For Soil at Universiti Teknologi MARA Pahang Jengka

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Abstract*:* Universiti Teknologi MARA (UiTM) Jengka, Malaysia was established in 1988 covers an area of about 1000 acres and surrounded by palm oil plantation. The soils are a mixture of red-yellow and yellow-grey podzolic in nature. Natural radionuclides occur everywhere and mostly found in the soil, rocks and water which then contribute to the radioactive decays of radon as one of the natural background radiation. Although the areas have been converted to learning institution, no recent data of natural radionuclides has been carried out. Result of this study would serve as baseline data for the people, workers and students who have been exposed to natural background radiation in this area. Five soil samples were taken randomly by using a hand auger approximately up to 20 cm depth. The samples were dried, grind and sieved to ensure homogeneity. The homogenized soil samples were then analysed by using Energy Dispersive X-ray Fluorescence Spectroscopy (EDXRF) for uranium (^{238}U), thorium (^{232}Th) and potassium(^{40}K) concentrations. Activity concentration of ^{238}U varies from 19.81 to 29.0 Bq/kg with an average value of 24.2 ± 1.1 Bq/kg, ^{232}Th varies from 17.8 to 51.0 Bq/kg with an average value of 30.9 ± 1.6 Bq/kg and ^{40}K varies from 243.5.0 to 540.6 Bq/kg with an average value of 381.1 ± 9.8 Bq/kg respectively. It was found that, the average values for ^{38}U, ^{232}Th, ^{40}K is still in considerably safe to be exposed as compared to the world average concentrations 33 Bq/kg, 40 Bq/kg and 420 Bq/kg respectively. Therefore, the assessment of the radiological risk distribution at university campus is essential as a guideline data in order to take precaution steps in prolong time.

Keywords: EDXRF, UiTM Jengka, radionuclides, soil

Protein Hydrolysates Extracted from Fish Sources in Selangor

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Abstract: Fisheries industry produces probably almost 32 million tons of waste annually. These large quantities of waste need appropriate management to avoid chemical and microbial deteriorations if improper handling. An interesting possibility is to hydrolyze the waste to obtain fish protein hydrolysates (FPH)-containing proteins or peptone. Due to protein hydrolysate (FPH) limitation in the human industry because of taste defects, this fish peptone is very useful in microbial growth media in the fermentation industry. Peptones are a water-soluble mixture of polypeptides and amino acids are widely used in microbial biomass. The objectives of this study to extract protein hydrolysate from *Moolgarda seheli* and *Rastrelliger kaagurta* by using acid hydrolysis and alkaline hydrolysis. The extracted peptones were tested as growth media of *L. acidophilus*. The protein concentration measured using Bradford method showed that *Rastrelliger kaagurta* had the highest protein concentration using acid hydrolysis while *Moolgarda seheli* using alkaline hydrolysis. The extracted peptones as growth media showed the best growth of *L. acidophilus*. In conclusion, the fish peptones are successfully extracted and have potential to be used as growth media for *L. acidophilus.*

Keywords: protein hydrolysate, fish peptone, microbial growth media, acid hydrolysis, alkaline hydrolysis

Leaf Anatomy and Micromorphology of *Rhinacanthus nasutus* (L.) Kurz (Acanthaceae) From Peninsular Malaysia

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Abstract: Acanthaceae family has been used traditionally for medicinal purposes especially amongst the native communities in Peninsular Malaysia. It is also known as one of the potential plant families that can be used to cure diseases. Nowadays, many taxonomists have difficulties during the identification of the Acanthaceae species due to its morphological similarities and when there is an incomplete part of plants obtained from the field sampling. But until now, there is no comprehensive study that has been documented especially on the Acanthaceae family, specifically for *Rhinacanthus nasutus*. To avoid incorrect species identification, a systematic study that involved the leaf anatomy and micromorphology parts are being used for the identification and classification of plants in the Acanthaceae. Therefore, the main objective of this present study is to identify the leaf anatomical and micromorphological characteristics that can be used in plant identification and also for supportive data in plant classification. The leaf anatomical and micromorphological studies that are conducted on *R. nasutus* involve several procedures such as cross-section using a sliding microtome, and observation under a light microscope and scanning electron microscope. The anatomical and micromorphological characteristics observed include patterns of petiole and midrib vascular bundles, presence of cystolith cells in lamina,midrib and petiole, type of stomata (amphistomatic) and the presence of trichomes. In conclusion, results showed that anatomical and micromorphological characteristics have taxonomic significance that can be used in the identification and classification especially at the species level.

Keywords: Acanthaceae, *Rhinacanthus nasutus*, taxonomic significant, traditional medicine

The Impact of Recreational Activity on Water Quality and Characterisation of Bacteria from Recreational River Water in Kuching, Malaysian Borneo

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Abstract: Humans have been using river water different purposes including leisure activities, agriculture, transportation, drinking water and generating electricity through hydroelectric dams. These activities can affect the health of the river and also its surrounding environments. The objectives of this study are to assess the impact of recreational activity on water quality of Jangoi River in Padawan, Sarawak. Water quality determination based on Malaysian Water Quality Index-Department of Environment (WQI) was carried out at three sampling stations on two different days. Six water quality parameters were measured; pH, dissolved oxygen, biological oxygen demand, chemical oxygen demand, total suspended solids and ammonia. The results showed that the WQI at each station have excellent water quality with WQI values ranging from 88 to 92%. One-way ANOVA analysis showed that the WQI parameters for all stations are not significantly different from each other thus suggesting that recreational activities at Jangoi river do not affect its water quality. Samples of water from the river were analyzed for the presence of bacteria. The isolates were analysed by using $(GTG)_5$-Polymerase Chain Reaction (PCR). Upon construction of the dendogram, the representatives of five isolates were identified by using 16S rRNA PCR and DNA Sequencing. Achromobacter, Stenotrophomonas and Bacillus dominated the population of bacteria in the river. The Antibiotic Susceptibility Test was done to determine the susceptibility of each isolate towards selected antibiotics by using disk diffusion assay. The bacteria showed resistance against tetracycline, ciprofloxacin, erythromycin, chloramphenicol and ampicillin. The findings in this study suggested that there is a need to continuously monitor the antibiotic resistant patterns of bacteria in recreational rivers to predict emerging MAR bacteria as well as preventing its widespread since these bacteria may pose health hazards to the public.

Keywords*:* Jangoi River, water quality, antibiotic resistance bacteria, $(GTG)_5$-PCR and 16S rRNA sequencing

Daily Activity Patterns of Three Female Orangutans *(Pongo pygmaeus)* in Captivity

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Abstract: Orangutan has been facing a rapid population decrease globally from habitat loss due to deforestation, hunting, and diseases. Conservation efforts have been carried out since the 19th century to ensure the survivability of the species, which includes saving the orangutan from the wild and taking them into captivity for care. This study aims to determine the activity pattern of three captive female orangutans - Baboon, Careena and April aged 33, 13 and 10 respectively at Bukit Merah Orang Utan Island. Behavioural observation of the orangutans was conducted via scan and focal sampling for a total number of 42 days. From the results, it was found that there are some significant differences in the behaviours displayed at different times of the day and between the three individuals. Inactive behaviours which include idle, sit and lie were displayed significantly the most by the animals. The inactive behaviour was also found to be significantly higher in the morning compared to in the afternoon. The three orangutans also spent the longest time playing in the morning with April displayed play behaviour significantly longer compared to Baboon and Careena. The results of this study can be utilised to further enhance our understanding on the behaviour pattern of captive orangutans in ensuring the effectiveness of their conservation programme.

Keywords: daily activity; behaviour; orang utan; focal sampling; scan sampling

Isolation Bacteriophage of *Pseudomonas aeruginosa* and evaluation of their activity against onions

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Abstract: The ability of agriculture to continually provide food to a growing world population is of crucial importance. Bacterial diseases of plants have continually reduced production since the advent of crop cultivation practices. Bacteriophages are important microorganisms in combating bacteria as they have the properties to lyse the host while they done completing their cycle of life. Therefore, it gives a new promising field namely as phage therapy to be explore and use in agricultural practices. The aims of this study are to isolate the bacteriophage and *Pseudomonas aeruginosa*, to enumerate total number of bacteriophage and to evaluate it activity in combating *P. aeruginosa*. This study is accomplish using plaque assay and evaluating bacteriophage activity on onion skin. Sample uses contain a total of 3.13 X 10^2, 2.4 X 10^2 PFU/ml of bacteriophage in filtered and unfiltered, respectively. The purified phage plaque produced clear, with 1.0-3.0 mm in diameter plaques and exhibit well-defined edges in bacterial lawn. Furthermore, result indicate that the present of bacteriophage able to control the plant disease cause by *P. aeruginosa* in the onion skin test. As a conclusion phage therapy has a potential to be used to fight plant disease.

Keywords: Bacteriophage, *P. aeruginosa*

Structural Characterization of Cytotoxic Exopolysaccharides Produced by *Bifidobacterium Pseudocatenulatum* ATCC 27919 Cultivated in Aloe Vera Medium

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Abstract: Different cultivation medium by probiotic bacteria has been hypothesized to produce different molecular structure of exopolysaccharides (EPS). The present study, human colorectal adenocarcinoma (Caco-2) cell line was used to access the cytotoxic property of EPS produced by the probiotic *Bifidobacterium pseudocatenulatum* ATCC 27919 cultivated in aloe vera and commercial media (MRS). The cytotoxicity was carried out using MTS assay. The monomer repeating units of EPS was identified using thin-layer chromatography (TLC) and their molecular structures were characterized through flourier-transform infrared (FT-IR) and nuclear magnetic resonance (NMR) spectroscopies techniques as well as CHNS elemental analysis. Exopolysaccharides obtained from aloe vera and commercial media were found to be toxic to Caco-2 cells at a tested concentration of 1 mg/ml and 40 hrs incubation with percentage cell viability of 65% and 38%, respectively. Result obtained was compared to 48% of the 4 µM as positive control (dexamethasone). The monomer repeating units of the hydrolysed EPS molecular structures of both media was identified to be glucose through TLC analysis. This monomer of the EPS was further confirmed by the FTIR and NMR spectroscopic analysis. The arrangement of the glucose units in the EPS molecular structure was proposed to exhibit α-(1→4) glycosidic linkage for the backbone and α-(1→6) glycosidic linkage for the branch based on NMR structural characterization as well as literature values. This study demonstrates that the carbon profiles of the EPS produced *B. pseudocatenulatum* ATCC 27919 cultivated in aloe vera, and commercial media have no difference.

Keywords: Exopolysaccharide, EPS structure, Extraction, Bifidobacterium, Cytotoxicity, Repeating unit

Preliminary Antimicrobial Effects of Jerangau Merah (*Boesenbergia Stenophylla*) Against Pathogenic *Klebsiella pneumoniae, Vibrio cholerae* and *Shigella flexneri*

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Abstract: The food and waterborne pathogens; *Klebsiella pneumoniae*, *Vibrio cholerae* and *Shigella flexneri* have been the culprit for the food poisoning, diarrhoea and bacteraemia. It can be treated by using a combination of antibiotics. However, the emergence of multiple antibiotic resistance (MAR) due to the overuse and misuse of antibiotics had made the treatment difficult. Hence, the search for an alternative, safe and cost-effective antimicrobial agent is crucial. *Boesenbergia stenophylla* or known by the locals as "Jerangau Merah", is a rare ginger species belongs to the Zingiberaceae family. It was commonly known to have therapeutic effects against food poisoning, stomachache, diarrhoea, and fever. This study aims to extract and characterize the phytocompounds in *B. stenophylla* for their antimicrobial activities against these pathogens. Soxhlet extraction was utilized to produce the crude extracts from the stem and rhizome using hexane and ethyl acetate as the solvent. Antimicrobial susceptibility tests (AST) using disk diffusion (Kirby-Bauer) methods were then conducted to determine their preliminary antimicrobial effects against the pathogenic bacteria. From disk diffusion assay, the pathogenic bacteria observed to be susceptible to all extracts tested, especially *V. cholera* which was notably being most sensitive to the extracts. The rhizome and stem extracted with n-hexane exhibited great antimicrobial activities against *V. cholerae* with an average inhibition zone size of 11.33 mm and 11 mm. The rhizome extracted with ethyl acetate showed great antimicrobial activities [9 mm] against *K. pneumonia* compared to the other extracts. Apart from that, the stem extracted with h-hexane and ethyl acetate and rhizome extracted with ethyl acetate shared the similar activities [9 mm] against *S. flexneri*. This preliminary study showed that *B. stenophylla* possess antimicrobial properties against pathogenic bacteria. Hence, these crude extracts of *B. stenophylla* should be intensively studied to serve as the potential antimicrobial agents against these pathogens in future.

