

**BEYOND 2021:  
BUILDING SUSTAINABLE SCIENCE**

# **PROGRAMME BOOK**

## **4<sup>th</sup> International Conference on Molecular Biology & Biotechnology 2021 (ICMBB2021)**

in conjunction with the 27<sup>th</sup> Scientific Meeting of  
the Malaysian Society for Molecular Biology & Biotechnology

**1-3 JUNE 2021**



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## **MESSAGE FROM Prof. Dr. Lau Yee Ling President, MSMBB**

Dear colleagues and friends,

As the president of The Malaysian Society of Molecular Biology and Biotechnology (MSMBB), I take great pride in welcoming all the attendees of the 4<sup>th</sup> International Conference on Molecular Biology and Biotechnology 2021 (ICMBB2021) in conjunction with the 27<sup>th</sup> Scientific Meeting of MSMBB. 4<sup>th</sup> ICMBB2021 is a major scientific conference organized by MSMBB. From 1-3 June 2021, there will be plenary and invited lectures by outstanding speakers each day. As this is an on-line conference, the programme is only conducted in the morning to minimize screen fatigue. This conference has been designed to provide an arena for participants to share and exchange knowledge, generate new ideas and establish collaboration. There will be many opportunities for early career scientists to present their work in oral and short flash poster presentations.

We look forward to an excellent online meeting with great scientists from different countries around the world and sharing new and exciting results in Molecular Biology and Biotechnology.

*Lau Yee Ling*



**MESSAGE FROM  
Dr. Amirah Amir  
Chair, Organizing Committee  
ICMBB2021**

On behalf of the Organizing Committee, it is my great pleasure to welcome you to the 4<sup>th</sup> International Conference on Molecular Biology & Biotechnology 2021 (ICMBB2021), 1-3 June 2021. This conference is carried out in conjunction with the 27<sup>th</sup> Scientific Meeting of the Malaysian Society of Molecular Biology & Biotechnology (MSMBB).

Last year, due to the COVID-19 pandemic, we were forced to cancel our conference. Consequently, the 4<sup>th</sup> ICMBB committee decided to move forward with a virtual conference considering the continued uncertainty surrounding the pandemic.

Nonetheless, we are very excited to embark on this new online edition for the first time. The theme this year is Beyond 2021: Building Sustainable Science. In a world where maintaining balance is becoming more challenging, pursuing sustainable science is important to support long-term ecological balance. It is pertinent that science is geared towards solving problems to ensure the development of effective interventions to meet the needs of present and future generations, while protecting the environment.

The conference programme that we have prepared for you is a result of the efforts poured in by many people. I would like to thank the ICMBB2021 Organizing Committee for all their hard work, commitment, and dedication in organizing this conference. I would like to express my deepest gratitude to the distinguished keynote speakers for being able to spend time and share their expertise with us. Finally, the conference would not be possible without the excellent abstract submission by presenters, support from non-presenting participants and the contributions from our sponsors. Thank you all!

Although we are physically separated, I hope that this online conference will be able to provide a platform for participants to connect with colleagues, share and exchange knowledge, generate new ideas and establish collaboration. We hope you find the conference both enjoyable and informative. Until we meet again in person, take care and stay safe.

With best wishes

*Amirah Amir*

## PROGRAMME

DAY 1: TUESDAY, 1 <sup>st</sup> June 2021		
Time	Item	
9.00 - 9.10 am	Participants login to Zoom (HALL 1) - <a href="#">ENTER HALL 1</a>	
<b>ICMBB 2021 Opening Ceremony, Keynote Session &amp; Technical Talk</b>		
9.10 - 9.20 am	<b>Opening Remarks</b> Chair of the organizing committee, Dr. Amirah Amir <a href="#">ENTER HALL 1</a>	
9.20 - 9.50 am	<b>Keynote 1- Beyond 2021: Building sustainable science</b> Prof. Datuk Wira Dr. Raha Abdul Rahim Universiti Teknikal Malaysia Melaka <a href="#">ENTER HALL 1</a>	
9.50 - 10.05 am	<b>Technical Talk 1- Large Scale 3D Bioreactor Technology: Linear Scale Up of Mesenchymal Stromal Cell Expansion with TideXcell™ System</b> Jonathan Han Wei Lim Esco Micro (M) Sdn. Bhd. <a href="#">ENTER HALL 1</a>	
10.05 - 10.20 am	<b>Technical Talk 2- PacBio HiFi Sequencing: Sustainable Technology for Sustainable Science</b> Zuwei Qian Research Instruments Sdn. Bhd <a href="#">ENTER HALL 1</a>	
10.20 - 10.25 am	Participants dispersing to Hall 1 and 2	
	<b>HALL 1 - <a href="#">ENTER HALL 1</a></b>	<b>HALL 2 - <a href="#">ENTER HALL 2</a></b>
<b>CONCURRENT SESSION 1</b>	<b>O1. Agricultural &amp; Aquaculture Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Assoc. Prof. Dr. Crystale Lim Siew Ying</i>	<b>O2. Medical Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Assoc. Prof. Dr. Jamal Hussaini</i>
10.25 - 10.55 am	<b>Plenary 1- It's not in our DNA: Non-transformative gene silencing in orchids</b> Prof. Dr. Jennifer Harikrishna University of Malaya, Malaysia <a href="#">ENTER HALL 1</a>	<b>Plenary 2 – Functional nanodomains of cardiomyocytes in heart failure</b> Prof. Dr. Julia Gorelik Imperial College London, UK <a href="#">ENTER HALL 2</a>
10.55 - 11.15 am	<b>Invited 1- Moving GenomeSelect™ to the field – highs and lows</b> Dr. David Ross Appleton Director of Sime Darby Plantations <a href="#">ENTER HALL 1</a>	<b>Invited 2- Understanding the endometrium: the “Black box of implantation”</b> Dr. Madhuri Sonal Salker Tübingen University, Germany <a href="#">ENTER HALL 2</a>
11.15 - 11.20 am	<b>Short break</b>	
11.20 - 11.30 am	<b>O11-Attenuation of <i>Macrobrachium rosenbergii</i> nodavirus through codon-deoptimization of virus functional genome</b> Dr. Low Chen Fei Universiti Kebangsaan Malaysia <a href="#">ENTER HALL 1</a>	<b>O21-CRISPR-mediated generation of <i>in vitro</i> breast cancer models to study P53 gain of function mutation</b> Ms. Asmaa Abuhamad Universiti Putra Malaysia <a href="#">ENTER HALL 2</a>

11.30 - 11.40 am	<b>O12-Transcriptomic analysis of <i>Chlorella sorokiniana</i> for pigment production under moderate light intensity</b> Dr. Siti Nor Ani Azaman Universiti Putra Malaysia <a href="#">ENTER HALL 1</a>	<b>O22-Development and evaluation of 1'-acetoxychavicol acetate-loaded nanostructured lipid carrier for prostate cancer therapy</b> Ms. Bavani Subramaniam University of Malaya <a href="#">ENTER HALL 2</a>
11.40 - 11.50 am	<b>O13-Growth promotion of sweet potato by IAA-producing rhizobacteria</b> Dr. Farzana Yasmin Lincoln University College <a href="#">ENTER HALL 1</a>	<b>O23-Tocotrienol-rich fraction lowers the ratio of phospho NF-κB to NF-κB in retinal tissue of diabetic rats</b> Mr. Muhammad Zulfiqah Sadikan Universiti Teknologi MARA <a href="#">ENTER HALL 2</a>
11.50 - 12.00 pm	<b>O14-Potential muscle activity disturbance in <i>Penaeus monodon</i> during acute hepatopancreatic necrosis disease (AHPND) infection: inference through gene expression, calcium concentration, and microRNA</b> Ms. Aileen See Siou Ning University of Malaya <a href="#">ENTER HALL 1</a>	<b>O24-<i>Plasmodium knowlesi</i> duffy binding protein alpha region II (PkDBPαII) from Peninsular Malaysia and Malaysian Borneo exhibit different immune responses in animal models</b> Ms. Ummi Kalthum Azlan Universiti of Malaya <a href="#">ENTER HALL 2</a>
12.00 - 12.10 pm	<b>O15-GCMS-based metabolomics and effect of fatty acids dietary supplementation on the survival and innate immunity response of hybrid grouper against vibriosis</b> Ms. Maya Erna Natnan Universiti Kebangsaan Malaysia <a href="#">ENTER HALL 1</a>	<b>O25-<i>In Silico</i>-SELEX Reveals PRDBDapt17 as the potential aptamer against progesterone receptor DNA binding domain</b> Ms. Navien Tholasi Nadhan Universiti Sains Malaysia <a href="#">ENTER HALL 2</a>
12.10 - 12.20 pm	Q&A panel <a href="#">ENTER HALL 1</a>	<b>O26-Ultrasensitive and Label-free Fluorescent Nanobiosensor for the Detection of miRNA in Breast Cancer Progression</b> Mr. Wong Zheng Wei University of Nottingham Malaysia <a href="#">ENTER HALL 2</a>
12.20 - 12.35 pm		Q&A panel <a href="#">ENTER HALL 2</a>
12.35 pm	End of Session 1. Participants reconvene in <b>HALL 1</b> <a href="#">ENTER HALL 1</a>	
<b>Poster presentation (BREAKOUT ROOMS, Room A to F)</b>		
2.00 – 4.00 pm	Poster presentations <a href="#">ENTER HALL 1</a>	
4.00 pm	End of Day 1	

**DAY 2: WEDNESDAY, 2<sup>nd</sup> June 2021**

Time	Item
9.00 - 9.10 am	Participants login in to Zoom (HALL 1) - <a href="#">ENTER HALL 1</a>
<b>Keynote Session &amp; Technical Talk</b>	
9.10 - 9.30 am	<b>Presentation by EduSTEM 2019 winners</b> <a href="#">ENTER HALL 1</a>
9.30 - 10.00 am	<b>Keynote 2- The Triumphs and Vicissitudes Of Biotechnologies On Malaria Control</b> Prof. Dr. Georges Snounou Université Pierre et Marie Curie (Paris VI), France <a href="#">ENTER HALL 1</a>
10.00-10.15 am	<b>Technical Talk 3- Primer Dimers? Late Ct? Poor Detection Limit? Say Goodbye To These Problems With PCR Biosystems!</b> Megan Bello, Cheong Zhin Whee Impaco PLT <a href="#">ENTER HALL 1</a>
10.15 - 10.25 am	Participants dispersing to Hall 1 and 2
	<b>HALL 1 - <a href="#">ENTER HALL 1</a></b>
	<b>HALL 2 - <a href="#">ENTER HALL 2</a></b>
<b>CONCURRENT SESSION 2</b>	<b>O3. Environmental Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Assoc. Prof. Dr. Chia Suet Lin, Eddie</i>
	<b>O4. Industrial &amp; Food Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Dr. Yeo Siok Koon</i>
10.25 - 10.55 am	<b>Plenary 3 - Mechanism of Functional Homeostasis in Bacterial Complex System</b> Prof. Dr. Hiroyuki Futamata Shizuoka University, Japan Bioremediation <a href="#">ENTER HALL 1</a>
	<b>Plenary 4 - Active edible coatings/films for perishable foods preservation: potential, present limits and future prospects illustrated by some case studies</b> Prof. Dr. Pascal Degraeve Claude Bernard University Lyon 1, France <a href="#">ENTER HALL 2</a>
10.55 - 11.15 am	<b>Invited 3 - The application of Antarctic microorganism on hydrocarbon bioremediation process</b> Assoc. Prof. Dr. Siti Aqlima Ahmad Universiti Putra Malaysia, Malaysia. <a href="#">ENTER HALL 1</a>
	<b>Invited 4 - Omics Technologies: Elucidating Relationships between Microbes and Cancer and Future Applications</b> Prof. Dr. Chong Pei Pei Taylor's University, Malaysia <a href="#">ENTER HALL 2</a>
11.15 - 11.20 am	<b>Short break</b>
11.20 - 11.30 am	<b>O31-Bacterial diversity analysis in mangrove ecosystem of Johor using minion sequencing</b> Assoc. Prof. Dr. Roshan Mascarenhas Newcastle University Medicine Malaysia (NUMed) <a href="#">ENTER HALL 1</a>
	<b>O41-Targeting double genes in multiplex PCR: an innovation in PCR technology for the authentication of food products</b> Dr. M. A. Motalib Hossain Universiti of Malaya <a href="#">ENTER HALL 2</a>

11.30 - 11.40 am	<p><b>O32-Eco-friendly silver nanoparticles (AgNPs) fabricated by green synthesis using marine polychaete, <i>Marphysa moribidii</i></b>  Assoc. Prof. Dr. Wan Iryani  Wan Ismail  Universiti Malaysia Terengganu  <a href="#">ENTER HALL 1</a></p>	<p><b>O42-Production of spray-dried sea cucumber (<i>Cucumaria frondosa</i>) by-products hydrolysate powder</b>  Dr. Chang Lee Sin  Universiti Kebangsaan Malaysia  <a href="#">ENTER HALL 2</a></p>
11.40 - 11.50 am	<p><b>O33-Preliminary synthesis of P(3HB-3HV) using glycerin pitch as main carbon source from <i>Cupriavidus malaysiensis</i> USMAA1020</b>  Ms. Rozina Kakar  Universiti Sains Malaysia  <a href="#">ENTER HALL 1</a></p>	<p><b>O43-Nutritive bambara groundnut powdered drink mix: consumer acceptability, physicochemical characterization, and storage stability</b>  Ms. Tan Wen Chian  UCSI University  <a href="#">ENTER HALL 2</a></p>
11.50 - 12.00 pm	<p><b>O34-Immobilisation of oil degrading bacteria on cellulose triacetate beads formed from kapok fibres and their role in oil spill remediation</b>  Mr. Joel Zachariah  UCSI University  <a href="#">ENTER HALL 1</a></p>	<p><b>O44-Detection of animal species in food chain by multiplex PCR-restriction fragment length polymorphism (RFLP) assay</b>  Mr. Syed Muhammad Kamal Uddin  University of Malaya  <a href="#">ENTER HALL 2</a></p>
12.00 - 12.10 pm	<p><b>O35-Bioprospecting and molecular identification of waste transformer oil-degrading bacteria for bioplastic production</b>  Mr. Shehu Idris  Universiti Sains Malaysia  <a href="#">ENTER HALL 1</a></p>	<p><b>O45-Elucidation of anthocyanin biosynthesis pathway in <i>Cosmos caudatus</i> Kunth.</b>  Mr. Darvien Gunasekaran  Universiti Kebangsaan Malaysia  <a href="#">ENTER HALL 2</a></p>
12.10 - 12.25 pm	Q&A panel <a href="#">ENTER HALL 1</a>	Q&A panel <a href="#">ENTER HALL 2</a>
12.25 pm	End of Day 2	

## DAY 3: THURSDAY, 3<sup>rd</sup> June 2021

Time	Item	
9.00 - 9.10 am	Participants log into Zoom Hall 1 and 2	
	<b>HALL 1 - <a href="#">ENTER HALL 1</a></b>	<b>HALL 2 - <a href="#">ENTER HALL 2</a></b>
<b>CONCURRENT SESSION 3</b>	<b>O5. Medical Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Assoc. Prof. Dr. Siti Hamimah</i>	<b>O6. Microbial Biotechnology &amp; Molecular Biology</b> <i>Chairperson: Assoc. Prof. Dr. Dharmani Devi Murugan</i>
9.10 - 9.40 am	<b>Plenary 5 - Chitosan hydrogel biomaterial from fish scales for topical wound healing application</b> Prof. Dr. Mohd. Effendy Abdul Wahid Universiti Malaysia Terengganu <a href="#">ENTER HALL 1</a>	<b>Plenary 6- Understanding Alzheimer's Disease through yeast studies</b> Prof. Dr. Ian Macreadie School of Science, RMIT University, Australia <a href="#">ENTER HALL 2</a>
9.40 - 10.00 am	<b>Invited 5- Single cell proteomic analysis of COVID-19 patient samples by mass cytometry</b> Assoc. Prof. Dr. James Badger Wing Osaka University, Japan <a href="#">ENTER HALL 1</a>	<b>Invited 6- Beneficial endophytic actinomycetes</b> Assoc. Prof. Dr. Arinthip Thamchaipenet Department of Genetics, Faculty of Science, Kasetsart University, Thailand <a href="#">ENTER HALL 2</a>
10.00 - 10.05 am	<b>Short break</b>	
10.05 - 10.15 am	<b>O51-Cold gas spray hydroxyapatite coatings with thermally grown interlayer titanium oxide on Ti-6Al-4V</b> Ms. Norarney Ahmad Universiti Sains Malaysia <a href="#">ENTER HALL 1</a>	<b>O61-Phage enzybiotics secreted from <i>Lactococcus lactis</i> as potential antimicrobials</b> Dr. Adelene Song Universiti Putra Malaysia <a href="#">ENTER HALL 2</a>
10.15 - 10.25 am	<b>O52-Morindone from <i>Morinda citrifolia</i> as potential antiproliferative agent on colorectal cancer cell lines</b> Ms. Chee Cheok Wui Universiti Malaya <a href="#">ENTER HALL 1</a>	<b>O62-Mutation on Newcastle Disease Virus V protein, yes or no?</b> Ms. Tham May Ling Universiti Putra Malaysia <a href="#">ENTER HALL 2</a>
10.25 - 10.35 am	<b>O53-Tocotrienol-rich Fraction (TRF) improves gross liver morphology and liver histological changes in non-alcoholic fatty liver disease (NAFLD) mice model</b> Mr. Mohd Danial Bin Mohd Efendy Goon Universiti Teknologi MARA <a href="#">ENTER HALL 1</a>	<b>O63-Recombinant cell penetrating peptides and intrabodies targeting inner membrane-bound mutated KRAS antigen</b> Mr. Jeremy Ng UCSI University <a href="#">ENTER HALL 2</a>

10.35 - 10.45 am	<b>O54-Generation of DNA aptamers against envelope 2 (E2) protein of Chikungunya virus by <i>in vitro</i> systematic evolution of ligands for exponential enrichment (SELEX) for diagnostic application</b> Ms. Anna Andrew Universiti Sains Malaysia <b><a href="#">ENTER HALL 1</a></b>	<b>O64-Screening of selected ageing-related proteins that extend chronological life span in yeast <i>Saccharomyces cerevisiae</i></b> Ms. Lee Jee Whu Universiti Sains Malaysia <b><a href="#">ENTER HALL 2</a></b>
10.45 - 10.55 am	<b>O55-Expression of specific biomarkers toward microfold cells differentiation in 3D culture of Caco-2 and Raji B cells</b> Mr. Mizanurfakhri Ghazali Universiti Teknologi MARA <b><a href="#">ENTER HALL 1</a></b>	<b>O65-Determination of the metabolic difference in hemolytic and non-hemolytic <i>Listeria monocytogenes</i> by Phenotype MicroArray™ Technology</b> Ms. Yap Phui Chyng Universiti of Malaya <b><a href="#">ENTER HALL 2</a></b>
10.55 - 11.10 am	Q&A panel <b><a href="#">ENTER HALL 1</a></b>	Q&A panel <b><a href="#">ENTER HALL 2</a></b>
11.10 - 11.20 am	Back to Hall 1	
<b>Prize Presentations &amp; Closing Ceremony (HALL 1) - <a href="#">ENTER HALL 1</a></b>		
11.20 - 11.45 am	Awards ceremony – EduSTEM, EduSTEMX, Distinguished Scientist Award, Young Scientist Award, Best Poster awards	
11.45 - 11.55 am	Closing address by President of MSMBB, Professor Dr. Lau Yee Ling	
<b>END OF CONFERENCE</b>		

**3-MINUTE POSTER PRESENTATION  
(3MPP)**

Access the posters and the video presentations of the participants by clicking on the links below:

Agricultural and Aquaculture		
<p><b>P101- In silico characterization of UGT76G1 protein In <i>Stevia rebaudiana</i> Bertoni accessions MS007</b>  <i>Ms. Nor Iswani Mokthar</i>  <i>International Islamic University Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P102- Investigation of the antibacterial potentials of the black soldier fly (<i>Hermetia illucens</i>) larvae</b>  <i>Ms. An Nie Tee</i>  <i>Universiti Tunku Abdul Rahman</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P103- In silico identification and characterization of kaurene synthase protein in <i>Stevia rebaudiana</i> MS007</b>  <i>Ms. Fathiah Rosilan</i>  <i>International Islamic University Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P202- Antagonistic and inhibitory potentials of some natural <math>\beta</math>-carboline alkaloids against 5-HT1A homology receptor as potent antidepressants</b>  <i>Mr. Yusuf Ayipo</i>  <i>Universiti Sains Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P203- Phytochemical composition and antioxidant potential of methanolic extract of filamentous <i>Anabaena</i> sp. and unicellular <i>Microcystis</i> sp.</b>  <i>Ms. Reem Abdulsalam Al-Nedawe</i>  <i>Universiti Putra Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P204- Suppressing cinnamate-4-hydroxylase (C4H) gene using RNA and CRISPR interference systems increases the expression of flavonoid-related genes in ginger and tobacco</b>  <i>Mr. Karlson Chou Khai Soong</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P205- Generation of superfolder green fluorescent protein variants as non-invasive reporters in plants</b>  <i>Mr. Wai Keat Toh</i>  <i>Universiti Tunku Abdul Rahman</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P206- Tandem mass tag-based quantitative proteomics analysis reveals the leaf response to drought in <i>Pandanus amaryllifolius</i></b>  <i>Mr. Muhammad Asyraf Mohd Amnan</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P207- Proteomic analysis of giant freshwater prawn, <i>Macrobrachium rosenbergii</i> eyestalks throughout different molting stages</b>  <i>Ms. Amy Raihanah Husain</i>  <i>Universiti Kebangsaan Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P208- Waterlogging affects morpho-physiology and group VII ethylene response factor gene expression in banana</b>  <i>Ms. Ee Yang Teoh</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P211- Metabolite profiling of 50% ethanolic extraction of <i>Clinacanthus nutans</i> by using GC-MS and LC-MS/MS and cytotoxicity analysis of succinic acid, betulinic acid and artemisinin on J774.2 macrophage cell line</b>  <i>Mr. Ravi Kumar Kalaichelvam</i>  <i>Universiti Sains Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P269- Transcriptome analysis of virus-host interactions between the lytic bacteriophage DchS1 and the soft-rot macerger, <i>Dickeya chrysanthemi</i></b>  Mr. Ming Wei Lew  AIMST University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P318- <i>Mallotus mollissimus</i> and <i>Solanum erianthum</i> carries potential phytochemical with antimicrobial properties</b>  Dr. Lucky Poh Wah Goh  Universiti Malaysia Sabah</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P319- In silico transcriptome-wide mining of transcription factor families in <i>Curcuma alismatifolia</i> (ornamental ginger)</b>  Dr. Sima Taheri  Universiti Malaya</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P320- Metabolome analysis of oil palm friable calli and its development</b>  Ms. Dalilah Abu Bakar  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P321- Classification of multifunctional and multisubunit oil palm acetyl-CoA carboxylase (ACCCase) via domain analysis</b>  Ms. Nadzirah Amiruddin  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P322- Variability in yield components and vegetative traits of 3-way crosses oil palm progenies</b>  Ms. Nor Azwani Abu Bakar  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P323- Optimization of protoplast isolation from oil palm <i>in vitro</i>-derived leaf and mesocarp</b>  Mr. Mohd Al Akmarul Fizree Md Piji  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P324- Preliminary analysis of QTLs associated with yield components in oil palm (<i>Elaeis guineensis</i> Jacq.) through association mapping</b>  Ms. Suzana Mustaffa  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P325- Oil palm tissue culture system for artificial inoculation study of <i>Ganoderma boninense</i></b>  Dr. Pei Lee Angel Lee  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P327- Production of recombinant iridovirus coat protein using a synthetic biology approach</b>  Associate Prof. Dr. Kenneth Rodrigues  Universiti Malaysia Sabah</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P328- <i>In vitro</i> proliferation of shoots and callus of <i>Talinum paniculatum</i> (Jacq.) Gaertn</b>  Mr. Shahril Efzueni Rozali  International University of Malaya-Wales</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P329- Identification of putative olfactory proteins from a key palm oil pollinating weevil, <i>Elaeiodobius kamerunicus</i></b>  Mr. Nabeel Muneim  Malaysian Palm Oil Board</p>	<a href="#">Poster</a>	<a href="#">Video</a>

Medical		
<p><b>P104- Antifungal and antimicrobial activity of <i>Solanum nigrum</i> and <i>Solanum torvum</i> mediated silver nanoparticles</b>  <i>Ms. Melannie Roberts</i>  AIMST University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P105- The effectiveness of crude palm oil in preventing Alzheimer's disease induced in rat</b>  <i>Ms. Siti Norliyana Che Mat Zubaidi</i>  Management and Science University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P106- CRISPR-Cas9 as a cancer therapy</b>  <i>Mr. Ali Adil</i>  Al-Furat Al-Awsat Technical University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P107- Elucidating the effectiveness of <i>Elaeis Guineensis</i> on sex hormone in PCOS induced rats</b>  <i>Ms. Vigneswary Thiruselvam</i>  Management and Science University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P108- Over-expression and purification of <i>Acinetobacter baumannii</i> Hfq protein in BL21 cells</b>  <i>Ms. Kanchana Appalasamy</i>  AIMST University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P109- Transcriptome analysis of <i>S. Typhi</i> treated with durian waste (rind) mediated silver nanoparticles</b>  <i>Ms. Savithri Shanmugam</i>  AIMST University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P110- Renal protective effects of <i>Trigonella foenum-graecum</i> seeds on morphine withdrawal rats</b>  <i>Ms. Sutha Sharminni</i>  Management and Science University</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P214- Effects of <i>trans</i>-resveratrol and RU-615 on human trabecular meshwork cells morphology and viability</b>  <i>Ms. Amy Suzana Abu Bakar</i>  Universiti Teknologi MARA</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P215- The toxicity level of raw titanium alloy sample (Ti-6Al-4V) on human periodontal ligament fibroblast</b>  <i>Mr. Mohammad Idham Abd Hamid</i>  Universiti Sains Malaysia</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P216- Effect of spironolactone towards proliferation of metastatic osteosarcoma cells HOS-143B</b>  <i>Ms. Farhana Khamarudin</i>  Universiti Teknologi MARA</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P217- Genome-wide SNP analysis of the evolutionary multidrug resistant <i>Mycobacterium tuberculosis</i> (MDR-TB) in Malaysia</b>  <i>Ms. Hui Wen Teh</i>  Universiti Sains Malaysia</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P218- Investigation of cytotoxins from Malaysian cobras (<i>Naja sumatrana</i> and <i>Naja kaouthia</i>) as a potential antineoplastic agent</b>  <i>Ms. Ho Phin Chong</i>  Universiti Malaya</p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P220- BPIFB1 role in the regulation of EMT associated genes in the gastric cancer cells</b>  <i>Ms. Anis Suraya Mohd Jamil</i>  Universiti Teknologi MARA</p>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P221- Cell-free supernatants from probiotics inhibit colon cancer cells proliferation</b>  <i>Ms. Ifeoma Dikeocha</i>  <i>University of Cyberjaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P223- Antibiotic resistance patterns of WHO priority pathogens isolated from acute pharyngitis patients in private primary care clinics</b>  <i>Ms. Christina Shook Cheng Chong</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P224- HMGCR expression in relation to HER2 status of breast cancer</b>  <i>Ms. Rosmaizan Drahman</i>  <i>Universiti Sains Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P225- Proteomic analysis reveals protective role of melatonin in tumour-prone <i>Drosophila melanogaster</i> lethal giant larvae mutants</b>  <i>Ms. Kar Cheng Wong</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P226- Evaluation of antidiabetic activity of methanolic extract of <i>Coccinia grandis</i> (Voight) and <i>Spondias mombin</i> (Linn) leaves in streptozotocin induced diabetic Sprague Dawley rats</b>  <i>Mr. Gobinath Ramachawolran</i>  <i>AIMST University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P227- Synthesis and characterization of azobenzene derivatives and azobenzene-imidazolium conjugates with selective antimicrobial potential</b>  <i>Ms. Halimah Funmilayo Babamale</i>  <i>Universiti Sains Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P228- Changes in inflammatory biomarker VCAM-1 and insulin levels during progression of premature atherosclerosis in rats</b>  <i>Ms. Maleeka Abdullah Hilmy</i>  <i>Management and Science University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P229- Investigation of upper respiratory carriage of bacterial pathogens and their antibiotic susceptibility profile in the Kinta Valley, Perak, Malaysia</b>  <i>Mr. Hing Huat Ong</i>  <i>Universiti Tunku Abdul Rahman</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P230- The anti-proliferative role of 15,16-dihydrotanshinone I (DHTS) extracted from <i>Salvia miltiorrhiza</i> in autosomal dominant polycystic kidney disease (ADPKD)</b>  <i>Ms. Rhubaniya Mahendran</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P231- Production truncated bacterial leukotoxin from <i>Aggregatibacter actinomycetemcomitans</i> via different types of expression system</b>  <i>Ms. Sook Kee Chong</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P232- Tocotrienol rich fraction (TRF) upregulates farnesoid X receptor (FXR) and modulates FXR target genes in the heart of high fat diet-fed mice</b>  <i>Dr. Nur Aliah Natasha Md Shahrulnizam</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P233- Evaluation of antioxidant and antidiabetic capacity of medicinal weeds, <i>Mimosa pudica</i></b>  <i>Ms. Nor Saffana Binti Baharuddin</i>  <i>Universiti Putra Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P234- Determining structural stability of glucose-6-phosphate dehydrogenase deficiency variants using molecular dynamics simulation</b>  <i>Mr. Naveen Louis</i>  <i>Universiti Teknologi Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P235- Comparative evaluation of commercially available NS1-based serological assays for the detection of anti-ZIKV IgG antibodies</b>  <i>Ms. Hooi Yuen Khoo</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P236- Perfluorooctane sulfonate (PFOS) exposure affects beating rate and brain natriuretic peptide (BNP) expression of cardiomyocytes</b>  <i>Ms. Siti Suhana Abdullah Soheimi</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P237- Downstream effects of berberine treatment in colorectal cancer cell line, HCT 116</b>  <i>Mr. Muhammad Azizan Samad</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P238- The association of small dense LDL cholesterol level with clinical risk factors of metabolic syndrome subjects in Selangor</b>  <i>Ms. Nur Atiqah Auni Razali</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P240- Establishment of reference interval for haematological parameter among Afghan population</b>  <i>Ms. Najia Sherzay</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P241- Differential lipocalin-1 levels in keratoconus in a Malaysian cohort</b>  <i>Mr. Jun Bin Ng</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P242- Deciphering the evolutionary divergence of Bleg1_2478 B3 metallo-<math>\beta</math>-lactamase from structural perspective</b>  <i>Ms. Shaw Xian Au</i>  <i>Universiti Putra Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P243- Tocotrienol-rich fraction (TRF) upregulates antioxidant genes of human endometrial stromal fibroblast cells of endometriosis</b>  <i>Ms. Nur Amira Md Amin</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P244- Preliminary evaluation of optimised PCR-based assay for the detection of pathogenic familial hypercholesterolaemia gene variants among Asian population</b>  <i>Ms. Norhidayah Rosman</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P245- Global gene expression of obese patients with knee osteoarthritis</b>  <i>Ms. Chiaw Lee Chiew</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P246- Interaction between in utero BPA exposure and postnatal trans fat diet on small intestine function of male Sprague Dawley rats</b>  <i>Ms. Sarah Zulkifli</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P247- Natural quinones induce ROS-mediated apoptosis and inhibit cell migration in PANC-1 human pancreatic cancer cell line</b>  <i>Mr. Prasad Narayanan</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P248- Cytotoxicity effects of allicin towards human oral squamous cell carcinoma (OSCC) cell lines, ORL-48 and SCC-15</b>  <i>Ms. Farrah Hazwani</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P249- Evaluation of cadmium treatment on ATP level, cell membrane integrity and cell viability in Caco-2 cell line</b>  <i>Mr. Fu Hou Wong</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P250- Apoptotic mechanisms of tocotrienol isomers towards oral squamous carcinoma cell lines, ORL-48</b>  <i>Ms. Atiqa Syazwani Ridzuan</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P251- Modulation of small interfering RNA in Newcastle disease virus persistently infected colorectal cancer cells</b>  <i>Mr. Lee Chin Chan</i>  <i>Universiti Putra Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P252- Expression of dominant AMPK gamma 1 subunit gene in post-mortem obese human perihepatic adipose tissue</b>  <i>Ms. Norainfarahin Zainal Aznam</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P253- Primer and probe conservation issue in the quantification of hepatitis B virus DNA</b>  <i>Ms. Chye Phing Teh</i>  <i>Sunway University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P254- Inhibitory effect of 1-DNJ towards on extracellular matrix proteins expression in osteosarcoma cells</b>  <i>Ms. Zulaika Roslan</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P255- Effect of hsa-miR-3131 transfection upon cell viability in imatinib sensitive and imatinib resistance chronic myeloid leukemia cells</b>  <i>Ms. Syarifah Faezah Syed Mohamad</i>  <i>Universiti Sains Islam Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P256- GAS5 associated CeRNA network in lower grade glioma</b>  <i>Ms. Jesminder Kaur</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P257- Synthesis and cytotoxic effects of novel paclitaxel (PTX)-loaded PLGA (Poly (lactic-co-glycolic acid) nanoparticle bio-conjugate with EGFR monoclonal antibody for triple negative breast cancer</b>  <i>Ms. Shalini Krishnan</i>  <i>Universiti Sains Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P258- Hyperglycaemia disrupts FKN and RANK-RANKL-OPG system in a pregnant rat model</b>  <i>Dr. Noor Eliza Hashim</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P301- Application of mesenchymal stem cell-derived secretome to promote full-thickness wound healing- an <i>in vivo</i> study</b>  <i>Dr. Jia Xian Law</i>  <i>Universiti Kebangsaan Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P302- Measurement of fatty acid beta-oxidation target protein using in-cell enzyme-linked immunosorbent assay (ELISA) in human fibroblast</b>  <i>Ms. Rosnani Mohamed</i>  <i>National Institute of Health</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P303- Pyrogallol induces antimicrobial effect and cell membrane disruption on methicillin resistant <i>Staphylococcus aureus</i> (MRSA)</b>  <i>Dr. Yik Ling Chew</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P304- Cervical cancer and next generation sequencing (NGS): a systematic review</b>  <i>Associate Prof. Dr. Nazefah Abdul Hamid</i>  <i>Universiti Sains Islam Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P305- Antimicrobial effect of <i>Quercus infectoria</i> and <i>Acorus calamus</i> in wound model</b>  <i>Ms. Sharmanee Thiagarajah</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P306- Detection of nuclear &amp; surface marker of pluripotency in human induced pluripotent stem cells by immunofluorescent microscopy</b>  <i>Ms. Nur Jannaim binti Muhamad</i>  <i>National Institute of Health</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P307- <i>In vitro</i> screening of selected ulam for the inhibition of CYP450 3A4 activity</b>  <i>Dr. Wan Rosalina Wan Rosli</i>  <i>University of Cyberjaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P308- Cytokilling effect of NK-92 cells on nasopharyngeal carcinoma (NPC) cell lines</b>  <i>Ms. Marini Marzuki</i>  <i>National Institute of Health</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P309- Cytotoxic effect of lapatinib on T84 human colonic epithelial cell line</b>  <i>Dr. Wan Nor I'zzah Wan Mohamad Zain</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P310- Drug repurposing for COVID-19 and understanding the molecular action pathways of SARS-CoV-2</b>  <i>Dr. Idris Adewale Ahmed</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P311- Knowledge, attitude and perception towards colorectal cancer among public</b>  <i>Assistant Prof. Dr. Sheiladevi Sukumaran</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P312- Nisin induces apoptosis of MG63 osteosarcoma cells while protecting non-neoplastic cells</b>  <i>Dr. Muhammad Fairuz Azmi</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P313- Air pollution skin effects and hospital admissions for eczema in Kuala Lumpur, Malaysia</b>  <i>Mr. Thavin Kumar Mathana Sundram</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P314- Real-time reverse transcription loop-mediated isothermal amplification for rapid detection of SARS-CoV2</b>  <i>Prof. Dr. Yee Ling Lau</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P315- Comparative proteomics profiling of serum of women with BI-RADS scores of 1 to 5 using gel-based approaches</b>  <i>Dr. Jaime Jayapalan</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P316- Effect of R92L and R92P mutations in ornithine transcarbamylase (OTCase) enzyme</b>  <i>Dr. Ernie Zuraida Ali</i>  <i>National Institute of Health</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P317- Wnt pathway gene expression in oral squamous cell carcinoma</b>  <i>Dr. Nyi Mas Siti Purwaningsih</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

Environmental		
<b>P212- Modification of Kapok fibres into porous beads for marine oil spill remediation efforts</b> <i>Mr. Zhi Yong Kang</i> <i>UCSI University</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P213- Physical and chemical preventive countermeasures of disinfectants used during the SARS-CoV-2 pandemic: Implications on toxicity and resistance development</b> <i>Mr. Najib Yahaya Sani</i> <i>Universiti Sains Malaysia</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P330- Food operators' perceptions on biodegradable food container usage at Subang Jaya: The relationship of environmental knowledge, concern, attitude and usage intention</b> <i>Ms. Kavita Chirara</i> <i>UCSI University</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P331- Pharmaceuticals and personal care products (PPCPs) residues in surface water bodies from Selangor (Malaysia): Occurrence and environmental risk assessment</b> <i>Assistant Prof. Dr. Eugenie Sin Sing Tan</i> <i>UCSI University</i>	<a href="#">Poster</a>	<a href="#">Video</a>

Industrial and Food		
<b>P268- The effects of extraction time and temperature on phenolic compounds and antioxidant capacity of Malaysian Trigona propolis aqueous extract using response surface methodology</b> <i>Mr. Abdullah Hagar</i> <i>International Islamic University Malaysia</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P332- Functionalization of medium-chain-length polyhydroxyalkanoates with methyl acrylate by free radical copolymerization using azobisisobutyronitrile</b> <i>Dr. Chong-Boon Ong.</i> <i>International University of Malaya-Wales</i>	<a href="#">Poster</a>	<a href="#">Video</a>

Microbial		
<b>P111- Isolation and characterisation of probiotic bacteria from livestock and kimchi and assessment of their antibacterial potentials</b> <i>Ms. Annie Mei Tin Low</i> <i>Universiti Tunku Abdul Rahman</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P259- Exopolysaccharides (EPS) from <i>Bifidobacteria pseudocatenalatum</i> induced apoptosis cell death in Caco-2 cells</b> <i>Ms. Husna Zulkipli</i> <i>Universiti Teknologi MARA</i>	<a href="#">Poster</a>	<a href="#">Video</a>
<b>P260- Optimization of milk fermentation incorporated with recombinant <i>Lactococcus lactis</i> NZ3900</b> <i>Ms. Yu Hsuan How</i> <i>UCSI University</i>	<a href="#">Poster</a>	<a href="#">Video</a>

<p><b>P261- Determination of total phenolic content and antibacterial activities of Malaysian traditional plants against selected pathogenic bacteria</b>  <i>Mr. Ibrahim Abuga</i>  <i>International Islamic University Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P262- Evaluating the specificity of a bacterial leukotoxin LtxA on targeting human integrin: Towards a potential therapeutic agent against LFA-1 mediated autoimmune diseases</b>  <i>Ms. Pei Yin Lee</i>  <i>UCSI University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P263- Isolation and characterization of prenyltransferase isomers from <i>Boesenbergia rotunda</i></b>  <i>Ms. Alicia Jia Huey Ng</i>  <i>Universiti Malaya</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P264- Identification and characterization of novel non-protein coding RNAs (npcRNAs) associated with global transcriptional regulator, Hfq in pathogenic bacteria <i>S. Typhi</i></b>  <i>Ms. Kishonthani Krusnamurthy</i>  <i>AIMST University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P265- Knocking-out the non-protein coding RNA gene (PmiR-137) in <i>Proteus mirabilis</i> to understand its role in pathogenesis</b>  <i>Ms. Abirami Sanniraj</i>  <i>AIMST University</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P267- Identification of cucumber-associated fungus by using recombinase polymerase amplification (RPA) method</b>  <i>Ms. Wan Hawa Najibah Wan Rasni</i>  <i>Universiti Sains Islam Malaysia</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P334- Molecular characterization and phylogenetic analysis of an <i>Enterococcus faecium</i> isolate from a clinical sample in Sabah, Malaysia</b>  <i>Associate Prof. Dr. Mohammad Zahirul Hoque</i>  <i>Universiti Malaysia Sabah</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P335- Prevalence and genetic diversity of PVL-positive <i>Staphylococcus aureus</i> nasal carriers among patients and healthcare-workers in a tertiary hospital in Selangor –Malaysia</b>  <i>Dr. Hassanain Al-Talib</i>  <i>Universiti Teknologi MARA</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>
<p><b>P336- Identification of lactic acid bacteria through phenotype and genotype based methods</b>  <i>Ms. Nur Ilida Mohamad</i>  <i>Malaysian Agricultural Research and Development Institute</i></p>	<a href="#">Poster</a>	<a href="#">Video</a>

## 4<sup>th</sup> ICMBB 2021 3-min Poster Presentation Live Q&A Session Schedule (1<sup>st</sup> June 2021)

The 3MPP judges will be asking their questions to the participants during these Q&A sessions.

If you have any questions about their research, you can get in contact with them using Zoom's private chat function during these sessions.

Molecular Biology

Biotechnology

### Session 1

Time	Breakout Room A <i>Chairperson:</i> <b>Dr. Alan Tan Yee Hock (UCSI)</b>	Breakout Room B <i>Chairperson:</i> <b>Asst. Prof. Yap Wai Sum (UCSI)</b>	Breakout Room C <i>Chairperson:</i> <b>Dr. Cheong Fei Wen (UM)</b>	Breakout Room D <i>Chairperson:</i> <b>Assoc. Prof. Dr Dharmani Devi (UM)</b>	Breakout Room E: <i>Chairperson:</i> <b>Assoc. Prof. Dr Siti Hamimah (UiTM)</b>	Breakout Room F <i>Chairperson:</i> <b>Assoc. Prof. Dr. Crystale Lim (UCSI)</b>
2:00PM – 2:05PM	P202- Antagonistic and inhibitory potentials of some natural $\beta$ -carboline alkaloids against 5-HT1A homology receptor as potent antidepressants  <i>Mr. Yusuf Ayipo Universiti Sains Malaysia</i>	P214- Effects of <i>trans</i> -resveratrol and RU-615 on human trabecular meshwork cells morphology and viability  <i>Ms. Amy Suzana Abu Bakar Universiti Teknologi MARA</i>	P224- HMGCR expression in relation to HER2 status of breast cancer  <i>Ms. Rosmaizan Drahman Universiti Sains Malaysia</i>	P234- Determining structural stability of glucose-6-phosphate dehydrogenase deficiency variants using molecular dynamics simulation  <i>Mr. Naveen Louis Universiti Teknologi Malaysia</i>	P231- Production truncated bacterial leukotoxin from <i>Aggregatibacter actinomycetemcomitans</i> via different types of expression system  <i>Ms. Sook Kee Chong UCSI University</i>	P212- Modification of Kapok fibres into porous beads for marine oil spill remediation efforts  <i>Mr. Zhi Yong Kang UCSI University</i>
2:05PM – 2:10PM	P203- Phytochemical composition and antioxidant potential of methanolic extract of filamentous <i>Anabaena</i> sp. and unicellular <i>Microcystis</i> sp.  <i>Ms. Reem Abdulsalam Al-Nedawe Universiti Putra Malaysia</i>	P215- The toxicity level of raw titanium alloy sample (Ti-6Al-4V) on human periodontal ligament fibroblast  <i>Mr. Mohammad Idham Abd Hamid Universiti Sains Malaysia</i>	P225- Proteomic analysis reveals protective role of melatonin in tumour-prone <i>Drosophila melanogaster</i> lethal giant larvae mutants  <i>Ms. Kar Cheng Wong Universiti Malaya</i>	P235- Comparative evaluation of commercially available NS1-based serological assays for the detection of anti-ZIKV IgG antibodies  <i>Ms. Hooi Yuen Khoo Universiti Malaya</i>	P260- Optimization of milk fermentation incorporated with recombinant <i>Lactococcus lactis</i> NZ3900  <i>Ms. Yu Hsuan How UCSI University</i>	P213- Physical and chemical preventive countermeasures of disinfectants used during the SARS-CoV-2 pandemic: Implications on toxicity and resistance development  <i>Mr. Najib Yahaya Sani Universiti Sains Malaysia</i>

2:10PM – 2:15PM	P204- Suppressing cinnamate-4-hydroxylase (C4H) gene using RNA and CRISPR interference systems increases the expression of flavonoid-related genes in ginger and tobacco  <i>Mr. Karlson Chou Khai Soong Universiti Malaya</i>	P216- Effect of spironolactone towards proliferation of metastatic osteosarcoma cells HOS-143B  <i>Ms. Farhana Khamarudin Universiti Teknologi MARA</i>	P226- Evaluation of antidiabetic activity of methanolic extract of <i>Coccinia grandis</i> (Voight) and <i>Spondias mombin</i> (Linn) leaves in streptozotocin induced diabetic Sprague Dawley rats  <i>Mr. Gobinath Ramachawolran AIMST University</i>	P236- Perfluorooctane sulfonate (PFOS) exposure affects beating rate and brain natriuretic peptide (BNP) expression of cardiomyocytes  <i>Ms. Siti Suhana Abdullah Soheimi Universiti Teknologi MARA</i>	P261- Determination of total phenolic content and antibacterial activities of Malaysian traditional plants against selected pathogenic bacteria  <i>Mr. Ibrahim Abuga International Islamic University Malaysia</i>	P330- Food operators' perceptions on biodegradable food container usage at Subang Jaya: The relationship of environmental knowledge, concern, attitude and usage intention  <i>Ms. Kavita Chirara UCSI University</i>
2:15PM – 2:20PM	P205- Generation of superfolder green fluorescent protein variants as non-invasive reporters in plants  <i>Mr. Wai Keat Toh Universiti Tunku Abdul Rahman</i>	P217- Genome-wide SNP analysis of the evolutionary multidrug resistant <i>Mycobacterium tuberculosis</i> (MDR-TB) in Malaysia  <i>Ms. Hui Wen Teh Universiti Sains Malaysia</i>	P227- Synthesis and characterization of azobenzene derivatives and azobenzene-imidazolium conjugates with selective antimicrobial potential  <i>Ms. Halimah Funmilayo Babamale Universiti Sains Malaysia</i>	P237- Downstream effects of berberine treatment in colorectal cancer cell line, HCT 116  <i>Mr. Muhammad Azizan Samad Universiti Malaya</i>	P262- Evaluating the specificity of a bacterial leukotoxin LtxA on targeting human integrin: Towards a potential therapeutic agent against LFA-1 mediated autoimmune diseases  <i>Ms. Pei Yin Lee UCSI University</i>	P331- Pharmaceuticals and personal care products (PPCPs) residues in surface water bodies from Selangor (Malaysia): Occurrence and environmental risk assessment  <i>Assistant Prof. Dr. Eugenie Sin Sing Tan UCSI University</i>
2:20PM – 2:25PM	P206- Tandem mass tag-based quantitative proteomics analysis reveals the leaf response to drought in <i>Pandanus amaryllifolius</i>  <i>Mr. Muhammad Asyraf Mohd Amnan Universiti Malaya</i>	P218- Investigation of cytotoxins from Malaysian cobras ( <i>Naja sumatrana</i> and <i>Naja kaouthia</i> ) as a potential antineoplastic agent  <i>Ms. Ho Phin Chong Universiti Malaya</i>	P228- Changes in inflammatory biomarker VCAM-1 and insulin levels during progression of premature atherosclerosis in rats  <i>Ms. Maleeka Abdullah Hilmy Management and Science University</i>	P238- The association of small dense LDL cholesterol level with clinical risk factors of metabolic syndrome subjects in Selangor  <i>Ms. Nur Atiqah Auni Razali Universiti Teknologi MARA</i>	P263- Isolation and characterization of prenyltransferase isomers from <i>Boesenbergia rotunda</i>  <i>Ms. Alicia Jia Huey Ng Universiti Malaya</i>	P268- The effects of extraction time and temperature on phenolic compounds and antioxidant capacity of Malaysian Trigona propolis aqueous extract using response surface methodology  <i>Mr. Abdullah Hagar International Islamic University Malaysia</i>

2:25PM – 2:30PM	P207- Proteomic analysis of giant freshwater prawn, <i>Macrobrachium rosenbergii</i> eyestalks throughout different molting stages  <i>Ms. Amy Raihanah Husain Universiti Kebangsaan Malaysia</i>	P220- BPIFB1 role in the regulation of EMT associated genes in the gastric cancer cells  <i>Ms. Anis Suraya Mohd Jamil Universiti Teknologi MARA</i>	P229- Investigation of upper respiratory carriage of bacterial pathogens and their antibiotic susceptibility profile in the Kinta Valley, Perak, Malaysia  <i>Mr. Hing Huat Ong Universiti Tunku Abdul Rahman</i>	P240- Establishment of reference interval for haematological parameter among Afghan population  <i>Ms. Najia Sherzay Universiti Teknologi MARA</i>	P264- Identification and characterization of novel non-protein coding RNAs (npcRNAs) associated with global transcriptional regulator, Hfq in pathogenic bacteria <i>S. Typhi</i>  <i>Ms. Kishonthani Krusnamurthy AIMST University</i>	P332- Functionalization of medium-chain-length polyhydroxyalkanoates with methyl acrylate by free radical copolymerization using azobisisobutyronitrile  <i>Dr. Chong-Boon Ong. International University of Malaya-Wales</i>
2:30PM – 2:35PM	P208- Waterlogging affects morpho-physiology and group VII ethylene response factor gene expression in banana  <i>Ms. Ee Yang Teoh Universiti Malaya</i>	P221- Cell-free supernatants from probiotics inhibit colon cancer cells proliferation  <i>Ms. Ifeoma Dikeocha University of Cyberjaya</i>	P230- The anti-proliferative role of 15,16-dihydrotanshinone I (DHTS) extracted from <i>Salvia miltiorrhiza</i> in autosomal dominant polycystic kidney disease (ADPKD)  <i>Ms. Rhubaniya Mahendran Universiti Malaya</i>	P241- Differential lipocalin-1 levels in keratoconus in a Malaysian cohort  <i>Mr. Jun Bin Ng Universiti Malaya</i>	P265- Knocking-out the non-protein coding RNA gene (PmiR-137) in <i>Proteus mirabilis</i> to understand its role in pathogenesis  <i>Ms. Abirami Sanniraj AIMST University</i>	P255- Effect of hsa-miR-3131 transfection upon cell viability in imatinib sensitive and imatinib resistance chronic myeloid leukemia cells  <i>Ms. Syarifah Faezah Syed Mohamad Universiti Sains Islam Malaysia</i>
2:35PM – 2:40PM	P211- Metabolite profiling of 50% ethanolic extraction of <i>Clinacanthus nutans</i> by using GC-MS and LC-MS/MS and cytotoxicity analysis of succinic acid, betulinic acid and artemisinin on J774.2 macrophage cell line  <i>Mr. Ravi Kumar Kalaichelvam Universiti Sains Malaysia</i>	P223- Antibiotic resistance patterns of WHO priority pathogens isolated from acute pharyngitis patients in private primary care clinics  <i>Ms. Christina Shook Cheng Chong UCSI University</i>	P259- Exopolysaccharides (EPS) from <i>Bifidobacteria pseudocatenalatum</i> induced apoptosis cell death in Caco-2 cells  <i>Ms. Husna Zulkipli Universiti Teknologi MARA</i>	P242- Deciphering the evolutionary divergence of Bleg1_2478 B3 metallo- $\beta$ -lactamase from structural perspective  <i>Ms. Shaw Xian Au Universiti Putra Malaysia</i>	P267- Identification of cucumber-associated fungus by using recombinase polymerase amplification (RPA) method  <i>Ms. Wan Hawa Najibah Wan Rasni Universiti Sains Islam Malaysia</i>	P256- GAS5 associated CeRNA network in lower grade glioma  <i>Ms. Jesminder Kaur Universiti Malaya</i>

2:40PM – 2:45PM			<p>P232- Tocotrienol rich fraction (TRF) upregulates farnesoid X receptor (FXR) and modulates FXR target genes in the heart of high fat diet-fed mice</p> <p><i>Dr. Nur Aliah Natasha Md Shahrulnizam</i></p>	<p>P243- Tocotrienol-rich fraction (TRF) upregulates antioxidant genes of human endometrial stromal fibroblast cells of endometriosis</p> <p><i>Ms. Nur Amira Md Amin Universiti Teknologi MARA</i></p>		<p>P257- Synthesis and cytotoxic effects of novel paclitaxel (PTX)-loaded PLGA (Poly (lactic-co-glycolic acid) nanoparticle bio-conjugate with EGFR monoclonal antibody for triple negative breast cancer</p> <p><i>Ms. Shalini Krishnan Universiti Sains Malaysia</i></p>
2:45PM – 2:50PM			<p>P233- Evaluation of antioxidant and antidiabetic capacity of medicinal weeds, <i>Mimosa pudica</i></p> <p><i>Ms. Nor Saffana Binti Baharuddin Universiti Putra Malaysia</i></p>			<p>P258- Hyperglycaemia disrupts FKN and RANK-RANKL-OPG system in a pregnant rat model</p> <p><i>Dr. Noor Eliza Hashim Universiti Malaya</i></p>

## Session 2

Time	Breakout Room A <i>Chairperson:</i> <i>Asst. Prof. Dr. Pui Liew Phing</i> <i>(UCSI)</i>	Breakout Room B <i>Chairperson:</i> <i>Assoc. Prof. Dr. Eddie Chia</i> <i>(UPM)</i>	Breakout Room C <i>Chairperson:</i> <i>Assoc. Prof. Dr. Siti Sarah</i> <i>Othman</i> <i>(UPM)</i>	Breakout Room D <i>Chairperson:</i> <i>Assoc. Prof. Dr. Jamal</i> <i>Houssaini</i> <i>(UiTM)</i>	Breakout Room E <i>Chairperson:</i> <i>Assoc. Prof. Dr. Yeo Siok Koon</i> <i>(Taylor's University)</i>
3:00PM – 3:05PM	P318- <i>Mallotus mollissimus</i> and <i>Solanum erianthum</i> carries potential phytochemical with antimicrobial properties  <i>Dr. Lucky Poh Wah Goh</i> <i>Universiti Malaysia Sabah</i>	P244- Preliminary evaluation of optimised PCR-based assay for the detection of pathogenic familial hypercholesterolaemia gene variants among Asian population  <i>Ms. Norhidayah Rosman</i> <i>Universiti Teknologi MARA</i>	P301- Application of mesenchymal stem cell-derived secretome to promote full-thickness wound healing- an <i>in vivo</i> study  <i>Dr. Jia Xian Law</i> <i>Universiti Kebangsaan Malaysia</i>	P311- Knowledge, attitude and perception towards colorectal cancer among public  <i>Assistant Prof. Dr. Sheiladevi Sukumaran</i> <i>UCSI University</i>	P111- Isolation and characterisation of probiotic bacteria from livestock and kimchi and assessment of their antibacterial potentials  <i>Ms. Annie Mei Tin Low</i> <i>Universiti Tunku Abdul Rahman</i>
3:05PM – 3:10PM	P319- In silico transcriptome-wide mining of transcription factor families in <i>Curcuma alismatifolia</i> (ornamental ginger)  <i>Dr. Sima Taheri</i> <i>Universiti Malaya</i>	P245- Global gene expression of obese patients with knee osteoarthritis  <i>Ms. Chiaw Lee Chiew</i> <i>Universiti Malaya</i>	P302- Measurement of fatty acid beta-oxidation target protein using in-cell enzyme-linked immunosorbent assay (ELISA) in human fibroblast  <i>Ms. Rosnani Mohamed</i> <i>National Institute of Health</i>	P312- Nisin induces apoptosis of MG63 osteosarcoma cells while protecting non-neoplastic cells  <i>Dr. Muhammad Fairuz Azmi</i> <i>Universiti Teknologi MARA</i>	P101- In silico characterization of UGT76G1 protein In <i>Stevia rebaudiana</i> Bertoni accessions MS007  <i>Ms. Nor Iswani Mokhtar</i> <i>International Islamic University Malaysia</i>
3:10PM – 3:15PM	P320- Metabolome analysis of oil palm friable calli and its development  <i>Ms. Dalilah Abu Bakar</i> <i>Malaysian Palm Oil Board</i>	P246- Interaction between in utero BPA exposure and postnatal trans fat diet on small intestine function of male Sprague Dawley rats  <i>Ms. Sarah Zulkifli</i> <i>Universiti Teknologi MARA</i>	P303- Pyrogallol induces antimicrobial effect and cell membrane disruption on methicillin resistant <i>Staphylococcus aureus</i> (MRSA)  <i>Dr. Yik Ling Chew</i> <i>UCSI University</i>	P313- Air pollution skin effects and hospital admissions for eczema in Kuala Lumpur, Malaysia  <i>Mr. Thavin Kumar Mathana Sundram</i> <i>UCSI University</i>	P102- Investigation of the antibacterial potentials of the black soldier fly ( <i>Hermetia illucens</i> ) larvae  <i>Ms. An Nie Tee</i> <i>Universiti Tunku Abdul Rahman</i>
3:15PM – 3:20PM	P321- Classification of multifunctional and multisubunit oil palm acetyl-CoA carboxylase (ACCase) via domain analysis  <i>Ms. Nadzirah Amiruddin</i> <i>Malaysian Palm Oil Board</i>	P247- Natural quinones induce ROS-mediated apoptosis and inhibit cell migration in PANC-1 human pancreatic cancer cell line  <i>Mr. Prasad Narayanan</i> <i>Universiti Malaya</i>	P304- Cervical cancer and next generation sequencing (NGS): a systematic review  <i>Associate Prof. Dr. Nazefah Abdul Hamid</i> <i>Universiti Sains Islam Malaysia</i>	P314- Real-time reverse transcription loop-mediated isothermal amplification for rapid detection of SARS-CoV2  <i>Prof. Dr. Yee Ling Lau</i> <i>Universiti Malaya</i>	P103- In silico identification and characterization of kaurene synthase protein in <i>Stevia rebaudiana</i> MS007  <i>Ms. Fathiah Rosilan</i> <i>International Islamic University Malaysia</i>

3:20PM – 3:25PM	P322- Variability in yield components and vegetative traits of 3-way crosses oil palm progenies  <i>Ms. Nor Azwani Abu Bakar Malaysian Palm Oil Board</i>	P248- Cytotoxicity effects of allicin towards human oral squamous cell carcinoma (OSCC) cell lines, ORL-48 and SCC-15  <i>Ms. Farrah Hazwani Universiti Teknologi MARA</i>	P305- Antimicrobial effect of <i>Quercus infectoria</i> and <i>Acorus calamus</i> in wound model  <i>Ms. Sharmanee Thiagarajah UCSI University</i>	P315- Comparative proteomics profiling of serum of women with BI-RADS scores of 1 to 5 using gel-based approaches  <i>Dr. Jaime Jayapalan Universiti Malaya</i>	P104- Antifungal and antimicrobial activity of <i>Solanum nigrum</i> and <i>Solanum torvum</i> mediated silver nanoparticles  <i>Ms. Melannie Roberts AIMST University</i>
3:25PM – 3:30PM	P323- Optimization of protoplast isolation from oil palm <i>in vitro</i> -derived leaf and mesocarp  <i>Mr. Mohd Al Akmarul Fizree Md Piji Malaysian Palm Oil Board</i>	P249- Evaluation of cadmium treatment on ATP level, cell membrane integrity and cell viability in Caco-2 cell line  <i>Mr. Fu Hou Wong UCSI University</i>	P306- Detection of nuclear & surface marker of pluripotency in human induced pluripotent stem cells by immunofluorescent microscopy  <i>Ms. Nur Jannaim binti Muhamad National Institute of Health</i>	P316- Effect of R92L and R92P mutations in ornithine transcarbamylase (OTCase) enzyme  <i>Dr. Ernie Zuraida Ali National Institute of Health</i>	P105- The effectiveness of crude palm oil in preventing Alzheimer's disease induced in rat  <i>Ms. Siti Norliyana Che Mat Zubaidi Management and Science University</i>
3:30PM – 3:35PM	P324- Preliminary analysis of QTLs associated with yield components in oil palm ( <i>Elaeis guineensis</i> Jacq.) through association mapping  <i>Ms. Suzana Mustaffa Malaysian Palm Oil Board</i>	P250- Apoptotic mechanisms of tocotrienol isomers towards oral squamous carcinoma cell lines, ORL-48  <i>Ms. Atiqa Syazwani Ridzuan Universiti Teknologi MARA</i>	P307- <i>In vitro</i> screening of selected ulam for the inhibition of CYP450 3A4 activity  <i>Dr. Wan Rosalina Wan Rosli University of Cyberjaya</i>	P317- Wnt pathway gene expression in oral squamous cell carcinoma  <i>Dr. Nyi Mas Siti Purwaningsih Universiti Teknologi MARA</i>	P106- CRISPR-Cas9 as a cancer therapy  <i>Mr. Ali Adil Al-Furat Al-Awsat Technical University</i>
3:35PM – 3:40PM	P325- Oil palm tissue culture system for artificial inoculation study of <i>Ganoderma boninense</i>  <i>Dr. Pei Lee Angel Lee Malaysian Palm Oil Board</i>	P251- Modulation of small interfering RNA in Newcastle disease virus persistently infected colorectal cancer cells  <i>Mr. Lee Chin Chan Universiti Putra Malaysia</i>	P308- Cytokilling effect of NK-92 cells on nasopharyngeal carcinoma (NPC) cell lines  <i>Ms. Marini Marzuki National Institute of Health</i>	P334- Molecular characterization and phylogenetic analysis of an <i>Enterococcus faecium</i> isolate from a clinical sample in Sabah, Malaysia  <i>Associate Prof. Dr. Mohammad Zahirul Hoque Universiti Malaysia Sabah</i>	P107- Elucidating the effectiveness of <i>Elaeis Guineensis</i> on sex hormone in PCOS induced rats  <i>Ms. Vigneswary Thiruselvam Management and Science University</i>

3:40PM – 3:45PM	<p>P269- Transcriptome analysis of virus-host interactions between the lytic bacteriophage DchS1 and the soft-rot macerger, <i>Dickeya chrysanthemi</i></p> <p>Mr. Ming Wei Lew AIMST University</p>	<p>P252- Expression of dominant AMPK gamma 1 subunit gene in post-mortem obese human perihepatic adipose tissue</p> <p>Ms. Norainfarahin Zainal Aznam Universiti Teknologi MARA</p>	<p>P309- Cytotoxic effect of lapatinib on T84 human colonic epithelial cell line</p> <p>Dr. Wan Nor I'zzah Wan Mohamad Zain Universiti Teknologi MARA</p>	<p>P335- Prevalence and genetic diversity of PVL-positive <i>Staphylococcus aureus</i> nasal carriers among patients and healthcare-workers in a tertiary hospital in Selangor – Malaysia</p> <p>Dr. Hassanain Al-Talib Universiti Teknologi MARA</p>	<p>P108- Over-expression and purification of <i>Acinetobacter baumannii</i> Hfq protein in BL21 cells</p> <p>Ms. Kanchana Appalasamy AIMST University</p>
3:45PM – 3:50PM	<p>P327- Production of recombinant iridovirus coat protein using a synthetic biology approach</p> <p>Associate Prof. Dr. Kenneth Rodrigues Universiti Malaysia Sabah</p>	<p>P253- Primer and probe conservation issue in the quantification of hepatitis B virus DNA</p> <p>Ms. Chye Phing Teh Sunway University</p>	<p>P310- Drug repurposing for COVID-19 and understanding the molecular action pathways of SARS-CoV-2</p> <p>Dr. Idris Adewale Ahmed Universiti Malaya</p>	<p>P336- Identification of lactic acid bacteria through phenotype and genotype based methods</p> <p>Ms. Nur Ilida Mohamad Malaysian Agricultural Research and Development Institute</p>	<p>P109- Transcriptome analysis of <i>S. Typhi</i> treated with durian waste (rind) mediated silver nanoparticles</p> <p>Ms. Savithri Shanmugam AIMST University</p>
3:50PM – 3:55PM	<p>P328- <i>In vitro</i> proliferation of shoots and callus of <i>Talinum paniculatum</i> (Jacq.) Gaertn</p> <p>Mr. Shahril Efzueni Rozali International University of Malaya-Wales</p>	<p>P254- Inhibitory effect of 1-DNJ towards on extracellular matrix proteins expression in osteosarcoma cells</p> <p>Ms. Zulaika Roslan Universiti Teknologi MARA</p>			<p>P110- Renal protective effects of <i>Trigonella foenum-graecum</i> seeds on morphine withdrawal rats</p> <p>Ms. Sutha Sharmini Management and Science University</p>
3:55PM – 4:00PM	<p>P329- Identification of putative olfactory proteins from a key palm oil pollinating weevil, <i>Elaeidobius kamerunicus</i></p> <p>Mr. Nabeel Muneim Malaysian Palm Oil Board</p>				

# KEYNOTE 1



## Beyond 2021: Building sustainable science

Raha Abdul Rahim<sup>1,2</sup>

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Economic viability, environmental protection and social equity have been identified as the three pillars of sustainability. Science is critical to tackle complex challenges for humanity such as the impacts of climate change, biodiversity loss, food security, pollution and poverty reduction; as it lays the foundation for new approaches and solutions. How can science best fulfil these commitments? How can we create dynamic connections between knowledge and action? Sustainability science promotes cross-disciplinary approaches to advance the understanding of human-environment interactions and systems, and how these interactions affect the challenge of sustainability (Nada Al-Nashif, UNESCO's Assistant Director-General for Social and Human Sciences).

A fundamental challenge facing science educators at the Higher Education Institutions is how to develop and support the implementation of project-based, technology-rich science curriculum and demand-driven research connectivity that is consistent with international calls for a "new approach" to science education. In this presentation, I will highlight some initiatives promoted by relevant ministries to elevate the importance of interrelationship and interdisciplinary factors and taking into account these factors when seeking solution strategies. The role of biotechnology and molecular biology in advocating sustainable science will also be discussed. Lastly, we will address the need of educators to ingrain the right values and technical know-hows to the future generation.

**Keywords:** Sustainable science, interdisciplinary and cross-disciplinary, demand-driven research.

## KEYNOTE 2



### The Triumphs and Vicissitudes of Biotechnologies on Malaria Control

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The disease we now call malaria had been recorded by all civilisations throughout human history. Then as now, malaria significantly impacts development and exacts a severe public health burden. A confluence of biotechnological advances in the 1970's has propelled a search for a vaccine against the highly adaptable and diverse parasites, which still remains elusive. Nonetheless, the elaboration of novel advanced biotechnological tools over the recent years are giving researchers the opportunity to probe hitherto inaccessible mechanisms of the parasites' life cycle. In this lecture, I wish to present an overview of the strategies adopted for malaria research and for control programmes, and to discuss how such biotechnological advances contributed to shape these strategies, and the consequences that this has had in the past and could potentially have in future.

**Keywords:** Biotechnology, History, Malaria, Parasitology, Research

## It's not in our DNA: Non-transformative gene silencing in orchids

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**Introduction:** The uncovering of the mechanism of RNA-mediated gene silencing led to a precise technology for application in crop protection and targeted modifications in plants. RNA silencing through the direct application of double stranded RNA (dsRNA), a non-transgenic approach using ectopically applied dsRNA, or RNA sprays, has been demonstrated to provide effective crop protection and to be a powerful and rapid reverse genetic tool to study gene function and for validation of target sequences for gene silencing. **Methods:** dsRNAs targeting orchid virus and orchid endogenous mRNAs were synthesised in an RNase deficient strain of *E. coli*, and used for RNA silencing by direct application of dsRNA to orchid plants and flowers. **Results:** Application of dsRNA based on the coat protein of Cymbidium mosaic virus (CymMV), a major pathogen affecting commercial orchid production operations and hobbyists, effectively protected tissue cultured orchid plantlets from the virus and so has potential for use to protect plantlets during transplantation and pruning. In separate experiments, the use of dsRNA to silence endogenous plant genes to determine gene function and for potential use in the modification of flower phenotype were explored. Experiments with dsRNAs based on R2R3 MYB transcription factor mRNA sequences from orchids showed that these were able to alter phenotypes of orchid flower cell shape and anthocyanin content. **Conclusion:** Non-transformative dsRNA-mediated gene silencing provides a useful tool for crop protection and for fundamental studies of gene function without the expense, time or need to introduce new DNA or alter plant DNA.

**Keywords:** dsRNA, flower, gene silencing, MYB, orchid

## PLENARY 2

### Functional nanodomains of cardiomyocytes in heart failure

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**Introduction:** Heart failure (HF) is a major contributor to the cardiovascular disease burden and impacts significantly to global health expenditure. A host of pathological remodelling changes are consistently observed in HF patients; that includes the alterations in beta adrenergic receptors ( $\beta$ ARs), ion channels, in particular L-type calcium channels (LTCCs),  $\text{Ca}^{2+}$  handling proteins, and proteins mediating cell-cell coupling. In HF, a progressive loss of T-tubules results in molecular remodelling and in the development of triggers of arrhythmia (early and delayed after-depolarizations, EADs and DADs). In cardiac myocytes, receptors are coupled to effector molecules and ion channels in nanodomains. **Methods:** Using novel cutting edge methodology including scanning ion conductance microscopy (SICM), scanning patch clamp technique, SICM/FRET combination we uniquely resolved surface topography of the live myocyte at nanoscale and then activate adrenoceptors in precise locations identified, with either imaging of cAMP changes in the vicinity or ion channel recording. **Results:** Particularly we focused on the T-tubules and the caveolae and on the relationship between  $\beta$ -Adrenoceptors and L-type  $\text{Ca}^{2+}$  channels. We studied how the disturbance of these microdomains affects cell function in ventricular myocytes from a rat model of infarct and from human patients with several myopathies. Further, we attempted to restore the normality of nanodomain organisation to indirectly influence the calcium channels and improve contraction. **Conclusion:** This work gives an understanding of how signalling operates at nanoscale resolution in living cells. This will translate to new methods of restoring proper organisation of nanodomains for treatment of failing hearts.

**Keywords:** Cardiomyocytes, heart failure, ion channels, beta-adrenoceptors

# PLENARY 3

## Mechanism of Functional Homeostasis in Bacterial Complex System

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**Introduction:** Controlling microbial communities is vital for sustainable agriculture, human health care, wastewater treatment and bioremediation. However, we do not know yet why/how engineered microbial communities and whole microbial systems have been maintained functionally. **Methods:** Synthetic bacterial communities (SBCs) were constructed with phenol-degrading bacteria and phenol as sole carbon source under chemostat conditions to unveil the mechanism of functional homeostasis because microbial ecosystems are too complex to analyze the mechanism. While some SBCs collapsed, an SBC maintained phenol degrading activity although phenol-supply stoppage was set in several times. Population dynamics of bacterial strains were monitored by real time-quantitative PCR (qPCR) targeting gene encoding large subunit of phenol hydroxylase in the SBC. Kinetic parameters for phenol of the SBC were tracked by an oxygen electrode. Transcriptional levels of phenol hydroxylase and catechol dioxygenase of bacterial strains were analyzed by reverse transcription-qPCR (RT-qPCR). **Results:** The kinetic parameters for phenol of the SBC changed before and after the phenol-supply stoppage, which suggests a change in functional roles of strains in the SBC. The RT-qPCR analyses revealed that all strains shared phenol and survived independently before the phenol-supply stoppage. After the stoppage, a strain would incur the cost for degradation of phenol and catechol, whereas other strains seemed to be cheaters using metabolites, indicating the development of the metabolic network. **Conclusion:** These results indicated that it is important for the management and redesign of microbial communities to understand the flexibility of metabolism of bacterial communities.