Keywords: *Boesenbergia stenophylla*; antimicrobial susceptibility test; *Klebsiella pneumoniae*; *Vibrio cholerae*; *Shigella flexneri*

Diversity of Microorganisms in Stingless Bee Brood Cell

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Abstract: The main microorganisms living in stingless bee colonies are yeasts, molds, and bacteria. Newly emerged adult worker bees are inoculated with microorganisms when they begin to feed. More than 6,000 microbial strains were explored within stingless bee communities and very limited on *Heterotrigona itama.* However, the knowledge about this biodiversity is very limited only for a few stingless bee species. Our aim in this study is to determine the diversity of the most common microorganisms associated with the larval provision from the brood cell of *H. itama.* The microorganism from larval provision in the brood cell of stingless bee *H. itama* were isolated and identified through molecular 16S rRNA gene sequencing. Numerous species of bacteria, fungi and yeast were calculated from brood cell. The colony forming units (CFU/ml) of bacteria are 1.59×10^8, fungi (1.2×10^6), yeast (1.1×10^7) and 9.0×10^8CFU/ml for lactic acid bacteria. The microbial identification of the larval food from the *H. itama* brood cell showed the presence of five bacteria including lactic acid bacteria (LAB), three fungi and two yeast species. The species of the bacterial encountered are *Lactobacillus* sp., *Bacillus* sp., *Bacillus subtilis*, *Acinetobacter radioresistens* and *B. amyloliquefaciens* while *Monascus ruber*, *Aspergillus nomius* and *Aspergillus flavus* are the fungi encountered. Meanwhile, yeast that were identified are *Rhodotorula mucilaginosa* and *Candida* sp. The microorganisms encountered in this study may be of both beneficial and detrimental importance to stingless bee community. Further research is recommended to understudy the possible implication of the microorganisms in stingless bee larvae development and *in vitro* rearing.

Keywords: Microflora, *Heterotrigona itama*, bacteria, fungus, yeast

Do Metal Ions Affect the Binding Behavior of Antimalarial Drugs to Human Serum Albumin: Fluorescence Spectroscopic Investigation

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Abstract: Influence of six metal ions *viz*. Mg^{2+}, K^{+}, Ca^{2+}, Mn^{2+}, Cu^{2+} and Ba^{2+} on the binding affinity of human serum albumin (HSA) towards three antimalarial drugs, namely, sulfadoxine (SDN), mefloquine (MEF) and lumefantrine (LUM) was investigated using fluorescence quenching titrations. The effects of metal ions (Mn^{2+}, Cu^{2+} and Ba^{2+}) were found similar on the affinity of HSA towards SDN, MEF and LUM. Values of the association constant, K_a for SDN/MEF/LUM−HSA interactions in the presence of these metal ions were found to decrease significantly in the order: $Mn^{2+} > Cu^{2+} > Ba^{2+}$. On the other hand, the presence of Mg^{2+}, K^{+}, Ca^{2+} affected the binding affinity for these drugs differently. Whereas a slight increase in the K_a value of the SDN−HSA complex was seen in the presence of Mg^{2+}, Ca^{2+} produced a similar effect on the LUM−HSA system. For MEF−HSA and LUM−HSA systems, effects of K^{+} and Mg^{2+} were found similar, showing the decrease in the K_a value, being more effective with K^{+}, however, this decrease was more significant than Mn^{2+}, Cu^{2+} and Ba^{2+}. These results suggested interference of metal ions with drug-protein interactions either through binding to the protein near the drug binding site or weakening the drug-protein binding due to metal ion-drug complexation. As a conclusion, these findings will be useful in understanding the effect of metal ions on the binding of antimalarial drugs to human serum albumin, which may help in future clinical application.

Keywords: Antimalarial drugs; human serum albumin; metal ions; fluorescence spectroscopy.

Cell Viability, Physicochemical and Sensory Characteristics of Probiotic Coconut Juice During Cold Storage

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Abstract: Probiotic fermentation has gained considerable attention in the pharmaceutical and food industry, and the use of milk-based products has prevented vegetarians, allergic to protein and lactose, intolerant consumers from their consumption. Nevertheless, there is a genuine interest in the production of crop juice-based probiotic beverages with probiotics potentials. The objective of this study focused on the development and storage of probiotic coconut juice using lactic acid bacteria (LAB) as a starter, and determination of physicochemical parameters, viability, antibacterial and sensory test of the samples. The viability of the probiotic, physicochemical and sensory test of stored probiotic coconut juice employing LAB (*Lactobacillus casei* ATCC 393, Lactobacillus plantarum ATCC20174, *Lactobacillus rhamnosus* ATCC 7469 and *Lactococcus lactis* IO-1) as a single starter culture was studied. There was an increase in total acidity production and a decrease in pH, (°Brix), phenolic, antioxidant and tannin content during the refrigerated condition. At weeks 3 and 4, coconut juice inoculated with *L. lactis* IO-1 samples had the highest total acidity (1.32%). However, the level of phenolic compound, antioxidant, and tannin content reported a slight decrease during storage. The probiotic strains were viable throughout the refrigerated storage. *L. lactis* IO-1 showed greater viability compared to other strains (8.426 log CFU/ml). There were no significant differences in all the samples in terms of taste, aroma, colour, and appearance. It could be inferred from this study that high acidity and presence of inhibitor phenolic compounds in probiotic coconut juice have no negative impact on the viability of probiotics and the antibacterial potential of the samples throughout storage. Hence, probiotic fermentation could provide an alternative outlet for coconut juice utilization and may produce a novel probiotic beverage for consumers, especially for sport nutrition.

Keywords: Coconut juice; probiotic; antioxidant; sensory test

Inhibitory Action of Topical Antifungal Creams Against *Candida albicans* Biofilm

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Abstract: Candidiasis is an infection caused by Candida fungi, especially *Candida albicans* that generates high healthcare costs worldwide. Factors that heighten the risk of candidiasis include cancers, steroids, stress, antibiotic usage and diabetes. Excessive use of antifungal agents often causes fungal resistance and leads to failure of antifungal therapy. Susceptibility of *C. albicans* biofilm towards existing topical antifungal creams needs to be further investigated. The objective of this study was to evaluate the effects of miconazole nitrate, econazole nitrate, ketoconazole and tolnaftate-based antifungal creams against *C. albicans* biofilm. *C. albicans* ATCC MYA-2876 biofilm was developed in microplate assay in the absence and presence of antifungal creams. All antifungal creams were evaluated in the range between 156.25µg/ml and 5000µg/ml. Biofilm biomass and biofilm viability were measured using crystal violet assay and resazurin assay respectively. Results demonstrated that all antifungal creams effectively inhibited *C. albicans* biofilm. Treatment with miconazole nitrate-based antifungal cream significantly ($p<0.05$) reduced biofilm biomass and biofilm viability at all test concentrations. Correlation between biofilm biomass and biofilm viability in the presence of miconazole nitrate-based antifungal cream was also found to be significant ($p<0.05$). The findings of the present study suggest that the most efficient agent against *C. albicans* biofilm is miconazole nitrate-based antifungal cream.

Keywords: *Candida albicans;* candidiasis; biofilm; antifungal cream

Antimicrobial and Antifungal Activity of Chitosan Prepared from Cuttlebone Against Pathogens Causing Skin Infection

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Abstract: The discovery of new antibiotics for infectious diseases has become challenging due to the rise of antimicrobial resistance. Meanwhile, chitosan has been considerably used in many branches of research. It has been discovered to have some good benefits in medicals, pharmaceuticals and food technologies. The effect of the chitosan is influenced by their sources. In this study, chitosan was prepared from the cuttlebone of *Sepia* sp. by chemical method and analysed by using FT-IR spectrophotometer for the confirmation presence of its functional groups. There are three types of reactive functional groups in the chitosan which are amino group and primary and secondary hydroxyl group attached to the C-2, C-3 and C-6 positions respectively. The chitosan has a high cationic property due to the presence of its amino group. The bacteriostatic activity of chitosan occurs due its positive charged in acidic concentration that interact with the negative charged residue of carbohydrates, lipids and proteins located on the cell surface of bacteria. The antimicrobial and antifungal activity of chitosan from cuttlebone were analysed against two different bacterial strains (*Escherichia coli* and *Staphylococcus aureus*) and a fungal strain, *Candida albicans* by disc diffusion and minimum inhibitory concentration (MIC) methods. For the disc diffusion method, the concentrations used are 100 mg/ml and 50 mg/ml while 20, 40, 60, 80, and 100 mg/ml concentrations are used for MIC test. The results showed that this chitosan from *Sepia* sp. has concentration dependent antibacterial and antifungal activity with higher antifungal activity compared to antibacterial activity against all tested organisms and may become a new potential agent for antibiotic discovery.

Keywords: Cuttlebone; chitosan; antimicrobial activity

Efficiency of Commercial Disinfectants Against *Salmonella typhimurium* Biofilm

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Abstract: Salmonellosis remains one of the most common foodborne diseases, constituting a worldwide major public health concern. The main sources of infection for humans are contaminated poultry products such as chicken, turkey and quail. *Salmonella typhimurium* is known to form a heterogeneous biofilm that is commonly found in infected hosts. Susceptibility of *S. typhimurium* biofilm towards existing commercial disinfectants needs to be further investigated. The objective of this study was to evaluate the effects of sodium hypochlorite, sodium dodecyl-benzene sulfonate, benzalkonium chloride and chloroxylenol-based disinfectants against *S. typhimurium* biofilm. *S. typhimurium* ATCC14028 biofilm was developed in microplate assay in the absence and presence of commercial disinfectants. All commercial disinfectants were evaluated in the range between 3.125% and 100%. Biofilm biomass and biofilm viability were measured using crystal violet assay and resazurin assay respectively. Results demonstrated that all commercial disinfectants effectively inhibited *S. typhimurium* biofilm. Treatment with chloroxylenol-based disinfectant significantly ($p<0.05$) reduced biofilm biomass and biofilm viability at all test concentrations. Correlation between biofilm biomass and biofilm viability in the presence of chloroxylenol-based disinfectant was also found to be significant ($p<0.05$). The findings of the present study suggest that the most efficient agent against *S. typhimurium* biofilm is chloroxylenol-based disinfectant.