**Keywords:** Microbial ecosystem, Complex system, Bacterial community, Homeostasis

## PLENARY 4

### Active Edible Coatings/Films for Perishable Foods Preservation: Potential, Present Limits and Future Prospects Illustrated by some Case Studies »

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Besides limiting drying and oxidation of the superficial zones of perishable foods due to their gas barriers properties, edible coatings/films can be suitable carriers of antimicrobial and/or antioxidant agents. The possibilities to add antimicrobial and/or antioxidant biomolecules (e. g. lysozyme, nisin, plant phenolics...) and even, although more rarely, to add living bioprotective lactic acid bacteria in coatings/films have thus been considered in order to extend the shelf life and/or improve the safety of perishable foods. The potential advantage of using active coatings/films to deliver such agents over their direct spraying on the surface of perishable foods lies in their capacity to improve the stability of active agents before their application and/or to control their release from coatings/films to the superficial zone of foods following their application. In this context, the formulation of coatings/film-forming suspensions can be defined to design edible coatings/films matrices with a structure favoring (i) the preservation of the activity of active biomolecules or of the viability and metabolic activity of bioprotective lactic acid bacteria and/or (ii) the controlled release of active molecules/metabolites. This will be illustrated by two case-studies:

- the possibility to change the properties of gelatin films and the kinetics of release of lysozyme added in these films by enzymatic crosslinking with microbial transglutaminase
- the possibilities offered by alginate-caseinate aqueous two-phase systems to prepare coatings with a microstructure maintaining both the viability and antagonistic activity against *Listeria* spp. strains of bioprotective lactic acid bacteria.

**Keywords:** edible coatings, edible films, antimicrobial activity, food preservation, controlled release

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## PLENARY 5

### Chitosan hydrogel biomaterial from fish scales for topical wound healing application

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It was estimated that the fish processing industry generates between 18 and 30 million tons of fish wastes annually, of which 4% are fish scales. Hence a study was conducted to extract chitin from tilapia fish scales for chitosan hydrogel from the sequence of chemical processes involving demineralization, deproteinization, and deacetylation. The product was applied as wound healing gel and evaluated using full-thickness wounded skin with 8 mm diameter in Swiss albino mice model. Eighteen clinically healthy mice were divided into two groups; Group 1 as Control Group without any treatment, and Group 2 as Treatment Group that was applied with chitosan hydrogel treatment once daily. Observation and measurement of wound contraction were recorded daily for 21 days. Three mice from each group were euthanized, and the skin was dissected for histology evaluation of the wounded skin on days 7, 14, and 21 post wounding. The wounded skins treated with chitosan hydrogel showed better reconstruction healing than the control group. They generally attained full wound closure and over 95% of collagen density within two weeks post wounding. The absence of pathological abnormalities in the organs obtained by necropsy indicates its biocompatibility with no side effects to the hosts. All parameters observed were significant ( $p < 0.05$ ) in comparison to the control group. The accelerated wound healing shown with higher collagen deposition, short epithelialization, and rapid wound closure suggests a significant positive effect of chitosan hydrogel to be an effective wound healing agent.

**Keywords:** fish scales, chitin, chitosan hydrogel, Swiss albino mice, wound healing



## PLENARY 6

### Understanding Alzheimer's disease through yeast studies

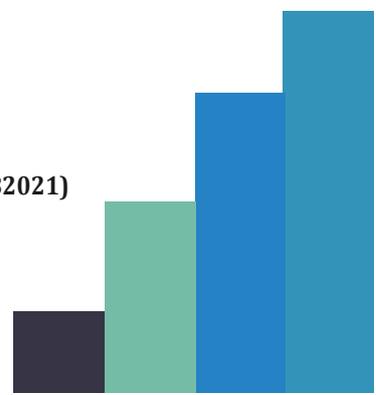
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**Introduction:** Alzheimer's disease (AD), the leading cause of dementia, is age-related and associated with a neurotoxic 42 amino acid peptide, amyloid beta ( $A\beta$ ) that is a proteolytic product of a natural human protein called APP.  $A\beta$  levels increase with age and are observed in AD patients as brain plaque composed of amyloid fibrils. **Methods:** Yeast, the simplest eukaryote, can be used to study  $A\beta$ , to explore ways to remove it and to find agents that may increase or reduce its toxicity. Yeast were engineered to express native  $A\beta$ , or  $A\beta$  fused to green fluorescent protein (GFP) to aid its visualisation. **Results:**  $A\beta$  oligomers, but not fibrils are toxic to yeast (and neuronal cells). Simvastatin, the common drug prescribed for lowering cholesterol levels, is the best drug to prevent AD (and Parkinson's disease). In yeast simvastatin, reduces  $A\beta$  levels, suggesting it may act through increasing a protein clearance mechanism. Some compounds like tyramine and aluminium increase the toxicity of  $A\beta$  possibly accounting for the sporadic appearance of AD. **Conclusion:** Yeast represents a convenient model for the development and testing of compounds that may have utility in prevention of Alzheimer's disease.

**Keywords:** Alzheimer's disease, amyloid beta, model organism, toxic peptide, yeast biotechnology



# TECHNICAL TALK 1

## Large Scale 3D Bioreactor Technology: Linear Scale Up of Mesenchymal Stromal Cell Expansion with TideXcell™ System

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**Introduction:** In recent years, cell therapies have received much attention in the field of regenerative medicine and potential treatments, especially mesenchymal stromal cells (MSC) – derived therapies. Commercial bioreactors are expected to generate 400- 500B cells per annum to meet high dosages requirements. Esco Aster utilizes Tide Motion-based platforms for the expansion of anchorage-dependent cells to achieve sufficient therapeutic quantities cellular products. **Methods:** Here, we performed upstream process development in a series of Tide Motion bioreactors that offer a culture environment with high dissolved oxygen and low shear stress to cells. P4 bone marrow MSCs were recovered in planar cultures, seeded into a small benchtop bioreactor, the CelCradle, before harvesting and inoculation to the TideXcell™ bioreactor with 1L packed bed volume. Cells were cultured for 7 days in TideXcell before harvesting with the automated, closed TideXcell™ Harvesting System (TXLHS). Critical quality attributes (identity, purity, potency and safety) of the final cell product were inspected. **Results:** Within a culture period of 15 days, MSCs expanded by 9.6 doubling population levels, achieving 2 billion cells from an initial cell count of 2.5 million cells. With the TXLHS, 97.7% harvesting efficiency was achieved with a cell viability of 93.8%. The harvested cells demonstrated trilineage differentiation and MSC phenotypes as per ISCT criteria. T-cell suppression assay and IDO quantification also demonstrated intact immunomodulatory capabilities of the expanded MSCs. **Conclusion:** Overall, we present the scale up process of MSCs via the Tide Motion platform. Furthermore, the quality of cells are assessed to ensure high therapeutic quantities of MSCs for clinical and commercialization.

**Keywords:** Mesenchymal stromal cells, Tide Motion bioreactors, Cell therapy, Upstream and downstream processing

# TECHNICAL TALK 2

## PacBio HiFi Sequencing: Sustainable Technology for Sustainable Science

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Recent improvements in sequencing chemistry and instrument performance combine to create a new PacBio data type of highly accurate long reads – HiFi reads. These reads have the accuracy comparable to short read NGS but with 50-100 times longer read length. This technical improvement has resulted in overwhelming enthusiasm from the scientific community. HiFi has become the go-to technology for genomic research as evidenced by adoption by many high profile international projects. In this presentation I will highlight what advancement this technology has rendered in medicinal, agricultural, industrial, environmental and microbial areas.

**Keywords:** highly accurate long-read sequencing, sequencing, genomics, HiFi

# TECHNICAL TALK 3

## Primer Dimers? Late Ct? Poor Detection Limit? Say Goodbye To These Problems With PCR Biosystems!

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**Introduction:** With the global spotlight on qPCR as a result of the COVID-19 pandemic, the fundamentals of dye-based qPCR will be explored with one of the signature products from PCR Biosystems, qPCRBIO SyGreen Mix. The combination of a strategically engineered Taq DNA Polymerase with antibody-mediated hot start technology significantly reduces the formation of primer dimers as well as non-specific amplification. Our buffer chemistry has undergone stringent screening of the various concentrations of magnesium, enhancers and additives to determine the optimal amount of each component that will best enhance our enzyme. The results of our formulation show early Ct values which demonstrates the ability of our enzyme to extend at a rapid rate. Our data also shows how our polymerase is market-leading with its sensitivity. Overall, our mix is both robust and reliable for a range of applications including absolute quantification, high throughput qPCR, relative gene expression analysis, and detection from a low copy number of targets.

## Moving GenomeSelect™ to the Field – Highs and Lows

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**Introduction:** After seven years of research, starting from a single oil palm genome sequence, Sime Darby Plantation planted the first commercial-scale field with GenomeSelect™ palms in 2016. Since then, we have observed commercial yield data and developed ways to scale up planting to satisfy all seed requirements in Sime Darby Plantation. This talk will present the highs and lows of the journey to realising commercial value from genomics tools in this very important crop. **Methods:** Following 2<sup>nd</sup> gen sequencing of a reference oil palm, GWAS methods were applied to test populations of commercial palms in order to develop genomic selection models that can be applied to commercial seed production. The first planting was split into two locations; coastal and inland to determine possible environment effects. **Results:** Coastal yield of GenomeSelect™ palms has been encouraging while inland yields indicate significant impact of rainfall and water supply on yields. Controlled trials confirm the positive impact of genomic selection models, which have now been applied in parental selection for commercial seed scale up. **Conclusion:** the application of genomic selection techniques for commercial oil palm seed production has shown significant promise and will certainly be improved based on the large amount of data now available.

**Keywords:** Oil palm, genomic selection, crop improvement

# Understanding the Endometrium: the “Black Box of Implantation”

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Miscarriage is the commonest complication of pregnancy. Most miscarriages happen in the first 12 weeks of pregnancy. In recent years, evidence was found indicating that endometrial decidualization represents an ingenious strategy to meet this challenge. Decidualization (a specific phase during days 20-27 menstrual cycle) is characterized by transformation of endometrial fibroblasts into specialized epithelioid cells. Importantly, decidualization is not an all-or-nothing phenomenon. Instead, decidualizing endometrial cells transit through a distinct functional phenotype upon transformation into decidual cells. This transitional pathway is characterized initially by an acute pro-inflammatory response, lasting several days. Endometrial stromal cells release ‘alarmins’, like IL-33, which is a potent activator of the innate immune system and has emerged as an important driver of this transient inflammatory process. Acquisition of a mature decidual phenotype curtails the inflammatory response through induction of anti-inflammatory soluble decoy receptors and increased local cortisol production. Decidual factors such as LEFTY2 contribute to the active closure of the ‘window of receptivity’. Importantly, new evidence points to decidual cells being exquisitely responsive to embryo signals, especially trypsin-like proteases, and engage in active rejection by triggering menstruation-like shedding mediated by a decidual stress response. Taken together, these observations illustrate how the decidualization pathway contributes to the functional transition of the endometrium from a nonreceptive (early-secretory phase) to a receptive (mid-secretory phase) and then a selective (late-secretory phase) state. A greater understanding of the etiology of implantation is pivotal to improving reproductive outcomes, but human studies are hampered by ethical and technical challenges. However, a combination of informative animal models and novel in vitro systems is beginning to throw new light on what has previously been considered the implantation “black box”.

**Keywords:** Miscarriage, Endometrial decidualization, endometrial fibroblast, reproductive outcome.

## Application of Antarctic Microorganisms in Diesel Bioremediation Process

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Antarctica offers perennially cold, sub-zero temperatures due to the extreme climate of the continent. The presence of recalcitrant petrogenic hydrocarbons in Antarctica is generally associated with extreme conditions that impede the natural attenuation of hydrocarbon components. These pollutants have caused major perturbations in the Antarctic ecosystem, suggesting that conventional bioremediation approaches are largely ineffective at present. The purpose of this study is to evaluate the hydrocarbon-degrading ability of marine and soil bacteria consortia to assimilate diesel fuel as the sole carbon source, using statistical optimisation of growth conditions and diesel degradation. Concurrently, the obtained data were implemented in a scale-up bioreactor design study, with additional investigation on the effects of soil washing duration, agitation speed, soil to water ratio, surfactant concentration and aeration mode. In this study, the bacterial community isolated from soil successfully degraded up to 95% of a 1.75% v/v diesel, while the marine bacterial community have ability to degrade up to 80% of 1% v/v diesel. A scale-up study using the fabricated soil washer and bioreactor *in situ* Antarctic settings showed that optimised conditions for soil washing were at 40 rpm soil agitation, 3 h washing time, 1:5 soil to water ratio and 1% w/v SDS. The data obtained suggest that the Antarctic bacterial community has a potential for use in low-temperature bioremediation applications of diesel pollution.

**Keywords:** Antarctic, Bioremediation, Diesel

## Omics Technologies: - Elucidating Relationships between Microbes and Cancer and Future Applications

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Cancer is known as a disorder with multi-factorial causes. Throughout the last few decades, different microbes have been shown to have causal links to carcinogenesis. Some microbes are direct carcinogens through the expression of viral oncogenes whereas others are indirect carcinogens through toxins accumulation or chronic inflammation. Through next-generation sequencing technologies and transcriptomic studies, researchers were able to pinpoint the specific genes whose aberrant expression leads to multiple mutations. Through a combination of NGS, gene knockdowns and immunofluorescence studies, we found that HPV infection could induce APOBEC3B upregulation which in turn leads to mutations in various genes in breast carcinoma. We postulate that HPV infection and estrogen receptor expression together with APOBEC3B exists in a tri-partite relationship which promotes early-stage breast carcinogenesis. Recently, the gut microbiota has been shown to affect local immunity, systemic immunity, as well as microbe-specific immune programming, and dysbiosis of microbiota is associated to various cancers. An important achievement in cancer treatment in the last decade has been the introduction of immune checkpoint blockade or (ICB) immunotherapy, including anti-CTLA-4 and anti-PD-1/PD-L1 inhibitor drugs. Interestingly, but not surprisingly, gut microbes were found to be able to profoundly influence the potency of immunotherapy and some chemotherapies with immunestimulatory functions. Using NGS, certain species of gut microbiota were shown to be associated with poor response to cancer immunotherapy, while other species were related to good prognosis. These findings have important implications for not only cancer immunotherapy but also development of microbiota-based therapies as an adjunctive treatment in the future.

**Keywords:** Cancer, Microbiota, Immunotherapy, NGS, Omic Technologies

## Single Cell Proteomic Analysis of COVID-19 Patient Samples by Mass Cytometry

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**Introduction:** The devastating outbreak of SARS-CoV2 and the associated COVID-19 has had a severe impact on the global community. While recent advances in vaccination have given some hope of respite the proven ability of the virus to mutate and potentially generate vaccine resistant strains indicates that there can be no relaxation of our urgent efforts to better understand the effects of this disease. A critical part of this effort is to understand the changes to the immune system of infected patients since both viral clearance and most symptoms of the disease are mediated by the immune system. Recent advances in single cell technologies, such as mass cytometry (also known as CyTOF) have revealed high levels of heterogeneity among immune cells. **Methods:** Mass cytometry was used to assess the single cell proteome of millions of cells from the blood of patients with COVID-19. **Results:** Wide ranging changes to a variety of cell populations occur. Simultaneous assessment of changes to both common populations and such as classical monocytes, and rare sub-populations of FOXP3 expressing regulatory T-cells and T-follicular helper cells was observed **Conclusion:** Simultaneous assessment of wide ranging cell populations may indicate how they interact during COVID-19 and suggest that differences between regulatory T-cell subsets among moderate, severe, and critical patient groups may be a factor in pathogenesis.

**Keywords:** Mass cytometry, Immunology, Regulatory T-cells, COVID-19.

## Beneficial Endophytic Actinomycetes

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**Introduction:** Endophytic actinomycetes residing *in planta* provide plant growth promoting (PGP) benefit by enhancement of growth and protection plants from abiotic and biotic stresses. **Methods:** Endophytic actinomycetes were isolated from agricultural, economical, and medicinal plants in Thailand. Their PGP traits were determined and demonstrated to promote growth and stress tolerance in crops. **Results:** A new genus and seven new species of endophytic actinomycetes were validated. Novel bioactive compounds were identified. Many of them possess PGP traits including phytohormone and siderophore secretion, phosphate solubilisation, ACC-deaminase, chitinase, and anti-microbial production. These traits were proven to promote plant growth, protect plants from phytopathogens, and increase plant stress tolerance *in planta*. Molecular plant-actinomycete interaction using transcriptome analysis towards salinity stress have been demonstrated. **Conclusion:** Extensive understanding of the interaction of endophytic actinomycetes with plants will sustainably enable application of these endophytes as added value biofertilizer and biocontrol agents for green agriculture in the future.

**Keywords:** actinomycete, endophyte, new species, PGP, stress

## Attenuation of *Macrobrachium rosenbergii* Nodavirus through Codon-Deoptimization of Virus Functional Genome

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**Introduction:** White tail disease (WTD) in the giant freshwater prawn, *Macrobrachium rosenbergii* has been affecting the aquaculture production of the species in several countries, which include Taiwan, China, India, Thailand, Australia and Malaysia. WTD affects larval, post-larval and early juvenile stages of *M. rosenbergii*, which could cause up to 100% mortality of the infected prawn. The disease is caused by *Macrobrachium rosenbergii* nodavirus (MrNV), a non-enveloped virus containing bipartite positive sense single stranded RNA genome. To-date, there is no effective prophylactic and therapeutic agent available to control its outbreak. **Methods:** This study evaluated the attenuation of MrNV through genome-wide multiple point mutation, which deoptimized the codon usage of the MrNV RNA2. A total number of 125 synonymous codon substitutions were introduced into the viral RNA2. Viral genes (wild-type RNA1, RNA2 and mutant RNA2) were *de novo* synthesized and harboured by pUC57 plasmid. Viral genes were expressed through *in vitro* transcription using T7 promoter, which were subsequently transfected into confluent Sf9 cells. Then, the pathogenicity of these infectious clones in the transfected cells were compared. **Results:** Cytopathogenic effects recorded in Sf9 cells transfected with the wild-type MrNV clones include cytoplasmic swelling and aggregation of the infected cells into clumps of various sizes. While cells transfected with mutant MrNV clones observed insignificant cytoplasmic swelling and aggregation. **Conclusion:** Results indicated that codon-deoptimization of viral RNA2 attenuated the MrNV. Further analysis is currently being conducted to evaluate its potential as live-attenuated viral vaccine against WTD in *M. rosenbergii*.

**Keywords:** *Macrobrachium rosenbergii* nodavirus, reverse genetics, viral vaccine, codon deoptimization

## Transcriptomic Analysis of *Chlorella sorokiniana* for Pigment Production under Moderate Light Intensity

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**Introduction:** *Chlorella* can produce an unusually wide range of metabolites under various nutrient availability, carbon source, and light availability. Manipulation of light intensity could induce the formation of secondary metabolites such as pigments, and carotenoids in *Chlorella*. Besides, other metabolic pathways also affected; such as lipids, starch, carbohydrate and isoprenoids biosynthesis pathways. This study was carried out to gain knowledge about how these biosynthetic pathways could be regulated in response to moderate light intensity. **Methods:** De Novo transcriptome profiling of *C. sorokiniana* growth under moderate light intensity was conducted to study the effect of physiological condition towards genetic changes. **Results:** The moderate light intensity used to induce pigment formation caused a total of 937 genes were upregulated, and 1124 genes were downregulated. Genes that were upregulated involved in carotenoids production (specifically lutein biosynthesis), fatty acid biosynthesis, TAG accumulation, and the majority of the carbon fixation pathways. Conversely, starch biosynthesis, sucrose biosynthesis, and isoprenoid biosynthesis were downregulated. **Conclusion:** Novel insights into the pathways that link the enhanced production of pigments in *C. sorokiniana* grown under moderate light intensity is presented.

**Keywords:** *Chlorella sorokiniana*, de-novo transcriptome profiling, metabolic pathways, pigments

## Growth Promotion of Sweet Potato by IAA-Producing Rhizobacteria

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**Introduction:** Plant growth promoting rhizobacteria (PGPR) are beneficial bacteria that living on the surface of roots, providing plant growth regulators or phytohormone such as indole-3-acetic acid to improve plants growth and fixed nitrogen to plants. This could increase crop productivity and lower N fertiliser input this study was conducted to determine the effect of IAA-producing rhizobacteria isolates on growth of sweetpotato.

**Methods:** A pot experiment was conducted in the glasshouse of Universiti Putra Malaysia. Vine cuttings of sweet potato was grown in two kg of sterilized sandy soil The bacterial treatments consisted of: i) Control, ii) SP1 iii) SP2 and iv) *Azospirillum* sp. SP7. An inoculum concentration of  $10^9$  cfu/ml was applied into the respective pots. Each pot was inoculated at planting and two weeks after planting with five ml inoculum/pot/application. Plants were harvested at 30 days after planting. **Results:** The results showed that inoculation with IAA producing rhizobacteria significantly improved the early growth of sweet potato plants. Plants inoculation with SP1 and SP2 increased growth (tops and roots), nutrient uptake (N, P, K, Ca and Mg) of the sweet potato plants. Bacterial population and IAA concentration in soil. **Conclusion:** This study indicated that the bacterial strains have the potential plant growth promoters and may be used as bioenhancers.

**Keywords:** Sweet potato, Plant growth promoting rhizobacteria, Indole-3-acetic acid, *Azospirillum* sp., Bioenhancers

## Potential Muscle Activity Disturbance in *Penaeus monodon* during Acute Hepatopancreatic Necrosis Disease (AHPND) Infection: Inference through Gene expression, Calcium concentration, and MicroRNA

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**Introduction:** Diseases have brought a huge impact in global shrimp aquaculture which leads to major economic losses. Acute Hepatopancreatic Necrosis Disease (AHPND) is new strain of *Vibrio parahaemolyticus* bacteria (*VpAHPND*) that would colonise in shrimp gut and release the toxins to damage the hepatopancreas. This disease can also cause the shrimp mortality with 35 days and hence, it will cause devastating losses in global shrimp production. However, no studies have investigated whether this disease will cause any shrimp muscle damage or functioning. **Method:** In our study, we challenged *Penaeus monodon* shrimp with *VpAHPND* bacteria using an immersion method. Dystrophin gene was chosen as regulatory gene for determine the muscle integrity and was quantified using qRT-PCR. Determination of calcium concentration and btamiR-4286 and dre-miR-107b miRNAs expression were conducted to verify the expression of dystrophin gene. **Results:** The results showed that the dystrophin gene was highly expressed during AHPND infection when lowest calcium concentration was detected at 6-hour post-infection (hpi). While the highest calcium concentration was determined at 36 hpi, was verified by higher bta-miR-4286 miRNA expression and lower dre-miR-107b miRNA expression in *VpAHPND*-infected samples compared to uninfected samples. **Conclusion:** Upregulated dystrophin gene expression led to suggestion that AHPND is not only damage the shrimp gut and hepatopancreas, but also affect the shrimp muscle functioning. This was supported by calcium concentration and miRNA expression in AHPND infected *P. monodon* shrimp samples. Therefore, we deduced a strong interactive relationship between dystrophin gene expression, calcium concentration and miRNA expression in shrimp muscle tissue triggered by *VpAHPND* bacterium.

**Keywords:** Acute Hepatopancreatic Necrosis Disease (AHPND), Dystrophin gene, Calcium concentration, MicroRNAs, Apoptosis

## GCMS-based Metabolomics and Effect of Fatty Acids Dietary Supplementation on the Survival and Innate Immunity Response of Hybrid Grouper against Vibriosis

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**Introduction:** Grouper is one of the high market value marine fish that well received in Malaysia. However, due to it easy exposure to infectious diseases such as bacteria, the mass mortality of this fish culture poses a major problem in aquaculture industry. **Methods:** Metabolite profiles from survived control and challenged fingerlings against *Vibrio vulnificus* infection were determined by gas chromatography-mass spectrometry (GCMS). Based on GCMS analysis, several metabolites from fatty acid group showed significant roles regarding differential metabolites between the control and challenged fingerlings. Hence, the fish feed dietary was prepared with the addition of these fatty acids to determine the effectiveness of fatty acid as an immunostimulants on survival, growth, and innate immune response of hybrid grouper (*Epinephelus fuscoguttatus* x *Epinephelus lanceolatus*) fingerlings against vibriosis infection. **Results:** Several metabolites from fatty acid group such as oleic acid, stearic acid, palmitic acid and behenic acid had been identified to be highly abundant in survived *E. fuscoguttatus* during the preliminary experimental infection against *V. vulnificus*. After six weeks of feeding experiment, fingerlings fed with oleic acid showed the highest specific growth rate (SGR) compared to other dietary. Moreover, after challenged with *V. vulnificus*, fingerlings with oleic acid dietary observed the highest survival rate (60.7%) as compared to control (42.9%) ( $p < 0.05$ ). Whereas, in immunology assay; lysozyme activity, respiratory burst activity and phagocytic activity of fingerlings fed with oleic acid showed highly significant differences ( $p < 0.05$ ) compared to fingerlings fed with control dietary. **Conclusion:** The finding suggested that oleic acid as modulator used in fish dietary elevated the survival and innate immune response of hybrid grouper which give a potent effect in fish disease resistant.

**Keywords:** fatty acid, metabolites, immune response, hybrid grouper, vibriosis

## CRISPR-Mediated Generation of *In Vitro* Breast Cancer Models to Study P53 Gain of Function Mutation

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**Introduction:** Breast cancer (BC) is the second leading cause of cancer-related deaths among women. Aggressive BC is commonly linked to P53 gene mutations. The predominant P53 mutation is missense that can result in either loss of functions or acquisition of novel pro-oncogenic functions (gain-of-function mutation). Establishing robust in vitro models to interrogate mutated P53 molecular properties and functions is essential. In this study, we embarked on generating three different in-vitro BC models by using CRISPR-mediated gene editing tool. **Methods:** Using the T47D BC cell line that carries the L194F gain-of-function mutation, we targeted P53 in the pooled cells population by stably expressing the Cas9 and P53-targeting sgRNA using the lentiviral transduction approach. The P53 targeting efficiency was assessed using Western blotting. The second model was generated by transiently transfecting the T47D cells with plasmid that encodes for the Cas9 and P53-targeting sgRNA, followed by single cell isolation, clonal expansion, and screening for complete P53 knockout using Western blotting. For the third model, we employed new CRISPR variant called Prime Editing to revert T47D L194F mutation. **Results/Conclusions:** We have successfully established the first and second in-vitro BC models that can be subsequently utilized to study P53 gain-of-function mutations molecular properties and roles in BC. Nonetheless, for the 3<sup>rd</sup> model, we are still screening for edited single cell-derived clones. We found that the efficiency of Prime Editing technology is very low. Given the fact that this technology was just recently developed, there are definitely plenty of rooms for improvisations and further developments.

**Keywords:** Breast cancer, Gene editing, Mutp53, CRISPR, Prime Editing

## Development and Evaluation of 1'-Acetoxychavicol Acetate-Loaded Nanostructured Lipid Carrier for Prostate Cancer Therapy

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**Introduction:** Previous studies have established 1'-acetoxychavicol acetate (ACA), a phytoconstituent extracted from the rhizomes of *Alpinia conchigera* Griff (Zingiberaceae), as an anti-cancer compound with cytotoxic properties on many cancer types. ACA has been demonstrated to induce apoptosis-mediated cell death by deregulation of the NF- $\kappa$ B signalling pathway on cancer cells, while minimally affecting normal cells. However, ACA is a hydrophobic ester with poor rate of dispersion, lack of bioavailability and non-specific tumour targeting *in vivo*. **Methods:** To overcome these problems, a nanostructured lipid carrier (NLC) system was formulated to encapsulate ACA and improve the latter's aqueous solubility. In addition, to encourage targeted delivery towards tumours, the NLC was modified with AMD3100 octahydrochloride, an antagonist of the CXCR4 receptor which is overexpressed on many cancer cell lines. **Results:** Formulation and optimization of the NLC has availed nanoparticles of ideal physico-chemical properties. *In vitro* studies of the NLC on PC-3 prostate cancer cells have demonstrated time-based cellular uptake in addition to significant cytotoxicity, anti-migration and anti-invasion properties. Furthermore, the formulations have exhibited significant anti-tumour efficacy in nude athymic (*Nu/Nu*) mice models with minimal physiological and toxic effects on the animals. Post-*in vivo* immunohistochemistry analysis and cytokine quantification provided evidence that the NLCs downregulated NF- $\kappa$ B related tumour markers and pro-inflammatory cytokines. **Conclusion:** This NLC system was found to have great potential in promoting the anti-tumour effects of ACA in prostate cancer therapy and can possibly be translated to other forms of cancer.

**Keywords:** nanostructured lipid carrier; 1'-acetoxychavicol acetate; AMD3100; targeted delivery; prostate cancer

## Tocotrienol-Rich Fraction Lowers the Ratio of Phospho NF- $\kappa$ B to NF- $\kappa$ B In Retinal Tissue of Diabetic Rats

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**Background and Aim:** Diabetic retinopathy (DR) is the second commonest microvascular complication in diabetes mellitus. It is characterized by chronic inflammation associated with increased transcription factor, nuclear factor kappa B (NF- $\kappa$ B), expression. Palm oil-derived tocotrienol-rich fraction (TRF), a potent antioxidant and anti-inflammatory substance, may provide protection against DR development. Therefore, we investigated the effect of TRF on retinal NF- $\kappa$ B and phospho-NF- $\kappa$ B expression in rats with streptozotocin (STZ)-induced DR. **Methodology:** Sprague-Dawley rats weighing 200-250 grams were grouped into normal control rats (NC) and diabetic rats. NC was intraperitoneally injected with citrate buffer, whereas diabetic rats received intraperitoneally streptozotocin (55 mg/kg body weight). STZ-treated rats with blood glucose of more than 16 mmol/L were considered diabetic. Diabetic rats were further subgrouped into diabetic-control (DC) and diabetic-treated (DT) groups. N and DC group received vehicle treatment, whereas DT received TRF treatment (100 mg/kg body weight) via oral gavage daily for 12 weeks. At the end of experimental period, rats were euthanized, and retinal tissues were collected for measurement of NF- $\kappa$ B p65 and phospho-NF- $\kappa$ B p65 (Ser536) using enzyme-linked immunosorbent assay (ELISA). **Results:** Greater phospho-NF- $\kappa$ B and ratio of phospho- to total NF- $\kappa$ B were detected in DC compared to NC (1.85-fold,  $p < 0.001$  and 1.58-fold,  $p < 0.05$  respectively), whereas lower expression of the same parameters was observed in DT compared to DC (1.65-fold,  $p < 0.01$  and 1.57-fold,  $p < 0.05$  respectively). Total NF- $\kappa$ B expression was comparable in all groups. **Conclusion:** Oral TRF may provide protective effect against DR by reducing the activation of retinal transcription factor (NF- $\kappa$ B) in streptozotocin-induced diabetic rat.

**Keywords:** Diabetic Retinopathy, Tocotrienol-Rich Fraction, Streptozotocin, NF- $\kappa$ B and Inflammation.

## ***Plasmodium knowlesi* Duffy Binding Protein Alpha Region II (PkDBP $\alpha$ II) from Peninsular Malaysia and Malaysian Borneo Exhibit Different Immune Responses in Animal Models**

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**Introduction:** The *Plasmodium knowlesi* Duffy Binding Protein  $\alpha$  region II (PkDBP $\alpha$ II) from Peninsular Malaysia and Malaysian Borneo has been shown to occur as distinct haplotypes, and the predominant haplotypes from these geographical areas demonstrated differences in binding activity level to human erythrocytes in erythrocyte binding assays. This study aimed to determine the effect of genetic polymorphisms in PkDBP $\alpha$ II to immune responses in animal models. **Method:** The recombinant PkDBP $\alpha$ II (~45 kDa) of Peninsular Malaysia (PkDBP $\alpha$ II-H) and Malaysian Borneo (PkDBP $\alpha$ II-S) were used in mice and rabbit immunization. The profiles of cytokine IL-1ra, IL-2, IL-6, IL-10, tumour TNF- $\alpha$  and IFN- $\gamma$  in immunized mice spleen were determined via ELISA. Purified immunized rabbit sera were used to perform merozoite invasion inhibition assay. **Results:** The PkDBP $\alpha$ II-immunized mice sera of both groups showed high antibody titre and similar IgG subtype distribution pattern: IgG1 > IgG2b > IgG2a > IgG3 > IgG2c. Higher regulation of IL-1ra and IL-6 were observed in the PkDBP $\alpha$ II-H group, with IL-6 level significantly higher than PkDBP $\alpha$ II-S group ( $P \leq 0.05$ ). Merozoite inhibition assay using purified anti-PkDBP $\alpha$ II antibodies showed significant inhibition rate in the PkDBP $\alpha$ II-H group than PkDBP $\alpha$ II-S group ( $P \leq 0.05$ ). **Conclusion:** PkDBP $\alpha$ II has been shown to be immunogenic and the PkDBP $\alpha$ II haplotype from Peninsular Malaysia exhibited higher immune responses than the Malaysian Borneo haplotype, suggesting that polymorphisms in the PkDBP $\alpha$ II affect the level of immune response in the host.

**Keywords:** *Plasmodium knowlesi*, PkDBP $\alpha$ II protein, immunogenicity, genetic polymorphism

## ***In Silico*-SELEX Reveals PRDBDapt17 as the Potential Aptamer against Progesterone Receptor DNA Binding Domain**

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**Introduction:** Aptamers are single-stranded DNA or RNA oligonucleotides generated by SELEX that exhibit high binding affinity and specificity against a wide variety of target molecules based on their unique tertiary structural conformation. The tediousness and rigor associated with certain steps of the conventional SELEX intensify the efforts to adopt *in silico*-SELEX in developing DNA aptamers. That said, we report an *in silico* selection of DNA aptamer to the DNA binding domain of progesterone receptor (PR) using ssDNA sequences derived from human progesterone response elements (PREs). PRDBD plays a vital role in the progression of breast cancer, which makes it a promising diagnostic biomarker and potential therapeutic target. **Methods:** Sixty-four different near-native ssDNA analogs of the corresponding PRE sequences were subjected to secondary and tertiary structural determination. Docking of the ssDNA sequences was carried out against PRDBD using PatchDock. The sequence with the highest binding score was selected as the candidate and further subjected to *in vitro* validation using ELASA. **Results:** Among the candidates, we selected the ssDNA sequence (PRDBDapt17; 5'-AGAACAGCGTGTCT -3'), which showed the highest docking scores of 11334 as a promising PRDBD binding aptamer. The PRDBDapt17 revealed a higher binding affinity towards PRDBD in ELASA. **Conclusion:** In conclusion, PRDBDapt17 is identified as the potential aptamer using the *in silico*-based aptamer selection.

**Keywords:** *in silico*, aptamer, progesterone receptor DNA binding domain, docking, ELASA

## Ultrasensitive and Label-free Optical Nanobiosensor for miRNA Detection in Breast Cancer

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**Introduction:** Breast cancer accounts for 30% of all female cancers and 15% of all cancer-related mortalities. Early detection is known to improve the prognosis and overall survival-rate of breast cancer. Hence, extensive research has been focused on microRNAs (miRNAs) as diagnostic and prognostic biomarkers, for their regulatory role in post-transcriptional gene expression. In breast cancer patients, the expression of miRNA-155 is commonly upregulated as compared to healthy individuals. Herein, we present a nanobiosensor to detect miRNA-155, comprising hybridization chain reaction (HCR) and DNA-stabilized silver nanoclusters (AgNCs), that serve as an enzyme-free amplification strategy and label-free fluorescent detection probes, respectively. **Methods:** Under mild conditions, DNA probes were mixed with miRNA-155 to initiate HCR, followed by the addition of reduced silver salt to form fluorescent AgNCs. Gel electrophoresis was performed to validate the performance of HCR, and a spectrofluorometer was used to measure the fluorescence emission from AgNCs. **Results:** The HCR-AgNCs nanobiosensor showed high selectivity towards the miRNA-155, with capabilities to detect single-base mismatch. Furthermore, the HCR-AgNCs nanobiosensor displayed high sensitivity with a wide linear range between 100 fM and 10 nM, and a LOD of 7 fM. In real sample analysis, the nanobiosensor exhibited exceptional reproducibility and stability with human serum samples. **Conclusion:** In comparison to current breast cancer detectors, the HCR-AgNCs nanobiosensor displayed relatively better performance at a miniscule fraction of cost, effort and time required. Furthermore, the highly-responsive HCR-AgNCs nanobiosensor potentially offers a non-invasive and safe approach towards the clinical detection miRNA-155 and point-of-care early diagnosis of breast cancer.

**Keywords:** Biosensor, Breast Cancer, Hybridization Chain Reaction, MicroRNA, Silver Nanoclusters

## Bacterial Diversity Analysis in Mangrove Ecosystem of Johor Using Minion Sequencing

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**Introduction:** Mangrove sediments provide rich habitat for diverse bacterial population predominantly members of phyla Proteobacteria, Firmicutes and Actinobacteria. Actinobacteria are predominantly Gram-positive bacteria that make up largest bacterial phyla. Due to their adaptation to challenging habitats they produce abundant bioactive compounds like antibiotics, cytotoxins and enzymes. The increase in pollution of water bodies, emerging antibiotic resistance and loss of habitat makes it important to study bacterial diversity in less explored ecosystems of different geographical areas. Mangrove ecosystem in Johor has witnessed disturbance due to rapid development. Therefore, we sought to measure bacterial abundance, diversity using molecular approach. **Methods:** We sequenced bacterial 16S rRNA gene to identify taxonomical groups using Oxford Nanopore Technologies MinION sequencing. Samples were collected from Mangrove sediments from upstream and downstream from Sungai Melayu, Pulau Kukup locations. Samples were barcoded to allow multiplexing in the same sequencing run and sequencing data was analysed using EPI2ME software. **Results:** Recorded abundant Proteobacteria such as *Erythrobacter litoralis*, *Erythrobacter vulgaris*, *Sulfurovum aggregans*, *Paracoccus marcusii* and Actinobacteria such as *Ilumatobacter fluminis*, *Ilumatobacter nonamiensis* with variable diversity. *Bacteroidetes* like *Flavobacterium haorarii* was detected in less abundance. Upstream vs downstream analysis of bacterial diversity shows low Proteobacteria and high Actinobacteria in downstream suggesting influence of human activity, pollution in shaping the microbial flora. **Conclusion:** Human activity such as aquaculture, release of household wastewater and agricultural waste poses higher selection pressure and thus some Actinobacteria could have enriched due to their ability to produce bioactive compounds against xenobiotics but pose threat to their diversity.

**Keywords:** Actinobacteria, MinION-sequencing, mangrove sediments, water quality

## Eco-friendly Silver Nanoparticles (AgNPs) Fabricated by Green Synthesis Using Marine Polychaete, *Marphysa moribidii*

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**Introduction:** Silver nanoparticles (AgNPs) have received significant attention because of their antimicrobial activity. However, current methods are expensive and have detrimental effects on the environment. Biological methods e.g., using marine polychaete (*Marphysa moribidii*), which are abundantly found in Malaysian seashore may offer the alternative solution. Therefore, we aim to synthesize and optimize AgNPs production from the polychaete and measure their antibacterial ability. **Methods:** The synthesis process was initiated by adding the aqueous polychaete extract with silver nitrate (AgNO<sub>3</sub>). Optimization procedures e.g., polychaete size, AgNO<sub>3</sub> concentration, pH and temperature were conducted to increase the AgNP stability, yield, and characteristics. The color changes were observed visually and through surface Plasmon resonance (SPR) using UV-Vis spectroscopy. The AgNP formation validation was performed using scanning and transmission electron microscopy (SEM and TEM), Fourier transform infrared (FTIR), and X-ray diffraction (XRD). The antibacterial assessment was carried out using the optimized AgNPs on several bacteria. **Results:** Optimized conditions for obtaining high yield and stable synthesized AgNPs were polychaetes with 6-8 mm of body width, 1 mM AgNO<sub>3</sub> with polychaete crude extract of pH 9, preheated at 90 °C for 15 minutes before incubation at 30 °C (150 rpm) for 24 hours, and stored at 4 °C for long-term stability. The analyses were confirmed by an analysis of color variations from pinkish to yellowish-brown, as well as the appearance of SPR bands at 398–400 nm using ultraviolet-visible spectroscopy. The AgNPs were characterized by SEM, TEM, FTIR, and XRD and showed a significant effect (p < 0.05) in inhibiting the bacteria. **Conclusion:** The eco-friendly biosynthesized and optimized AgNPs with antibacterial activity were successfully synthesized and characterized in the study.

**Keywords:** eco-friendly, green synthesis, marine polychaete, nanobiotechnology, optimization, silver nanoparticles

## Preliminary Synthesis of P(3HB-3HV) Using Glycerin Pitch as Main Carbon Source from *Cupriavidus malaysiensis* USMAA1020

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**Introduction:** Deposition of petrochemical plastic waste in the environment is an evolving challenge in today's world. Researchers have established utterly eco-friendly plastics such as Polyhydroxyalkanoate (PHAs) to discover alternative products. PHA extracted from bacterial cells show commercial properties like polypropylene. Today, the industrialized world is exceptionally dependent on non-renewable fuel sources for commercial procedures and manufacturing structural materials such as plastics, adhesives, coatings, and foams. The present obstacles are the substitute of standard plastics from a non-sustainable source with an eco-friendly resource. Moreover, petrochemical plastics have not just decomposed in nature for many decades, also produced toxins via the destruction process. *Cupriavidus malaysiensis* USMAA1020, a Gram-negative bacterium able to produce biodegradable polymer P(3HB-co-3HV). **Methods:** In this study glycerin pitch was used as carbon source. The biosynthesis of P(3HB-co-3HV) was performed into 50 ml mineral medium in 250 ml Erlenmeyer flasks whereas inoculum (0.10 g/l) was added. The incubation period for this shake flask fermentation was 48 hours at 200 rpm. The presence of 3HB and 3HV was confirmed by the gas chromatography technique following with freeze-dryer and methanonylisis. Experiments performed on different parameters include concentrations of glycerin pitch, 1-pentanol, ammonium sulfate, and different precursors with 1-pentanol: Besides, different oleic acid concentrations were used as a secondary carbon source to enhance the production of PHA. **Results:** It was found that among various mixtures, 2% glycerin pitch, 1.1 g/l ammonium sulphate, 1-pentanol 0.06 wt% and oleic 0.5 wt %C yields PHA content 65%, 3HB (95 mol %), 3HV (4 mol %), RCDW (4 g/l), and PHA concentration (6 g/l.) respectively. **Conclusion:** This study found that glycerin pitch, a byproduct of the biodiesel industry, is a low-cost carbon source capable of producing copolymer.

**Keywords:** PHA, biodegradable plastics, glycerin pitch, biowastes, polymer P(3HB-co-3HV).

## Immobilisation of Oil Degrading Bacteria on Cellulose Triacetate Beads Formed from Kapok Fibres and Their Role in Oil Spill Remediation

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Oil spills occur almost daily in various regions in the world and pose a threat to all living organisms. Although global oil spill trends have decreased throughout the decades, its pernicious impacts cannot be nullified. Microbial remediation has gained much attention in the recent years and the remediation strategy discussed in this study is the immobilization of *Acinetobacter venetianus* RAG-1, an oil-degrading bacteria on porous cellulose triacetate beads (PCTBs) formed from Kapok fibres. *Acinetobacter venetianus* also produces an emulsan that was quantified through precipitation and dialysis. Cellulose triacetate powder (DS =  $2.88 \pm 0.137$ ) was produced from homogenous acetylation, then characterized through back titration and FTIR. Two types of PCTBs were produced through a solvent exchange method and observed through SEM. The absorption capacity and reusability of both beads and raw fibres were analyzed, showing that untreated Kapok fibres (UKF) had 7 times higher oil sorption than both of the PCTBs. Cell viability was conducted after bacterial immobilization for the UKF ( $3.05 \times 10^7$  CFU/g  $\pm$   $2.56 \times 10^7$ ) and one of the PCTBs ( $1.31 \times 10^7$  CFU/g  $\pm$   $7.03 \times 10^6$ ). However, there was no significant statistical differences in bacterial immobilization on UKF and PCTBs. Although UKF has a higher surface area compared to the PCTBs, there is no statistical significance in terms of better bacterial immobilization on UKF. We conclude that despite UKF showing better adsorption, PCTBs would potentially function better *in-situ* to adsorb and degrade oil from the marine environment.

**Keywords:** *Acinetobacter venetianus*, Bioremediation, Kapok fibre (*Ceiba pentandra*), Porous Beads

## Bioprospecting and Molecular Identification of Waste Transformer Oil-degrading Bacteria for Bioplastic Production

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**Introduction:** One of the major impediments to commercialization of biodegradable plastic is the high cost of substrate. Consequently, there is a continuous search for effective microorganisms and cheaper carbon substrates to reduce the high production cost of these ecofriendly materials. **Methods:** In this study, transformer oil-degrading bacteria were isolated from the environmental samples comprising soil, wastewater, and sediment. The isolation was accomplished using mineral salt medium (MSM) supplemented with 1% waste transformer oil as the sole carbon source. The isolates were screened for polyhydroxyalkanoates (PHA) production using Nile red staining and fluorescence Microscopic techniques. Accumulation of PHA granules were confirmed using Transmission electron microscopy. The oil degradation analysis was accomplished using solvent extraction and gravimetric methods. Bacterial identification was achieved using 16S DNA sequence homology according an established protocol. **Results:** A total of sixty-two (62) transformer oil-degrading bacteria were isolated from the different samples. Sixteen 16(26%) isolates showed a positive result when subjected to qualitative test using Nile red fluorescence microscopy. The bacteria identified belong to four different taxonomic genera of *Acinetobacter*, *Bacillus*, *Proteus*, and *Serratia*. The percentage oil degradation observed among the different isolates ranged between 19.58% to 57.51%. Gas chromatographic analysis of the polymer revealed the presence of medium chain length polyhydroxyalkanoate (mcl-PHA) monomers. **Conclusion:** The findings of this work have further highlighted the diversity of the bacteria capable of utilizing waste stream such as waste transformer oil. Consequently, the isolates can be explored as agents of converting waste transformer oil into bioplastics.

**Keywords:** Bioprospecting, transformer oil, bioplastic, polyhydroxyalkanoates.

## Targeting Double Genes in Multiplex PCR: An Innovation in PCR Technology for the Authentication of Food Products

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Nowadays, consumers' concern about the authenticity of food products is increasing due to the occurrence of food adulteration scandals worldwide. Specifically, food adulteration is of serious religious, health and economic concern. Consequently, researchers have paid more attention to the development of polymerase chain reaction (PCR) based methods for food authentication. However, existing PCR assays are mainly based on a single and a long DNA marker which often breaks down under food processing treatments. Instead of targeting a single gene, double genes targeting short-amplicon length PCR assay would be more reliable because where two different targets are present if one target is broken down due to heat treatment the second target will complement the missing target. It is highly unlikely that both targets would be broken down under food processing. We, for the first time, developed double gene targeting short-amplicon length multiplex PCR assay for discriminating bovine, buffalo and porcine materials in a single assay platform. Mitochondrial cytb and ND5 genes were targeted and all targets were amplified from raw, boiled, autoclaved and microwaved cooked meat under pure and mixed matrices. The detection limit was 0.02 ng DNA under pure states and 0.1% meat in admixtures. Screening of Malaysian meatball products revealed all beef products were buffalo positive in which 35% were totally replaced. In contrast, all pork products were found uncontaminated from beef and buffalo. Thus, this novel assay demonstrated sufficient merits to be used by regulatory bodies for food authentication in any samples even under degraded conditions.

**Keywords:** Multiplex PCR, Double gene-targets, DNA degradation, Food products, Authentication

## Production of Spray Dried Sea Cucumber (*Cucumaria frondosa*) By-Products Hydrolysate Powder

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**Introduction:** Sea cucumber is one of the valuable marine animals which is an important nutritious food source. However, approximately 50% biomass (by weight) in the form of visceral are discarded as waste during the processing of sea cucumber, causing an environmental threat. **Methods:** This study was aimed to transform these sea cucumber (*Cucumaria frondosa*) by-products (SC<sub>byp</sub>) into value-added product. Two enzymes (alkaline protease and exopeptidase) were used to hydrolyse the SC<sub>byp</sub> and release protein hydrolysate and the characteristics of the spray-dried protein hydrolysate powder were examined. **Results:** The production of SC<sub>byp</sub> hydrolysate powder was feasible, in which the powder that was treated with maltodextrin (SCh<sub>byp</sub>MD) exhibited better stability than powder without the addition of maltodextrin (SCh<sub>byp</sub>), with the former possessing significantly ( $p \leq 0.05$ ) lower moisture content ( $5.50 \pm 0.60\%$  dw) and water activity ( $0.25 \pm 0.02$ ). The SCh<sub>byp</sub>MD also demonstrated significantly ( $p \leq 0.05$ ) lower pH ( $5.33 \pm 0.06$ ), higher total soluble solids ( $5.07 \pm 0.12^\circ$  Brix) and water absorption index ( $82.33 \pm 2.20\%$  dw) and brighter ( $L^* = 47.51 \pm 1.86$ ) than SC<sub>byp</sub> and SCh<sub>byp</sub>. Interestingly, the hydrolysates contained all the 9 essential amino acids, corresponding to 39.81% and 36.66% of total amino acids in SCh<sub>byp</sub> and SCh<sub>byp</sub>MD, respectively. Thermal profiles indicated that melting point of SCh<sub>byp</sub>MD was higher ( $114.9^\circ\text{C}$ ) than that of SCh<sub>byp</sub> ( $94.2^\circ\text{C}$ ), due to the protective effect of maltodextrin. **Conclusion:** Converting waste into product not only preserve the environment but also could be potentially profitable to the industry as it can be applied as functional ingredients, animal feed or in nutraceutical product.

**Keywords:** Enzyme, Hydrolysate, Marine, Powder, Protease

## Nutritive Bambara Groundnut Powdered Drink Mix: Consumer Acceptability, Physicochemical Characterization, and Storage Stability

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**Introduction:** Underutilized crops that have increased resilience to climate change and inherent good nutritional composition are highlighted among scientists in recent years. Therefore, this study aimed to develop and characterize a nutritive powdered drink mix using Bambara groundnut (BGN) that is drought-tolerant crop. **Methods:** BGN powder was blended with soy powder at 0% (0B100S), 10% (10B90S), 20% (20B80S) and 30% (30B70S). Consumer acceptability of this BGN powder was assessed using a 9-point hedonic liking scale. The physicochemical properties (pH, color measurement, proximate analysis, protein and fiber analyses) of the product were determined. The storage stability of the product was determined by enumerating the fungal and bacteria upon storage six months under ambient room temperature. **Results:** Sample 10B90S was the most preferred sample with the highest mean values for aroma ( $6.22 \pm 1.28$ ), flavor ( $6.92 \pm 1.31$ ), grittiness ( $6.78 \pm 1.31$ ), and overall acceptability ( $6.98 \pm 1.15$ ). The concentration of total dietary fiber increased significantly as the BGN percentage in the beverage increased. The insoluble, soluble, and total dietary fiber of sample 10B90S were  $11.23 \pm 0.024\%$ ,  $5.31 \pm 0.031\%$ , and  $16.53 \pm 0.043\%$ , respectively. The samples' water activity and microbial enumeration did not have significant ( $p > 0.05$ ) change after six months of storage. **Conclusion:** In conclusion, BGN blended with soy powder (10B90S) was acceptable by consumers and could be marketed as a functional food that has improved nutritional values.

**Keywords:** Bambara Groundnut, Physicochemical, Hedonic liking scale, Storage stability, Proximate analysis

## Detection of Animal Species in Food Chain by Multiplex PCR-Restriction Fragment Length Polymorphism (RFLP) Assay

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**Introduction:** The adulteration or misrepresentation of food products is commonplace in the society. Detection of meat species in food products is important for economic, religious and medical perspectives. Among the DNA-based methods, polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) techniques are especially applicable in meat speciation because they utilize the sequence variations existing within a selected region of target DNA and allow very closely related species' differentiation with the use of selected restriction enzymes. It offers PCR products authentication through the analysis of restriction-digested products. **Methods:** We developed a simple multiplex PCR-restriction fragment length polymorphism (PCR-RFLP) assay using species-specific primer sets to authenticate highly consumed species such as beef, buffalo, chicken, duck, goat, sheep and pork simultaneously in food products. Short-length amplicons were used targeting mitochondrial cytochrome b (cytb) and NADH dehydrogenase subunit 5 (ND5) genes. Species-specificity was assured through cross-amplification reaction with 25 non-target species. PCR products authentication was performed by digesting with three restriction enzymes namely *FatI*, *BfaI*, and *HPY188I*. **Results:** Distinctive fingerprints were obtained for each of the seven targets. The assay could detect as low as 0.5% (w/w) meat in admixed states and food products and it retained its stability under heat treatments of boiling and autoclaving. A market survey on burger and frankfurter revealed a rampant substitution of beef with buffalo while chicken and porcine products were found pure. **Conclusion:** The developed assay could be conveniently used for differential detection of animal species as raw states as well as in meat products.

**Keywords:** PCR-RFLP, Meat products, Authentication, detection, Short target

## Elucidation of Anthocyanin Biosynthesis Pathway in *Cosmos caudatus* Kunth.

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**Introduction:** *Cosmos caudatus* Kunth. or “King’s salad”, contains high nutritional compounds. Although widely consumed for its medicinal value, information on phytochemical contents and their biosynthesis in the species is scarce. Among the exciting compounds are the anthocyanins that possess a dual role; an antioxidant and natural colorant. **Methods:** In this study, transcriptomic approaches with Illumina Hiseq, metabolomic analysis by Liquid chromatography-mass spectrometry (LC-MS), and anatomy description using light microscopy were used to identify the anthocyanin biosynthesis pathway in different tissues (leaf, stem, flower and root) of *C. caudatus*. **Results:** The transcriptomic analysis revealed nine main structural genes encoding enzymes in the anthocyanin biosynthetic pathway and the genes encoding the transcription factors relevant to the pathway. A total of 11 anthocyanins of cyanidin, pelargonidin, and delphinidin derivatives that are significantly abundant in the species were identified, correlating with the anthocyanin mainstream gene pathway. The occurrence of anthocyanin was further validated by light microscopy. Anthocyanin pigments in *C. caudatus* were detected at the epidermal layer of the leaf, stem, flower, and cortex of stem and root. **Conclusion:** A complete anthocyanin biosynthetic pathway in *C. caudatus* was elucidated using transcriptomics, metabolomics, and anatomical approaches in this study. To our knowledge, this is the first work that has delineated the complete anthocyanin biosynthetic pathway in Malaysia’s underutilized plant, *C. caudatus* Kunth. This study correlated multi-omics data that will help to integrate systems biology and synthetic biology for a detailed understanding of the molecular mechanism and characterization of the anthocyanin biosynthesis using heterologous expression studies.

**Keywords:** *Cosmos caudatus* Kunth; next-generation sequencing; liquid chromatography; anthocyanin; anatomy

## Cold Gas Spray Hydroxyapatite Coatings with Thermally Grown Interlayer Titanium Oxide on Ti-6Al-4V

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**Introduction:** Bioactivity and biocompatibility are important features in improving osseointegration for successful implants placement. Titanium alloy lacks bioactivity and Hydroxyapatite (HA) coating through modified cold gas spraying at room temperature has shown to improve bioactivity and enhance osseointegration. **Objectives:** This study aims to investigate, the morphology, and phase composition of HA coated Ti-6Al-4V with thermally grown titanium oxide as interlayer oxide. **Methods:** The Ti-6Al-4V wafer was oxidized in atmospheric conditioned at different temperature for thermally grown titanium oxide interlayer resulting in wavy surfaces prior to HA coating. The coating was produced by modified cold spray method which used low temperature processing. The thermally grown titanium oxide and coating was characterized by field emission scanning electron microscopy (FESEM) and X-ray diffraction. **Results:** The thermally grown titanium oxide layer maintain its morphology at different temperature. The mixed oxide phase showed reducing wavy structures as the temperature increases with occurrence of rutile and anatase peaks. There is no change in HA phases after coating formation by cold gas spray. The hardness value (HV) increased with increasing the oxidation temperature. **Conclusion:** The thermally grown titanium oxide at 550°C has shown the highest hardness value which prevent the severe crack on the morphology of coated HA.

**Keywords:** Ti-6Al-4V, Hydroxyapatite, Cold Gas Spray

## Morindone from *Morinda citrifolia* as Potential Antiproliferative Agent on Colorectal Cancer Cell Lines

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**Introduction:** Colorectal cancer (CRC), ranked the third most prevalent cancer worldwide is associated with p53 and KRAS mutation. Crucial role of phytochemical compounds as chemoprevention for CRC is definite, as there is strong correlation between dietary factors and colorectal risk. Anthraquinone compounds which are found in abundance in *Morinda citrifolia* demonstrate various pharmacological properties.

**Methods:** Three CRC cell lines, HCT116, LS174T, HT29 cells and normal colon cell line, CCD841 CoN cells were treated with eight anthraquinone compounds obtained from the roots of *Morinda citrifolia* at various concentrations. The cell cytotoxicity and antiproliferation effect of anthraquinones were determined by using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) analysis and xCELLigence Real Time Cell Analyzer (RTCA), respectively. Cell cycle analysis was performed with flow cytometry. The gene expression level of p53 and KRAS gene following anthraquinone treatment was evaluated with RT-qPCR and RNA sequencing. **Results:** Based on the MTT analysis, damnacanthal and morindone exhibited significant antiproliferative effects in HCT116 and HT29 cells. The real time impedance measurement showed that the proliferation rate of HCT116 and HT29 cells decreased in dose- and time-dependent manner following treatment with damnacanthal and morindone. Damnacanthal induces G1 cells accumulation in HCT116 cells while morindone induces G1 cells accumulation in HT29 cells. Both RT-qPCR and RNA sequencing data reported that morindone downregulates the p53 and KRAS gene expression in HT29 and HCT116 cells, respectively. **Conclusion:** Therefore, morindone may act as a competitive antiproliferative agent in treating CRC.

**Keywords:** *Morinda citrifolia*, morindone, anthraquinone, colorectal cancer, antiproliferative activity.

## Tocotrienol-rich Fraction (TRF) Improves Gross Liver Morphology and Liver Histological Changes in Non-alcoholic Fatty Liver Disease (NAFLD) Mice Model

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**Introduction:** Non-alcoholic fatty liver disease (NAFLD) is a major cause of liver disease worldwide with an estimated prevalence around 37% in Malaysia. It encompasses a spectrum of manifestations strongly associated with the presence of oxidative stress and excessive fat accumulation in the liver. Palm tocotrienol-rich fraction (TRF) has reported as a potential agent in ameliorating the liver of NAFLD subjects. Therefore, this study aimed to determine the effect of TRF supplementation on NAFLD parameters of animal model **Methods:** Twenty-one B6.Cg-LepOb/J (*ob/ob*) male mice were randomly divided into three groups comprised of high-fat diet (HFD; 60% kcal from fat) only, HFD with vehicle palm-kernel oil (PKO; 200mg/kg/day), HFD with TRF (TRF; 200 mg/kg/day) for six weeks. Body weight and food intake were measured each week. After six weeks, mice were euthanized and abdominal circumference and random blood glucose were measured. Liver span were measured prior to being assessed grossly and histologically using haematoxylin and eosin (H&E) and Masson Trichrome staining. **Results:** No differences were observed on abdominal circumference and random blood glucose reading in all groups ( $p>0.05$ ). TRF group recorded with smallest liver span compared to other groups ( $p<0.05$ ). Based on gross liver analysis, TRF groups were less steatotic compared to HFD only and PKO. NAFLD activity score (NAS) was less in TRF group with lower severity of steatosis, lobular inflammation and fibrosis compared to HFD and PKO. **Conclusion:** TRF exhibited profound histological improvement in *ob/ob* mice in comparison with HFD only group.

**Keywords:** non-alcoholic fatty liver disease, liver steatosis, knockout mice, high-fat diet, tocotrienols-rich fraction,

## Generation of DNA aptamers against envelope 2 (E2) protein of Chikungunya virus by *in vitro* systematic evolution of ligands for exponential enrichment (SELEX) for diagnostic application

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**Introduction:** Chikungunya virus (CHIKV) causes febrile illnesses in human and these cases have rapidly expanded across the globe in recent years. The current antibody-based tests for CHIKV such as ELISA have a variety of limitations associated with the molecules such as batch-to-batch variation, high cost and less stable. Aptamers are single-stranded DNA or RNA that have high affinity and specificity against a wide variety of target molecules. Compared to antibodies, aptamers are cheaper, produced *in vitro*, no batch-to-batch variations and thus serve as a good molecular recognition element for the development of diagnostic tests for CHIKV. **Methods:** Cloning, expression and purification of the recombinant CHIKV E2 was carried out and its identity was verified with western blot analysis. The purified protein was subjected to 9 SELEX cycles, the resulting nucleic acid pools were cloned and sent for sequencing. The secondary structure of the aptamer was predicted using Mfold web server and the performance of the aptamer was determined by enzyme-linked aptamer assay (ELAA). **Result:** The 24kDa recombinant E2 proteins were successfully cloned and purified. The protein was reactive against anti-CHIKV positive sera and anti-CHIKV polyclonal antibody with no cross reactivity with anti-dengue positive pool sera. Sequencing result revealed there were 6 potential candidates of DNA aptamers. DNA aptamer candidate with the highest frequency (61.9%) showed two loops in their predicted secondary structures. ELAA analysis revealed a binding affinity (Kd) of 177.5 nM and limit of detection was 3.3 nM. **Conclusion:** DNA aptamers were successfully generated and it has great potential as a feasible tool in CHIKV detection.

**Keywords:** Chikungunya virus, E2 protein, DNA aptamer, SELEX

## Expression of Specific Biomarkers toward Microfold Cells Differentiation in 3D Culture of Caco-2 and Raji B Cells

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### Abstract

**Introduction:** Microfold cells (M cells) are specialized epithelial cells found in follicle-associated epithelia (FAE) of the Peyer's patches, involved during transcytosis of enterocytes pathogen invasion. Differentiation of M cells induces expression of receptors which is recognized by specific M cells markers including alpha 5, beta 1 and Sialyl Lewis A antigen (CA19-9). However, studies on the expression of these markers in 3-dimensional culture system are lacking. Hence, this study aims to investigate the expression of the markers in two types of 3D culture model. **Methods:** The M cells differentiation were carried out in Transwell plate and in alginate hydrogel beads, whereby Caco-2 cells were seeded for 14 days prior to co-culture with Raji B cells. Polarity of the cell monolayer was measured as the transepithelial electric resistance (TEER). At post-21 days of co-culture, total cellular proteins were extracted using RIPA buffer (1X) for Western Blot analysis. **Results:** The TEER value of 270  $\Omega\text{cm}^2$  referred to the highly polarised monolayer. The alpha 5 expression was highest in Transwell compared to monolayer however its expression in alginate beads was lower than monolayer culture. Meanwhile, beta 1 expression was reduced in both 3D co-culture systems when compared to monoculture. Interestingly, CA19-9 was not expressed in both monoculture and 3D culture system. **Conclusion:** Both types of 3D culture systems were supportive towards the M cells differentiation, indicated by presence of alpha 5 and beta 1 integrins although at different level of expression. Thus, both integrin proteins are suitable as markers for M cells.

**Keywords:** microfold cells, 3D system, CA19-9, alpha 5 integrin, beta 1 integrin.

## Phage enzybiotics secreted from *Lactococcus lactis* as potential antimicrobials

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**Introduction:** Phage therapy is a potential alternative solution to the global antimicrobial resistance problem currently plaguing mankind. Bacteriophages are specific viruses which can lyse bacteria cells through the production of lysin enzymes that breaks down specific bonds in the peptidoglycan of the target bacteria. These lysins, also known as enzybiotics, can be broadly categorized into virion associated peptidoglycan hydrolases (VAPGH) or endolysins. The former locally degrade the bacteria cells during entry of the phage while the latter lyse the cells during release of new progenies at the end of the replication cycle. *Staphylococcus aureus* is an opportunistic pathogen which causes diseases ranging from skin infections to life-threatening meningitis and bacteremia. It is further complicated by emergence of drug resistant *S. aureus*, especially Methicillin Resistant *S. aureus* (MRSA). **Methodology:** In this study, lysins from the staphylococcal Phage 88 was cloned and expressed in *Lactococcus lactis*. *L. lactis*, a generally regarded as safe (GRAS) bacteria have been extensively used for decades in the food industry but more recently has become a model for genetic engineering in lactic acid bacteria. **Results:** The recombinant lysins secreted from *L. lactis* showed lysis activity on plate assays as well as inhibition of *S. aureus* growth in turbidity reduction assay. Additionally, the cell free extracts of the recombinant *L. lactis* was able to inhibit the growth of *S. aureus* by up to 4-log reductions. **Conclusion:** This study implies that the incorporation of recombinant probiotics secreting phage lysins in food starter cultures or cosmetic products may garner added value by inhibiting undesirable pathogens.

**Keywords:** phage therapy, endolysins, VAPGH, *Lactococcus lactis*, MRSA, antibiotic resistance

## Mutation on Newcastle Disease Virus V protein, Yes or No?

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**Introduction:** Newcastle disease virus (NDV) is a negative, single-stranded RNA virus which targets specifically towards avian species causing severe economic losses during an outbreak. The V protein was identified as one of the virulence factors of NDV that antagonises the host innate immunity for successfully viral replication in the host cells. However, detailed investigation of recombinant NDV expressing mutated V protein is scarce. Therefore, V protein was chosen as the factor to study the relation of mutation and pathogenicity. **Methods:** Using overlapping PCR, site-directed mutagenesis was carried out to introduce four premature-stop codon at the V reading frame respectively. The virus was then rescued, propagated in embryonated chicken eggs followed by pathogenicity analysis. **Results:** Only three out of four mutant viruses were successfully rescued. However, the substituted thymine was mutated into cytosine in mutant virus. Therefore, the stop codon was substituted with other amino acids and the V protein was no longer truncated. As a result, pathogenicity of the mutant viruses was not reduced due to substitution of the desired mutation into another nucleotide. **Conclusion:** It appears that an intact V protein is important for viral replication and pathogenicity. This study explored the possibility of V protein mutation in NDV through exploiting genetic engineering and warrants a further investigation on modifying a mutation for successful virus replication.

**Keywords:** *Paramyxoviridae*, Newcastle disease virus, V protein, C terminal, pathogenicity

## Recombinant Cell Penetrating Peptides and Intrabodies Targeting Inner Membrane-Bound Mutated KRAS Antigen

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**Introduction:** KRAS is an effector GTPase molecule responsible for signal transduction from ligand-bound epidermal growth factor receptor (EGFR) to the nucleus. The occurrence of specific somatic point mutations in the KRAS gene impairs its ability to regulate signal transduction, and are considered early drivers of carcinogenesis. Targeting this antigen however poses a problem as KRAS proteins are localized along a cell's inner membrane and are not easily accessible. In order to overcome this obstacle, two concepts using (i) cell penetrating peptides (CPPs) and (ii) adenoviruses were introduced. In this study, two different internalization mechanisms, namely endocytosis and viral transduction, were applied for the delivery of anti-mutant KRAS single-chain variable fragment (scFv). **Methods:** The fusion of scFv with an enhanced green fluorescence protein (eGFP) and Antennapedia-PTD (Antp), a CPP, was achieved through SOE-PCR. The first Antp-scFv-eGFP construct was successfully expressed in *E. coli* (BL21) at a concentration of 0.085 mg/ml. The second scFv-eGFP construct was cloned into an adenoviral vector and recombinant adenoviral particles were harvested from HEK293 cells. Both Antp-scFv-eGFP and adenoviral scFv-eGFP constructs were treated on SW480 and HeLa cells. **Results:** Mutant KRAS scFv binding efficiency between both approaches were compared based on eGFP localization and intensity, where the intrabodies approach was found to exhibit a higher (3 folds) signal intensity compared to the former. **Conclusion:** In conclusion, the intrabodies approach was evidently concluded to be a more reliable method as its construction was quicker, easier reproducibility, and the intrabodies produced contains a higher green fluorescence intensity.

**Keywords:** KRAS antigen, inner membrane, cell penetrating peptides, intrabodies, eGFP localization and intensity

## Screening of Selected Ageing-Related Proteins that Extend Chronological Life Span in Yeast *Saccharomyces cerevisiae*

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**Introduction:** Identification of ageing-related proteins sheds light on mechanisms modulating ageing. Ageing-related proteins play roles in various cellular processes such as eliciting heterochromatin silencing, combating oxidative stress, and modulating signal transduction pathways amongst many others, giving rise to longevity extension.

**Methods:** In this study, an overexpression screen of ageing-related proteins was performed in *Saccharomyces cerevisiae* using an adapted outgrowth kinetics chronological life span (CLS) assay. The selected CLS-extending proteins were characterized in terms of their stability, stress response during chronological ageing, and effect on cell proliferation through western blotting, colony forming unit (CFU) count and 96-well plate based growth assay respectively. **Results:** We identified seven proteins that extended yeast chronological life span (CLS) from the screen of ageing-related proteins. The top three CLS-extending proteins, Ptc4, Zwf1, and Sme1, promoted the highest survival percentage and shorter doubling time of yeast outgrowth compared to the control. The CLS-extending proteins contributed to thermal and oxidative stress responses differently. The overexpression of Ptc4 or Zwf1 also induced rapid cell proliferation during yeast growth. **Conclusion:** Overall, the proteins are likely involved in different mechanisms of actions in stress response and/or cell division or growth pathways to extend CLS.

**Keywords:** Ageing; Life span; Stress response; Cell proliferation; *Saccharomyces cerevisiae*

## Determination of the metabolic difference in hemolytic and non-hemolytic *Listeria monocytogenes* by Phenotype MicroArray™ Technology

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**Introduction:** *Listeria monocytogenes* causes a severe foodborne disease known as listeriosis with high mortality rate, especially in immunocompromised individuals. Listeriosis is developed through the production of several virulence factors such as listeriolysin O (LLO), hydrolytic enzymes, invasion associated protein, transcriptional activator etc. These virulence factors allow the escape of *L. monocytogenes* from phagocytes and multiply intracellularly to an infectious dose. **Methods:** *L. monocytogenes* ATCC19111 (hemolytic) and *L. monocytogenes* ATCC15313 (non-hemolytic) were selected to profile the metabolic differences. Four PM assay (PM1 to PM4) including carbon, nitrogen and sulphur-phosphorus assay were applied. The PM assay was validated by the growth of *L. monocytogenes* using optical density at 600nm. **Results:** There are significant metabolism differences among both *L. monocytogenes*, particularly in carbon metabolism. Hemolytic *L. monocytogenes* metabolized 19% (36/190) and non-hemolytic *L. monocytogenes* metabolized 18% (35/190) of carbon sources solely, and 19 carbon sources were shared by them. Among the shared carbon sources, non-hemolytic *L. monocytogenes* has a higher respiration rate. Although *L. monocytogenes* did not metabolize the carbon solely in PM test, the carbon was shown to play supporting role in their growth, in the validation test. The nine carbon sources only utilized by hemolytic *L. monocytogenes* were suspected to be involved in the stimulation of virulence factors production. **Conclusion:** Phenotype MicroArray™ (PM) Technology is a simple and bioinformatic for physiological differences determination in different bacteria strains. Carbon is the main sources for the metabolism of *L. monocytogenes* which certain substrates are responsible for the expression of virulence genes and hence their production.

**Keywords:** *Listeria monocytogenes*, Phenotype MicroArray™, Bioinformatic

***In Silico* Characterization of UGT76G1 Protein in *Stevia rebaudiana* Bertoni Accessions MS007**

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*Stevia rebaudiana* is a member of the Asteraceae family which is being consumed as an artificial sweetener. *Stevia* has been identified to be safe for human consumption and has been used as an alternative sweetener for diabetic and obese patients. This study used an *in silico* analysis of the transcriptome dataset of *Stevia rebaudiana* accession MS007 to describe the structure and gene content involved in the production of UGT76G1 protein. Homologous search using BLASTp resulting high similarity to UDP-glycosyltransferase 76G1-like *Helianthus annuus* (ID: XP\_021973845.1) as the highest percentage of identity. Protein family search using InterPro showed the presence and entry of IPR002213 available at positions 89 to 246. The phylogenetic tree was constructed by selecting 14 out of 100 protein sequences from BLASTp using MEGA X software. The phylogenetic tree analysis showed the same protein family which is Asteraceae. The protein structure prediction of primary, secondary and tertiary of UGT76G1 protein was computed using ProtParam ExPASy, PSIPRED and Phyre2. The tertiary structure prediction of UGT76G1 protein scored 100.0% confidence by the single highest scoring template and coverage of 98% and the dimension of the model is (Å) of X: 52.453, Y: 61.270, and Z: 48.102. The findings of this study will lead to a deeper understanding of the characteristics of UDP-glycosyltransferase 76G1 (*S. rebaudiana* MS007) and enhance target recognition mechanisms, resulting in a better understanding of protein-protein interaction in *Stevia rebaudiana* MS007.