Keywords: *Salmonella typhimurium;* salmonellosis; biofilm; disinfectant

Inhibition Properties of *Actinobacteria* Extracts Towards β–lactam Resistance

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Abstract: *Actinobacteria* is one of the most valuable sources of natural products with agricultural, biotechnological, industrial and medicinal importance. They are top producers of antibiotics and have the ability to produce a wide variety of secondary metabolites. The rapid development of resistance bacteria stresses the need to find new adjuvant or resistant modifying agents to combat the growing number of resistant pathogens. In this study, 85 *Actinobacteria* extracts that were grown in ISP 2 medium were studied for their ability to potentiate the activities of oxacillin against Methicillin-resistant *Staphylococcus aureus* (*MRSA*) ATCC 43300, a strain that confers resistance to β–lactam drugs. The anti-*Staphylococcal* activities of the extracts were evaluated using microtiter resazurin based assay and the minimum inhibitory concentration of the selected antibiotics was initially determined. A 50% sub-inhibitory concentration of the antibiotics was used in combination with the extract to evaluate β–lactamase inhibition potential. The results from this study showed that majority of the isolates were able to grow on ISP 2 instead of other ISP media used in this study. One *Actinobacteria* extracts from G3C38 isolate identified as *Streptomyces griseorubens* able to enhance the activity of oxacillin at a concentration of 4ug/mL. In addition, the active extracts displayed weak inhibitory activities (<20% cell growth inhibition) when tested against the same resistant strain in the absence of the antibiotic. This implied that *Actinobacteria* extracts may contain active metabolites that can act as β–lactamase inhibitors and restore the effectiveness of penicillin derivative antibiotics.

Keywords: *Actinobacteria; Staphylococcus aureus*; β–lactamase; β–lactam; oxacillin

Antibacterial activity and organic acid formation by *Lactobacillus* sp. originated from pickled guava and papaya

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Abstract: *Lactobacillus* sp. is part of lactic acid bacteria (LAB) and known to be able to produce several antibacterial compounds including organic acids that are able to inhibit many types of pathogenic bacteria. The antibacterial activity of LAB with the ability to inhibit growth of pathogenic bacteria associated with foodborne illness is seen as a natural way to improve food safety. This study was carried out to isolate and identify LAB from local pickled guava (*Psidium guajava*) and papaya (*Carica papaya*) and to evaluate their antibacterial activity against selected foodborne pathogens. Standard method was used for the isolation of LAB, while identification was done based on their morphological characteristics, biochemical reactions and polymerase chain reaction (PCR) amplification of 16S rRNA gene and sequencing. The antibacterial activity study was done using cell free supernatant (CFS) of the identified LAB against selected Gram-positive and Gram-negative foodborne pathogens by microtiter plate method. Determination of the organic acid formation in the CFS that are responsible for the antibacterial activity of the LAB was also conducted using HPLC. The results showed that a total of three LAB from the genus *Lactobacillus* have been successfully isolated and identified as *Lactobacillus plantarum* (LABP1), *Lactobacillus reuteri* (LABR) and *Lactobacillus paracasei* (LABC). The antibacterial activity of CFS of all three *Lactobacillus* sp. was due to organic acid production. The lactic acid was the most abundant organic acid produced by all *Lactobacillus* sp. in growth media when evaluated by High Performance Liquid Chromatography (HPLC) method. Other organic acids including acetic acid, citric acid, tartaric acid and succinic acid were also detected in significantly lower amount than lactic acid.

Keywords: lactic acid bacteria; cell free supernatant; antibacterial; pickled fruits; foodborne pathogen

Identification and Characterization of *Lactobacillus* spp. from Animal Milk as Potential Probiotic Bacteria

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Abstract: Species of the genera *Lactobacillus* is among the lactic acid bacteria most commonly applied in industry due to their important roles as starters in healthy fermented foods. This study attempted to isolate and characterize *Lactobacillus* spp. with increased potential for use as probiotic with health profit using molecular and biochemical methods. A total of 228 samples received in the form of glycerol stocks were revived on MRS agar plates for phenotype identification. The respective colonies were subjected to Gram stain, catalase and oxidase test. Further identification was carried out via molecular means. Biochemical tests for probiotic properties include bile salt tolerance, acid tolerance and bile salt hydrolase (BSH) activity tests. Out of 228 samples, only 34 isolates exhibited Gram positive bacilli with negative oxidase and catalase activity which phenotypically indicated as *Lactobacillus*. Primers Lac1 and Lac2 was used for 16S rRNA gene amplification which then generated 231 base pair PCR products. As for *bsh* gene, for the purpose of determining strains that possess bile salt hydrolase, forward primer *bsh1* and reverse primer *bsh2* were applied that resulted in amplification of 104 base pair PCR products. Twelve out of 34 samples showed bands for *bsh* gene. These samples were further examined and were observed to have good ability to withstand the exposure to 0.3% bile salts for 3 h, with the highest resistance rate of 89.31%. All the tested strains also showed good capacity to survive under low pH condition with the highest survival rate noted at 90.14%. They also displayed BSH activity to different levels. In conclusion, the current study has successfully identified several *Lactobacillus* spp. isolates to be used as potential probiotic strains. Furthermore, this project provided an important opportunity to advance the understanding and make an important contribution to the field of food biotechnology in regard to probiotics.

Keywords: *Lactobacillus*, probiotic, animal milk, bile salt hydrolase, *bsh* gene

Antibiofilm And Cytotoxicity Properties of Green Synthesized Iron Oxide Nanoparticles

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Abstract: *Staphylococcus aureus* can attach to most foreign objects and create biofilm on medical devices surfaces. *S. aureus* is known to be resistant to multiple types of drugs and the ability to form biofilm that makes the infections harder to eradicate. Nowadays, iron oxide nanoparticles (IONPs) have been intensively studied regarding their antibacterial and antibiofilm activity. The small size of the IONPs enables them to directly interact with microbial cells by several mechanisms. This study aims to investigate the antibiofilm activity and cytotoxicity properties of green synthesized IONPs through leaf extract of neem (*Azadirachta indica*) against *S. aureus* and breast cancer cells (MCF-7) respectively. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) was determined by microdilution broth method. The antibiofilm activity of IONPs was further evaluated using minimum biofilm inhibitory concentration (MBIC) assay. The morphology of *S. aureus* biofilm after treatment with $MBIC_{90}$ of IONPs was observed under SEM. The cytotoxicity of IONPs was tested on MCF-7 cells via WST-1 assay. From this study, IONPs showed antibacterial activity with MIC at 6.25 mg/ml and MBC value at 25 mg/ml. The antibiofilm activity of IONPs displayed a dose-dependent pattern with $MBIC_{50}$ and $MBIC_{90}$ were at 1.56 mg/ml and 12.5 mg/ml respectively. SEM images of sample treated with IONPs at $MBIC_{90}$ showed significantly reduced biofilm formation with abnormal morphology of *S. aureus* observed, thus indicating good antibiofilm action. The IONPs exhibited toxicity to MCF-7 cells with a dose dependent pattern and half maximal inhibitory concentration (IC_{50}) was found at 89 µg/ml. The finding from this study suggested that the green synthesized IONPs may provide a potential antibacterial and antibiofilm agent against *Staphylococcus aureus*.

Keywords: *Staphylococcus aureus*, iron oxide nanoparticle, antibiofilm, cytotoxicity

Probiotic Properties of Lactic Acid Bacteria from Three Species of Stingless Bees in Malaysia

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Abstract: Stingless bee is a natural type of bee that exists in almost every continent. The honey produced by this bee has been widely used across time and space. There are approximately 50 species of stingless bee have been identified in Malaysia. Despite the extensive studies on lactic acid bacteria (LAB), the data on LAB isolated from stingless bee is limited. Moreover, there is a huge demand for novel LAB strains as potential probiotic. This study reports the isolation and identification of LAB from three species of stingless bee which were *Heterotrigona itama*, *Geniotrigona thoracica* and *Tetragonula laeviceps* and also assessing the *in vitro* probiotic activity of the isolates. A total of 28 LAB isolates were successfully isolated and were further tested by *in vitro* probiotic characterization. Among the isolates, four isolates (HIT11, GTH3, GTH6 and TLA4) demonstrated good probiotic properties. Acidity tolerance in pH 2 and pH 3 from GTH6 isolates showed highest survivability with 81.55% and 62.21% respectively. As for bile salt and simulated gastric juice tolerance, GTH3 and HIT11 revealed good results with 96.72% and 93.64% respectively. This study reported that TLA4 exhibited good survival in surface hydrophobicity test with 87.96%. These four LAB isolates were further identified by 16s rRNA gene sequence and BLASTN database analysis. Results from the analysis identified that isolates HIT11 and GTH3 as *Fructobacillus tropaeoli* with sequences similarity 99.51% and 98.80% respectively. Isolate GTH6 was identified as *Weisella paramesenteroides* (with 99.24%) while isolate TLA4 was identified as *Lactobacillus plantarum* with 99.25% similarity. This study demonstrated that Malaysian stingless bees are a highly potential valuable reservoir for discovering new strains of LAB to be as probiotic candidates.

Keywords: Stingless Bees; Lactic Acid Bacteria; *In Vitro* Probiotic Test

Isolation and Identification of Amylase Producing *Bacillus* Spp. from Local House Waste Contaminated Soil

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Abstract: Amylase is an enzyme that breaks the starch molecules into dextrins and smaller glucose units. Amylase can be obtained from microorganisms in which the *Bacillus* species (*B.subtilis*, *B.licheniformis* and *B.amyloliquefaciens*) is most commonly use in the industrial production of amylase. The local house waste contaminated soil was used as a source to isolate different strains of amylase producing *Bacillus* and other bacteria producing amylase to support industrial need. The soil samples were collected from two locations in Selangor, Malaysia. The isolation of amylase producing *Bacillus* spp. was initiated with heat treatment to select aerobic endospore forming bacteria (AEFB). Starch hydrolysis test was performed to screen for potent amylase producer. The amplification of 16SrDNA region were performed and the sequences were used for *Bacillus* spp. identification through BLAST analysis for identification of *Bacillus* spp. A total of 12 bacterial isolates were successfully isolated from the soil samples. However, only eight isolates named as A1, A3, B1, B2, B3, C1, C4 and C6 were amylase producing *Bacillus* spp. The BLAST result showed that A1 was found to be *B. cereus JKR62* with 100% homology whereby the probable identity of A3 was *B. amyloliquefaciens LEM97* and *B. subtilis H-70* with 99% homology. Furthermore, B1 showed 99% homology with three different *Bacillus* strains which was *B. cereus BVC77, B. thuringiensis serovar morrisoni* and *B. anthrasis* isolate 1111TES13M4 whereas B2 and B3 showed 99% similarities with *B. amyloliquefaciens AR-2* and *B. amyloliquefaciens ARC225* respectively. Moreover, all the isolates from site C (C1, C4, and C6) were identified as *B. subtilis b+, B. subtilis IARI-V-7* and *B.subtilis DL47* respectively. In conclusion, this study demonstrated that amylase producing *Bacillus* spp. could be isolated from local house waste contaminated soil whereby these isolates can be further used for production of amylase to support the industrial need.

Keywords: House-waste contaminated soil; *Bacillus* spp; aerobic endospore forming bacteria (AEFB); Amylase

Efflux Pump Inhibitor Potential of Schiff Base Ligands Derived from Phenylenediamine and Its Metal Complexes Against *Klebsiella pneumoniae*

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Abstract: Synthesizing new Schiff base complexes has become an interesting strategy in developing alternative treatments to combat the prevalence of multi-drug resistance (MDR) bacteria. These complexes are considered as "privileged ligands" due to their facile preparation and its capability to combine and coordinate with other metals. Despite of its versatility, their biological potential as antibacterial agent and resistant modifiers in bacteria remains understudied. Hence, this research screened 40 Schiff base complexes that consist of the ligands: Salicylaldehyde Ortho- phenylenediamine (SalOPD), Ortho-Vanillin Ortho-phenylenediamine (OVanOPD), Ortho-Vanillin Meta-phenylenediamine (OVanMPD), Ortho-Vanillin 2,4,6-trimethyl- m-phenylenediamine [OVan(Me)MPD], Ortho-Vanillin 4-chloro-1,3-diaminobenzene [OVanMPD(Cl)] including the metal complexes (copper, nickel, cobalt and zinc) for their antibacterial activity and efflux pump inhibitor potential against *Klebsiella pneumoniae* ATCC 700603 using the resazurin microtiter based format. Among all the complexes, Cu_4[OVan(Me)MPD] showed the highest antibacterial activity with 64.2% inhibitory against *K. pneumoniae*. On the other hand, Co_4[OVan(Me)MPD] displayed the highest inhibition percentage of 86.5% against *K. pneumoniae* when treated in combination with chloramphenicol (20 µg/mL). The activity observed maybe due to the steadiness of the metal ion formed between ligand and metal that resulted in the increase in lipophilicity which then improves the cell permeability of the complexes. The results suggest that tetranuclear complexes may potentially be developed into antibacterial agent as well as efflux pump inhibitors in the future.