**Keywords:** *Stevia*, UGT76G1, phylogenetic, structure prediction.

## Investigation of the Antibacterial Potentials of the Black Soldier Fly (*Hermetia illucens*) Larvae

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**Introduction:** As a sustainable approach of waste management, the black soldier fly larvae (BSFL) are commonly used for bioconversion of organic waste. The ability to survive in nutrient-rich environment heavily colonized by microorganisms suggests that BSFL have antimicrobial potentials. This study aimed to investigate the potential antibacterial strategies of BSFL, which could be mediated by their microbiota or endogenous chemical compounds. **Methods:** Both the internal and surface larval microbiota were isolated and identified via the 16S rDNA sequencing. The antibacterial activities of the larval isolates were then evaluated via the cross-streak test. The larvae were also subjected to sequential solvent extraction and the inhibitory activities of the resulting crude extracts tested via the resazurin microplate assay (REMA). **Results:** The identities of the larval isolates were *Providencia rettgeri*, *Escherichia coli*, *Morganella morganii*, *Bacillus cereus*, *Alcaligenes faecalis*, *Staphylococcus* spp., *Staphylococcus sciuri*, *Brachybacterium* sp. and *Corynebacterium casei*, where the former five were internal bacteria and the latter four were surface bacteria. In the cross-streak test, only *B. cereus* yielded an inhibition zone of about 14 mm against MRSA. The growth of MRSA in REMA was inhibited by the chloroform, hexane and methanol extracts; the latter two were also inhibitory against *E. faecalis*. The growth of *S. flexneri* was inhibited by the ethanol (3.75 mg/mL) and methanol (1.875 mg/mL) extracts; the latter was also active against *S. aureus*. All the inhibitions observed were at 7.5 mg/mL, unless otherwise stated. **Conclusion:** The findings of this study suggest that BSFL are potential source of antimicrobial agents.

**Keywords:** Black soldier fly larvae, *Hermetia illucens*, Antibacterial activity, larval microbiota, larval crude extracts

## ***In Silico* Identification and Characterization of Kaurene Synthase Protein in *Stevia rebaudiana* MS007**

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*Stevia rebaudiana* (Sr), belonging to Asteraceae family is a plant native to Paraguay. It is currently being used as a healthier alternative for sugar. Sr produces steviol glycosides (SGs), a group of secondary metabolite compounds that is responsible for its sweetening taste. SGs act as sweetener due to the presence of two major compounds, Stevioside and Rebaudioside A. Biosynthesis of these compounds involves enzymes such as geranylgeranyl pyrophosphate (GPPS), copalyl diphosphate synthase (CPPS), kaurene synthase (KS) and kaurene oxidase (KO) in the pathway. In this study, the identification and characterization of *Stevia rebaudiana* MS007 kaurene synthase (SrKS) were done by *in silico* analysis of the transcriptomic dataset. Homology search from BLASTx resulting in SrKS from query Cluster-31069.42907 (Sr MS007) of transcriptomic dataset shows the highest similarity percentage identity (99.62%). ExPasy tools were used to translate the nucleotide sequence into protein sequence. The protein domain is predicted by protein domain search analysis using Interpro and shows IPR005630 (terpene synthase metal-binding domain) available at positions 454 to 719 and IPR001906 (terpene-synthase-N-terminal-domain) at position 222 to 411 as the domains. In constructing the phylogenetic analysis tree, multiple sequence alignment was initially done using MUSCLE and MEGA-X was used as phylogenetic tree analysis tools. Cluster-31069.42907 shows the relationship between the ancestors, based on the bootstrap value. Bootstrap value of *Helianthus annuus* and *Stevia rebaudiana* is 100% as both the sequences are from the Asteraceae family. This study contributes to a deeper understanding of *S. rebaudiana* MS007 Kaurene synthase through *in silico* analysis.

**Keywords:** *Stevia rebaudiana*, Kaurene synthase, Steviol glycosides, Rebaudioside A, Stevioside

## Antifungal and Antimicrobial Activity of *Solanum nigrum* and *Solanum torvum* Mediated Silver Nanoparticles

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**Introduction:** *Solanum nigrum* known called as European black nightshade is native for few countries such as America, Australia and South Africa. It is a common herbal plant which is indigenous to India. *Solanum torvum* commonly known as pea eggplant. The herbs of *Solanum* species have found to be effective against numerous pathogenic fungi and bacteria infection. **Methods:** This study focused on the evaluation of antimicrobial and antifungal activity of silver nanoparticles (AgNPs) by using leaf extract. Several pathological bacterial strains and fungal strains such as *Candida* species were used to study the antimicrobial and antifungal activity of *Solanum sp.* **Results:** The zone of inhibition obtained by disc diffusion method and dilution method indicates the inhibition of microbial and fungal growth. The synthesized *Solanum nigrum* and *Solanum torvum* based silver nanoparticles were found to have antimicrobial and antifungal properties. **Conclusion:** These results indicate the potential applications of the medicinal plants to the field of nanotechnology.

**Keywords:** *Solanum nigrum*, *Solanum torvum*, silver nanoparticles, antimicrobial, antifungal

## The Effectiveness of Red Palm Oil in Preventing Alzheimer's Disease Induced in Rat

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**Introduction:** Alzheimer's disease is a chronic irreversible neurodegenerative brain disorder. In a brain of Alzheimer's disease patient, there is disposition of senile plaque in the extracellular space of the brain and neurofibrillary tangles (NFT) within the intracellular space of neuron. One of the causes that lead to these formation is high level of ROS within the brain that finally induce and increase the formation of NFT and senile plaque. Hence, this study was carried out to determine the effectiveness of red palm oil (RPO) in preventing the Alzheimer's disease induced in rat as RPO is one of the natural sources that rich with anti-oxidant. **Methods:** Forty male Sprague-Dawley rats were divided into 5 groups (n=8) that comprised of two groups that were administered by RPO daily (200 and 400 mg/kg), induced by D-Galactose only (negative control), donepezil administration (0.25 mg/kg) (positive control) and normal saline (control). This pre-treatment groups were given RPO through oral gavage. Y-maze spontaneous alternation test was done every week to evaluate the spatial working memory of the rats in exploring new area. After 21 days, the blood sample was collected to measure the level of GSH, MDA, SOD, TAC and dopamine through Elisa test kit. **Results:** Results showed low level of MDA and high level of dopamine, GSH, SOD and TAC in rats treated with RPO and donepezil compared to the rats that were induced with D-Galactose only after 21 days of pre-treatment ( $p < 0.05$ ). On the other hand, the group of rats that were treated with RPO and donepezil also showed significant improvement in exploring new area ( $p < 0.05$ ). **Conclusions:** Red palm oil has showed significant evidence of anti-oxidant effect in attenuating the oxidative stress in Alzheimer's disease by lowering down the level of MDA and improving the spatial memory of the rats.

## Review: CRISPR-Cas9 as a Cancer Therapy

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Cancer is a hereditary disorder caused by a series of genetic and epigenetic errors. It is one of the leading causes of death worldwide and still a major social and economic challenge. According to data, about 8.5 million people die each year as a result of cancer's lethality, and cancer rates are expected to rise by 50% in the next ten years, resulting in around 15 million deaths. There are many forms of cancer such as single or several gene alterations, chromosomal abnormalities, and translocations. Although, several approaches have been used to diagnose cancer, but they are still insufficient in cancer combating. Thus, scientists are investigating a variety of emerging methods for early cancer detection. Therefore, one of the most recent, simple, and effective technologies that has been used during the last few years in gene editing and cancer therapy is; Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-associated protein-9 (Cas9), a unique RNA domain-containing endonuclease-based genome engineering technology. In simple, CRISPR/Cas9 have been developed from a bacterial defense mechanism against virus infection. Recently, this technique showed its effectivity in the treatment of cancer and gene editing. CRISPR/Cas9 use the homology-directed repair and non-homologous end joining pathways to edit the genome. Moreover, CRISPR/Cas9 can also be used to quickly engineer immune cells and oncolytic viruses for cancer immunotherapy. In general, this paper reviewed this influential mechanism and its components. Also, this paper shows the pros and cons of this mechanism in details. Specifically, in this paper, we highlight the possible uses and recent developments of CRISPR/Cas9 in cancer treatment, as well as the difficulties that might be faced during clinical studies. In this regard, we hope to contribute to optimizing work CRISPR/Cas9 as well as focusing on showing the possible future directions of this technology.

**Keywords:** CRISP, Cancer, Modern Technology, Cas9, Therapy.

## Elucidating the effectiveness of *Elaeis Guineensis* on sex hormone in PCOS induced rats

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**Introduction:** *Elaeis Guineensis* is commonly known as palm oil which is known to have many medicinal uses as they are rich in nutritional values. Several studies have reported that the nutritional content of the palm oil showed a positive effect on improving PCOS. Therefore the current study is intended to identify the mechanism of *Elaeis Guineensis* on improving induced PCOS in rats. **Methods:** Forty Sprague Dawley rats were divided into 5 experimental groups with 8 rats in each group. The drugs and the palm oil were given to the rats orally for 28 days. The rats were given 1mg/kg of Letrozole diluted with 0.9% NaCl to induce PCOS (4 groups). Negative control group were not given any induction or treatment. Positive control group were given 100mg/kg of Metformin dissolved in 0.9% NaCl followed by letrozole. Group 1 and Group 2 were given 200mg/kg and 400mg/kg of palm oil respectively followed by letrozole. Group 3 were only given Letrozole. The Estrous cycle of the rats were monitored throughout the research. At the end of the research period the rats were sacrificed and the blood samples were collected to evaluate the serum level of sex hormones such as LH, FSH, Estrogen, Progesterone and testosterone using ELISA kit. The ovaries were removed to study on the histopathology of PCOS. **Results:** LH, testosterone and Estrogen level in group 2 (400mg/kg) showed a significant decrease compared to other groups ( $p < 0.05$ ). FSH and Progesterone level in group 2 (400mg/kg) increased significantly ( $p < 0.05$ ). The number of cyst decreased and the number of primary follicle, antral follicle, graafian follicle and corpus luteum were increased in group 2 (400mg/kg). **Conclusion:** From this study it is evident that *Elaeis Guineensis* has the ability to improve the level of sex hormones and tissue symptoms of PCOS.

## Over-Expression and Purification of *Acinetobacter baumannii* Hfq Protein in BL 21 Cells.

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**Introduction:** *Acinetobacter baumannii* is a coccobacillary gram-negative bacteria that survives well in hospital environment. It readily infects human by silencing immune responses. The strain is often multidrug resistant; thus, new strategies are required to combat the pathogen. Recently, non-protein coding RNAs emerged as a mediator of bacterial virulence regulation and performing their function by binding to RNA chaperone Hfq protein, forming ribonucleoprotein complex. In this study, we would like to establish a method to identify novel npcRNAs by sequencing cDNA library of Hfq protein bound RNA of *A. baumannii*. **Methods:** The Hfq gene from *A. baumannii* was amplified and cloned into pET-28b+ vector. Ligated mixture was transformed into TOP-10 cells and this transformed bacterial colony was screened by antibacterial (Kanamycin) selection and then further confirmed using PCR technique. The recombinant plasmid was transformed into *E. coli* BL21 and induced with IPTG for Hfq over-expression. **Results:** The over expressed Hfq protein was purified using Ni-NTA affinity chromatography. A highly purified Hfq protein was obtained by elucidation and confirmed by SDS PAGE analysis. The purified Hfq protein were mixed together with npcRNA of *A.baumannii* to identify all the possible npcRNA binding to Hfq protein and sent it for sequencing. **Conclusion:** We had successfully purified Hfq protein from *A. baumannii*. The identification and characterization studies will be carried out by RNA binding study for the selection of the npcRNA that binds to the protein.

**Keywords:** *Acinetobacter baumannii*, Hfq, npcRNA, over-expression, protein

**Acknowledgement:** We would like to acknowledge Ministry of Higher Education for financing this work under Fundamental Research Grant Scheme (FRGS) FRGS/1/2018/STG05/AIMST/02/1

## Transcriptome analysis of *S. Typhi* treated with durian waste (rind) mediated silver nanoparticles

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**Introduction:** *Durio zibethinus* is a climacteric, seasonal tropical fruit of Southeast Asia which has high nutritional value and rich bioactive properties. Many research have been done in exploring the potential food value of the edible and non-edible parts of durian. Yet, during durian season, a huge amount of durian waste in the form of seeds and rind or shell were disposed which leads to environmental pollution. In the present research, we aimed to study the transcriptome of *S. Typhi* treated with durian waste (rind) mediated silver nanoparticles. **Methods:** The synthesized silver nanoparticles were incubated with *S. Typhi* and the total RNA was extracted. These total RNA were sequenced via Illumina HiSeq 2000 platform. The fastQ format transcriptome sequences were analysed using bioinformatics software tools such as Trimmomatic and Bowtie2. Un-annotated intergenic regions were screened for the possible novel ncRNA candidates using Artemis. Differential expression of exponential phase and synthesized durian waste (rind) mediated silver nanoparticles in *S. Typhi* transcriptomes were analysed using HTSeq and DESeq software. **Results:** A total of 4290 coding genes, 1533 and 2131 showed significantly up and down regulations, respectively. The metabolic pathways of selected significantly differential expression mRNAs were studied. **Conclusion:** This preliminary transcriptome analysis data reveals interesting insights in gene regulation of *S. Typhi* treated with durian rind silver nanoparticles.

**Keywords:** silver nanoparticles, transcriptome, *S. Typhi*, *Durio zibethinus*

**Acknowledgement:** We would like to acknowledge Ministry of Higher Education for financing this work under Fundamental Research Grant Scheme (FRGS) FRGS/1/2015/SKK08/AIMST/02/1

## Renal Protective Effects of *Trigonella Foenum-Graecum* Seeds on Morphine Withdrawal Rats - A Review

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Morphine is an opioid drug that widely used for treating chronic pain caused by post-operations and cancer. It is considered as gold standard opioid therapy because it has the potential to exhibit analgesic property. However, prolonged morphine administration can trigger induce tolerance to its analgesic effect. Thus, a higher dose of morphine is needed in order to overcome the tolerance and attain the same pharmacological effect. But, over time, morphine withdrawal can occur, if the amount of opioid drug intake is not sufficient to get the desired pharmacological effect or when changed to the use of other opioid drug therapy. Simultaneously, there are several adverse effects when morphine is abused. This is because a high dose of morphine administration is capable of triggering the generation of reactive oxygen species (ROS) and reactive nitrogen species (RNS). Thereby, it can lead to a condition called oxidative stress that can induce damage to the cells. Since, the liver performs its role in drug metabolism and the kidney in detoxification, both these organs can be highly affected due to morphine administration. On the other hand, the plant called fenugreek, which has the scientific name *Trigonella-Foenum Graceum*, is well known for its antioxidative properties. The presence of polysaccharides, flavonoids, polyphenols along with minerals such as calcium, zinc and magnesium, primarily support the role of fenugreek seeds as an antioxidant. Hence fenugreek seed extract, may have a renal protective effects on the morphine withdrawal rats.

**Keywords:** Morphine, Fenugreek, Oxidative stress, *Trigonella-Foenum Graceum*, kidney

## Isolation and Characterisation of Probiotic Bacteria from Livestock and Kimchi and Assessment of Their Antibacterial Potentials

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**Introduction:** Probiotics are microorganisms that are not harmful to the consumers but rather, they confer health benefits. They are mainly bacteria and are usually found in the animal gastrointestinal tracts and fermented foods. The aim of this study was to isolate and characterise potential probiotics from several of these sources. **Methods:** The samples tested include chicken intestines and gizzards, pig intestines, cow intestines and faeces, and kimchi, which were homogenised in saline and then cultured on the de man, Rogosa and Sharpe (MRS) agar. The resulting bacterial isolates were assessed for their antibacterial potentials and then identified by the 16S rDNA sequencing. **Results:** Among the isolates obtained include *Lactobacillus pentosus*, *Lactobacillus reuteri*, *Lactobacillus fermentum*, *Leuconostoc mesenteroides*, *Lactobacillus sakei*, and *Lactobacillus plantarum*. The former three were from livestock sources while the rest were from kimchi. In the well diffusion assay, the culture filtrates of *L. pentosus*, *L. plantarum*, *L. mesenteroides*, and *L. fermentum* were shown to be inhibitory against laboratory strains of *Escherichia coli* O157:H7, *Salmonella typhimurium*, and *Shigella* sp. Some of these were also inhibitory against the bacteria isolated from the milk of a goat with mastitis. Their inhibitory effects diminished post-neutralisation, thus suggesting the role of the organic acids produced in these. The probiotic isolates were preliminarily shown to be able to tolerate 0.3% bile but only two were acid-tolerant (pH 2). **Conclusion:** The outcomes from this study may contribute to development of novel probiotic consortia that can be commercialised for use in animal feed in livestock farming.

**Keywords:** Probiotics, *Lactobacillus*, Livestock, Kimchi, Antibacterial activities

## Antagonistic and Inhibitory Potentials of some Natural $\beta$ -Carboline Alkaloids against 5-HT<sub>1A</sub> Homology Receptor as Potent Antidepressants

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**Introduction:** Serotonin antagonists and reuptake inhibitors (SARIs) are atypical antidepressants with pharmacological application on major depressive disorder, and oftentimes, co-administered with selective serotonin reuptake inhibitors (SSRIs) to mitigate SSRI-induced aftereffects such as insomnia and sexual dysfunction. Only few of this important drug class are available and not without serious side effects including priapism and hyponatremia symptoms. Natural  $\beta$ -carboline alkaloids are reported with spectrum of neuropharmacology against several psychiatric disorders including anxiety and depression. However, their potentials as SARIs remain underexplored. This study is aimed at identifying potent SARIs among 55  $\beta$ -carboline alkaloids from natural products. **Methods:** Maestro Glide docking, Swiss ADMET and VEGA ToxRead mutagenic simulations. **Results:** Selectively, monoacetylarenarine B, arenarine B, cordysin E, ingenine E and eudistomidin A show strong binding affinity as docking scores, -5.713, -5.865, -6.204, -5.815 and -6.011 kcal/mol respectively compared to the positive controls, fluoxetine, trazodone and WAY100635 with -6.126, -5.980 and -5.196 kcal/mol respectively. The negative controls, albendazole and metformin display lowest scores, -3.835 and -1.601 kcal/mol respectively, thereby validating the docking protocols. The selected compounds occupy similar binding pockets of 5-HT<sub>1A</sub> homology receptor and interact with pharmacologically essential residues in the receptor active site, Asp 116, Asn 386 and Phe 362 referenced to the antidepressant standards. The phytochemicals, from *Arenaria kansuensis*, *Psilocybe* mushrooms, *Acanthostrongylophora ingens*, *Annona foetida* and *Eudistoma* spp., possess good ADMET, druggability and mutagenicity parameters ideal of lead-like candidates. **Conclusion:** The study models a faster, cheaper and environmental friendly approach to identify potent SARIs from natural  $\beta$ -carboline alkaloids for further experimental studies.

**Keywords:** 5-HT<sub>1A</sub> receptor, molecular docking,  $\beta$ -carboline alkaloid, natural products, antidepressant

## Phytochemical Composition and Antioxidant Potential of Methanolic Extract of Filamentous *Anabaena* sp. and Unicellular *Microcystis* sp.

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**Introduction:** Cyanobacteria (blue-green algae) are a diverse group of photosynthetic, prokaryotic micro-organisms found in fresh and marine waters. They produce a diversity of secondary metabolites having potential activities such as antibacterial, anticancer, antiviral, antioxidant, and other pharmacologically active compounds. Phytonutrients and pigments present in cyanobacteria have been shown to act as antioxidants, which facilitate the formation of the body's defence mechanism against free radical damage to cells. **Methods:** In this study, methanolic extract of *Anabaena* sp. and *Microcystis* sp., which are indigenous Malaysian cyanobacteria species was evaluated for their total phenolic contents (TPC), total flavonoid contents (TFC), carotenoids, and antioxidant activity. TPC, TFC and carotenoids were analysed spectrophotometrically while 2,2-diphenyl-1-picrylhydrazyl (DPPH) and ferric reducing antioxidant power (FRAP) assays were carried out to determine the antioxidant activity. **Results:** the results showed that the methanolic extract of *Anabaena* sp. contains higher TPC ( $43.05 \pm 7.2$  mg GAE/g) and TFC ( $99.83 \pm 3.56$  mg QE/g) while *Microcystis* sp. methanolic extract showed higher amount of carotenoids ( $9.890 \mu\text{g/g}$ ) and higher antioxidant potential through DPPH assay ( $54.04 \pm 0.347$  %). **Conclusion:** The present study revealed that *Anabaena* sp. and *Microcystis* sp. are excellent sources of natural products representing both filamentous and unicellular classes of cyanobacteria respectively which could be explored for various purposes specifically for human health and well-being.

**Keywords:** *Anabaena* sp., *Microcystis* sp., phytochemical, antioxidant

## Suppressing Cinnamate-4-hydroxylase (C4H) Gene Using RNA and CRISPR Interference Systems Increases the Expression of Flavonoid-related Genes in Ginger and Tobacco

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**Introduction:** *Boesenbergia rotunda*, commonly known as fingerroot ginger, produces valuable compounds, including panduratin A, pinostrobin, and pinocembrin. However, the low abundance of these compounds in nature limits their industrial applications. Cinnamate-4-hydroxylase (C4H) is a vital enzyme located in the first branching point in the flavonoid biosynthetic pathway. The re-direction of the metabolic flux after silencing the branching pathway may enhance flavonoid production in plants. This study demonstrated how C4H silencing affects flavonoid-related genes in *B. rotunda* and *Nicotiana tabacum* cell suspension cultures. **Methods:** The partial cDNA of *C4H* isolated from *B. rotunda* was cloned into an RNAi vector. To construct a CRISPRi vector, sgRNA sequences targeting the promoter region of *C4H* were designed. Both constructed vectors were introduced into the established *B. rotunda* and *N. tabacum* cell suspension cultures. The putative transformants were analysed using PCR. The expression of *C4H* and flavonoid-related genes were determined using qPCR. **Results:** RNAi and CRISPRi silencing vectors targeting *C4H* were successfully constructed and introduced into *B. rotunda* and *N. tabacum* cell suspension cultures. About 50% of *B. rotunda* and *N. tabacum* regenerants were transformed. Both RNAi and CRISPRi vectors effectively reduced *C4H* expression. **Conclusion:** This study showed that C4H is a key enzyme in modulating flavonoid production.

**Keywords:** Metabolic Engineering, Flavonoids, CRISPRi, Gene silencing, Cell suspension culture

## Generation of Superfolder Green Fluorescent Protein Variants as Non-invasive Reporters in Plants

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**Introduction:** Green fluorescent protein (GFP) is the most widely used non-invasive reporter proteins to-date. However, the interference of plant auto-fluorescent compounds with GFP fluorescence when excited at 480 nm, remains a major complication in plant research. Hence, improvements in expression efficiency and fluorescent intensity are required for GFP to be a useful marker in intact plants. Recently, superfolder GFP (sfGFP) has been developed as a robust folding reporter. **Methods:** To enhance the performance of sfGFP as a reporter protein in plants, site-directed mutagenesis and random mutagenesis were performed. The engineered *sfGFP* variants were cloned, expressed, and subsequently purified. Purified sfGFP variants were then subjected to fluorescence spectroscopy to identify their respective excitation and emission spectra. Lastly, the engineered *sfGFP* variants were separately cloned into a plant expression vector and *Agrobacterium*-mediated transient transformation of *Nicotiana benthamiana* leaves was performed. **Results:** Through site-directed mutagenesis at S65 and/or T203, a total of three sfGFP variants, namely sfGFPuv, sfYFP and sfYFPuv were generated. Next, using yellow fluorescent proteins (YFPs) Venus and EYFP as references, *sfYFPuv* was subjected to further site-directed mutagenesis to generate *esfYFP*. Moreover, using *sfYFPuv* as template, an exceptional brighter variant, *esfYFPuv* was obtained through random mutagenesis. A novel point mutation which caused the exceptional brightness in *esfYFPuv* was revealed through DNA sequencing. **Conclusions:** A total of five sfGFP variants, namely sfGFPuv, sfYFP, sfYFPuv, esfYFP and esfYFPuv were constructed and were proven to be functional *in planta*. Lastly, a novel mutation that may enhance GFP brightness under UV excitation was discovered.

**Keywords:** *Agrobacterium*-mediated transient transformation, fluorescent protein, reporter gene, sfGFP

## Tandem Mass Tag-Based Quantitative Proteomics Analysis Reveals Prospective Drought Response Mechanism in *Pandanus amaryllifolius*

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**Introduction:** Drought is one of the major threats to the agricultural sector and food security. Drastic changes in morphology and molecular mechanisms are crucial for plant survival under unfavourable environments. *Pandanus amaryllifolius*, a moderate drought-tolerant plant, is well known for its ability to survive in prolonged low-level soil moisture conditions. Understanding the molecular regulation of drought stress signalling in this plant is important to help guide the rational design of crop plants to counter these environmental challenges. This study aimed to determine the morpho-biochemical and protein changes of *P. amaryllifolius* in response to drought stress. **Methods:** *P. amaryllifolius* plants were subjected to drought treatment by withholding water for 4, 7, 10, and 14 days. The 7-day drought-treated plants were then re-watered. Morphological changes, such as plant height, relative water content (RWC), relative electrolyte leakage (REL), and antioxidant enzyme activities, including superoxide dismutase, peroxidases, ascorbate peroxidase, catalase, glutathione reductase, proline, and malondialdehyde (MDA), were recorded. Total protein of the leaf samples was extracted, labelled with tandem mass tags reagent, and analysed by LCMS/MS. **Results:** Drought stress significantly affected the morpho-biochemical of plants. The RWC and height for drought-treated plants were significantly reduced, while REL, antioxidant enzymes activities, proline, and MDA were significantly increased. Of the 1,415 identified proteins, 134 proteins were significantly changed in each treatment comparison. These proteins are predominantly involved in carbohydrate metabolism, metabolism of cofactors and vitamins and genetic information processing. **Conclusion:** This study provides an important and valuable drought-responsive proteome dataset for the future crop improvement programme.

**Keywords:** Drought stress, antioxidants, liquid chromatography mass spectroscopy, tandem mass tags, pandan

## **Proteomic Analysis of Giant Freshwater Prawn, *Macrobrachium rosenbergii* Eyestalks throughout Different Molting Stages**

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**Introduction:** Giant freshwater prawn or *Macrobrachium rosenbergii* is a native species of Malaysian freshwaters. This species has been farmed for commercial purposes in Malaysia since the 80s, nevertheless, our national production for the past years were not impressive. It is said that poor growth performance such as growth retardation and heterogenous growth among individuals in the same proximity are the setbacks for the industry to obtain maximum production for the year. Since molting is the principle of growing for this species, comprehensive understanding of molting cycle mechanism on molecular level is important. **Methods:** In this study, differentially expressed proteins (DEPs) throughout different molting stages of *M. rosenbergii* were studied using high-throughput proteomic approach. Three molting stages of post-, inter- and pre-molt were involved with three biological replicates for each, making it in total of nine samples. **Results:** Overall, a total of 369 proteins were identified from the samples and 17 proteins were significantly up- or down- regulated from all nine samples. DEPs in pre-molt are hypothesized to be assisting the ecdysis to happen, thus, focuses on these proteins are crucial. Out of 17 DEPs, 6 DEPs were found in pre-molt stage namely ribosomal protein S3A, crustacean calcium-binding protein 23-like, elongation factor 1-gamma-like, putative clotting protein, uncharacterized protein LOC119585594 and Histone 2A. **Conclusion:** Here, we presented the proteins that could potentially help in speeding up the molting cycles in *M. rosenbergii*. These findings are advantageous to the species farming industry as they eventually may perhaps will be useful in growth strategy planning.

**Keywords:** Giant freshwater prawn, molting, ecdysis, eyestalks, proteomic

## Waterlogging Affects Morpho-physiology and Group VII Ethylene Response Factor Gene Expression in Banana

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**Introduction:** Flooding reduces plant growth and yield, causing significant agricultural losses. Flooding (submergence and waterlogging) disturbs stomatal conductance, carbon dioxide assimilation, and photosynthesis rate in plants. Understanding the flooding responses and adaptation mechanisms in plants is thus indispensable. Ethylene response factor (ERF) transcription factors (TFs) are crucial regulators of flooding and low oxygen responses. However, the signalling and regulation of ERFVII TFs during waterlogging stress are not well understood. Hence, this study aimed to determine the morphological and biochemical changes of bananas under waterlogging stress and analyse the expression of ERFVII TFs. **Method:** The morphological and biochemical changes of waterlogged-banana roots (*Musa acuminata* cv. Berangan) were assessed at 0, 1, 3, 5, 7, 14, and 24 days. These include total biomass, leaf area, aerenchyma formation, and antioxidant enzyme activities, such as catalase and ascorbate peroxidase. The selected ERFVII TFs and hypoxia-responsive genes were analysed using semi-quantitative RT-PCR. **Results:** Waterlogging stress affected the growth of banana plants. The leaf area was reduced after 3 days of waterlogging (DOW). New adventitious roots and aerenchyma were formed after 3 and 7 DOW, respectively. The antioxidant enzyme activities, lipid peroxidation, and hydrogen peroxide content were highest at 7 DOW. The hypoxia-responsive genes and ERFVII genes showed the highest gene expression after 3 DOW. **Conclusion:** This study provides an insight into how waterlogging stress impacts the morphological changes and ERFVII gene expression profiles of banana.

**Keywords:** Abiotic stress, Banana, Crop improvement, Waterlogging, ERFVII

## Metabolite Profiling of 50% Ethanolic Extraction of *Clinacanthus nutans* by Using GC-MS and LC-MS/MS and Cytotoxicity Analysis of Succinic Acid, Betulinic Acid and Artemisinin on J774.2 Macrophage Cell Line

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**Introduction :** *Clinacanthus nutans* (Burm f.) Lindau (*C. nutans*) or commonly known as belalai gajah or Sabah snake grass, is a well-known traditional medicine in South East Asia. It consists of abundant phytomedicinal properties such as anti-viral, anti-bacterial and anti-inflammation. This work aimed to profile the phytochemical compounds in 50% ethanolic extracts of *C.nutans* and to identify the cytotoxic effect of 3 selected compounds on J774.2 macrophage cell. **Methods:** Metabolite profiling of the extracted *C.nutans* was carried out using GC-MS and LC-MS/MS analysis. MTT assay was carried out to measure the cytotoxicity of the 3 compounds in J774.2 at concentrations ranging from 1- 100  $\mu$ M at 24-, 48- and 72- h of incubation. **Results:** More than 100 compounds were profiled by both chromatography analysis, identifying an abundance in artemisinin, betulinic acid and succinic acid. Based on the MTT assay, artemisinin and betulinic acid caused a significant decrease ( $p < 0.05$ ) in J774.2 cell viability at a concentration and time-dependent manner. However, in succinic acid, at concentrations of 1 $\mu$ M and 5 $\mu$ M there were significant ( $p < 0.05$ ) increases in J774.2 cell viability in a time-dependent manner until 48 h. However, a decrease in cell viability was observed at 72 h for all concentration. Nevertheless, all the concentrations of succinic acid at 24-, 48- and 72 h incubation time exhibited a  $> 80\%$  cell viability. **Conclusion:** This study provides informative data on the existing metabolites in 50% ethanolic extracts of *C.nutans* and showed cytotoxicity effect of the compounds on J774.2 macrophage cell.

**Keywords:** *Clinacanthus nutans*; anti-proliferative; succinic acid; artemisinin; betulinic acid

## Modification of Kapok Fibres into Porous Beads for Marine Oil Spill Remediation Efforts

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Marine oil spills are widely reported in recent years and bioremediation is proposed to be an environmentally friendly approach to clean these spills. However, maintaining high biomass of oil-degrading bacteria is a challenge. Here, we propose a carrier that enables immobilization of bacteria and rapid oil absorption as a solution. This carrier consists of porous cellulose triacetate beads (PCTBs) derived from cellulose triacetate powder (DS value of 2.75 to 3.02) obtained through the acetylation of kapok fibres. The effect of cellulose-to-solvent ratio (% w/v) and precipitation solution used during the synthesis of these beads was investigated and characterized through FTIR and SEM. PCTBs with both 12.5% and 16.67% w/v precipitated in distilled water showed greater crude oil absorbency of  $2.4850 \pm 0.1326$  g/g and  $1.9852 \pm 0.2343$  g/g, respectively in artificial seawater surface compared to those precipitated in a mixture of methanol and water owing to its macropores (>50nm). The reusability test on PCTBs also showed no significant reduction in absorption capacity after 5 reabsorption cycles. Raw kapok fibres exhibited a greater absorption capacity ( $38.4943 \pm 1.3737$  g/g) compared to PCTBs due to its larger surface area, but the reabsorption ratio of fibres declined in continuous cycles. The next step is to determine successful immobilization of oil-degrading bacteria on these PCTBs and this will be carried out in a different study. To conclude, PCTBs can potentially play a very important role in bioremediation to achieve simultaneous absorption and biodegradation as beads occupy less space and are easier to handle compared to fibres.

**Keywords:** Kapok Fibres, Carriers, Porous Cellulose Beads, Cellulose Triacetate.

## Physical and Chemical Preventive Countermeasures of Disinfectants Used during the SARS-CoV-2 Pandemic: Implications on Toxicity and Resistance Development

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The novel human coronavirus (CoV) 2019 known as COVID-19, similar to previous CoVs infections outbreaks has posed a serious and an unprecedented challenge on the entire health care system in the world that needs aggressive preventive and easily accessible measures, policies for effective regular disinfection. Rampant use of disinfectants may pose toxicity to human, environmental hazards and, in some cases, decrease effectiveness and development of resistance due to other ingredients in the disinfectant agents. This review comprehensively highlights the effects of physical and chemical countermeasures and their related potential toxicity on human and environment. The study reveals that physical inactivation especially the effects of temperature, humidity and light mostly ultraviolet-C (UV-C), have significantly demonstrated proven efficacy in reducing the spread of CoV infections. Similarly, chemical countermeasures especially alcohol- and iodine-based disinfecting agents have shown potentials inhibition against the survival of the viruses and other pathogenic micro-organisms on surfaces. Large number of disinfectants were reported to contain corrosive chemicals that are toxic to humans especially children and destroy the environment due to unhealthy accumulation and pollution, and other additional ingredients having potentials to develop resistance and decrease effectiveness of the disinfectants. This review summarizes the importance of physical and chemical preventive countermeasures currently in use against CoV infections for further modifications and translational study to design improved disinfecting agents.

**Keywords:** SARS-COV-2, disinfectants, toxicity, resistance, physical & chemical agents, viral inactivation,

## Effects of Trans-Resveratrol and RU-615 on Human Trabecular Meshwork Cells Morphology and Viability

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**Introduction:** Steroid-induced ocular hypertension (SIOH) is a close representation of primary open-angle glaucoma with elevated intraocular pressure (IOP). Human trabecular meshwork cells (HTMC) regulate IOP by maintaining the drainage of the aqueous humour. Trans-resveratrol (TR) is a polyphenolic compound with potent anti-oxidant and anti-inflammatory effects, whereas RU-615 belongs to benzimidazole group, a class of heterocyclic, aromatic organic compounds that have anti-microbial and anti-hypertensive activities. Both agents were shown to reduce the IOP of SIOH rats, however, their mechanisms are yet to be investigated. The use of HTMCs is important in studying IOP lowering effects of potential antiglaucoma agents. Therefore it is important to ensure the concentrations chosen are safe to use on HTMCs. **Methods:** Passage 5 primary HTMCs were divided into 7 groups and treated with resveratrol and RU-615 with or without dexamethasone (Dexa) for 7 days. These cells were then subjected to morphological assessment daily followed by MTS assay on day-7 of treatment. **Results:** Vehicle treated HTMCs were generally wide, large and flat with spindle-like shape. Treatment with TR and RU-615 with or without Dexa for 7 days did not alter much of the morphology, however the shape of HTMCs treated with TR 12.5  $\mu$ M alone showed more elongated appearance. The cell viability revealed no significant differences ( $p \geq 0.05$ ) between the vehicle-treated group and those treated with TR and RU-615 with or without Dexa. **Conclusion:** Treatment of HTMC with TR 12.5  $\mu$ M and RU-615 0.1 mM with or without Dexa 100 nM are safe and non-toxic to the HTMCs viability.

**Keywords:** Cell viability, Resveratrol, RU-615, Human Trabecular Meshwork Cells, MTS assay

## The Toxicity Level of Raw Titanium Alloy Sample (Ti-6Al-4V) on Human Periodontal Ligament Fibroblast

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**Introduction:** Titanium alloy is one of the biomaterials that has been widely used for medical implant especially in orthodontics and orthopaedics. It is important to know the toxic dose of titanium before developing any implants. The unknown toxicity level of titanium implants might trigger the host inflammatory response leading to failure of osseointegration, causing implant rejection. Therefore, the purpose of this study was to determine titanium toxicity level using raw titanium alloy sample (Ti-6Al-4V) on human periodontal ligament fibroblast cell (hPDLFc). **Methods:** Conditioned medium (CM) was prepared by immersing 2g raw Ti-6Al-4V in 20 ml DMEM medium for 1000mg/ml initial concentration of CM solution. hPDLFc were exposed to different concentrations of raw Ti-6Al-4V (1000, 500, 250, 125, 62.5, 31.25, 15.63, 7.81, 3.9, 1.95 mg/ml) for 24 h and the cell viability were assessed by Alamar Blue assay. **Results:** After 24 h, Ti-6Al-4V sample at concentrations 125, 62.5, 31.25, 15.63, 7.81, 3.9, and 1.95mg/ml showed increased hPDLFc cell viability. 122% cell viability which was the highest, was observed in cells treated with 125mg/ml Ti-6Al-4V. While at 250, 500, and 1000mg/ml Ti-6Al-4V concentrations, the cell viability was reduced and the lowest cell viability was observed at 1000mg/ml which was -81%. **Conclusion:** The different concentrations of raw Ti-6Al-4V affected the hPDLFc viability. The toxic level of raw Ti-6Al-4V based on this experiment is 250mg/ml. Ti-6Al-4V content in implants should be at a non-toxic level to ensure successful implant placement.

**Keywords:** Human periodontal ligament fibroblast cell, Ti-6Al-4V

## Effect of Spironolactone towards Proliferation of Metastatic Osteosarcoma Cells HOS-143B

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**Introduction:** Osteosarcoma (OS) is a primary malignant bone tumour affecting mostly children and adolescents. Previous study reported its ability in inducing the expression of Natural Killer Group 2 member D ligand (NKG2DL) in cancer cells, suggesting possible role towards cancer immune reactions. Thus, the aim of this study is to investigate the effect of SPIR towards proliferation of normal osteoblast cells (hFOB) and highly metastatic OS cells (HOS-143B). **Methods:** Both hFOB and HOS-143B cells were treated with SPIR at different concentrations ranging from 5 to 40  $\mu$ M. Cytotoxicity level of SPIR was determined at post- 24, 48 and 72 hours using the Cell Proliferation Assay. **Results:** SPIR exerted its effect in a dose-dependent manner for the hFOB cells at all incubation time, with viable cell percentage ranging from 95% to 35% following the dose increment. Meanwhile, at post- 24 hours and 48 hours, the SPIR exerted effect in HOS-143B was independent of the doses, indicated by the similar pattern of high percentage (85% and above) of viable cells at all doses. **Conclusion:** SPIR exerted a more consistent effect towards the normal cells compared with the cancer cells. However, despite being dose independent, SPIR exerted low cytotoxicity towards HOS-143B indicated by the high percentage of viable cells at all doses with the optimum reaction time of 48 hours. In conclusion, SPIR exerted an overall positive effect towards proliferation of both normal osteoblast and OS cancer cells when used below its cytotoxic doses.

**Keywords:** osteosarcoma, spironolactone, cell proliferation assay, immune cells, natural killer (NK) cell ligand

## Genome-wide SNP Analysis of the Evolutionary Multidrug Resistant *Mycobacterium tuberculosis* (MDR-TB) in Malaysia

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**Introduction:** Tuberculosis (TB) control has been a constant battle, and this is beleaguered by the increasing cases of multidrug-resistant tuberculosis (MDR-TB). Understanding the underlying factors of MDR-TB would augment our understanding and could potentially pave the trajectory towards an effective treatment. In this study, we have identified mutations potentially associated with drug resistance in MDR-TB using Next-Generation Sequencing (NGS) approach. **Methods:** A total of 24 available genomes sequences of clinical strain of *Mycobacterium tuberculosis* (MTB) were subjected to NGS sequence analysis. The obtained variants were filtered by using the existing protein-coding genes in MTB, obtained from NCBI. Selected candidates were singled out and subjected to protein structural prediction analysis. **Results:** Using H37Rv genome as the reference, overall sequences ranging from 4.2Mb to 4.3Mb were acquired. A deletion was detected for heparin-binding hemagglutinin (HBHA) and forkhead-associated (FHA) domain (FHAA), respectively. Both protein-coding genes that contains a deleted segment were consistently present in most of the isolates. These deleted segments may potentially change the structural conformation of the proteins. The deletion in HBHA protein is speculated to cause a reduction in the adherence of MTB to epithelial cell, hence inhibit autophagy and facilitate apoptosis in macrophage that promotes MTB infection. Deletion in the segment in FHAA protein, may led to potential downregulation of cell growth, causing the cell wall to be impermeable to the antibiotics thus inducing antibiotic resistance. **Conclusion:** These findings suggest that the mutation in both HBHA and FHAA proteins may confer antibiotic resistance.

**Keywords:** *Mycobacterium tuberculosis* (MTB), multidrug resistant, next generation sequencing (NGS), protein structure prediction

## Investigation of Cytotoxins from Malaysian Cobras (*Naja sumatrana* and *Naja kaouthia*) as A Potential Antineoplastic Agent

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**Introduction:** Cancer is a leading cause of death worldwide. The pursuit of novel antineoplastic agents has reinvigorated interest in natural proteins and peptides for target-specific and effective treatments of cancer. With this, cobra venoms are one of the promising natural resources with antineoplastics potential. Here, we investigated the antineoplastic potential of cobra venom and their purified cytotoxins of two Malaysian cobras, *Naja sumatrana* (equatorial spitting cobra) and *Naja kaouthia* (monocled cobra) on three types of cancer and non-cancerous cell lines, i.e., breast (MCF-7 and 184B5), A549, NL20 (lung), PC-3 and RWPE-1 (prostate). **Methods:** The cytotoxins were purified via sequential fractionation using ion-exchange chromatography, followed by C18 reverse-phase high-performance liquid chromatography (HPLC). The protein homogeneity was validated with sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and identified through liquid chromatography-tandem mass spectrometry (LCMS/MS). The cytotoxicity was determined with MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay and the half-maximal inhibitory concentration (IC<sub>50</sub>) of the cytotoxins towards cell lines were determined. **Results:** The cytotoxins exhibited cell-type specificity, by showing a more potent cytotoxicity against A549 (IC<sub>50</sub> < 1.5 µg/ml) and PC-3 (IC<sub>50</sub> = 3–4 µg/ml) compared to MCF-7 (IC<sub>50</sub> = 9–12 µg/ml). In comparison, these cytotoxins also demonstrate different selectivity towards cancer and non-cancer cell lines, with the most promising selectivity observed in the lung cell line (Selective Index > 2). However, the cytotoxins were not selective in breast and prostate cell lines (SI < 2). **Conclusion:** The findings suggest that the cytotoxins of both Malaysian cobras may serve potential as a prospective antineoplastic candidate despite the need for further studies to address its limitations and challenges.

**Keywords:** snake venom, cobra cytotoxin, anticancer

## BPIFB1 Role in the Regulation of EMT Associated Genes in the Gastric Cancer Cells

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**Introduction:** Bacterial/Permeability-Increasing Fold Containing Family B Member 1 (BPIFB1), is a member of the BPI-fold family of protein differentially expressed in various types of cancers. Overexpression of BPIFB1 protein has been reported to down-regulate the expression of E-cadherin (CDH1). CDH1 is an epithelial marker regulating the epithelial to mesenchymal transition (EMT) of cancer cells, hallmark of invasion and metastasis stage of cancer. The loss of CDH1 expression leads to EMT and alter the expression of mesenchymal markers such as CDH2 and VIMENTIN as well as other EMT associated genes such as Snail 1 (SNAI1). This study aims to investigate the effect of BPIFB1 overexpression in the mesenchymal marker gene expression *in-vitro* in GC cells that have been previously transfected to overexpressed BPIFB1 expression. **Methods:** Three different GC cell lines were used in this study, AGS, HGC-27 and MKN-45 cells. Expression analysis was carried out via qRT-PCR to determine target genes expression and comparative expression analysis was done using the transfected and non-transfected GC cells with normalization to the standard reference gene  $\beta$ -ACTIN (*ACTB*). **Results:** The results showed that overexpression of BPIFB1 leads to the differential expression in the EMT associated genes in the AGS, HGC27 and MKN45 GC cells. **Conclusion:** The data generated from this study can be used to provide more insight on the role of BPIFB1 protein as the transcriptional regulator for the EMT process in GC cells.

**Keywords:** Bacterial/Permeability-Increasing Fold Containing Family B Member 1 (BPIFB1), Gastric cancer (GC), Epithelial Cadherin (CDH1), Snail 2 (SNAI2), Epithelial-to-mesenchymal transition (EMT).

## Cell-Free Supernatants from Probiotics Inhibit Colon Cancer Cells proliferation

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**Introduction:** Probiotics are live microorganisms which when administered in adequate amounts provide health benefits to the consumer. Patients with colorectal cancer benefits from the consumption of probiotics as it helps to reduce colorectal cancer spread and progression through various mechanisms. The cytotoxic effect of the cell free supernatant of *Propionibacterium freudenreichii* and *Faecalibacterium prausnitzii* was investigated in vitro using HCT116 colon cancer cell line. **Methods:** MTT cell viability assay was used to check the cytotoxicity and inhibitory effects of Cell free supernatant of *P. freudenreichii* and *F. prausnitzii* against human colorectal cancer cells (HCT116). The cells were seeded at 5000 cells/well overnight after which they were exposed to both probiotic supernatants singly and as a cocktail at different concentrations. and 5-FU standard chemotherapeutic drug at different concentrations then incubated at 37°C and 5% CO<sub>2</sub> for 12, 24, 48 and 72h. Afterwards, 10µl MTT solution was added to the wells and reincubated for 3 hours. 100µl of DMSO was used to lyses the cells to expose the formazan crystal formed and the absorbance was measured at 570 nm. **Results:** Cell free supernatant of *P. freudenreichii* and *F. prausnitzii* exhibited cytotoxic effects on HCT116 cells in a time dependent and dose dependent manner. The cells that were treated with the highest concentration of the CFS had the lowest viability rates across all the time points. **Conclusion:** The result gotten from this study shows that probiotics are efficient against colorectal cancer cells even when no live cells are present.

**Keywords:** Probiotics; Colorectal cancer; *Propionibacterium freudenreichii*; *Faecalibacterium prausnitzii*; MTT assay

## Antibiotic Resistance Patterns of WHO priority pathogens isolated from Acute Pharyngitis Patients in Private Primary Care Clinics

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**Introduction:** The World Health Organization (WHO) has developed a global priority pathogen list (PPL) with 12 antibiotic-resistant bacteria. Acute pharyngitis (AP) is a common reason for primary care consultation and antibiotics are often prescribed by general practitioners (GPs) for AP patients in Malaysia. However, there is limited primary care antibiotic resistance surveillance data available in Malaysia. Therefore, this study aims to investigate the prevalence and antibiotic resistance profiles of WHO global priority pathogens specifically towards last-resort drugs in AP patients in the community.

**Methods:** A cohort of 205 AP patients visiting private primary care clinics in Klang Valley, Malaysia was selected. Throat swabs were taken and bacterial identification were done using Matrix-Assisted Laser Desorption/Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS). Disc diffusion or broth microdilution were performed on 237 PPL isolates found in 153 AP patients following standard guidelines. **Results:** *Staphylococcus aureus* (n=89), *Streptococcus pneumoniae* (n=62), *K. pneumoniae* (n=49), *Acinetobacter baumannii* (n=7), *Pseudomonas aeruginosa* (n=6) and *Enterobacter* spp. (n=24) were found among the WHO PPL. Results showed 23 out of 62 *S. pneumoniae* isolates were penicillin-non-susceptible and more than half of *S. aureus* isolates were penicillin-resistant (n=52/89) although penicillin V has been recommended for AP management in Malaysia. Alarmingly, all 5 community-acquired methicillin-resistant *S. aureus* (MRSA) throat isolates found were also vancomycin-resistant *S. aureus* (VRSA), indicating the spread of VRSA in the Malaysian community. **Conclusion:** In conclusion, this study demonstrates that these pathogens are acquiring trends for resistance towards last-resort antibiotics, therefore, these data obtained can be useful to improve antibiotic stewardship in Malaysia. (250 words)

**Keywords:** Acute pharyngitis, antibiotic resistance, community-acquired, private primary care, WHO global priority pathogens list

## HMGR Expression in Relation to HER2 Status of Breast Cancer

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**Introduction:** 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGR) is the rate-limiting enzyme in cholesterol biosynthesis pathway that has been associated with cancer development. The association between HMGR and HER2 has been established, however, the role of HMGR in HER2 positive breast cancer progression remains unknown. This study aims to evaluate the HMGR expression in relation to HER2 status of breast cancer. **Methods:** Cell lines MDA-MB-453, MDA-MB-361, MDA-MB-231 and MCF-7 were grown in DMEM medium with 4% FBS and 1% antibiotic. The cells were subcultured in petri dishes and protein were extracted upon reaching confluency. Western blotting was performed on the protein extracts targeting HMGR protein at 98 kDa. In addition, tissue block samples of breast cancer patients diagnosed in Hospital USM were selected for IHC staining of HMGR. Besides, the HMGR mRNA levels were also studied using patient samples with IHC scored HER2 0, HER2 1+, HER2 2+ and HER2 3+. **Results:** High basal protein expression of HMGR was observed in MDA-MB-453 (HER2 moderate overexpression) compared to the other breast cancer cell lines. Moreover, the percentage of IHC HER2 3+ samples with high protein expression of HMGR was 91.7 % (33 out of 36 cases), which was higher compared to 69.4% (25 out of 36 cases) of high HMGR expression in IHC HER2 0 & 1+ samples. qPCR analysis showed the mRNA level of HMGR increased in IHC HER2 3+ breast cancer samples as compared to the other HER2 breast cancer subtypes. **Conclusion:** Overall, increased HMGR protein and mRNA expression was seen in HER2 overexpression breast cancer. Further study should be carried out to examine the molecular interactions between HMGR and HER2 positive breast cancer in relation to tumour progression of HER2 positive breast cancer.

**Keywords:** HMGR, HER2 status, breast cancer, cholesterol biosynthesis

## Proteomic Analysis Reveals Protective Role of Melatonin in Tumour-Prone *Drosophila melanogaster* lethal giant larvae Mutants

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**Introduction:** *Lethal giant larvae (lgl)* is the first neoplastic tumour suppressor gene identified in *Drosophila melanogaster* and it encodes protein that regulates cell polarity and epithelial integrity. The aberrant expression of human homolog of *lgl*, *Hugl*, is associated with the progression of multiple cancers, including colorectal cancer. However, molecular characterisation of *lgl* mutant flies is still lacking. In this study, the proteome profile of intestinal tissues of *lgl* mutant flies and the effects of melatonin treatment were investigated. **Methods:** *Drosophila melanogaster* flies were cultured and categorised into three groups: (i) wild type; (ii) *lgl* mutant; and (iii) *lgl* mutant treated with melatonin. Total protein isolated from the intestinal tissues was subjected to two-dimensional gel electrophoresis and silver-staining. The gel images were analysed using Progenesis SameSpots software. Protein spots of interest were digested for mass-spectrometry analyses and subsequently identified using MASCOT search engine against *Drosophila* entries in the Swiss-Prot database. **Results:** A total of 40 protein spots were detected with significant differences ( $p < 0.01$ ) in abundance between the groups of flies. Among these, upregulation of eukaryotic initiation factor 4A and actin-79B, and downregulation of glutathione S-transferase S1 were observed in *lgl* mutants. Interestingly, the reversal changes in these proteins were observed in those flies under melatonin treatment. **Conclusion:** The results indicate changes in protein expression in *lgl* mutant flies and normalisation upon treatment with melatonin, thus suggesting a protective effect of melatonin in tumour-prone *Drosophila melanogaster lgl* mutant.

**Keywords:** *Drosophila melanogaster*, lethal giant larvae, intestine, proteomics, melatonin

## Evaluation of Antidiabetic Activity of Methanolic Extract of *Coccinia grandis* (voight) and *Spondias mombin* (Linn) Leaves in Streptozotocin Induced Diabetic Sprague Dawley Rats.

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**Introduction:** Medicinal plants are well documented for treating diabetes mellitus. However, scientific evidence on antidiabetic activity of *Coccinia grandis* and *Spondias mombin* leaves from Malaysian origin have not been significantly reported so far. Present study is to evaluate the antidiabetic potential of methanolic extract of *Coccinia grandis* (MECG) and *Spondias mombin* (MESM). **Methods:** Antidiabetic activity of MECG and MESM was evaluated in streptozotocin induced diabetic rats by administering glibenclamide (20 mg/kg) as standard drug, (125, 250 and 500 mg/kg) individually and combined doses (125 mg/kg + 125 mg/kg, 125 mg/kg + 250 mg/kg, and 125 mg/kg + 500 mg/kg) for 28 days. **Results:** Qualitative analysis of MECG and MESM showed the presence of reducing sugar, tannins, alkaloids, phenols and flavonoids and HPLC analysis indicated presence of quercetin and rutin. Blood glucose, serum cholesterol triglycerides, low density lipoproteins (LDL), very low-density lipoproteins (VLDL), alanine aminotransferase (ALT), aspartate aminotransferase (AST), were significantly ( $p < 0.05$ ) decreased while, high density lipoproteins (HDL) were increased in MECG, MESM and glibenclamide treated rats compared to diabetic control and combined doses treated rats. Furthermore, histopathological study of pancreas in MECG, MESM and glibenclamide treated rats showed significant regeneration of  $\beta$ -cells of islets of Langerhans compared to diabetic control and combined doses treated rats. No changes observed in combined dose treated rats. **Conclusion:** This study provided evidences for significant antidiabetic activity of MECG and MESM.

**Keywords:** *Coccinia grandis*, *Spondias mombin*, antidiabetic activity, type 2 diabetes, histopathology.

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## Synthesis and Characterization of Azobenzene Derivatives and Azobenzene-Imidazolium Conjugates with Selective Antimicrobial Potential

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**Introduction:** Five new non-fluorinated and fluorinated azo derivatives, as well as a new series containing five azo-imidazolium conjugates of varying alkyl chain length in the imidazolium head group were prepared and characterized. **Methods:** Fourier Transform Infrared, Nuclear Magnetic Resonance spectroscopy, and elemental microanalysis were employed to characterize the synthesised compounds. Antimicrobial activities of these compounds against pathogenic Gram positive bacterium *Staphylococcus aureus* and Gram negative bacteria *Escherichia coli*, *Salmonella enterica* serovar Typhimurium, as well as yeasts *Candida albicans* and *Saccharomyces cerevisiae* were evaluated using the disc diffusion method. **Results:** The azo derivatives and their imidazolium conjugates were selectively active against the tested microorganisms with zone of inhibition diameters ranging from 10-21 mm. Their biological efficacy was dependent on the chain length and level of fluorine substitution. The presence of long alkyl chains is essential for the azo derivatives to exhibit microbial efficacy. Active azo-imidazolium conjugates on *Staphylococcus aureus* contained 16 and 18 carbons in the alkyl chains while Gram negative strains exhibited a cut-off effect at chain length C16. **Conclusion:** Difference in antimicrobial behavior of the azo derivatives could be due to the different cell wall between the Gram positive and negative bacteria. Fluorination had no effect on the activity against *E. coli* and *Salmonella*. However, a clear correlation between the level of fluorine substitution and the antimicrobial activity against *Staphylococcus aureus*, *Candida albicans* and *Saccharomyces cerevisiae* was observed.

**Keywords:** azo-imidazolium conjugates, fluorinated azo derivatives, *E. coli*, *Staphylococcus aureus*, *Candida albicans*.

## Changes in Inflammatory Biomarker Vcam-1 and Insulin Levels during Progression of Premature Atherosclerosis in Rats

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**Introduction:** Atherosclerosis is an inflammatory disease which can cause various systemic complications. Obesity is a traditional biomarker and one of the major risk factors contributing to atherosclerosis. The study aims to assess changes in inflammatory marker serum VCAM-1 and metabolism marker serum insulin levels during progression of premature atherosclerosis alongside traditional markers. **Methods:** 10 healthy Sprague Dawley rats were randomly divided into a high fat diet group (n=5) and a normal diet group (n=5). Animals were observed for a period of 16 weeks. BMI, blood lipid profiling and fasting blood glucose levels were assessed weekly as traditional biomarkers. Systemic markers serum VCAM-1 and insulin levels were determined by ELISA. HOMA-IR index was calculated and histological analysis of aorta was used to measure intima media thickness. **Results:** The study found that there was a significant difference in BMI  $t(8)=7.483$ ,  $p<0.001$ , LDL-C  $t(8)=8.551$ ,  $p<0.001$ , HDL-C  $t(8)=-14.213$ ,  $p<0.001$ ,  $p<0.001$ , AI  $t(8)=14.803$ ,  $p<0.001$ , VCAM-1  $t(8)=9.506$ ,  $p<0.001$  and fasting blood glucose levels  $t(8)=10.450$ ,  $p<0.001$  between groups. Strong positive correlations were observed for VCAM-1 with body weight ( $r=0.97$ ,  $p<0.001$ ) and atherogenic index ( $r=0.94$ ,  $p<0.001$ ). HDL levels had strong negative correlations with VCAM-1 ( $r=-0.93$ ,  $p<0.001$ ). A strong positive correlation was observed between LDL levels and HOMA-IR index ( $r=0.81$ ,  $p=0.005$ ), IMT and VCAM-1 ( $r=0.87$ ,  $p=0.001$ ). **Conclusion:** Inflammatory marker VCAM-1 showed significant increase among the HFD. The increase in serum insulin in the HFD was not significant. Therefore, VCAM-1 can pose as a potential systemic biomarker alongside traditional biomarkers for better prediction of premature atherosclerosis progression.

**Keywords:** Biomarker, Atherosclerosis, VCAM-1, Insulin, Obesity, ELISA

## Investigation of Upper Respiratory Carriage of Bacterial Pathogens and Their Antibiotic Susceptibility Profile in the Kinta Valley, Perak, Malaysia

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**Introduction:** Some normal microbiota in the human upper respiratory tract can be potentially pathogenic when they overgrow or translocate; the latter could lead to pneumonia, septicaemia and meningitis. The occurrence of these pathogens can be investigated via the respiratory carriage studies, which are limited in Malaysia and therefore, their prevalence remains poorly understood. This study aimed to investigate the upper respiratory carriage of *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Neisseria meningitidis*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* among the Kinta Valley population. **Methods:** Nasal, oropharyngeal, and nasopharyngeal swabs ( $n = 563$  samples) from 236 subjects aged 2-90 years were collected. Detection of the fastidious target bacteria (*S. pneumoniae*, *H. influenzae*, and *N. meningitidis*) was by multiplex PCR on the swab DNA extracts. The presence of non-fastidious targets (*S. aureus*, *K. pneumoniae*, and *P. aeruginosa*) was assessed by culture on selective media followed by their respective species-specific PCR assays.

**Results:** The carriage rates of *S. pneumoniae*, *S. aureus*, *H. influenzae*, *K. pneumoniae*, *N. meningitidis* and *P. aeruginosa* were 44%, 33%, 16%, 11%, 1.3% and 0.8%, respectively. In the Kirby-Bauer assay, 86% and 14% of the *S. aureus* isolates obtained were resistant to penicillin and tetracycline, respectively. Among the *S. pneumoniae* isolates, 54% and 42% were resistant to trimethoprim/sulphamethoxazole and tetracycline, respectively.

**Conclusion:** The carriage rate for *S. pneumoniae* is the highest among the study population. The recent inclusion of the pneumococcal conjugate vaccine in the National Immunisation Programme has the potential to reduce this carriage in the community.

**Keywords:** Bacterial carriage, Upper respiratory tract, *Streptococcus pneumoniae*, Antibiotic susceptibility, Epidemiology

## The Anti-Proliferative Role of 15, 16-Dihydratanshinone I (DHTS) Extracted from *Salvia miltiorrhiza* in Autosomal Dominant Polycystic Kidney Disease (ADPKD)

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**Introduction:** Autosomal polycystic kidney disease (ADPKD) is a kidney disorder caused by mutations in polycystin proteins resulting in cystic formation in kidney. Tolvaptan, a vasopressin-2-receptor (V2R) antagonist, is the only FDA approved drug currently for ADPKD but it demonstrates serious side effects such as hepatotoxicity. Dihydratanshinone I (DHTS) extracted from *Salvia miltiorrhiza* has been shown previously to stop proliferation in cancers. Given that ADPKD also involves cell proliferation, the present study aims to repurpose this natural compound for ADPKD treatment. **Methods:** The cell viability of ADPKD cells (WT 9-12), normal kidney cells (HK2), and hepatocellular carcinoma cells, (HepG2, positive control cell line) treated with various concentration of DHTS, metformin and tolvaptan (positive control drugs) was assessed using crystal violet viability assay on day 3 and day 6 of treatment. The cells were treated daily (Model 1), every two days (Model 2), and every three days (Model 3). The DHTS concentration(s) that significantly reduced the WT 9-12 cell viability with minimal inhibitory effect on HK2 cells ( $\leq 50\%$ ) will be further analyzed with sulforhodamine B (SRB) cytotoxic assay and real time cell analyser (RTCA). **Results:**  $5\mu\text{M}$  ( $p < 0.05$ ) and  $10\mu\text{M}$  ( $p < 0.001$ ) DHTS treatment from Model 2 significantly inhibited the WT 9-12 viability in the preliminary studies with minimal cytotoxic effects on HK2. (SRB assay and RTCA results will be obtained before conference) **Conclusion:** DHTS showed promising anti-proliferation effects on ADPKD cell in this study. Although the side effects of DHTS is yet to be determined, this natural compound can be gentler alternative than tolvaptan for ADPKD treatment.

**Keywords:** ADPKD, treatment, DHTS, proliferation

## Production Truncated Bacterial Leukotoxin from *Aggregatibacter Actinomycetemcomitans* via Different Types of Expression System

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**Introduction:** *Aggregatibacter actinomycetemcomitans* is the primary causative agent of aggressive periodontitis. It selectively kills human leukocytes through the surface-located leukotoxin (LtxA), a member of the Repeat in Toxin (RTX) Family which acts as a pore-forming protein. LtxA recognizes lymphocyte function-associated receptor (LFA-1) of the hematopoietic leukocytes. The activated LFA-1 is up-regulated in most leukocytic diseases including hematological malignancies and autoimmune disorders. LtxA-mediated lysis of neutrophils results in the production of abundant hypercitrullinated proteins which act as neoantigens that are associated with Rheumatoid Arthritis (RA). How LtxA confers specificity towards activated LFA-1 is not fully understood due to the hitherto of the structural information. The structural study of LtxA is challenging due to the nature of recombinant LtxA is inactive in the form of inclusion body when it was expressed in the common expression host of *Escherichia coli*. **Methods:** Towards the structural analysis of LtxA, recombinant productions of various trimmed variants were attempted in both pCold and pET47 expression systems. Expression optimizations were performed to fine-tune the expression level and solubility. **Results:** All constructs expressed the LtxA, upon comparing the expression level and solubility, a truncated LtxA variant (461-900 aa) was found to be partially soluble. **Conclusion:** The recombinant production of LtxA has yielded a significant outcome, it is being used as the candidate for structural study via protein crystallization. Ideally, the structural information would serve as a blueprint in designing an alternative therapeutic strategy for combating periodontitis and leukocytic disorders.

**Keywords:** Leukotoxin, Repeat in Toxin Family, LFA-1.

## Tocotrienol Rich Fraction (TRF) Upregulates Farnesoid X Receptor (FXR) and Modulates FXR Target Genes in the Heart of High Fat Diet-Fed Mice

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**Introduction:** Cardiovascular Disease (CVD) is the number one cause of mortality due to non-communicable disease and high fat diet as one of the major risk factors for CVD development. FXR have been found to be expressed in the heart and is reported to exert anti-inflammatory and anti-atherosclerotic effects following its activation thus enhances cardiac remodeling and reduction in blood pressure. Tocotrienol-rich fractions (TRF) possess cardioprotective effects such as anti-atherosclerosis, anti-inflammatory, antioxidant activities, anti-thromboembolic and anti-adipogenic. However, it is not known whether TRF activates FXR and its target genes in high fat diet (HFD) animal model. **Methods:** A total of 21 Leptin deficient Jax male mice were randomly divided into HFD only (control), HFD with PKO (vehicle control) and HFD with TRF (TRF supplementation). After 6 weeks of treatment, heart tissues were extracted for real time polymerase chain reaction (qRT-PCR) to measure *fxr*, *shp*, *stat3*, *sod1*, *sod2* and *gpx1* expression from all animals. **Results:** Our findings demonstrated a significant increase in *fxr* expression of HFD+TRF and HFD+PKO group respectively by 3.18±0.61 folds and 10.0±2.05 folds as compared to control. A significantly reduced expression of *stat3* in both HFD+PKO (0.49±0.048) and HFD+TRF (0.53±0.053) groups, while increased *gpx1* expression was observed in HFD+TRF group (1.789±0.164 fold). No significant differences were noted in *shp*, *sod1* and *sod2* expression between HFD+TRF and control. **Conclusion:** Our results suggest that in HFD mice, the cardioprotective effect of TRF could be mediated by *fxr* signalling pathway through downregulation of inflammatory gene (*stat3*) and not through *shp* dependent-target genes.

**Keywords:** Tocotrienol-Rich Fraction, High fat diet, nuclear receptor FXR

## Evaluation of Antioxidant and Antidiabetic Potential of Medicinal Weeds, *Mimosa pudica*

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**Introduction:** *Mimosa pudica* is one of the common weeds used in ayurvedic medicine in treating diabetes. Preliminary screenings in previous studies found this species to possess bioactive compounds with potential antidiabetic effects due to its antioxidative content. This study aimed to optimize the solvent extraction parameters of *M. pudica* using response surface methodology in order to enrich the accumulation of antioxidants in the extracts. This study also examined the effects of *M. pudica* extract on the cell viability and glucose uptake ability in 3T3-L1 adipocyte cell line. **Methods:** A series of 17 runs were performed in solvent extraction of dried *M. pudica* aerial parts by manipulating three factors; extraction duration, water bath temperature and ethanol concentration. Then, the pre-adipocyte cell line was exposed to *M. pudica* extract at different concentrations of between 0.05 - 0.80 mg/ml to assess its cell viability level. 2-NBDG glucose analogue was used to measure the glucose uptake ability of matured adipocyte cells treated with *M. pudica* extract. **Results:** The results indicated highest ethanol concentration used as solvent had the greatest impact on the accumulation of antioxidant compounds in the extract. The highest TPC and TFC value recorded were 94.015 mg GAE and 1212.63 mg QE using 100% ethanol, three-fold and five-fold respectively higher as compared to using 50% ethanol. The lowest IC<sub>50</sub> value recorded was 19.92 µg/ml using 100% ethanol as compared to 975.02 µg/ml using 50% ethanol. The optimized extraction factors value for duration, temperature and solvent concentration were 82 minutes, 40°C and 100% ethanol respectively. In the cell viability assay, all extract concentrations treatment recorded viability level of above 50%. Extracts at concentration of 0.05 and 0.10 mg/ml were used to proceed in glucose uptake assay using 2-NBDG analogue. The results showed 2-NBDG uptake in cells treated with 0.10 mg/ml extract combined with insulin were more than 200% as compared to control group. **Conclusion:** These initial findings suggest that future research could fruitfully explore the compound and mechanism involved in *M. pudica* which could benefit in the treatment of diabetes.

**Keywords:** *Mimosa pudica*, antioxidant, antidiabetic, adipocyte, medicinal weeds.

## Determining Structural Stability of Glucose-6-Phosphate Dehydrogenase Deficiency Variants Using Molecular Dynamics Simulation

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**Introduction:** Glucose-6-phosphate dehydrogenase is responsible for replenishing the NADPH supply in erythrocytes, which protect against free radical induced oxidate stress. G6PD deficiency is the most common enzyme deficiency disorder. More than 186 variants are linked with G6PD deficiency by decreasing the activity or stability of the enzyme. G6PD dimerization is responsible for structural stability and catalytic efficiency. Despite geostatistical studies highlighting the incidence of many variants in Southeast Asia (SEA), there is still a gap in knowledge for these variants in a structural and a biochemical context. The structural-functional relationship of G6PD variants were unraveled by employing molecular dynamics simulation (MDS) to validate existing biochemical data. **Methods:** A complete G6PD dimer was constructed by using AutoDock 4.2 and AutoDock Vina to dock G6PD ligands, hence creating a complete dimer. The MDS package Gromacs 2018.1 was used to study the protein. SEA variants V291M (Viangchan), L128P (Vanua Lava) and H32R (Gaohe) were chosen and created by *in silico* site-directed mutagenesis using PyMOL. Trajectory analyses were performed to understand the structural changes exhibited by the mutants. **Results:** H32R was loosely packed which indicates poor catalytic activity, and all three mutants had higher number of hydrogen bonds towards their substrates and cofactors. **Conclusion:** Biochemical studies have shown that H32R exhibits a 90% reduction in catalytic activity and variants with low catalytic activity have greater affinities to their substrate and cofactors which is a compensatory mechanism. This establishes a structural and functional link that was formed by validating *in silico* and *in vitro* findings.

**Keywords:** Glucose-6-phosphate Dehydrogenase Deficiency, Computational Biology, Molecular Docking Simulation, Molecular Dynamics Simulation, Dimerization

## Comparative Evaluation of Commercially Available NS1-based Serological Assays for the Detection of Anti-ZIKV IgG Antibodies

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**Introduction:** Zika virus (ZIKV) is an emerging mosquito borne virus which belongs to the *Flavivirus* genus similar to the well-known DENV and JEV. Up to February 2018, there are 87 countries reporting mosquito borne ZIKV transmission and recent increase cases of birth defect microcephaly and neurologic complications Guillain-Barré syndrome (GBS) related to ZIKV. Although it is known theoretically that diagnosis of ZIKV infection can be carried out by molecular and serological approaches. However, serological diagnosis of ZIKV infection is challenging due to high cross-reactivity between flaviviruses. **Methods:** In this study, we evaluated 6 commercially available anti-ZIKV IgG ELISA kits. A total of 70 pre-characterized serum samples were selected as the panel samples for the evaluation. The diagnostic accuracy of each ELISA kit was determined through a comparison with the gold standard, Foci Reduction Neutralization Test (FRNT). **Results:** The ELISA kits that obtained the most accurate readings are the kit from Euroimmun followed by Abcam. The readings were comparable with the FRNT results. Although cross-reactivity (25%, n=3) with DENV was identified in ZIKV FRNT, our study proposed a diagnostic testing algorithm that is able to distinguish ZIKV infection from secondary DENV infection. **Conclusion:** Considerable insight has been gained concerning serological diagnosis of ZIKV infection by commercially available ELISA kits. The framework described here is both simple and universal. This approach is suitable for the screening of ZIKV infection among the healthy blood donors in dengue endemic regions.

**Keywords:** flavivirus, vector-borne diseases, diagnostic, serology, FRNT.

## Perfluorooctane Sulfonate (PFOS) Exposure Affects Beating Rate and Brain Natriuretic Peptide (BNP) Expression of Cardiomyocytes

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**Introduction:** Perfluorooctane Sulfonate (PFOS) is non-biodegradable synthetic compounds widely used in manufacturing household products. Exposure to PFOS demonstrated to increase the risk of cardiovascular diseases. This study aimed to investigate the effects of PFOS exposure on cardiomyocytes beating rate and cardiac markers. **Methods:** Primary neonatal cardiomyocytes cultured were exposed to PFOS with concentration from 10 to 125  $\mu\text{M}$  to determine its effective concentration ( $\text{EC}_{50}$ ). Cells were cultured and divided into unexposed (control), PFOS-exposed, Endothelin-1-exposed and combination of PFOS with Endothelin-1-exposed. All cells were subjected for beating rate assessment assay and stained for cardiac marker F-actin and hypertrophy marker (Brain natriuretic peptide, BNP). **Results:** In this study,  $\text{EC}_{50}$  was determined at 50  $\mu\text{M}$  in 48-hour treatment ( $n=4$ ,  $p<0.05$ ). PFOS-exposed groups ( $60 \pm 2$  beats/min) showed significant increase in beating rate compared control ( $43 \pm 3$  beats/min); ( $n=6$ ,  $p<0.001$ ). Reduction in F-action expression were indicated in PFOS-exposed ( $21 \pm 4$  % intensity) and Endothelin-1-exposed ( $25 \pm 2$  % intensity) compared to control ( $44 \pm 7$  % intensity); ( $n=4$ ,  $p<0.001$ ). Meanwhile, increased in BNP expression were indicated in PFOS-exposed ( $16 \pm 2$  % intensity) and Endothelin-1-exposed group ( $15 \pm 3$  % intensity) compared to control ( $0.4 \pm 0.1$  % intensity); ( $n=4$ ,  $p<0.05$ ). **Conclusion:** Our findings indicate that PFOS may affect the normal function of cardiomyocytes and lead to the development of cardiac hypertrophy.