Keywords: Schiff Base Ligands; Phenylenediamine; Efflux Pump Inhibitor; *Klebsiella pneumoniae*

Anti-*Staphylococcus aureus* Activity of Butanol Extract Isolated from Endophytic Fungus *Aspergillus flavus* IBRL-C8

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Abstract: Endophytes are microorganisms that reside in the internal tissues of living plants without causing any immediate overt negative effects on the hosts. Endophytic fungus *Aspergillus flavus*-C8 was isolated from medicinal plants namely johar leaves (*Cassia siamea* Lamk). The objective of this study was to extract, fractionate and determine the anti-*Staphylococcus aureus* activity of the butanol extract. The endophyte was grown in Yeast Extract Sucrose (YES) medium at 30ºC with 120 rpm of agitation. After 20 days of incubation, the fermentation broth was extracted with ethyl acetate and followed by butanol to obtain the polar extract. The antibacterial activities were tested using two Gram-positive bacteria (*Staphylococcus aureus* and *Bacillus subtilis*) and two Gram-negative bacteria (*Escherichia coli* and *Klebsiella pneumonia*). The butanol extract was applied on disc (diameter 6 mm) at 1 mg per disc using disc diffusion method. Microdilution method was performed on all susceptible tested bacteria to determine the Minimal Inhibitory Concentration (MIC) value. The Minimal Lethal Concentration (MLC) value was determined through the spread plate method. To observe *S. aureus* growth after exposure to butanol extract, time kill assay was conducted. The active extract was fractionated using TLC with the solvent system of chloroform:methanol (9:1, v/v) and anti-*S. aureus* activity was detected *via* bioautography detection. The butanol extract isolated from *A. flavus* IBRL-C8 only inhibited Gram-positive bacteria, with the clear zone range from 9.7 to 11 mm. The MIC and MLC values were 125 µg/ml. The time kill of *S. aureus* indicated a growth decrease after 32 hours of incubation period. A total number of seven spots were detected on the TLC plate. There were some active spots detected which were represented by clear zones. These results suggested that butanol extract isolated from *A. flavus* IBRL-C8 can be a potential source of anti-*Staphylococcus aureus* agent.

Keywords: Endophytic fungi, MIC, MLC, anti-*Staphylococcus aureus*

Antimicrobial activity of *Strobilanthes crispus* leaves aqueous extract against tested human pathogens

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Abstract: *Strobilanthes crispus* is plant species from the family of Acanthaceae, known as 'pecah kaca' or 'jin batu' among Malaysian. *Strobilanthes crispus* is bush-like plants that geographically distributed from Madagascar to Malay Archipelago. The *S. crispus* leaves are anti-diabetic, diuretic, laxative agents, antimicrobial agents and have wound healing properties which usually used as traditional medicine by old folk. The study aimed to investigate the antimicrobial activity of *S. crispus* leaves aqueous extract against tested human pathogens that is *Staphylococcus aureus*, *Escherichia coli*, *Bacillus cereus*, *Salmonella typhimurium*, *Candida albicans* and *Aspergillus brasiliensis*. The antimicrobial properties of *S. crispus* leaves aqueous extract can be measured through the disc diffusion test. The inhibitory action of *S. crispus* leaves aqueous extract was visible against *E. coli*; at 50% v/v, the diameter of zone inhibition was 7.3 mm and at 100% v/v the diameter was 8.7 mm. Whereas, no inhibitory action was observed against *Staphylococcus aureus*, *Bacillus cereus*, *Salmonella typhimurium*, *Candida albicans* and *Aspergillus brasiliensis* at all concentrations. Hence, these conclude that *S. crispus* leaves aqueous extract have antimicrobial properties against *E. coli*. Thus, this suggest the potential of *S. crispus* leaves aqueous extract as new antimicrobial agent in pharmaceutical industry.

Keywords: *Strobilanthes crispus*; aqueous extract; antimicrobial activity; disc diffusion method; human pathogens.

Surveillance of *Burkholderia* sp. in Bukit Merah Orang Utan Island (BMOUI), Perak

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Abstract: A soil bacterium known as *Burkholderia pseudomallei* is the causal agent of melioidosis. It represents one of the most common infectious causes of death in zoo animals, leading to biological diversity loss. Due to close contact with soil, Orang Utan in Bukit Merah Orang Utan Island, Perak also has the potential to get infected with melioidosis. However, research regarding this infection in animals is minimal and no updated reports were available to access this problem. Since Malaysia is an endemic region of melioidosis and the conservation of endangered Orang Utan is paramount, a study was carried out to isolate the organism from soil in BMOUI. This is a surveillance of the soil and culture method, which is the gold standard for *B. pseudomallei*. The soil samples were collected from the area treated and non-treated with quicklime powder. The putative soil-isolated organisms were examined for *B. pseudomallei* via bacteriological methods, including culture on Ashdown agar, biochemical oxidase and catalase tests and Gram-staining. The putative soil-isolated organisms were then run for species identification in VITEK automated ID system and subsequently confirmed by PCR and 16S rRNA sequencing. Thirty-seven out of 50 BMOUI soil samples were successfully grown on Ashdown agar which was observed to show mixed bacterial colony growth with various colony morphology. Six of the isolates labelled as P2(25), P5(2), P5(3), P5(5), P6(1) and P6(6)2 showed pinkish purple colour with wrinkled characteristics similar to *B. pseudomallei* colony morphology after incubation for 48 hours. The results showed that all putative soil-isolated organisms were Gram-negative bacteria, positive for oxidase test and negative for catalase test. In the VITEK automated ID system and PCR sequencing analysis, no *B. pseudomallei* was identified however, *B.cepacia* group was successfully recovered from the soil in BMOUI. As many serious infections related to these bacteria have recently been reported, the presence of these opportunistic pathogens in the soil of BMOUI must be of concern. From these preliminary findings, we postulate the use of quicklime as a preventive measure that successfully prevents the growth of *B. pseudomallei* in BMOUI, hence it should be implemented in other conservation centers.

Keywords Orang Utan; *Burkholderia*; melioidosis; soil; conservation

Comparative Evaluation of Antiseptic Wipes and Chlorohexidine Gluconate Bathing Solution against Bacteria Causing Nosocomial Infections

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Abstract: Nosocomial infections among critical patients in intensive care units are associated with significant morbidity and mortality globally, including in Malaysia. Both Chlorhexidine gluconate (CHG) bathing solution and commercially available antiseptic wipes were used for patients prior to surgical or medical intervention. A controversy was reported on the inhibitory effects of antiseptic wipes and CHG bathing solution on the bacteria causing nosocomial infections. This study was conducted to evaluate the antimicrobial effects of the antiseptic wipes and CHG bathing solution on nosocomial bacteria (methicillin-resistant *S. aureus* (MRSA), *Acinetobacter baumannii, Escherichia coli, Klebsiella* spp. and *Pseudomonas aeruginosa*). The antibacterial effectiveness of antiseptic wipes impregnated with 2% CHG and bathing solution 4% CHG were assessed using agar well diffusion method. Microtiter plate assay was used to estimate the minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC). The CHG from antiseptic wipes was aseptically extracted by squeezing method. The CHG bathing solution revealed excellent inhibitory effects against all study bacteria with inhibition zones [15 mm (*A. baumannii*), 17 mm (*Klebsiella* spp.), 20 mm (*Pseudomonas aeruginosa*), 23 mm (*Escherichia coli*) and 25 mm (MRSA). In contrast, antiseptic wipes were effective against *E. coli* only with 15 mm inhibition zone. The MIC of CHG bathing solution was 0.03% for all study bacteria except for *P. aeruginosa*, which was 0.06%; however, the MIC of the antiseptic wipes against MRSA and *E. coli* were 0.13% and 0.5%, respectively. The MBC of CHG bathing solution against MRSA, *A. baumannii* and *E. coli* were 4%, 0.25% and 0.5% respectively. The MBC of antiseptic wipes couldn't be determined since all study bacteria showed uncountable colonies even with the highest concentrations. In conclusion, CHG bathing solution showed a stronger antibacterial effect than antiseptic wipes against nosocomial bacteria. Using CHG bathing solution will significantly reduce the risks of acquiring multidrug resistant organisms and developing nosocomial infections.

Keywords: Antimicrobial, antiseptics, bathing solution, nosocomial, Chlorhexidine gluconate.

Cellulolytic bacterial fermented *Moringa* leaf potential as a protein source in aquaculture feed

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Abstract: The production cost of animal farming is alarmingly high and unprofitable, especially for small scale farmers. In the aquaculture industry, the feed itself contributes more than 70% of total production cost due to the high price of fish meal which is commonly used as their protein source. There are quite a few plants with high protein content, but the high non-digestible cellulose content restricts their utilization in monogastric animals. This study is to analyze the potential of *Moringa* sp. leaves, a high protein, mineral and vitamin content plant species, to be used as fish meal substitute. Solid state fermentation of the leaves was conducted using cellulolytic bacteria as its starter culture. The cellulose and glucose contents were measured for a week. The formulated feed pellets using *Moringa* fermented leaves were then used to feed *Cherax quadricarinatus* juveniles for 20 days. The weight and length of the species were measured before and after treatment to determine their growth rate. Commercial and non-fermented *Moringa* leaf pellets were used as controls. The cellulose content of fermented leaves was reduced more than 80% and 49% increment of glucose level after 7 days of fermentation. *C. quadricarinatus* fed with fermented leaves showed the highest growth rate significantly. Therefore, it can be a suggestive conclusion that cellulolytic bacterial solid state fermented *Moringa* leaves has high potential to be used as a protein source in aquaculture feed.

Keywords: Cellulolytic bacteria; *Moringa* sp. leaf; *Cherax quadricarinatus*; aquaculture feed

Bioremediation of Textile Wastewater Using *Pleurotus pulmonarius*

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Abstract: The textile industry is a main producer of water pollution worldwide due to the high amounts of wastewater it produces on a daily basis. Conventional methods to treat textile wastewater usually involve high energy and costs. As an alternative, bioremediation using white rot fungi is commonly proposed due to its ligninolytic enzymes such as laccase, lignin peroxidase and manganese peroxidase which are able to break down pollutants in the textile wastewater. In this study, the white rot fungi *Pleurotus pulmonarius* was used to treat textile wastewater obtained from a textile laboratory in Shah Alam, Malaysia. Shake flask fermentation was implemented with the parameters of pH 3, agitation rate of 120 rpm and temperature of 40°C to decolourise the dyes in the textile wastewater, as well as reduce the heavy metals in the wastewater. *P. pulmonarius* showed promising results with a total of 59.45% of dyes decolourised and the heavy metal reduced determined by Inductive Coupled Plasma (ICP) analysis was 34.54%, 76.82%, 38.17% and 41.94% of copper, iron, manganese and zinc respectively after 144 hours of incubation. However, the biochemical oxygen demand (BOD) of the textile wastewater had increased after the treatment with *P. pulmonarius,* and the cells were not viable starting at the 72nd hour. With further optimisation, *P. pulmonarius* could prove to be a promising alternative to the treatment of textile wastewater in the efforts to reduce water pollution.

Keywords: *Pleurotus pulmonarius;* White Rot Fungi; Bioremediation; Textile Wastewater.