**Keywords:** Perfluoroalkyl compound, Perfluorooctane sulfonate, Peralkyl substance, Hypertrophy, Cardiovascular Disease

## Downstream Effects of Berberine Treatment in Colorectal Cancer Cell Line, HCT 116

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**Introduction:** Colorectal cancer (CRC) is one of the most common cancer which is associated with the increment of telomerase expression and activity. Telomerase is the enzyme that functions to maintain the length of telomere which contributes to the unlimited proliferative potential in cancer cells. **Methods:** HCT 116 cell cycle distribution was analysed at 24, 48 and 72 hours of culture. Screening of telomerase inhibitors (boldine, silymarin and berberine) on HCT 116 was done to determine the compound with the lowest concentration that caused 50% inhibition (IC<sub>50</sub>). TeloTAGGG PCR ELISA was used to determine the telomerase activity. Protein levels were determined by western blot, while RNA levels as well as the relative telomere length were determined by Real Time-PCR. **Results:** The highest S phase percentage occurred at 48 hours. It was revealed that berberine had the lowest IC<sub>50</sub>. Berberine decreased the telomerase activity in HCT 116 by simultaneous downregulation of *TERT* and *TERC* levels, which resulted in a decrease of the TERT protein level subsequently caused telomere attrition. Berberine induced G<sub>0</sub>/G<sub>1</sub> arrest through upregulation of cyclin D1 (CCND1) and downregulation of cyclin-dependent kinase 4 (CDK4) protein and RNA levels, and its effect on the cell cycle was time-dependent. Hydrogen peroxide concentration increased in berberine-treated HCT 116 due to the increment of superoxide dismutase (*SOD*), and decrement of catalase (*CAT*) levels subsequently caused damage to the nuclei. **Conclusion:** In summary, our research has shown the downstream effects of berberine in HCT 116, in which it has inhibited the proliferative ability of the cells.

**Keywords:** colorectal cancer, HCT 116, berberine, telomerase, telomere

## The Association of Small Dense LDL Cholesterol Level with Clinical Risk Factors of Metabolic Syndrome Subjects in Selangor

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**Introduction:** Low density lipoproteins (LDL-c) has been shown to be strongly associated with Metabolic Syndrome (MetS). MetS is strongly associated with atherosclerosis of which small dense LDL-c (sdLDL-c) has been shown to be the atherogenic lipid in the formation of atherosclerotic plaques. However, the determination of sdLDL-c among these subjects have not been widely studied. The aim of this study is to determine the correlation between sdLDL-c in MetS and risk factors of MetS. **Methods:** Fifty-five MetS subjects diagnosed by Joint Interim Statement criteria 2009 were recruited from Primary Care Clinic UiTM Selayang from July 2020 until January 2021. Demographic data and anthropometric measurements were collected and blood samples were analyzed for direct LDL-c concentration on an automated platform c501 and applied to the sdLDL equation by Srisawasdi to derive sdLDL-c level. **Results:** The mean sdLDL-c level among MetS subjects were (1.93±0.77 mmol/L) which was well above the sdLDL cut-off (<1.27 mmol/L). SdLDL-c showed positive correlation with triglycerides (TG) (r=0.53, p<0.01) and systolic blood pressure (BP) (r=0.33, p<0.05). Multiple Linear Regression analysis showed that only TG and systolic BP are the significant factors (R square=0.395, p<0.05) where 39.5% of the variations in sdLDL-c level can be explained by TG and systolic BP. There were no significant correlations between sdLDL-c and high density lipoproteins, fasting blood sugar and waist circumference. **Conclusion:** sdLDL-c is elevated among subjects with MetS, having positive correlation with TG and systolic BP. This suggests that sdLDL can potentially be a useful marker in assessing risk for atherogenesis.

**Keyword:** sdLDL-c, Metabolic syndrome, direct LDL, lipid profile, automated platform

## Establishment of reference interval for haematological parameter among Afghan population

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**Introduction:** The reference interval of haematological parameters is widely affected by race, gender, age and environmental factors. The reference interval used for haematological parameters in Afghanistan are usually the one that are estimated for western population. Therefore, this study was conducted to establish the reference values of haematological parameters for healthy adult males and females among the residents of Kabul city, and to compare these values with mostly used values in local laboratories in Kabul city. **Methods:** The research was designed as a cross sectional study and the samples were collected as per non-random sampling method. Blood samples were collected from the students and employees of Kabul University, Afghanistan. In this study, 166 males and 125 females, aged 18 to 45 years old were included. **Results:** Reference range for haemoglobin was determined between 13.5 g/dl to 18g/dl for male and 11 to 17 g/dl for female, for RBC the reference range was established 4.5 to 7 million per microliter for male and 4 to 6 million per microliter for female. For haematocrit the reference range was established from 36 to 56% and 30 to 54% for female. For MCV the reference range was 73 to 91 fl for male and 64.5 to 94 fl for female, MCH was 24.5 to 35.5 pg for male and 23 to 33 pg for female and MCHC was determined, 32.5 to 38g/l for male and 32.5 to 37.5g/l for female. **Conclusion:** Reference interval for haematological parameters for Afghan population are different from the western parameters.

## Differential Lipocalin-1 Levels in Keratoconus in a Malaysian Cohort

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**Introduction:** Keratoconus is an eye disorder characterised by corneal thinning. It is suggested that degenerative processes, inflammatory mediators and biochemical signalling are involved in the pathogenesis of keratoconus. Lipocalin-1 (LCN1) is a major protein component in tears which functions as an extracellular lipid binding protein in tears. Interestingly, LCN1 has been implicated in the prevention of dry eyes and removal of harmful lipophilic molecules. This study aims to identify differentially expressed proteins in Malaysian keratoconus patients and controls. **Methods:** Tear samples were collected from keratoconus patients ( $n = 7$ ) and normal controls ( $n = 8$ ). Proteins were separated using two-dimensional gel electrophoresis (2DE) and were detected using modified glutaraldehyde silver stain. Differently expressed protein levels were detected based on maximum fold change of  $> 1.5$  and  $p$ -value of  $< 0.05$  using Progenesis. False discovery rate was used to verify for any false-positive readings from the data analysis. Differently expressed protein spots were isolated and identified by MALDI-ToF/ToF. **Results:** Of the 600 protein spots detected, eleven spots were differentially expressed ( $p < 0.05$ ). Three of those were identified as LCN1 and immunoglobulin J chain. LCN1 was lower in keratoconus patients compared to healthy controls ( $p < 0.05$ ). **Conclusion:** The differential protein expression of LCN1 suggested its importance in maintaining homeostasis and viscosity of tears. The protein profiling may be used to screen for keratoconus.

**Keywords:** Keratoconus, Lipocalin 1, Tears, Proteomics, Malaysia

## Deciphering the Evolutionary Divergence of Bleg1\_2478 B3 Metallo- $\beta$ -Lactamase from Structural Perspective

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**Introduction:** Metallo- $\beta$ -lactamase (MBL) is a hydrolytic enzyme that deactivates  $\beta$ -lactam antibiotics predominantly used in combating bacterial infections. Previously, a hypothetical protein, Bleg1\_2437 (currently named as Bleg1\_2478) with properties similar to B3 subclass MBL was found to be evolutionary divergent. With recently solved Bleg1\_2478 crystal structure, its key structural and binding features with ampicillin compared to a model B3 subclass MBL would be able to shed light on its evolutionary divergence. This is addressed in the present study through *in silico* molecular docking approach. **Methods:** Crystal structures of Bleg1\_2478 and L1 B3 MBL from *Stenotrophomonas maltophilia* (PDB ID: 1SML, chain A) were docked with ampicillin using AutoDock4.2.6 software. The key interactions and structural features involved in substrate binding were analysed. **Results:** Results showed that long loop structures at the N- and C-terminals of Bleg1\_2478 and L1 active sites played a key role in interacting with the aromatic side chain and penam ring of ampicillin respectively, stabilised mainly by hydrophobic interaction contributed by amino acids at the N-terminal region. The “door”, “ceiling” and “floor” architectures observed in L1 MBL were present in Bleg1\_2478 and are postulated to be important in substrate accommodation at the active site. However, Bleg1\_2478 does not possess certain interactions observed in L1 MBL-ampicillin complex at certain domains. **Conclusion:** Based on these results, Bleg1\_2478 may have further differences in active site structure and key interactions than other closely related members of MBL superfamily. Further comparison on their structures may be able to yield more details on its evolutionary divergence.

**Keywords:** Bleg1\_2478, metallo- $\beta$ -lactamase, substrate binding, molecular docking

## Tocotrienol-Rich Fraction (TRF) Upregulates Antioxidant Genes of Human Endometrial Stromal Fibroblast Cells of Endometriosis

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**Introduction:** Endometriosis is a common gynecological inflammatory disease defined by the presence of endometrial-like glands and stroma throughout the pelvic cavity. It is often associated with pain and infertility as 30 to 50% of infertile women had been diagnosed with endometriosis. Tocotrienol-rich fraction (TRF) possesses potent antioxidant and anti-inflammatory activities. Therefore, the objective of this study was to investigate the effects of TRF on the cell viability and antioxidant genes of endometrial stromal fibroblast (eSF) cells. **Methods:** eSF cells were isolated from the endometrium of patients with endometriosis (PEC). PECs were cultured and incubated with 25, 50 and 75µg/ml of TRF (LCT carrier) or ETRF (MCT carrier) for 48 hours. Cells were then subjected for MTS assay after incubation period. The differential in antioxidant genes expression were measured by Real-time PCR (qRT-PCR). **Results:** There are no significant differences in the cell viability for 25ug/ml TRF-treated and 25ug/ml ETRF-treated cells in comparison to untreated cells. However, 50 and 75µg/ml of both TRF supplementation showed significant reduction in cell viability up to 10%. Hence, 50 and 75ug/ml supplementation of TRF and ETRF may affect PEC cells viability. SOD1 and SOD2 were significantly upregulated in TRF-treated cells ( $2.0 \pm 0.40$  and  $1.7 \pm 0.11$ , accordingly). While no significant changes on SOD genes expression were observed in other groups. **Conclusion:** TRF at a concentration of 25ug/ml may activate the expression of antioxidant genes and alleviate the oxidative stress in PEC.

**Keywords:** Tocotrienol-Rich Fraction, Tocotrienols, Oxidative stress, Endometrial Stromal Fibroblast Cells, Endometriosis

## Preliminary Evaluation of Optimised PCR-based Assay for the Detection of Pathogenic Familial Hypercholesterolaemia Gene Variants among Asian Population

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**Introduction:** Familial hypercholesterolaemia (FH) is an inherited disorder characterised by elevation low-density lipoprotein cholesterol levels, which leads to premature coronary artery disease (PCAD). Identification of pathogenic FH variants via genetic confirmation, may prompt early initiation of statins, therefore preventing PCAD. Current method for molecular confirmation of FH is next-generation sequencing (NGS), which is costly and time-consuming. In this study, an optimised tetra-amplification refractory mutation system (T-ARMS) PCR assay was developed and evaluated as a viable alternative to genotype pathogenic FH variants of low-density lipoprotein receptor (*LDLR*) and apolipoprotein B (*APOB*) genes among Asian populations. **Methods:** The T-ARMS PCR assay diagnostic evaluation was performed using 16 NGS-confirmed patients' DNA with pathogenic FH variants, and 17 normal patients' DNA. This assay was designed to detect 12 pathogenic *LDLR* and *APOB* gene variants, at a standardised annealing temperature of 64.6°C and analysed using 1.5% agarose gel electrophoresis. **Results:** The preliminary evaluation of the PCR assay revealed 100% for both sensitivity and specificity. The assay was also able to distinguish between homozygous and heterozygous pathogenic variants amongst the tested samples, which were consistent with the earlier NGS results. **Conclusion:** The promising results of the initial diagnostic evaluation of the optimised T-ARMS PCR implied its potential application as a cheaper and more accessible alternative FH genetic confirmation method, which is suitable to be used among Asian population. Future studies on engaging a larger sample size and multi-centre testing should present a clearer picture of its diagnostic performance.

**Keywords:** Familial hypercholesterolaemia, pathogenic variant, *LDLR*, *APOB*, T-ARMS PCR.

## Global Gene Expression of Obese Patients with Knee Osteoarthritis

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**Introduction:** The development and progression of knee osteoarthritis (OA) are closely related to obesity. Limited evidence on focusing the gene expression profile of OA SDFs in obesity. The objectives of this study were to characterize the genes and pathways of OA synovium derived fibroblasts (SDFs) in non-obese and obese subjects (BMI>27.5kg/m<sup>2</sup>). **Methods:** Synovium were collected from subjects who underwent arthroplasty and arthroscopy procedures (MREC reference no: 20164-2398) and grouped as non-OA and non-obese (G1, n=3), non-OA and obese (G2, n=3), OA and non-obese (G3, n= 3) and; OA and obese (G4, n=3). SDFs were isolated from the OA and non-OA synovium with the enzymatic digestion method. Total RNA extracted from SDFs were used for Clariom™ S Pico Assay. **Results:** A total 97 gene was upregulated in OA obese SDFs compared to non-OA SDF. The top 10 genes upregulated in OA obese SDFs were PLA2G2A, FGL2, CRIP1, KRBOX1, CGNL1, HPSE, PRRG4, IL13RA2, EPB41L4A and OMG. Among these genes, PLA2G2A and FGL2 are involved in systemic inflammation. Immunofluorescence staining demonstrated a positive expression of VCAM1 in OA SDFs, which may play a role in the infiltration of inflammatory cells in OA SM. Pathway analysis based on the upregulated genes in G4 showed upregulation of protein-protein interactions in podocytes, VEGFA/VEGFR2 signalling pathways. **Conclusion:** Our study identified a spectrum of genes up- and down-regulated in G3 and G4. The pathways identified would allow us to elucidate further the specific cell adhesion molecules that facilitate inflammatory cells infiltration in OA synovium.

**Keywords:** Osteoarthritis, Obesity, Gene expression, Inflammation

## Interaction between *In Utero* BPA Exposure and Postnatal Trans Fat Diet on Small Intestine Function of Male Sprague Dawley Rats

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**Introduction:** Bisphenol A (BPA) level has been associated with higher body mass index children and adults, as well as gut inflammation. Studies reported conflicting findings on BPA exposure impact on the gastrointestinal function and the risk of obesity. Thus, this study aimed to investigate whether *in utero* BPA exposure and postnatal TFD poses synergistic effects on the small intestine morphology and increases the risk of obesity. **Methods:** Twelve pregnant Sprague Dawley rats were divided into two groups: vehicle control (P80) and BPA-exposed (BPA; 5 mg/kg/day) until end of gestation. Twenty-four male offsprings from the pregnant rats were weaned off at postnatal week (PNW) 3 and were fed with either normal diet (ND) or 25%kcal TFD from PNW3–13; grouped into P80-ND, P80-TFD, BPA-ND and BPA-TFD groups. Body weight (BW), WC, water and food intake of offsprings were measured weekly from PNW3 to PNW13. **Results:** Increase in BW and WC were observed as offsprings developed from weanlings (PNW3) to adults (PNW13), with significant differences in BW observed between P80-TFD vs BPA-ND from PNW11 ( $470.7 \pm 13.1$  vs  $431.2 \pm 11.1$  g;  $p < 0.05$ ) to PNW13 ( $521.5 \pm 15.1$  vs  $469.8 \pm 13.9$  g;  $p < 0.01$ ). Additionally, P80-ND consistently showed significantly higher food and water intake than BPA-TFD from PNW7–12. However, for histology, no significant differences were observed in villi length and width, and crypt length between all groups. **Conclusion:** Our findings suggest that prenatal BPA with and without postnatal TFD may have no significant effects on the small intestinal architecture which could lead to obesity development.

**Keywords:** *in utero* BPA exposure, postnatal trans fat diet, obesity, small intestinal function

## Natural Quinones Induce ROS-Mediated Apoptosis and Inhibit Cell Migration in PANC-1 Human Pancreatic Cancer Cell Line

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**Introduction:** Pancreatic cancer is a malignancy with poor prognosis and high mortality rates worldwide. Thymoquinone, plumbagin, and juglone, are *natural quinones*, widely reported for promising anticancer effect on different cancer cells. However, the cytotoxic activity and their anti-metastatic effects are unknown against human pancreatic cancer cell line (PANC-1). **Methods:** Cytotoxic activity of quinones was evaluated on PANC-1 cells through MTT cell viability assay. Next, apoptosis was assessed through morphological changes, AO/EB staining and further confirmed by Annexin-V-FITC staining assay. ROS generation was quantified by DCFDA fluorescent probes. Anti-migratory effect was studied by wound healing (scratch) assay and MMP-9 assay. **Results:** Cell viability significantly decreased in a dose-dependent manner with the IC<sub>50</sub> value of 5.72, 5.74 and 22.22  $\mu$ M respectively for juglone, plumbagin and thymoquinone after 24-hour treatment. *Typical apoptotic morphology was demonstrated in treated PANC-1 cells compared to control.* Flow cytometry analysis following Annexin V-FITC and PI staining demonstrated the potency of quinones to induce early and late apoptosis in treated cells. ROS accumulation confirmed the involvement of the mitochondrial intrinsic pathway. Wound healing potential of all three quinones were demonstrated by inhibiting cell migration in a time-dependent manner. Only juglone dose-dependently reduced MMP-9 expression in treated PANC-1 cells, which was in accordance with its effect on cell migration whereas plumbagin and thymoquinone showed no effect. **Conclusion:** In conclusion, thymoquinone, plumbagin, and juglone significantly inhibited cell growth and induced ROS-mediated apoptosis in PANC-1 cells. In addition, they could be potent anti-metastatic agents due to their anti-migratory effect against PANC-1 cells.

**Keywords:** pancreatic cancer, quinones, cell viability, apoptosis, anti-metastatic

## Cytotoxicity effects of Allicin towards human oral squamous cell carcinoma (OSCC) cell lines, ORL-48 and SCC-15

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**Introduction:** Oral squamous cell carcinoma (OSCC) has been a contributing factor to 90% to 95% of oral malignancies. The 5-year survival rate for patients with oral cancer has been stagnant at 50% for decades. Despite many advances in treatment and prognosis, the main solution for oral cancer is chemotherapy and surgery. The genotoxic drug, cisplatin has been introduced as an alternative for the treatment. However, cisplatin has been studied to give out repercussions such as nausea, diarrhea, pain and vomiting. Therefore, a more reliable anticancer agent has to be discovered. Allicin (diallylthiosulfinate) has been known for decades for its antioxidant, antimicrobial, antifungal and anti-inflammatory activities. Serving as an anticancer agent is also allicin's most prominent advantage and has been studied in numerous types of cancer cells. In a dose-dependent manner, allicin has been studied to inhibit proliferation on cancer cells. Unfortunately, not many studies reported on oral cancer cell lines. Hence, this paper will provide an overview of the research framework to investigate cytotoxicity effects of allicin in oral cancer cell lines, ORL-48 and SCC-15 in comparison with cisplatin. **Methods:** Pure compound allicin at final concentration of 10 µg/ml, 15 µg/ml, 20 µg/ml, 25 µg/ml, 50 µg/ml, 75 µg/ml and 100 µg/ml was diluted and used in the experiment. The in vitro cytotoxicity test was determined by WST-1 assay. **Results and conclusion:** The expected findings may reveal the cytotoxicity effects of allicin towards oral cancer cell lines, ORL-48 and SCC-15.

**Keywords:** oral cancer, allicin, OSCC, cytotoxicity, cisplatin.

## Evaluation of Cadmium Treatment on ATP Level, Cell Membrane Integrity and Cell Viability in *Caco-2* Cell Line

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**Introduction:** Human exposure to heavy metals via food, water, and air pollution may partially explain the higher incidence of non-communicable diseases. Cadmium is one of the most hazardous heavy metals for human health. This study aimed to evaluate cell viability, ATP level and cell membrane integrity in *Caco-2* treated with cadmium. **Methods:** *Caco-2* cells were cultured in DMEM (5 mM galactose) and treated with different cadmium concentration (0.25, 1, 2.5, 5, 7.5, 10 and 20)  $\mu\text{g/ml}$  for 24, 48, 72 and 192 hours. ATP level, cell viability and membrane integrity were measured using CellTiter-Glo Luminescent Cell Viability and Mitochondria ToxGlo Assay. **Results:** ATP level decreased once cadmium concentration was increased (48.6% - 6.9% at 24 hours; 21.09% - 1.09% at 48 hours; 15.76% - 0.47% at 72 hours; and 13.3% - 0.63% at 96 hours). Cell viability test indicated  $\text{IC}_{50}$  of 171  $\mu\text{M}$ , 100.52  $\mu\text{M}$ , 69.66  $\mu\text{M}$  and 72.86  $\mu\text{M}$  for 24, 48, 72, and 96 hours, respectively. Protease level decreased once cadmium concentration was increased (62.5% to 40.1% at 24 hours; 80.86% to 62.14% at 48 hours; 85.44% to 66.71% at 72 hours; and 69.97% to 57.22% at 96 hours). **Conclusion:** The results showed that regardless of cadmium concentration, ATP level decreased with longer exposure time. After cadmium exposure in *Caco-2*, ATP level decreased in a dose- and exposure time-dependent manner. A higher concentration of cadmium indicates the lower activity of protease released from the membrane-compromised cell. Cadmium demonstrated a biphasic dose-response phenomenon characterized by low-dose stimulation and high-dose inhibition.

**Keywords:** Cadmium, *Caco-2*, ATP, membrane integrity, protease level

## Apoptotic Mechanisms of Tocotrienol Isomers towards Oral Squamous Carcinoma Cell Lines, ORL-48.

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**Introduction:** Tocotrienol is a subgroup of Vitamin E and it is divided into four isomers known as alpha-, beta-, gamma-, and delta-tocotrienol. These compounds can be found in nature where their major source is palm oil. Recent studies showed that tocotrienol is effective in inducing apoptosis to other cancer cell lines such as cervix (HeLa cell line), lung (A549 cell line), brain (U87MG cell line) and neuroblastoma (SH-SY5Y cell line). This paper aims to investigate the effectiveness of tocotrienol isomers in inducing cell death of oral squamous carcinoma cell lines, ORL-48. **Methods:** The pure compounds of  $\gamma$ - and  $\delta$ -tocotrienols at the concentration of 50  $\mu\text{M}$ , 75  $\mu\text{M}$ , 100  $\mu\text{M}$ , 125  $\mu\text{M}$  and 150  $\mu\text{M}$  were used in the experiment. The *in vitro* cytotoxicity of tocotrienol isomers on ORL-48 was determined by using MTS Cell Proliferation Colorimetric Assay. The cell death mechanism of the isomers on ORL-48 was analysed by using TUNEL Assay. **Results and Conclusion:** The expected findings may reveal the toxicity of tocotrienol isomers on ORL-48, and the mode of cell death induced by the isomers on ORL-48. A review of relevant literature on anti-cancer properties of tocotrienol isomers also be presented in this paper.

**Keywords:** Vitamin E, tocotrienols, apoptosis, oral squamous carcinoma cell lines

## Modulation of Small Interfering RNA in Newcastle Disease Virus Persistently Infected Colorectal Cancer Cells

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**Introduction:** Newcastle disease virus (NDV) is an oncolytic virus that shows promising results in various cancer cell lines both *in vitro* and *in vivo*. During the course of infection, some cancer cells develop resistance to NDV infection while permitting the virus to replicate within the cells. Mechanism involved is yet to be elucidated. **Methods:** In this study, we aimed to develop several persistently NDV-infected (PI) colorectal cancer cell lines, including HCT116, RKO and LoVo to study the mechanism in the persistence of infection. These cancer cell lines were infected with recombinant NDV expressing green fluorescent protein, (rAF-GFP). After three rounds of infections, the NDV-resistance subpopulation in each cell lines emerged. **Results:** GFP expression of these PI cells were confirmed by flow cytometry. Virus released from these PI cells are infectious and able to form plaques on cancer cells. Annexin V/propidium iodide assay revealed that the PI cells elevated in level of apoptotic markers. Upregulation of pro-survival Bcl-2 proteins that detected in PI cells suggested that these proteins expression promoted cellular viability under viral persistent infection. Small RNA will be used to knockdown the elevated proteins to enhance the NDV therapeutic effect. **Conclusion:** This study describes the potential key players that contribute to PI development of NDV in colorectal cancer cells.

**Keywords:** Newcastle disease virus, colorectal cancer, persistent infection

## Expression of Dominant AMPK Gamma 1 Subunit Gene in Post-mortem Obese Human Perihepatic Adipose Tissue

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**Introduction:** Adenosine monophosphate (AMP)-activated protein kinase (AMPK), regulator of energy balance, is a heterotrimeric complex consisting of  $\alpha$  catalytic subunit and  $\beta$  and  $\gamma$  regulatory subunits. Theoretically, 12 possible complexes have been formed exhibiting differential tissue specificity, in muscle three complexes were identified ( $\alpha 2\beta 2\gamma 1$ ,  $\alpha 2\beta 2\gamma 3$ , and  $\alpha 1\beta 2\gamma 1$ ) whilst one in liver ( $\alpha 1\beta \gamma 1$ ). The aim of this study is to determine the dominant AMPK subunit genes present in perihepatic adipose tissue.

**Methods:** Perihepatic adipose tissue was collected from post-mortem cases (32 lean; 33 obese) at the National Institute of Forensic Medicine (IPFN), Hospital Kuala Lumpur. Total RNA was extracted from perihepatic adipose tissues with its quantity and integrity determined by bioanalyzer. Gene expressions of all AMPK subunits were studied by real-time polymerase chain reaction using SYBR-green as a fluorophore detection. Then, comparative  $2^{-\Delta\Delta Ct}$  method was used to calculate the relative expression of each target gene; with the expression levels of all genes normalized to that of GAPDH, RPLP0 and HPRT1. Mean differences were evaluated by Mann-Whitney test for two-sample comparison using SPSS 26.0 (SPSS Inc., USA).

**Results:** There were no significant difference of  $\alpha$  and  $\beta$  subunits gene expressions in both lean and obese individuals. For gamma subunits, gene expressions of  $\gamma 2$ - and  $\gamma 3$ -subunits were lower whilst only  $\gamma 1$ -subunit was significantly higher in obese ( $U = 367, p = .034$ ) compared to lean individuals.

**Conclusion:** Results show that the dominant AMPK subunit genes present in perihepatic adipose tissue among obese individuals is  $\gamma 1$ . This suggests that  $\gamma 1$ -subunit present in perihepatic adipose tissue is specific to obesity.

**Keywords:** AMPK, gamma subunit, adipose tissue, post-mortem, human

## Primer and Probe Conservation Issue in the Quantification of Hepatitis B Virus DNA

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**Introduction:** Current treatment strategies for chronic hepatitis B virus (HBV) infection aim at long-term suppression of the viral replication since a cure remains elusive. Its clinical management therefore relies greatly on routine monitoring of serum HBV DNA levels using a quantitative polymerase chain reaction (qPCR) assay. Designing a highly conserved oligo set for the qPCR assay can be challenging due to the high genetic heterogeneity of the virus. The ever-increasing number of HBV genomes deposited in the GenBank nucleotide database warrants a revisit to previous primer and probe designs. **Methods:** We examined primer and probe sets from 53 qPCR assays published in the past two decades for their coverage in 9,864 complete HBV genomes retrieved from the GenBank, as well as the primer and probe binding affinity through DNA thermodynamics analysis. **Results:** Of all the 53 qPCR assays, only 17% achieved  $\geq 80\%$  coverage. About 40% of the 53 assays covered less than 20% of the 9,864 genomes. In silico DNA thermodynamics analysis demonstrated reduced primer/probe binding affinity, which further increases the risk of viral load misdetection and underestimation for certain HBV variants. **Conclusion:** Taken together, there is a pressing need for improving available qPCR designs for the quantification of HBV DNA based on the updated genome data.

**Keywords:** HBV DNA quantification, nucleic acid testing, viral load, real-time PCR, qPCR assay

## Glycosylation Inhibitory Effect of 1-DNJ Towards Extracellular Matrix Proteins Expression in Osteosarcoma Cells

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**Introduction:** Rapid progression of cancer cells towards metastasis particularly in highly metastatic osteosarcoma is mainly attributable to cell migration involving interactions between cell-cell and cell-extracellular matrix (ECM). ECM proteins are regulated by glycosylation of integrins of which when aberrant, increases the rate of cancer cells migration and invasion. Inhibition of the aberrant glycosylation by 1-Deoxynojirimycin (1-DNJ) towards alpha-glucosidase reduced migration rate of melanoma cells. Thus, this study aims to investigate the glycosylation inhibitory effect of 1-DNJ towards ECM proteins osteosarcoma cells. **Methods:** Two types of osteosarcoma cells, MG63 and HOS143B were treated with 1-DNJ at concentration of 0.5mM. At post- 24 hours treatment, total cellular protein was extracted for Western blot (WB) analysis while scratch assay was performed on another set of treated cells. **Results:** WB result showed high level of expression of ECM proteins; collagen type II (COL II), fibronectin (FN), and vitronectin (VN) in 1-DNJ treated cells of both types compared to the control (non-treated). Scratch assay results revealed higher rate of cell migration in both MG63 and HOS143B treated cells compared with control. **Conclusion:** Results showed that inhibition with 1-DNJ intensified the effects of aberrant glycosylation in osteosarcoma cancer cells, as evidenced by increased ECM protein expression and cell migration rate. Nonetheless, osteosarcoma metastasis involves various cellular microenvironment factors which further investigation to elucidate the underlying mechanism between aberrant glycosylation and cancer cell progression. Various external factors may also involve in migration process hence further research is required to fully understand 1-DNJ's mechanism in OS cancer progression.

**Keywords:** 1-Deoxynojirimycin, Extracellular Matrix Proteins, cell migration, osteosarcoma cells, aberrant glycosylation

## Effect of hsa-miR-3131 Transfection Upon Cell Viability in Imatinib Sensitive and Imatinib Resistance Chronic Myeloid Leukemia Cells

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**Introduction:** Chronic myeloid leukemia (CML) is a myeloproliferative disorder characterized by the Philadelphia chromosome and the BCR-ABL fusion gene. Despite tyrosine kinase inhibitors (TKIs) wide application, TKIs resistance occurred in nearly 20-30% of chronic myeloid leukemia (CML) patients. Identification of new molecular therapeutic target to overcome TKI resistance is in demand. MicroRNAs (miRNAs) are small, noncoding, single-stranded RNAs that consist of 18 to 25 nucleotides that participate in various cellular processes by posttranscriptional regulating gene expression. microRNA has demonstrated potential as a biomarker for cancer diagnosis, prognosis, and therapeutic targets. In present study, our aim was to determine cell proliferation and viability of K562-s and K562-r cells transfected with hsa-miR-3131. **Methods:** Imatinib IC<sub>50</sub> for 24h and 48h in both cells were determined. miRNA targeting 3'UTR of ABL1 was verified using DIANA TOOLS, the micro-T CDS. **Results:** In-silico analysis shows that miR-3131 has a strong binding conformity with 3'UTR of ABL1 with the miTG score of 0.97. Hence, mir-3131 was selected to be transfected with both cells. The study included four groups which are the (hsa-miR-3131), (Imatinib), (hsa-miR-3131 & Imatinib), (no transfection control) and (miR-1 as the positive control). All groups were transfected and incubated for 24h, 48h and 72h for cell proliferation using MTS assay. Results of IC<sub>50</sub> for K562-s and K562-r cell for 24h were 45.3  $\mu$ M and 60.5  $\mu$ M, while for 48h IC<sub>50</sub> were 2.38  $\mu$ M and 23.47  $\mu$ M, respectively. Hsa-mir-3131 transfected into K562-s was able to inhibit cell proliferation at 72h with the lowest cell viability of 78%. Whilst the K562-r cell proliferation was highly inhibited when transfected with hsa-miR3131 during 48h with 83% cell viability. However, hsa-miR-3131 transfected K562-s cells did show an increase of inhibition of 8.9% with Imatinib addition compared when treated with Imatinib alone during 24h. **Conclusion:** Although hsa-mir-3131 may retain certain effect towards the CML cell proliferation, it is highly suggested to determine its molecular mechanism underlying CML cells proliferation.

## GAS5 Associated CeRNA Network in Lower Grade Glioma

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**Introduction:** Grade II and grade III lower grade gliomas (LGG) consist of astrocytic, oligo-astrocytic and oligodendroglia. Although LGG has a better survival rate compared to patients with glioblastoma multiforme (Grade IV glioma), it is a fatal disease of young adults because grade II lesions can eventually progress to high-grade glioma (Grade III and IV). Long noncoding RNA GAS5 has been identified as a tumour suppressor gene located at chromosome 1q25 with low levels of GAS5 expression associated with poor overall survival in cancers. GAS5 associated regulatory axis can be targeted as potential therapeutic targets or biomarkers in lower grade glioma. **Methods:** In this study, we grouped the TCGA-LGG dataset into high (n=125 samples) and low level (n=128 samples) of GAS5 expression, and using the bioinformatics methods, GAS5 associated competing endogenous RNA (ceRNA) network was constructed to identify GAS5 regulatory axis in lower grade glioma. **Results:** Gene set enrichment analysis showed low GAS5 group has high enrichment score in the epithelial mesenchymal transition (EMT) gene set. ceRNA network including genes from EMT gene set was established. EMP3, TNFRSF11B and TIMP3 genes were found to be upregulated in low GAS5 expression group. **Conclusion:** By analysing TCGA-LGG dataset, we identified EMP3, TNFRSF11B and TIMP3 are negatively regulated by GAS5. The ceRNA network can further be evaluated as potential therapeutic targets or potential biomarkers in LGG.

**Keywords:** Glioma, lncRNA, bioinformatics

## Synthesis and Cytotoxic Effects of Novel Paclitaxel (PTX)-loaded PLGA (Poly (lactic-co-glycolic acid) Nanoparticle Bio-conjugate with EGFR Monoclonal Antibody for Triple Negative Breast Cancer

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**Introduction:** Triple negative breast cancer (TNBC) is categorized as an aggressive subtype of breast cancer that expressed EGFR receptor. Currently, Paclitaxel is a standard chemotherapy drug that is used in treatment. Delivery of this drug can be improved for targeted therapy by binding to EGFR receptor. **Objective:** The aim of this study was to develop an efficient drug delivery system for specifically targeting the TNBC cells without affecting healthy cells by formulating the Paclitaxel (PTX)-loaded PLGA (Poly (lactic-co-glycolic acid) nanoparticle bio-conjugate with EGFR monoclonal antibody (mAb). **Methods:** The nanoparticles were synthesized by the using double emulsification solvent evaporation method. The integrity of mAb was confirmed by performing SDS page. Subsequently. Cytotoxicity of the PTX-loaded PLGA nanoparticles was tested in TNBC cell line (MDA-MB-231) with MTT assay. **Results and Discussion:** The sizes of the PTX-loaded PLGA nanoparticles were approximately 120 nm. The SDS PAGE analysis indicated that the mAb integrity remained the same after conjugation with nanoparticles. The cytotoxicity activity was confirmed by using MDA 231 cell line with MTT Assay with an inhibitory concentration (IC<sub>50</sub>) of 2 mg. Results indicated that the and antibody conjugated nanoparticles showed best specific targeting of the EGFR receptor in MDA 231 cells. **Conclusion:** Current study suggest that the anti-EGFR anchored PTX loaded nanoparticle may have the ability to target the TNBC cells and could potentially improve the therapeutic action of PTX.