Inhibition of *Corynebacterium pseudotuberculosis* biofilm by DNA synthesis and protein synthesis inhibitors

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Abstract: *Corynebacterium pseudotuberculosis* is the causative factor of caseous lymphadenitis, a ruminant disease that contributes to major economic loss in most sheep farming countries. The disease is associated with inflammation of the lymph node resulting in the formation of caseous cheesy material in the nodes and abscess formation in internal organs. A recent work has shown the biofilm formation by *C. pseudotuberculosis.* Multiple lines of work have shown that DNA synthesis and protein synthesis represent active biological processes taking place during biofilm formation. However, DNA synthesis and protein synthesis in *C. pseudotuberculosis* biofilm remain poorly understood. The objective of the present study was to determine the effects of DNA synthesis and protein synthesis inhibitors against *C. pseudotuberculosis* biofilm. Biofilm of *C. pseudotuberculosis* clinical isolate was developed in microplate assay in the absence and presence of inhibitors. Morphology of *C. pseudotuberculosis* biofilm and antimicrobial susceptibility were studied using field emission scanning electron microscope and microplate biofilm assay respectively. All inhibitors were evaluated in the range between 3.125µg/ml and 100µg/ml. Results demonstrated that *C. pseudotuberculosis* biofilm formed a three dimensional and heterogenous structure. Treatment with inhibitors (nalidixic acid-DNA synthesis inhibitor, streptomycin-protein synthesis inhibitor, tetracycline-protein synthesis inhibitor) substantially inhibited viability of *C. pseudotuberculosis* biofilm. Significant correlation of antimicrobial susceptibility between these inhibitors and other antimicrobials were also demonstrated herein. The findings of the present study suggest the potential use of nalidixic acid, streptomycin and tetracycline in the control of caseous lymphadenitis.

Keywords: *Corynebacterium pseudotuberculosis;* biofilm; caseous lymphadenitis; DNA synthesis; protein synthesis

Microwave-Assisted Synthesis, Characterization and Anticancer Activity of Tetranuclear Schiff Base Complexes

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Metallosalens have potential to specifically bind protein and interact with DNA due to its cationic character and propensity to undergo hydrolysis and redox reaction that promoting DNA cleavage. A hexadentate Schiff base 6,6'-((*1E,1'E*)-(1,3-phenylenebis(azanylylidene))bis(methanylylidene))bis-(2-methoxyphenol) (L) was synthesized via condensation of *o*-vanillin and *m*-phenylenediamine. Its tetranuclear Cu(II), Co(II) and Zn(II) complexes were obtained through microwave-assisted complexation with corresponding acetate salts in 1:2 ratio of L:M. The compounds were characterized through elemental analysis, molar conductivity, magnetic susceptibility, thermogravimetric analysis (TGA), IR, UV-Visible, ^{1}H and ^{13}C NMR spectroscopy. The ν(C=N), $\nu(C\text{-}O)_{phenolic}$ and $\nu(C\text{-}O)_{methoxy}$ peaks shifted to lower frequencies upon complexation, with appearance of new peaks assignable to ν(M-N) and ν(M-O) at 651-671 and 424-441 cm^{-1}, respectively, indicating that L coordinated to metal centres through its azomethine N, phenolic O and methoxy O. The $Cu_4(L)_2$ and $Co_4(L)_2$ complexes were paramagnetic with μ_{eff} of 1.85 and 3.84 B.M., respectively; whereas the $Zn_4(L)_2$ displayed the expected diamagnetism. The thermal decomposition of all complexes showed a two-stage process at around 100 °C and 300 °C. An anticancer investigation against human colorectal cancer (HCT116) cell lines revealed that the parent ligand possessed lower activity than its metal complexes. $Cu_4(L)_2$ exhibited the highest anticancer activity with IC_{50} of 6.56 ± 1.26 µM. The anticancer screening results obtained are relevant for identifying possible new agents against cancer and pathogens.

Keywords: Microwave-assisted synthesis; tetranuclear complexes; Schiff base; anticancer.

Detection of non-polar chemical compositions of *in-vitro* culture products of *Pogostemon cablin* via GC/MS

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Abstract: *In-vitro* tissue culture of *Pogostemon cablin* is one of the main techniques that have been used to obtain free-disease plants that are suitable for economic purposes especially in the essential oil industry. There are a few efforts to optimize *in-vitro* tissue culture of *P.cablin* have been made to enhance the yield of patchouli alcohol comparable to the mature plants. Most of the chemical compound of *P. cablin* was detected after soil plantation rather than during *in-vitro* culture since it is expected to have secondary metabolites due to maturity. Theoretically, culture products may not be able to derive many chemical constituents compared to mature plants. However, it is possible to detect the presence of other beneficial compounds from the culture plants. Therefore, the objective of this study is to provide substantial data required to support this possibility and become a platform for new findings. The experiment was carried out by yielding two types of *in-vitro* culture product which were callus and microshoot by using plant hormone. After three-week, high abundances of callus in 0.5 mg/L BAP and 3.0 mg/L NAA were sufficiently acquired by using nodes explant. While only a week required to obtain microshoot from foliar explant by using 0.5 mg/L BAP. Both plant samples were extracted by using hexane solvent for non-polar GC-MS analysis. There are six compounds detected in hexane–callus extraction samples. The highest abundance compound detected is silane (19.04%) and the lowest abundance is tetrasiloxane (8.88%). Only three compounds were found in microshoot which tetrasiloxane is the highest abundance (76.23%) and tetrasiloctane is detected lowest (2.37%). Tetrasiloxane which is significantly higher in the microshoot compared to the callus is found to have great beneficial properties such as non-toxic, high compatibility with the lipophilic with extraordinary water repellency and stability, that may conclude to play a major role for enhancing plant growth.

Keywords: *In-vitro* Plant Tissue Culture; *Pogostemon cablin;* Callus; Microshoot; GC-MS

Liver Ultrastructural Changes in Rat Model of Insulin Resistance

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Abstract: Liver sinusoidal endothelial cells (LSECs) are perforated with transcellular fenestrations that provide unimpeded access of substrates between sinusoidal blood and hepatocytes. Defenestration refers to the loss of fenestration number and/or decreasing in fenestration diameter which, can alter metabolic homeostasis. Insulin resistance has been reported to promote the accumulation of fat in the liver leading to fatty liver disease. However, the effect of insulin resistance, specifically on fenestrations is yet to be investigated. This study was conducted to observe changes in the fenestrations of LSEC in response to insulin resistance. Adult male Sprague-Dawley rats were divided into two groups (n=8) where the control group received 0.9% NaCl and the treatment group received dexamethasone injection (1mg/kg) i.p once daily for ten days. At day 11, all rats were anaesthetised using ketamine/xylazine followed by cardiac puncture. Rats were then humanely sacrificed, dissected and the livers were perfusion-fixed for electron microscopy. Fenestrations were examined using Quanta FEG450 Scanning Electron Microscope at 15000x magnification. Ten random images per sample were taken for analysis of fenestrations diameter and porosity using ImageJ software. Data were analysed using SPSS version 23.0 followed by Independent Samples t-Test to compare differences between group. Results showed that dexamethasone has induced insulin resistance by a significant reduction of body weight (Dexamethasone (D) =276.84 ±7.87 vs Control (C) =393.84±12.47g; p=0.00), increased fasting blood glucose (D=5.57 ±1.30 vs C=3.97±0.55mg/dl; p=0.02) and higher Homeostatic Model Assessment for Insulin Resistance (HOMA-IR) value (D=1.37±0.52 vs C=0.85±0.22; p=0.00) in treatment group compared to the control. Analysis of the liver images has shown that insulin resistance causes defenestration of LSEC where there is a significant decrease in fenestrations frequency (D=3.202±1.16 vs C=2.656±1.044; p=0.04) and endothelial porosity (D=2.17±0.74 vs C=1.77±0.9; p=0.049) but not fenestration diameter. In conclusion, this finding shows that insulin resistance can affect the integrity of liver endothelium specifically on fenestrations frequency and liver porosity which will consequently lead to serious implications on liver function as the main site for metabolism.

Keywords: Insulin resistance, hepatology, liver endothelium, fenestrations, electron microscopy

Optimization of Plasma RNA Extraction for NanoString nCounter miRNA Panel

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Abstract: Growing interest in biomedical studies has brought RNA from biofluids, including plasma as promising candidates for genetics profiling. The precision and reliability of an analysis in downstream application such as NanoString nCounter depend on the RNA quality, purity and level. In this project, NanoString nCounter miRNA panel was chosen due to rapid identification and ability to profile approximately 800 miRNAs per run which requires total RNAs from plasma with a minimum concentration of 33.3 ng/µL with 260/280 and 260/230 ratios of ≥1.8 for optimal results. Unlike tissues and cells, circulating RNAs in plasma are cell-free and are present in very small sizes. However, the abundance of proteins and inhibitors in the plasma as possible contaminants could diminish the effectiveness of molecular isolation techniques and pose challenges in RNA isolation and quantification. This could skew data collection and elucidation. Therefore, the main objective is to determine the optimized plasma RNA isolation protocol to overcome problems in RNA quality and purity with regards to NanoString nCounter requirement. Several optimization steps were performed, including the addition of one chloroform extraction step with extra washing steps instead of conducting only once following the actual protocol. After conducting these steps, the average 260/280 ratio falls between 1.7 to 1.8, slightly increased compared to the results before optimization which was around 1.4 to 1.6 since these steps of optimization help to remove excess impurities including phenol and salt. Furthermore, increasing the incubation time in certain steps, for instance, after sample homogenization with Trizol, during 95% ethanol precipitation and after RNase-free water addition have boosted the RNA recovery allowing RNA concentration of 15 ng/µL and above to be obtained. Hence, the optimized plasma RNA isolation protocol was determined since several issues related to plasma RNA concentration and purity were significantly improved by performing the additional steps in the protocol.

Keywords: Optimization; Plasma; RNA Extraction; NanoString

Phytochemical Screening and Quantification of Phenolic Content in *Vitex trifolia*'s Leaves Hydro-alcoholic Extract

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Abstract: *Vitex trifolia* (Verbenaceae) is a multi-purpose medicinal plant that is traditionally used in many Asian countries to treat inflammation, pain, and allergy. Its multi-pharmacological activity is attributed to the presence of various secondary metabolites, including phenolic compounds. The present study aims to evaluate the phytochemical composition of *V. trifolia*'s leaves hydro-alcoholic extract and to report for the first time, its phenolic content using a validated high-performance thin-layer chromatography (HPTLC). The preliminary phytochemical screening was carried out qualitatively. The HPTLC analysis was performed on glass-backed F_{254} silica gel plates using a two steps gradient elution method of the mobile phase. In the first step, the plate was developed with 100% methanol over a 40 mm of developing distance, while in the second step, n-hexane:ethyl acetate:acetic acid (20:9:1, v/v/v) ratios were used over 80 mm developing distance. Detection and quantification were performed by densitometric analysis at 254 nm. The method was validated in terms of linearity, precision, accuracy, the limit of detection (LOD), and limit of quantification (LOQ) according to the International Council for Harmonization of Technical Requirements for Pharmaceuticals for Human Use (ICH) guideline. The preliminary phytochemical screening of *V. trifolia*'s leaves hydro-alcoholic extract showed the presence of alkaloids, flavonoids, phenols, phytosterols, and terpenoids. The calibration plot was linear in the range of 2-10 µg/band (R^2=0.973±0.011). The intra-day and interday precision were found to be <10% relative standard deviation and the method average recovery rate was obtained 101.48±2.37%. Thus, the developed HPTLC method was proved to be linear, precise, and accurate. The LOD and LOQ of the methods were determined to be 2.01 µg/band and 6.08 µg/band, respectively. The total phenolic content of the extract was calculated from the calibration plot and found to be 136.94±4.02 mg gallic acid equivalent (GAE)/g of dried extract. This preliminary study revealed that *V. trifolia* has a considerable amount of phenolic compounds, which can potentially contribute to its anti-inflammatory, antioxidant, and anticancer activities. Further pharmacological investigations are being carried out to support the folkloric claims.

Keywords: *Vitex trifolia*; phytochemical screening; phenolic content; HPTLC.

Open Field Mirror Test as a Tool for the Assessment of Visual Impairment in Rats with Streptozotocin-Induced Diabetic Retinopathy

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Abstract: Visual function test provides clinical que towards symptoms of vision loss. However, it is quite difficult to determine in animal-based experimental research. Considering the limited visual behaviour test that is available and applicable in rodent-based DR research work, in this study, we explored an alternative which may be suitable to evaluate rodent visual function. Therefore, this study aims to evaluate the use of mirror test in open field arena as a visual function assessment tool in DR experimental rodent model. Male Sprague-Dawley rats (200-250 grams) were divided into diabetic rats (DV), that received intraperitoneal streptozotocin (55mg/kg body weight) for induction of diabetes and control (N) which similarly received citrate buffer. Rat blood glucose was weekly monitored and recorded and those with a blood glucose level of more than 20 mmoI/L have been included in this study. The visual-behaviour response of the rats was assessed at final week post induction after assessing general behaviour in open field arena. To assess, a mirror and reversed mirror were added in the open field arena. In the open field test, N showed higher number of zone crossings (3.73-folds, $p<0.001$), total distance travelled (2.02-folds, $p<0.001$), number of rearing (2.22-folds, $p<0.001$) and frequency of grooming (4.33-folds, $p<0.01$) but lower number of freezing episodes (2.47-folds, $p<0.001$) and number of faecal pellet (4.17-folds, $p<0.01$) compared to DV. N spent more time with higher zone entries toward mirrored compared to non-mirrored and reversed mirror zones ($p<0.05$ and $p<0.01$ respectively), whereas DV rats showed no preference to zones. N also showed higher freezing episodes within mirrored zone, compared to DV (2.00-folds, $p<0.05$). Hence, the visual-behaviour response test (combination of open field and mirror test) suggested findings of visual loss and may have a potential role as one of the visual function assessment tools in experimental DR rodents.

Keywords: diabetic retinopathy; visual function test; visual-behaviour response; open field test; mirror test

Development of An *in vitro* Caco-2 Intestinal Model to Study Lapatinib-Induced Changes in Gut Permeability

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Abstract: Lapatinib, a dual ErbB1 and ErbB2 tyrosine kinase inhibitor, is effective in ErbB2-positive breast cancer treatment. However, lapatinib is associated with toxicities particularly diarrhea. Although diarrhea can be tolerated, it can cause treatment interruption as well as reduce patients' compliance. The underlying mechanism of lapatinib-induced diarrhea remains unclear. Therefore, Caco-2 cell line was selected as it has the ability to differentiate into enterocytes-like phenotype and to form high barrier integrity, hence, it was chosen as a model to reflect human normal small intestinal epithelium. Caco-2 cells were seeded in a transwell insert for 21 days to form an intestinal epithelial monolayer. The formation and integrity of intestinal monolayer were evaluated by measuring transepithelial electrical resistance (TEER) and the monolayer morphology was confirmed by scanning electron microscopy (SEM). Cytotoxic effect of lapatinib on Caco-2 was determined using 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium (MTS) assay. Caco-2 was treated with lapatinib (0-100µM) and incubated for 24, 48, 72 and 96h. Median half-maximal inhibitory concentration (IC_{50}) of lapatinib over 24-96h was estimated. Then, Caco-2 was seeded in a 6-well plate and incubated with lapatinib median IC_{50} for 24, 48, 72 and 96h to observe any growth inhibitory, microscopically. Caco-2 showed optimum TEER reading on day-19 at 810.74±243.16 ohms/cm^2. The ultrastructure observed using SEM showed densely packed microvilli on the pore membrane. In MTS assay, no IC_{50} was observed at 24h, with 28.00±12.81µM at 48h, 29.00±2.51µM at 72h and 14.00±1.64µM at 96h while median IC_{50} over 48-96h was 28.00±2.51µM. Growth inhibitory by lapatinib was evidenced at 48, 72 and 96h. Overall, Caco-2 grown in transwell insert until day-19 is able to differentiate into a microvillus-like structure with established integrity. Meanwhile, lapatinib possessed cytotoxic effect on Caco-2 at 48-96h. Investigations on the effect of lapatinib on intestinal permeability are currently ongoing to determine the underlying mechanisms of lapatinib-induced diarrhoea.

Keywords: Caco-2; intestinal monolayer; lapatinib; cytotoxicity; morphology

The Effects of Oil Components and Homogenisation Conditions on The Physical Characteristics and Stability of Oil-in-Water Emulsion Formulations for Future Cosmetics Applications

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Abstract: Emulsions are thermodynamically unstable systems that require emulsifiers such as surfactants to provide kinetic stability to maintain their structure for a longer shelf-life. This work aims to study the effects of different oils, namely jojoba oil, grape seed oil, olive oil and waglinol on the droplet size distribution and stability of the emulsion formulations with Olivem 1000 as an emulsifying agent. For formulation development, nine formulations were designed containing different oils, waglinol and water at different homogenisation times of 5, 10 and 15 minutes. These formulations were prepared by hot mixing technique. Subsequently, all formulations were subjected to physical characteristics studies such as droplet size distribution and polydispersity index (PDI). In addition, all formulations were tested for stability using LUMiFuge stability analyser. The stability study was performed for one month to determine the tendency for sedimentation and creaming that produced unstable emulsions. Based on the findings, a few formulations showed a decrease in droplet size with an increase in homogenisation times up to 15 minutes. A decrease in droplet size resulted in a stable emulsion production, which is desirable to maintain its stability. Overall, Formulation 6 containing 10% grape seed oil, 7% Olivem 1000 and 83% water showed the smallest droplet size compared to other formulations. On the other hand, the most stable emulsion was Formulation 1 consisting of waglinol as oil with the homogenisation time of 5 minutes. In conclusion, Formulation 6 with 10 minutes homogenisation time was the preferable formulation due to its smallest droplet size, which is 3.468 ± 0.072 µm, and good stability with no separation upon storage for one month. These findings provide an insight on the formulation strategies that can be applied in the development of cosmeceutical products.

Keywords: Emulsion; particle size distribution, polydispersity index (PDI), Olivem 1000, oils, stability

Elicitation of total phenolics and flavonoids in *Trigonella foenum-graecum* using yeast extract elicitor

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Abstract: Oxidative stress caused by free radicals accounts for the development of a number of diseases such as inflammatory, neurological disorders and ischaemic diseases. The harmful effects of free radicals can be neutralized by antioxidative compounds, most of which are available primarily from plants. *Trigonella foenum graecum* which belongs to the family Leguminosae is one such medicinal plant which contains antioxidative compounds such as phenolics and flavonoid compounds. Benefits of antioxidants derived from plants has prompted the enrichment of antioxidative compounds through elicitation. Currently there exists a gap in enhancing antioxidative compounds in *in vitro* germinated *Trigonella foenum-graecum* plantlets by elicitation. Therefore, this study reports the effect of yeast extract (YE) elicitor on the total phenolic and flavonoid content and ultimately antioxidant activity of *in vitro* grown *Trigonella foenum-graecum* plantlets. *Trigonella foenum-graecum* plantlets obtained through *in vitro* seed germination for 5 weeks were selected for elicitation. MS media was treated with yeast extract elicitor of concentrations 5, 10, 15 and 20 mg/L for elicitation while MS media alone was used as control. Plantlets were subjected to elicitation for 48 hours. Elicited plantlets were oven-dried and extracted using methanol by rotary evaporation and the crude extract obtained was tested for total phenolics, flavonoids and antioxidative activity. Elicitor concentration of 10 mg/L YE resulted in the highest total phenolic content (15.88±0.13 mg GAE/g extract) and total flavonoid content (56.60±2.79 mg QE/g extract). The highest antioxidative activity was recorded in 5 mg/L YE (81.17±0.95 %). Moreover, elicited plantlets also exhibited a strong correlation between the DPPH scavenging activity and total phenolic content (r^2= 0.950) and total flavonoid content (r^2= 0.844). Due to the successful enhancement of phenolics and flavonoids by elicitation of *Trigonella foenum-graecum* plantlets *in vitro* with yeast extract, these elicited plantlets can be regarded as promising candidates for a plant-derived antioxidant compound.

Key words: *Trigonella foenum-graecum;* elicitation; yeast extract; phenolics; flavonoids; antioxidative activity

GuttaFlow Bioseal as Monocone Obturation Technique in Curved Root Canals. A Scanning Electron Microscopy Study.

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Abstract: The obturation with GuttaFlow Bioseal (GFB) in curved root canals is not clearly investigated due to the new generation of root filling material. This study compared the obturated surface area, extrusion of root filling material beyond the apical foramen and duration of obturation procedure in curved root canals using monocone obturation technique. Access cavity was prepared on twenty human mandibular molars. The root canal curvature of more than 10° determined according to Schneider's method was included. Samples were prepared using Hyflex CM rotary files and divided into two groups (n=10). Group 1 [gutta-percha (GP) cone and GFB] and Group 2 [GP cone and RoekoSeal Automix root canal sealer]. The duration of obturation procedure was recorded and the obturation radiograph was taken. Samples were bisected and the mesial roots were sectioned horizontally to obtain 3 root segments; apical, middle and coronal. All resected roots were mounted on brass stubs, sputter-coated with thin platinum coating and observed under scanning electron microscope (SEM) at 70x magnification. The SEM images were transferred to the SketchAndCalc Area Calculator software. There were no statistically significant differences on the obturated surface area and extrusion of root filling material between Group 1 and 2 irrespective of the status of root canal curvature. The duration of obturation procedure in severe root canal curvature between Group 1 and 2 exhibited statistically significant difference. The obturated surface area and extrusion of root filling material were not affected by the status of root canal curvature. The duration of obturation procedure with GFB in severe root canal curvature was slightly longer. Neither root filling material was able to seal the curved root canal of mandibular molars completely. Both root filing materials in the present study can be opted depending on the clinical cases, material availability and clinician preference.

Keywords: Curved Root Canal; Mandibular molars; GuttaFlow Bioseal; Monocone Obturation Technique; Scanning Electron Microscopy;

The Effect of Additional *Dadih* on Lactic Acid Bacteria and Nutritional value of Pudding as a Food Supplementation for Pregnant Women

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Abstract: Pregnant women need additional energy during pregnancy for the growth and development of the fetus. To fulfill these energy needs, Supplementary Feeding (SF) is needed. In this study, a pudding enriched with *dadih* was formulated. The study was conducted in November- December 2019 at the Nutrition Laboratory, Faculty of Public Health, Andalas University. The design of this study was True Experimental using a Completely Randomized Design (CRD) with two replications consisting of four, F0 formulas as the standard formula, F1, F2 and F3 as the treatment formula with the addition of dadih at 80, 90 and 100 grams, respectively. An analysis of nutritional value was performed, and the number of Lactic Acid Bacteria (LAB) was determinined. From the nutritional value analysis, per 100 grams of curd pudding F0 formula contains 11.59% carbohydrate, 1.24% protein, 1.09% fat, with a total of 61.13 calories; F1 formula contains 10.41% carbohydrate, 2.29% protein, 3.29% fat, with a total of 80.41 calories; F2 formula contains 10.12% carbohydrate, 4.74% protein, 3.32% fat, with a total 89.32 calories; and F3 formula contains 11.84% carbohydrate, 3.05% protein, 3.13% fat, with a total 87,73 calories. The LAB test results of Curd Pudding were: F0 at $3.1X10^3$ (Cfu/Gram); F1 at $1.7X10^9$ (Cfu/Gram); F2 at $2.4X10^9$ (Cfu/Gram) and F3 at $2.4X10^9$ (Cfu/Gram). The statistical analysis results of the organoleptic test and the highest average value as the chosen formula is F3 with a total 87.73 calories and the amount of LAB $2.4X10^9$ (Cfu/Gram), which is in accordance with SNI 281: 2009 that the minimum amount of BAL in fermented milk is 10^7 Cfu/Gram. It is recommended to consume dadih pudding as it contains a high nutritional value, also contains as well as LAB which are good for digestive system and able to increase the immune system of pregnant women.

Keywords: *Dadih*, Pudding, Lactic Acid Bacteria, Nutritional Value, Pregnant Women

Association of tumor necrosis factor-α (TNF-α) gene polymorphism and dengue in Sabah, East Malaysia population

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Abstract: Dengue is a growing pandemic infection especially in tropical country. Genetic variation such as single nucleotide polymorphism located at the promoter -308A of tumour necrosis factor-alpha (TNF-α) gene may affect transcription and increase cytokine production in dengue. No study has been conducted to investigate the association of this gene polymorphism in Sabah population. In this study, the association of TNF-α [-308 A/G (rs1800629)] gene polymorphism and dengue among Kadazan-Dusun and Bajau ethic groups in Sabah population was investigated. A case-control study was performed involving 84 dengue patients matched with 72 healthy controls of Kadazan-Dusun and Bajau ethnicities in Sabah. Dengue patients is defined as infected individuals as confirmed by IgM or IgG serology detection using acute serum samples. Controls is a healthy adult from the general populations matched with age, gender, and ethnics with the case. A total of three millilitres of venous blood was collected and genotyped using the real-time polymerase chain reaction (RT-qPCR). Statistical analysis is performed using Chi-square test and fisher exact test to examine the relationship between TNF-α gene (-308 A/G) polymorphism and dengue. A *p*-value of < 0.05 was considered statistically significant. No significant difference between dengue case and control in terms of age among the Kadazan-Dusun ethnicity (p=0.246) but was significantly different among the Bajau ethnicity (p=0.032). Furthermore, no difference between dengue case and control was observed in terms of gender for both ethnicities (p >0.05). Although, the frequency of -308A allele was higher in healthy control compared to dengue cases for both Kadazan-Dusun and Bajau ethnicities (OR= 1.60, 95% CI= 0.81–3.17 and OR=1.46, 95% CI =0.48–4.42, respectively), it was not statistically significant (p>0.05). The result suggests that TNF-α (-308 A/G) gene polymorphism is not associated with dengue among Kadazan-Dusun and Bajau ethnicities in Sabah population. Significance of study**:** Genetic biomarkers for dengue.

Keywords: Dengue infection; genetic; polymorphism; TNF-α; Sabah ethnicity

Knowledge, Attitude and Practice towards Tobacco Smoking Among Secondary School Students

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Abstract: Tobacco smoking has mostly adverse effects on human health and is a major cause of several medical conditions. Smoking activities are a serious public health concern and entail exposure to second-hand smokers. Smoking activities is not limited to adults, but nowadays practiced among teens and school kids as well which raise public interest. The long-term health risks associated with smoking are more difficult for teenagers to comprehend who are often more easily influenced by smoking. This study, therefore, aims to examine the level of knowledge, attitude and practices among secondary school students about tobacco smoking. The study was conducted in Bandar Tun Razak using the Global Youth Tobacco Survey (GYTS) questionnaires involving a total of 268 respondents of Form 4 students from four secondary schools. The data showed that 201(75%) students accepted that they know the substance of a cigarette, 267(99.6%) students are aware of the risk of smoking, 267 (99.6%) students are aware that smoking can cause cancer, and 260 (97%) students are aware that besides cancer, smoking can cause other diseases. 248 (92.5%) out of 268 students chose not to smoke, and the rest would smoke. Attitude wise, 105 (39.2%) students agree that not smoking will make them feel more comfortable in society, while 94 (35.1%) students feel that it will make them feel less comfortable in society, and 69 (25.7%) students are not sure about this. Moreover, results showed that about 71 (26.5%) students ever smoked and 41 (57.7%) of them started smoking at age of 11-12 years old while 52 (73.2%) of them smoked in public areas. Tobacco smoking among adolescents, especially school kids, should therefore be avoided and treated as a public emergency that needs to be addressed. Many governments and other organisations should be involved in protecting our next generation and improving the health and mortality of children.

Keywords: knowledge, attitude, practice, student, smoking

Exploring Extraction and Purification of Tannic Acid from *Camellia Sinensis* (Tea Leaves) for Potential Haemostatic Application in Dental Surgery

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Abstract: Evolution of naturally sourced haemostatic agents highlights opportunities for innovations in dental and surgical fields. With rapid developments in biotechnology, natural tannic acid sourced from *Camellia Sinensis* (tea leaves) has become more widely used in biomedicine. Apart from antimicrobial properties, tannic acid also offers beneficial effects for the haemostatic process resulting in significant reduction of bleeding time. Haemostasis is defined as a component of wound defence mechanism where vessel wall components and platelets act together with procoagulant and anticoagulant proteins to form a plug of cells and cross-linked fibrin. This terminology is imperative in dental extractions and dental surgery especially in the likelihood of any haemorrhage (bleeding). Preliminary clinical observation showed haemostasis can be achieved within 5 to 10 minutes after a dental extraction. We designed the present study to identify the best extraction method for pure and sustainable CSTA, and its bioactive compounds. The current study was improved from our preliminary CSTA extraction methods conducted in our pilot study to emphasise on sustainability by using locally sourced fresh *Camellia Sinensis* leaves and extraction via sustainable means to avoid hazardous health risks during extraction of CSTA. Bioactive compounds from the purified *Camellia Sinensis* extraction were observed via gas chromatography time-of-flight mass spectrometry (GC-TOF/MS). The modified pure CSTA opens up opportunities to signify its potential haemostasis properties and mechanism in dental surgical procedures. This study caters income generation in terms of university-industrial collaborations towards growth of the nation to achieve national and international Sustainable Developmental Goals (2030) by accelerating human capital development and productivity. Our aim to produce a novel CSTA haemostatic agent will also benefit the local tea industry in which it creates a potential agricultural-based biomedicine with worldwide marketability.

Keywords: haemostatic agent; tannic acid; *Camellia* Sinensis, tea leaves; tooth extraction.

Extracellular Metabolites Profile of Different Stages Colorectal Cancer Cell Lines

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Abstract: Metabolic footprinting involves the determination of extracellular metabolites of the cells. The objective is to identify the differential metabolites in extracellular colorectal cancer (CRC) cells and to determine the molecular changes that occur as CRC progresses. CRC cells at different stages ie; SW 1116 (stage A), HT 29 and SW 480 (stage B), HCT 15 and DLD-1 (stage C), and HCT 116 (stage D) were grown in culture medium. The media in which the cells were grown were subjected to metabolomics profiling using Liquid Chromatography Mass Spectrometry-Quadrupole Time of Flight (LCMS-QTOF). Statistical and metabolic pathway analysis were performed using Metaboanalyst software and identification of metabolites were determined by METLIN database. A total of 27 differential metabolites were identified in extracellular CRC cells of the more advanced stages compared with stage A. PLS-DA score plot showed a clear separation between stage A, and stage B, C, and D. Variable importance in projection (VIP) revealed 14 differential metabolites that were most significant in differentiating CRC cells of the advanced stages from stage A and these were 5-hydroxy-L-tryptophan, indoleacetaldehyde, 4,5-dimethylthiazole, 8-oxodiacetoxyscirpenol, bisnorbiotin, 5-amino-6-(5'phosphoribosylamino), uracil, glyceryl 5-hydroxydecanoate, sphinganine, 8,8-diethoxy-2,6-dimethyl-2-octanol, l-cystine, thiamine acetic acid, phytosphingosine, PE(20:4(5Z,8Z,11Z,14Z)/22:6(4Z,7Z,10Z,13Z,16Z,19Z)), and N-(2R-hydroxypentacosano-yl)-2S-amino-1,3S,4R-octadecanetriol. Altered metabolic pathways between the more advanced stages and stage A identified were tryptophan, sphingolipid, and tyrosine. This study highlights the importance of doing both fingerprinting and footprinting techniques to generate more complete understanding on the molecular changes that occur as CRC advances.

Keywords: Metabolomics, extracellular, metabolites, colorectal cancer, stages

Somatic Embryogenesis of *Hevea brasiliensis* Muell. Arg. RRIM 600

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Abstract: An efficient somatic embryogenesis protocol for sustainable natural rubber cultivation of *H. brasiliensis* was achieved by using leaf and petiole explants. For direct somatic embryogenesis, the explant was cultured on Murashige and Skoog (MS) media with 0.8 mg/L 2,4-dichlorophenoxyacetic acid (2,4-D) and 0.5 mg/L kinetin (KN). For indirect somatic embryogenesis, the callus was cultured on MS media with (1.0– 2.0 mg/L) 2,4-D together with (0.5 and 1.0 mg/L) KN in 24 hours of darkness. The induction of somatic embryos was achieved when callus cultured onto MS media with 0.3 mg/L GA_3 and 0.2 mg/L BA in 24 hours of darkness. Maturation of somatic embryos was achieved when the embryogenic callus cultured on MS media with 0.3 mg/L GA_3, 0.2-0.3 mg/L BA and 0.1 mg/L IAA in 16 hours of light and 8 hours of darkness.

Keywords: *Hevea brasiliensis*; RRIM 600; somatic embryogenesis; embryogenic callus; protocol; induction;

Transcriptomic Analysis Reveals to the Role of Cell Division During Mango Fruit Development

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Abstract: Mangoes comes in different sizes and consumer are often favour those with bigger, fleshy mango. Cell division process that happens during earlier stages of fruit growth plays an important role in determining the final size and shapes of the mango. To further understand the roles of cell division genes that play roles in the fruit development, transcriptome analysis was performed for the immature mango and ripen stages of mango. A total of 12,804 differentially expressed genes (DEGs) with 6,997 up-regulated and 5,807 down-regulated genes were identified in both stages respectively. Gene Ontology (GO) analysis indicated that DEGs were up regulated in cytoplasm and under biological process, transmembrane transport was enriched and in molecular function, oxidoreductase activity increases. While downregulated DEGs were found under ribosome biogenesis biological process, in ribosome and the molecular function of structural constituent of ribosome. The overexpression of genes involved in transmembrane transport indicates the high energy requirements for cell division and expansion process during earlier growth stages or the immature stage. Low expression of genes for ribosomal activity which are important for protein synthesis indicates that ripening mango growing process is slowing and stopping. The increase of approximately 35% changes of fruit weight and diameter between the two fruit growth stages have been in parallel to the transcriptome analysis. In conclusion, this study shows that high expression of cell division-related genes determines the final fruit size in mango fruit development.

Keywords: Mango, Cell division, Cell number, Transcriptome sequencing, Differentially expressed gene

Identification of MHC Class II-bound Peptides of *Shigella flexneri* 2a-infected Macrophages for Immunopeptidomics

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Abstract: *Shigella* is a Gram-negative rod-shaped intracellular bacterial pathogen that causes bacterial dysentery or shigellosis. *Shigella* contributes significantly to the global burden, as these bacteria is among the leading sources of diarrheal disease, especially among children less than 5 years old. Every year, up to 165 million shigellosis cases are reported worldwide. Antibiotics have been less effective in treating shigellosis due to the multi-drug resistance of *Shigella*. Therefore, an effective vaccine to prevent this disease is urgently needed. Macrophages are among the first immune cells that come in contact with *Shigella*. The aim of the present study is to determine the peptides presented by major histocompatibility complex (MHC) class II molecules of *Shigella*-infected macrophages. The MHC class II-associated peptides derived from *Shigella*-infected macrophages have the value of being the candidate for the epitope-based *Shigella* vaccine. To gain insight into this, THP-1 derived macrophages were infected with *Shigella flexneri* (*S. flexneri*) 2a at the multiplicity of infection of 10. The lysate was immunoprecipitated and analyzed by liquid chromatography-tandem mass spectrometry. The sequences retrieved were analyzed by bioinformatics tools. The *Shigella*-infected THP 1-derived macrophages were showed to sample peptides from source proteins of almost all subcellular localization and involved in various cellular functions but different proportions. Fifteen peptides from the *S. flexneri* 2a-infected macrophages were predicted localized at outer membrane proteins (OMPs) of *S. flexneri* 2a by PSORTb, CellO, and Gneg-mPLoc servers. Three of the OMPs-associated peptides were predicted as antigenic, non-allergenic, and non-toxic by respective bioinformatics tools. The finding reported in this study are novel and have not been tested as vaccine candidates against *Shigella*. This study offers a time and cost-effective way of identifying immunogenic antigens to be used as potential *Shigella* vaccine candidates. Moreover, this approach should easily be extendable to find new potential vaccine candidates for other pathogenic bacteria.

Keywords: macrophage; major histocompatibility complex; peptide; *Shigella*; immunopeptidome.

Mitochondrial Substrate Profiling of Polyethylene-Induced Osteoclasts Differentiation Supplemented with Tocotrienol-Rich Fraction.

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Abstract: Osteoclastogenesis process involves infusion of several activated macrophages to form multinucleated osteoclasts. This process is thought necessary for producing osteoclasts with an abundance of mitochondria inside, to accommodate its high energy-demanded function for pumping out protons and degrading enzymes. However, the metabolism profiles of osteoclasts following polyethylene-induced differentiation have never been studied. This study also profiled the metabolism of different mitochondrial substrates following TRF supplementation that inhibits osteoclastogenesis. Differentiation of mouse macrophage cell line (RAW 264.7) was induced in wells pre-coated with polyethylene particles in the presence of RANKL, with and without TRF supplementation. The metabolism of osteoclasts was studied by screening 31 mitochondrial substrates using Mitoplate S-1™. It was observed that different cells conditions showed different mitochondrial substrate oxidation profiles. Increased in reaction rate was observed in differentiated osteoclast as compared to the undifferentiated cells. There was reduction in reaction rate of specific substrate in osteoclasts supplemented with TRF in comparison to the corresponding controls. Higher rate of reaction suggests increase in proton (H^+) flows in the electron transport chain, indicated from the oxidation of those substrates that regulates mitochondrial metabolisms. In conclusion, there was increase in metabolism in osteoclasts following the differentiation induced by polyethylene. Supplementation with TRF reduced polyethylene-induced osteoclastogenesis possibly through modulating the substrate oxidation that regulate the metabolisms.

Keywords: Mitochondrial metabolisms, Polyethylene, Osteoclasts, TRF, Mitoplate S-1

Isolation and Identification of Pathogenic Bacteria in Satay at Kuala Pilah, Negeri Sembilan by Using MPN-PCR

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Abstract: Satay is one of the famous local street foods when made form marinated meats and grilling. Undercooked satay and poor hygienic practice by the satay hawker stall could lead to foodborne diseases such as pathogenic bacteria including *Salmonella* spp. and *Escherichia coli* O157:H7, which can cause foodborne disease like diarrhoea etc. There is reported cases of probability of eating meat that still contains surviving bacteria after heating is actually higher than the early assumption. This study aimed to isolate and identify the specific pathogenic bacteria between raw and undercooked satay for general profiling of microbial contaminants in satay from a hawker stalls around Kuala Pilah, Negeri Sembilan, Malaysia. The selective McConkey Agar and Tryptone Soya Agar (TSA) were used to obtain the positive result and further used for MPN dilution were counted and isolated for PCR amplification. The growth observed in Tryptone Soya Agar (TSA) were eliminated from isolation because the growth was too much too count (TMTC) for every plates cause it supports growth of many bacterial species. There is 60% probability of success in detecting prevalence of *Salmonella* spp. in raw satay samples through the PCR bands produced which showed same sizes (403 bp) which indicated the existence and commonness of *Salmonella* spp. in each positive sample. The MPN-PCR method is a good protocol in amplification of bacteria from environmental samples.

Keywords: Street food; Pathogenic bacteria; *Satay*; MPN-PCR.

In silico identification of antigenic proteins expressed in *Staphylococcus aureus*

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Abstract: *Staphylococcus aureus,* a Gram-positive bacterium is recognized as an opportunistic pathogen in humans and livestocks. It is known to form biofilm and cause a wide range of diseases such as endocarditis, toxic shock syndrome and osteomyelitis. Whole-cell proteome expression in *S. aureus* has previously been elucidated, however, antigenicity of *S. aureus* proteins remains not well investigated. The present work was performed to identify antigenic proteins expressed in *S. aureus* using *in silico* approach. The proteome information of *S.aureus* was retrieved from World-2DPAGE Repository. A total of 657 protein sequences of *S.aureus* were then downloaded from UniprotKB in FASTA format and used as queries in VaxiJen, CELLO, DEG, BLASTp, STRING and SWISS-MODEL programmes for antigenicity prediction, subcellular localization prediction, essentiality prediction, sequence similarity search, analysis of protein interaction network and 3D structural prediction respectively. Results demonstrated that 63% of *S. aureus* proteins were predicted as antigenic proteins. Majority of them were found to be associated with catalytic activity and metabolic processes. The antigenic *S. aureus* proteins such as 50S ribosomal protein L21 and an uncharacterized protein were identified as membrane proteins which essential for survival of *S. aureus,* non-host homologous and hub proteins in the protein interaction network which showed more functional linkages. Homology modelling of uncharacterized protein yielded a good model based on related structures from the Protein Data Bank. The findings of the present study suggest the potential use of the identified antigenic proteins in vaccine strategy against *S. aureus* infections.

Keywords: *Staphylococcus aureus;* antigenic; vaccine; *in silico*

Assessment of FTA Card Method in Detecting EgSHP Gene of Oil Palm Leaves

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Abstract: FTA card is a card that contains a unique filter paper which can capture nucleic acids and contains free radical traps to prevent the nucleic acids from denature in the room temperature. Thus, samples deposited onto FTA card can be directly used as DNA template in PCR without extracting the samples. This method is proven successful in collecting samples such as blood, bacterial culture suspension and plants. Nevertheless, dealing with plant materials can be quite challenging due to polysaccharides content that may inhibit *Taq* polymerase activity. This present study applies FTA card to store the oil palm tissue which can be directly amplified by PCR so that it can be a new alternative to extract DNA from plant. A 0.5g of crushed oil palm leaves were deposited onto each circle of FTA card and another 0.5g of same leaves were extracted using Dneasy plant mini kit. An attempt was made by amplifying the EgSHP gene by using a punch of FTA card and the analyte as DNA template. The amplicons then were ran on 2.0% metaphor agarose gel electrophoresis incorporated with Gelstar nucleic acid gel stain and observed under UV light after one hour. The size of PCR product from FTA card that was successfully amplified was in between 400bp to 800bp. The result was in line with 550 bp PCR product generated by EgSHP primer. However, there were no bands observed from the samples that were extracted using the kit. Hence, this study shows that the samples stored in FTA card can be reproducibly amplified by PCR. Therefore, the use of FTA card is a highly potential approach in studying the oil palm DNA.

Keywords: FTA card; oil palm leaves; direct PCR; gel electrophoresis; EgSHP gene

Elucidating the expression profile and *in-silico* analysis of iron-binding proteins of *S. flexneri* clinical isolates as vaccine construct

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Abstract: Shigellosis is an endemic disease covering worldwide including Malaysia, where the prevalence of the disease is reported to occur throughout the year. Until now there is no license of approved vaccine to eradicate the disease. Finding an effective vaccine is urgently needed. For pathogens, iron is a critically important micronutrient due to their important roles not only in bacterial survival but also for bacterial pathogenesis in vivo. Unfortunately, the bioavailability of iron within the infected host is usually low due to tight regulation deployed by the host. Bacteria respond to the fluctuation of iron availability by expressing the multiple iron-uptake systems to capture enough iron molecules. In this study, a virulence and mild virulence of *S. flexneri* 2a clinical isolates were used to compare the transcriptional profile of iron-binding proteins in response to the iron-deprived condition and in-silico analysis to explore potential antigenic epitope for target vaccine construct. Interestingly, most iron-binding proteins including FepA, FhuA, IutA, EfeU, and SitA were upregulated during the iron starvation. Besides, bioinformatics analysis showing that iron-binding outer membrane proteins FepA, FhuA, and IutA contain an antigenic region of epitopes capable of recognized by both B- and T-cells to mount humoral immunity as well as cell-mediated immunity response. This shows that iron-binding proteins could serve as a potential target vaccine construct to improves the current formulation of the vaccine against shigellosis disease. However, the efficacy and the effectiveness of these proteins need to be further evaluated through in-vivo study.

Keywords: Shigellosis; Iron-deprived; bacterial pathogenesis; iron-binding proteins; in-silico analysis

Assessment of FTA Card Method in Detecting EgSHP Gene of Oil Palm Leaves

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Abstract: FTA card is a card that contains a unique filter paper which can capture nucleic acids and contains free radical traps to prevent the nucleic acids from denature in the room temperature. Thus, samples deposited onto FTA card can be directly used as DNA template in PCR without extracting the samples. This method is proven successful in collecting samples such as blood, bacterial culture suspension and plants. Nevertheless, dealing with plant materials can be quite challenging due to polysaccharides content that may inhibit *Taq* polymerase activity. This present study applies FTA card to store the oil palm tissue which can be directly amplified by PCR so that it can be a new alternative to extract DNA from plant. A 0.5g of crushed oil palm leaves were deposited onto each circle of FTA card and another 0.5g of same leaves were extracted using DNeasy plant mini kit. An attempt was made by amplifying the EgSHP gene by using a punch of FTA card and the analyte as DNA template. The amplicons then were ran on 2.0% metaphor agarose gel electrophoresis incorporated with Gelstar nucleic acid gel stain and observed under UV light after one hour. The size of PCR product from FTA card that was successfully amplified was in between 400bp to 800bp. The result was in line with 550 bp PCR product generated by EgSHP primer. However, there were no bands observed from the samples that were extracted using the kit. Hence, this study shows that the samples stored in FTA card can be reproducibly amplified by PCR. Therefore, the use of FTA card is a highly potential approach in studying the oil palm DNA.

Keywords: FTA card; oil palm leaves; direct PCR; gel electrophoresis; EgSHP gene

Investigation on DNA Content of Oil Palm Leaves Tissues Stored onto FTA Card

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Abstract: Flinders Technology Associates (FTA) card is a model tool set employed to reduce the steps for the DNA samples collection, transportation, purification and storage. The main objective of this study was to investigate the DNA content of oil palm leaves tissues stored onto FTA cards and to identify its adequacy for downstream application. DNA was extracted from fresh samples as well as from samples stored onto FTA card using the DNeasy plant mini kit while the DNA was quantified by using a biophotometer. The extracted samples were amplified using Random amplified polymorphic DNA (RAPD) primer P15 (5'-TTGGCACGGG -3') and P12 (5'-TCTGGTGAGG-3'). The PCR products were separated by using agarose gel electrophoresis. The quantity of DNA extracted from fresh samples gave a yield range of 1690−2190 µg, and purity range of 1.75−1.93 while the samples stored onto FTA card gave a yield range of 1160−12000 µg and purity range of 1.66−1.70. The successful amplification was detected by the presence of PCR amplicons in between 800-1100bp on the agarose gel using RAPD P12 and P15 for both fresh samples and those stored onto FTA card. The present research work explains suitability of using FTA card for samples storage. It also gives an account on its application in DNA quantity determination and as alternative in using fresh samples. In addition, the FTA card reduces the risk of exposure to chemicals used in conventional methods and minimizes the cost and time.

Keywords: Oil Palm; Flinders Technology Associates; Polymerase Chain Reaction; Random Amplified Polymorphic DNA; Gel Electrophoresis