**Keywords:** Triple negative breast cancer (TNBC), PLGA Nanoparticles, EGFR monoclonal antibodies

## Hyperglycaemia Disrupts FKN and RANK-RANKL-OPG System in A Pregnant Rat Model

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**Introduction:** Diabetic pregnancy is linked to heightened inflammatory state, which is the root cause for various complications. Fractalkine (FKN) and RANK-RANKL-OPG system are inflammatory markers associated with angiogenesis and vascular calcification. This study aims to examine the effects of hyperglycaemia on pregnancy outcomes and its association with the levels these markers in maternal serum and placental tissue. **Methods:** Pregnant female *Sprague-Dawley* rats were injected with 45mg/kg body weight of Streptozotocin on gestational day (GD) 7 to induce hyperglycaemia. The control group was injected with the vehicle. The pregnancies were monitored until experimental endpoints at GD15 and GD21. Pregnancy outcomes were documented. Placenta and maternal plasma were collected for protein levels and mRNA expressions of FKN, RANK, RANKL and OPG. **Results:** Hyperglycaemia resulted in a significant reduction of maternal daily body weight despite an increased in daily food consumption. There was also an increase in foetal resorption and a reduction in foetoplacental weight ratio in the hyperglycaemic group. There was a significant increase in circulating FKN, RANKL and OPG together with increased placental FKN levels. OPG mRNA expression was also upregulated in the placental tissue. **Conclusion:** Maternal hyperglycaemia alters systemic and local FKN and RANK/RANKL/OPG system. These inflammatory markers are known to cause vascular remodeling and calcification in the peripheral artery disease. Disruption of these markers in maternal hyperglycaemia could be responsible for the adverse pregnancy outcomes observed in this study. Further investigation need to be done to evaluate the possibility of advanced aging and microcalcification in the placenta.

**Keywords:** Hyperglycaemia, FKN, RANK-RANKL-OPG, placenta, rat

## Exopolysaccharide (EPS) from *Bifidobacteria pseudocatenalatum* Induced Apoptosis Cell Death in Caco-2 Cells

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**Introduction:** Exopolysaccharide (EPS) is one of the bacterial components, predominantly studied in lactic acid bacteria (LAB). Its crucial roles are evidenced in probiotic activity including survival, adhesion, and anti-tumor/cancer effect. Several studies have also reported that LAB EPS exhibited highest cytotoxicity effect and mitigated colorectal cancer (CRC) cells proliferation when compared to other bacterial components. Besides LAB, another probiotic known as Bifidobacteria also inhabit the human colon and produce EPS likewise. However, the EPS has not been well explored. Thus, the aim of this study is to investigate its potential specifically in susceptibility to CRC treatment. **Methods:** *Bifidobacteria pseudocatenalatum* was cultured in rice wastewater medium. EPS was extracted and purified. Caco-2 cells were treated with EPS at concentrations 1, 5 and 10 mg/ml. Cytotoxicity level was determined at 24- and 48-hour time point using MTS assay. Apoptosis analysis were performed using Annexin V and cell cycle assay. 30  $\mu$ M Rapamycin was used as positive control. **Results:** EPS was able to inhibit Caco-2 cells proliferation in dose- and temporal-dependent manner. With viable cells at 44%, 5 mg/ml EPS at 48-hour time point was used for further experiments. The EPS-treated Caco-2 cells has highlighted an increase in early and late apoptosis induced cell death as compared to negative control ( $P < 0.001$ ). In addition, EPS also increased sub G2/M population of Caco-2 cells ( $P < 0.001$ ). **Conclusion:** These fundamental findings revealed potential anticancer properties of EPS through apoptosis in CRC. EPS is part of probiotics which naturally inhabits human colon; thus, the results may support the application of EPS as prospective therapeutic in the treatment of CRC in the future.

**Keywords:** Exopolysaccharide, Bifidobacteria, Colorectal cancer, Caco-2 cells, Apoptosis

## Optimization of Milk Fermentation Incorporated with Recombinant *Lactococcus lactis* NZ3900

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**Introduction:** *Lactococcus lactis* NZ3900 is a common food-grade recombinant strain used for protein expression and a potential delivery carrier for orally-administrated vaccines. However, the lactococcal strain could be susceptible to gastrointestinal digestion. Hence, milk could serve as a protective matrix and nutrient source for the recombinant *L. lactis*. This study aimed to optimize the formulation and fermentation condition of *L. lactis* NZ3900-fermented milk to achieve high viability and low syneresis. **Methods:** The milk was fermented using a recombinant *Lactococcus lactis* NZ3900 strain expressing a cancer peptide vaccine. The formulation and condition of milk fermentation were optimized using the Box-Behnken design. The effect of initial inoculum concentration (5, 10, 15% v/v), fermentation time (18, 24, 30 h), and fermentation temperature (23, 30, 37°C) on viability and syneresis of the *L. lactis*-fermented milk was investigated. Three commercial fermented milk served as control. **Results:** The predicted responses of maximum viability (9.56 log<sub>10</sub> CFU/mL) and minimum syneresis (59.6%) for *L. lactis* NZ3900-fermented milk was obtained by 11.2% (v/v) initial inoculum concentration, 30 h fermentation time, and 27 °C fermentation temperature. The viability of the *L. lactis* NZ3900 in fermented milk displayed higher as compared to all three of the commercial fermented milk. Furthermore, the syneresis of the *L. lactis* NZ3900 falls within the range of commercial fermented milk. **Conclusion:** This study demonstrated that milk acts as a good carrier for food-grade recombinant *L. lactis* NZ3900 and the *L. lactis* NZ3900-fermented milk has the potential to be developed as an orally-administrated approach for vaccine delivery.

**Keywords:** Fermentation, *Lactococcus lactis*, milk, recombinant vector, oral vaccine.

## Determination of Total Phenolic Content and Antibacterial Activities of Malaysian Traditional Plants against Selected Pathogenic Bacteria

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**Introduction:** Malaysia has vast species of medicinal plants that are traditionally used to combat diseases, thus, it has been counted as one of the 12 megadiverse nations with high rate of endemism. Many researches have been conducted on Malaysia medicinal plants as antibacterial agents. However, lack of scientific studies to prove the effectiveness of these plant materials is of great concern. **Methods:** The in vitro antibacterial activities of 5 Malaysian medicinal methanolic crude extracts were determined using broth dilution method against six different strains of pathogenic bacteria; *Escherichia coli* 0157:H7, *Escherichia coli* (ATCC 25922), *Listeria monocytogenes* (ATCC 19115), *Salmonella paratyphi* (ATCC 9150), *Salmonella typhi* (ATCC 14028), *Staphylococcus aureus* (ATCC 700699). Total phenolic content (TPC) was determined using Folin-Ciocalteu's (FC) method. The results were expressed as microgram of gallic acid equivalents per milligram extract ( $\mu\text{g GAE/mg extract}$ ). **Results:** Most of the extracts exhibited antibacterial activities against two or more tested bacteria with the lowest minimum inhibitory concentration (MIC) value of 31.25  $\mu\text{g/ml}$  obtained from the bark extract of *Cinnamomum verum* against *Listeria monocytogenes*. The total phenolic content (TPC) of each extract was calculated using the gallic acid calibration curve. Bark extract of *Cinnamomum verum* was observed to possess the highest total phenolic content of  $437.03 \pm 3.59 \mu\text{g GAE/mg}$ . **Conclusion:** Our findings suggest the possibility of using the bark extract of *Cinnamomum verum* as a new source of natural antibiotics in future.

**Keywords:** Methanolic crude extracts, antibacterial screening, Total phenolic content. Malaysian traditional plants.

## Evaluating the Specificity of a Bacterial Leukotoxin LtxA on Targeting Human Integrin: Towards A Potential Therapeutic Agent against LFA-1 Mediated Autoimmune Diseases

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**Introduction:** Leukotoxin (LtxA) is a bacterial protein secreted by an oral bacterium *Aggregatibacter actinomycetemcomitans* that possesses an intrinsic specificity to target the active form of lymphocyte function-associated antigen (LFA-1; CD11a/CD18). Due to this unique repertoire, Leukotoxin is currently being developed as a first-in-class biologic agent in treating LFA-1 related immune disorders. However, using native LtxA as a therapeutic agent would propel the immunopathogenesis of rheumatoid arthritis. Therefore, this study aims to engineer the LtxA to becoming a potential biologic agent that without the side effect to target the cells possessing the active form of LFA-1. **Methods:** The recognition domain of LtxA was fused with a vision tag Green Fluorescent Protein (GFP) using standard recombinant techniques. Protein expression was conducted and optimized by fine-tuning the expression parameters such as expression temperature, inducer concentration, and expression durations to maximize the expression level for LtxAR-GFP. The insoluble protein was solubilized in 8M urea and protein purification was performed under denatured condition via affinity chromatography. Subsequently, stepwise dialysis was performed for protein refolding. **Results:** The recombinant LtxAR-GFP protein was successfully expressed in *E. coli* as indicated by a presence of an over-expressed 85kDa protein. **Conclusion:** In this study, the recombinant construct constituted by the recognition domain of LtxAR fused and the GFP were successfully expressed. The construct will be used for further elucidation of the interaction of LFA-1 and LtxA.

**Keywords:** LtxA, LFA-1, immune disorders

## Isolation and Characterization of Prenyltransferase Isomers from *Boesenbergia rotunda*

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**Introduction:** Prenylated flavonoids exhibit beneficial effects on human health. Nevertheless, the low abundance of prenylated flavonoids in nature has limited their applications. Prenyltransferase (PT), an enzyme involved in the prenylation process is crucial in catalysing prenylflavonoids. To date, only a few flavonoid-related PT genes have been identified probably due to the membrane-bound nature of PTs. Hence, this study aimed to isolate and characterise PTs from a medicinal ginger, *Boesenbergia rotunda* (designated as *BrPT1*). **Methods:** The full-length cDNA of *BrPT1* isolated from *B. rotunda* using PCR was characterized by determining its molecular weight (MW) and isoelectric point (pI) using Compute MW/pI ([https://web.expasy.org/compute\\_pi/](https://web.expasy.org/compute_pi/)). The deduced amino acid sequence of *BrPT1* was aligned with other PTs using ClusterW before constructing a phylogenetic tree using the neighbourhood-joining method with a bootstrap value of 1000 using the Molecular Evolutionary Genetics Analysis version 10 (MEGAX). Conserved motif sequences were analysed using Multiple Em for Motif Elicitation (MEME) (<https://meme-suite.org/meme/tools/meme>), whereas transmembrane domains were predicted using TMHMM (<http://www.cbs.dtu.dk/services/TMHMM/>). **Results:** The isolated cDNA of *BrPT1* (1,197 bp) encodes a predicted 398 amino acid residues with a molecular weight of 44.6 kDa and pI of 9.86. *BrPT1* has 9 transmembrane domains. Phylogenetic and motif sequence analysis showed that *BrPT1* belongs to the HG family, sharing homologies with homogentisate PTs involved in tocopherol biosynthesis. **Conclusion:** The isolated *BrPT1* is a prenyltransferase localised in the plastid, predicted to be involved in the biosynthesis of tocopherol.

**Keywords:** Prenyltransferase, flavonoids, ginger, biotechnology

## Identification and Characterization of Novel non-protein coding RNAs (npcRNAs) associated with Global Transcriptional Regulator, Hfq in Pathogenic Bacteria *S. Typhi*

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**Introduction:** Most of cellular pathways involve in bacterial pathophysiology is regulator by non-protein coding RNAs (npcRNAs). In Gram negative bacteria the binding of Hfq protein and npcRNA facilitates its binding to the targeted mRNAs. Hfq gene is conserved in a wide variety of bacteria and it involved in many cellular functions such as stress adaptation and regulation of gene expression. **Methods:** The Hfq gene of *S. Typhi* was amplified and recombined in pET28b+ to be transformed into TOP10 cells. The bacterial with recombinant plasmid was screened by antibacterial selection and confirmed by sequencing. The recombinant plasmid was transformed into *E. coli* BL21 and induced the expression with IPTG. The over expressed Hfq protein was purified using Ni-NTA affinity chromatography. The purified Hfq protein will bind with *S. Typhi* npcRNAs to identify all possible Hfq protein binding npcRNAs. **Results:** Hfq gene had been successfully cloned into pET-28b(+) vector and transformed into TOP10 and BL21. the binding assay between total RNA and purified Hfq protein were carried out and the bound RNA were precipitated and sent for sequencing. **Conclusion:** The Hfq protein of *S. Typhi* was purified successfully and the Hfq bound RNAs were sent for Illumina Sequencing to identify the npcRNAs which is regulated by Hfq protein.

**Keywords:** *Salmonella enterica* serovar Typhi (*S. Typhi*), non-protein coding RNA, Hfq protein, over-expression.

**Acknowledgement:** We would like to acknowledge Ministry of Higher Education for financing this work under Fundamental Research Grant Scheme (FRGS) FRGS/1/2018/STG03/AIMST/02/2

## Knocking-out the Non-protein Coding RNA Gene (PmiR-137) in *Proteus mirabilis* to Understand Its Role in Pathogenesis

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**Introduction:** *Proteus mirabilis* is a Gram-negative, facultatively anaerobic rod-shaped bacterium, best known for its form of multicellular surface mobility termed swarming. *P. mirabilis* causes symptomatic urinary tract infections (UTI) such as cystitis and pyelonephritis, and also catheter-associated urinary tract infections (CAUTI). Our recent study revealed 240 Hfq-associated novel non-protein coding RNAs (npcRNAs) in *P. mirabilis*. One npcRNA of interest is PmiR-137, which is predicted to regulate virulence by association with the mRNA of fimbriae and flagella proteins. **Methods:** Plasmid pKD46 was transformed into *P. mirabilis* and screened using ampicillin marker. The deletion DNA fragment with kanamycin resistance gene, FRT sites and 100 bps of homologous sequence from the flanking regions of PmiR-137 gene was amplified by PCR and transformed into *P. mirabilis* with pKD46. To detect PmiR-137 mutants, the transformed colonies were selected on kanamycin plate and verified by PCR using FRT-specific primers. **Results:** The plasmid with lambda red-recombinase gene, pKD46 was successfully transformed into *P. mirabilis*. The deletion fragment was also successfully transformed into *P. mirabilis* with pKD46. Screening of colonies with FRT-specific primers resulted the PCR products with desired length. **Conclusion:** We obtained the PmiR-137 knock-out strain of *P. mirabilis*. The knock-out of the npcRNA gene will be further confirmed by sequencing analysis and the mutant strain will be used for functional characterization of npcRNA PmiR137.

**Keywords:** *Proteus mirabilis*, non-protein coding RNA, knock-out, lambda red-recombinase.

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## Identification of Cucumber-Associated Fungus by Using Recombinase Polymerase Amplification (RPA) Method

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**Introduction:** Agricultural crops often suffer from various diseases which causes great loss to the economy. A simple and rapid identification method of phytopathogen for an early warning and quick response is very important to aid in the disease management process. In this study, rapid identification method for species-specific diagnosis of fungi causing severe leaf blight in *Cucumis sativus* was established using recombinase polymerase amplification (RPA). **Methods:** *Fusarium incarnatum* and *Aspergillus japonicus* were isolated and identified from diseased leaves of *C. sativus*. The fungus was subjected to pathogenicity test to prove Koch's postulate and species-specific RPA primers for *F. incarnatum* and *A. japonicus* were designed based on sequence divergence within translation elongation factor 1 alpha (TEF-1a) and calmodulin (CaM) gene. **Results:** With incubation temperature of 37°C, fragments of TEF-1a and CaM gene were successfully amplified within 20 minutes. **Conclusion:** This method allows for rapid and sensitive detection of *F. equiseti* and *A. japonicus*, and will be useful in the disease management and rapid detection to prevent further spread of this pathogen.

**Keywords:** *Cucumis sativus*, pathogenic fungi, molecular diagnosis, recombinase polymerase amplification (RPA)

## The Effects of Extraction Time and Temperature on Phenolic Compounds and Antioxidant Capacity of Malaysian Trigona Propolis Aqueous Extract Using Response Surface Methodology

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**Introduction:** Propolis has been used in many applications such as foods additive, natural preservatives, biopharmaceuticals, and cosmetics products, due to its phytochemicals. **Methods:** The effect of extraction time and temperature on total phenolic content, total flavonoid content, and antioxidant activity were investigated for Trigona propolis aqueous extract using central composite design, response surface methodology. The influence of extraction temperature (X1:30–60°C) and time (X2:24–72 hours) on total phenolic content (Y1), total flavonoid content (Y2), and antioxidant capacity (DPPH (Y3), ABTS (Y4), and FRAP (Y5) were analysed. **Results:** The experimental results were satisfactorily fitted into a second-order polynomial model with regard to total phenolic content ( $R^2=0.9461$ ,  $p=0.0003$ ), total flavonoid content ( $R^2=0.9110$ ,  $p=0.0015$ ), DPPH ( $R^2=0.9482$ ,  $p<0.0001$ ), ABTS ( $R^2=0.9663$ ,  $p<0.0001$ ), and FRAP ( $R^2=0.9058$ ,  $p=0.0018$ ). The best extraction temperature and time were 43.75 °C and 52.85 hours. The predicted outcomes for total phenolic content, total flavonoid content, DPPH, ABTS, and FRAP were 104.30 mg GAE /100g, 6.95 mg QE/g, 3.24 mMTE/g, 2.59 mMTE/g, and 4.34 mMTE/g. The experimental values were close to the predicted values [ $100.41\pm 2.74$  mg GAE /100g,  $6.74\pm 0.08$  mg QE/g,  $3.17\pm 0.08$  mMTE/g,  $2.76\pm 0.14$  mMTE/g, and  $4.60\pm 0.14$  mMTE/g, respectively. **Conclusion:** The optimized parameters for the antioxidant potential of aqueous propolis extract can be incorporated in food additives, beverages, cosmetics, and pharmacological applications.

**Keywords:** Phenolic Content, Flavonoid Content, Antioxidant, Trigona Propolis, Response Surface Methodology.

## Transcriptome Analysis of Virus-Host Interactions between the Lytic Bacteriophage DchS1 and the Soft-Rot Macerger, *Dickeya chrysanthemi*

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**Introduction:** Bacteriophages have been used as a biocontrol agent for various crop diseases, including bacterial soft rot that is caused by *Dickeya chrysanthemi*. However, insights into the virus-host interactions are still lacking. Hence, this study aims to elucidate the genome-wide transcriptional response of *D. chrysanthemi* to a lytic phage (DchS1). **Methods:** A lytic phage strain against *D. chrysanthemi* (DchS1) was isolated from environmental sample using enrichment method. The strain was characterized using double agar overlay method, one-step growth curve, nuclease digestion, transmission electron microscopy and stability study. Total RNA was extracted from the culture of *D. chrysanthemi* infected with DchS1 at early, mid and late infection time points. **Results:** DchS1 was a double-stranded DNA phage from the *Myoviridae* family. The double agar overlay result showed clear plaques that indicate the lytic activity of DchS1 against *D. chrysanthemi*. The latent period and burst size were estimated to be 20 min and 209 plaque-forming units/cell, respectively. The phage showed highest survival rate at pH7, 29°C and 37°C, and after exposure to UV light for 5-10 min. Total intact RNA was successfully isolated from both the virus and host. The RNA samples will be sent for sequencing. **Conclusion:** The sequencing of the RNA samples and transcriptomic analysis will reveal the interactions between these organisms and uncover new candidates for antibacterial compounds and phage therapy.

**Keywords:** *Dickeya chrysanthemi*, bacteriophage, RNA extraction, transcriptome, virus-host

## Application of Mesenchymal Stem Cell-Derived Secretome to Promote Full-Thickness Wound Healing- An in Vivo Study

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**Introduction:** Diabetes mellitus (DM) is one of the most prevalent non-communicable diseases worldwide and one of the most common complications of DM is diabetic wound ulcer (DFU). Stem cells have been reported to promote wound healing via secretion of paracrine factors. In this study, we examined the role of adipose tissue-derived mesenchymal stem cell (ADSC) secretome on wound healing using a diabetic rat model induced with streptozotocin. **Methods:** Full-thickness wounds were created at the dorsum part 2 weeks after DM induction. The wounds were treated with ADSC secretome at day 0, 3 and 7, whilst the control group received DMEM medium. Gross examination was performed at day 4, 7 and 14, and the animals were euthanized at day 14 to collect the skin biopsy for histological and immunohistochemical (IHC) analysis. **Results:** Faster wound closure was observed in the animals treated with ADSC secretome ( $p < 0.05$ ). Hematoxylin and eosin staining revealed thicker epidermal layer in the secretome group ( $p < 0.05$ ) and Masson's trichrome staining showed less intense collagen deposition in the secretome group. The secretome group has higher mean histological score at  $10 \pm 1.73$  compared to the score of  $8.33 \pm 1.52$  in the control group, indicating more mature tissue architecture. IHC staining revealed higher expression of alpha-smooth muscle actin in the control group, indicating presence of more myofibroblasts that responsible for wound matrix deposition. **Conclusion:** ADSC secretome enhances the healing of DM wounds and this could be a new therapeutic strategy to treat DFU in the future.

**Keywords:** diabetes, wound healing, mesenchymal stem cells, secretome

## Measurement of Fatty Acid Beta-Oxidation Target Protein using In-Cell Enzyme-linked Immunosorbent Assay (ELISA) in Human Fibroblast

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**Introduction:** Fatty acid beta-oxidation (FAO) pathway plays an important role in energy homeostasis particularly in liver, heart and skeletal muscle. The most studied enzymes in this pathway were ACADM, ACADVL and HADHA. Measuring FAO enzyme activities are tedious, hence, we aimed to evaluate an alternative method using In-Cell ELISA. **Methods:** A commercial ATCC<sup>®</sup> fibroblast and 20 normal fibroblasts were used for precision study and determination of reference range. In-Cell ELISA method was used to quantify target proteins (ACADM, ACADVL and HADHA) in cultured cells. Human fibroblasts were cultured and seeded at ~40,000 cells per well on amine coated plate for overnight. The cells were fixed with 4% paraformaldehyde and permeabilized with blocking buffer, before incubated with primary and HRP labelled secondary antibodies. TMB peroxidase substrate was added into the plate and the reaction was stopped by adding hydrochloric acid solution after 30 min incubation. The absorbance was measured using a TECAN<sup>®</sup> spectrophotometer at 450 nm. The target proteins were normalized to cell amount, measured by Janus Green whole cell stain. **Results:** The coefficient variation of the intra- and inter-assays were less than 10% for all proteins. The reference range of ACADM, ACADVL and HADHA proteins in fibroblast cell were 2.201±0.463, 4.784±1.455 and 4.195±0.718 (n=20), respectively. From 6 suspected positive FAO disorder patients analysed by ELISA, two of them showed low level of ACADM protein and confirmed by western blot analysis. **Conclusion:** In-Cell ELISA is a precise and specific alternative method to measure level of FAO proteins in human fibroblast.

**Keywords:** Fatty acid oxidation, human fibroblast, ELISA

## Pyrogallol Induces Antimicrobial Effect and Cell Membrane Disruption on Methicillin Resistant Staphylococcus aureus (MRSA)

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**Introduction:** Pyrogallol is present naturally in numerous plants and it is also an important functional group in many polyphenol compounds. However, the antibacterial activity, efficacy and mechanism of pyrogallol towards MRSA strains had not been studied so far. **Methods:** Microbroth dilution method was used to determine the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC). Time-kill kinetic assay was adopted to determine the killing pattern of pyrogallol towards MRSA. The antibacterial mechanism was determined using scanning electron microscopy (SEM), Fourier Transform-Infrared (FT-IR) spectroscopy and crystal violet assay. **Results:** Pyrogallol exhibited strong antibacterial activity against MRSA with MIC and MBC 15.6 µg/mL. Pyrogallol could inhibit the exponential growth of MRSA and kill the bacterial cells at higher concentrations. Pyrogallol was found targeting the cell membrane fatty acids, proteins/peptides, polysaccharides/carbohydrates and peptidoglycan of cell walls in the antibacterial mechanism. This has been confirmed through SEM, FT-IR spectroscopy and crystal violet assay. **Conclusion:** This study suggested that pyrogallol has the potential to be used for inhibiting multidrug-resistant bacteria.

**Keywords:** Pyrogallol, Methicillin resistant Staphylococcus aureus, Antibacterial, Mechanism, Cell membrane

## Cervical Cancer and Next Generation Sequencing (NGS): A Systematic Review

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**Introduction:** Cervical cancer is one of the most common types of cancer frequently reported in women worldwide. It is ranked as the second most occurring cancer in women worldwide. Next Generation Sequencing (NGS) is one of the emerging technologies that can contribute towards precision medicine. In this study, we aim to determine the use of NGS using cervical cancer research. **Methods:** This systematic review was done using PubMed as the database of searching. Keywords used is 'cervical cancer' AND 'Next Generation Sequencing'. The search limits were languages (English), dates (year from 2005 until 2021) and types of articles (original articles). **Results:** A total of 63 articles were found to fit the criteria. From the list, further inclusion criteria were used including original articles, using human samples and not on genotyping of the viruses. A total of 7 studies met the inclusion criteria and the full text was obtained for further analyses. The studies used CIN1, CIN2, CIN3 and cervical carcinoma obtained either as fresh tissues or FFPE. From these studies, four studies reported on CpG methylation, while only one study reported on the genes that are expressed, miRNA and mutations, respectively. **Conclusion:** As a conclusion, the data obtained from this systematic review is hoped to help us to understand the molecular mechanisms underlying progression in cervical cancer.

**Keywords:** cervical cancer, genes, methylation, Next Generation Sequencing

## Antimicrobial Effect of *Quercus Infectoria* and *Acorus Calamus* in Wound Model

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**Introduction:** Wound infection is a global health concern especially in the tropical regions. It is crucial to ensure none or minimal bacterial growth for speedy recovery as well as to reduce risk of scarring. This research aimed to evaluate antimicrobial effect of plant-based extracts of *Quercus infectoria* and *Acorus calamus* in standard bacterial strains and to assess their efficacy for wound healing. **Methods:** The antimicrobial activity of plant-based extracts *Q. infectoria* and *A. calamus* against *Escherichia coli*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* were assessed using minimum inhibitory concentration resazurin assay. Six wounds were created using biopsy puncture on each Sprague Dawley (SD) rats and these wounds were treated using plant-based extracts. Wounds on five SD rats were assessed on second, fourth, seventh, twelfth and fifteenth day by measuring the progression of wound healing. **Results:** Both plant-based extracts showed a minimum inhibitory concentration of less than 1.0 mg/ml on all three bacterial strains. *A. calamus* showed significant wound healing ( $p < 0.05$ ) on the fourth day, while *Q. infectoria*, showed significant wound healing ( $p < 0.05$ ) on twelfth day. **Conclusion:** Methanolic extract of *Q. infectoria* and *A. calamus* demonstrated good wound healing properties. It exhibited potential to be developed into medicament for wound treatment and care.

**Keywords:** *Quercus infectoria*, *Acorus calamus*; Antimicrobial effect, Wound model

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## Detection of Nuclear & Surface Marker of Pluripotency in Human induced Pluripotent Stem Cells by Immunofluorescent Microscopy

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**Introduction:** Characterisation of pluripotent stem cells by its nuclear and surface markers is required to ensure high quality stem cells for downstream applications as well as to define & demonstrate its pluripotency. Immunofluorescent microscopy is used to detect and visualize the expression protein markers of pluripotency via antigen-antibody reaction. The aim of the study is to develop a method for visualisation of pluripotency in induced Pluripotent Stem Cells (iPSC) using immunofluorescent detection. **Methods:** Protocols carried out on generated (iPSC) colonies derived from neonatal foreskin fibroblasts (BJ)(ATCC) grown in feeder-free system. iPSC colonies are grown in chamber slides. The cells were fixed with 4% paraformaldehyde, permeabilised with 0.1% Triton X-100 and blocked with 1% horse serum. Colonies were incubated in combination of antibodies specific for nuclear (Oct4, Nanog and Sox2) and surface (Tra-1-60, Tra-1-81 and SSEA4) markers of pluripotency overnight. Then, colonies were incubated in secondary antibodies (DyLight 549, DyLight 488) for 1 hour before counter staining with DAPI for nuclear visualisation. Fluorescent signals were visualised using a ZEISS Axio Imager 2 microscope. Images were analysed using ImageJ software. **Results:** Nuclear transcription factors Oct4, Nanog and Sox2 and surface markers namely keratan sulfate antigen, Tra-1-60 and Tra-1-81 and glycolipid antigens SSEA4 were expressed in the BJ derived iPSC. Permeabilization of cells may disrupt certain detection of protein located extracellularly. **Conclusion:** We have developed a method for visualisation of pluripotency in iPSC by detection of fluorescent expression using specific combinations of nuclear & surface markers in single analysis.

**Keywords:** iPSC; Pluripotency; nuclear marker; surface marker

## ***In Vitro* Screening of Selected Ulam for the Inhibition of CYP450 3A4 Activity**

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**Introduction:** CYP3A4 is estimated to be involved in the metabolism of 50% of all available drugs and is a major enzyme in drug response by contributing 40% to 45% of all phase I metabolism. CYP3A4 has been shown to have many herb and food interactions that include St John's wort and grapefruit. Malaysia has a special group of traditional vegetables called ulam that may be consumed raw or cooked. Ulam is gaining popularity as people are moving toward healthier lifestyle by increasing vegetable intake. However, information on the inhibitory activities of ulam toward the activity of CYP3A4 is lacking. Therefore, the aim of this study was to investigate the inhibition of CYP3A4 activity in ulam to determine the food-drug interaction of ulam if they are administered concomitantly with drugs metabolised by CYP3A4. **Methods:** Four types of ulam namely *Cosmos caudatus* ("ulam raja"), *Melicope ptelefolia* ("tenggek burung"), *Centella asiatica* ("pegaga") and *Oenanthe javanica* ("selom") investigated. Each plant methanol extract were tested on the CYP3A4 enzyme activity with ketoconazole as controls. The abilities of these extracts to inhibit human CYP3A4 enzyme activity were analysed using P450-Glo™ CYP3A4 Assay (Luciferin-PPXE) DMSO Tolerant Assay. **Results:** *Centella asiatica* showed the most potent inhibitory activity against CYP3A4 with IC50 value of 23.99 µg mL<sup>-1</sup>, followed by *Melicope ptelefolia*, *Cosmos caudatus* and *Oenanthe javanica* with IC50 value of 34.67, 52.48 and 107.15 µg mL<sup>-1</sup>, respectively. **Conclusion:** The findings suggest that *Centella asiatica*, *Melicope ptelefolia* and *Cosmos caudatus* may contribute to food-drug interactions if they are administered concomitantly with drugs metabolised by CYP3A4.

**Keywords:** ulam, luminescent assay, CYP 3A4, inhibition, food-drug interaction

## Cytokilling Effect of NK-92 Cells on Nasopharyngeal Carcinoma (NPC) Cell Lines

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**Introduction:** Nasopharyngeal carcinoma (NPC) is a head and neck cancer typically associated with the Epstein-Barr virus (EBV). It is the fifth most common cancer in Malaysia, affecting males at a 3:1 ratio to females (2012-2016). Natural killer (NK) cells can kill virally-infected cells including cancer cells without prior sensitization, unlike cytotoxic T cells. **Methods:** The optimisation of *in vitro* growth curves and co-culture media of HK1, NPC43 and C666-1 (target cells) and NK-92 cell line (effector) were independently assessed using xCELLigence real-time cell adherence (RTCA) system for 168h. Cell viability and growth were measured as impedance, and expressed as cell index (CI) values. Cytotoxicity was measured by co-culturing target with differing effector cell concentrations for 72h, after initial target cell adhesion for 24h. 50% killing time (KT50) of target cells was determined to evaluate the efficient killing time of NK-92 on target cells. An imaging assay using GFP-transfected NPC cell lines was used to reflect the cytokilling effect of NK92. **Results:** Different optimal seeding densities were recorded in NPC cell lines ( $2.5 - 3.5 \times 10^4$  cells/well). The cell growth, morphology and adhesion of control NPC cell lines were unaffected in the co-culture media throughout 72h (co-culture treatment length). As target: effector (T:E) ratios increased, there was a decrease in the KT50 values and number of GFP cells in the targets. **Conclusion:** HK1, NPC43 and C666-1 cells can be effectively killed with NK-92 and its cytokilling can be monitored real-time by RTCA system.

**Keywords:** nasopharyngeal carcinoma, natural killer cells, xCELLigence, co-culture, cytokilling

## Cytotoxic Effect of Lapatinib on T84 Human Colonic Epithelial Cell Line

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**Introduction:** Lapatinib, an ErbB1/ErbB2 tyrosine kinase inhibitor (TKI) is effective in breast cancer treatment but is associated with diarrhoea. ErbB1 inhibition by lapatinib may interfere with the normal functioning in the intestine. The mechanism of lapatinib-induced diarrhoea remains unclear. This study aimed to determine the cytotoxic effect of lapatinib on T84 colonic epithelial cells and to evaluate the relationship between ErbB1 and tight junction protein zona occluden-1 (ZO-1) expressions and sensitivity to growth inhibition by lapatinib. **Methods:** T84 human colonic epithelial cell line was cultured using DMEM-F12 supplemented with 10% foetal bovine serum, 1% antibiotic-antimycotic and 2 mM L-glutamine in a 37°C incubator with 5% CO<sub>2</sub>. The half maximal inhibitory concentration (IC<sub>50</sub>) of lapatinib on T84 cells was evaluated via MTS assay. Regulation of lapatinib on ErbB1 and ZO-1 expression in T84 cells was determined via real-time PCR and immunofluorescence staining. **Results:** MTS results showed 50% inhibition by lapatinib on T84 cell growth at 26.48±1.64µM. Lapatinib downregulates ErbB1 and ZO-1 mRNA expressions in T84 cells. Decrease ErbB1 and ZO-1 staining intensities were also observed in lapatinib-treated cells. **Conclusion:** Lapatinib exhibited cytotoxic effect on T84 cell line that expressed ErbB1 and tight junction protein ZO-1. The cytotoxic effect on intestinal cells may explain ErbB1 TKI-induced diarrhoea in patients administered with the drug. Nevertheless, further investigations are required to confirm the findings.

**Keywords:** Lapatinib, ErbB1, ZO-1, T84 colonic epithelial cell line, diarrhoea

## Drug repurposing for COVID-19 and Understanding the Molecular Action Pathways of SARS-CoV-2

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**Introduction:** The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) which is responsible for the coronavirus disease 2019 (COVID-19) has become the greatest global public health crisis of the century with a profound impact on the global economy, politics, educational and health institutions as well as social changes. The pandemic has caused has so far affected more than 110 million individuals and more than 2.4 million confirmed deaths globally. Despite the recent presence of a few approved vaccines, more infectious variants and mutants of the virus are being discovered. Thus, the war against this pandemic is far from being won. Hence, developing a good therapeutic drug is of immense importance. **Methods:** Existing literature on molecular action pathways of SARS-CoV-2 infection were reviewed. The data on COVID-19 were collated from various resources and databases such as PubMed, Science Direct, Wiley, Springer, Taylor and Francis, Scopus, Infilbnet, Google, and Google Scholar. **Results:** Considering the multiple molecular signaling of action and replication of the COVID-19 virus, targeting multiple prospective targets seems reasonable. The repurposing of existing drugs will also shorten the time of drug discovery because the binding of SARS-CoV-2 viral particles to the host cell receptors is the key to its spread and pathogenesis. **Conclusion:** The development of strategies to control or prevent the binding thereby disabling the entry of the virus to the cells could be of great help towards combating the disease.

**Keywords:** COVID-19; Drug repurposing; Molecular Pathways; Therapeutics.

## Knowledge, Attitude and Perception towards Colorectal Cancer Among Public.

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In 2019, it was estimated that about 43,837 new patients were diagnosed to have colorectal cancer in Malaysia. Colorectal Cancer (CRC) is the second highest type of cancer among Malaysian. Overall 5years survival rate for colorectal cancer in our country is only 53% compared to United Kingdom, United States of America, and Singapore. The aim of this study was to analyse the association between sociodemographic and level of knowledge, awareness and perception towards CRC among Malaysian. This was a cross sectional survey with questionnaire divided into five major parts of health status, lifestyle, knowledge, awareness and perception. A total of 384 participants took part in this study. Predominant participants based on demographic factors were male (64.3%), aged 30-39 (31.5%), Malay ethnicity (45.1%), single (47.7%) and has a degree qualification (19.5%). The finding of this study showed that there were association between knowledge, attitude and perception that corelate with sociodemographic on CRC among public. The variables level of education ( $P \leq .000$ )\*\*\* was highly significant and correlated with knowledge on CRC, with higher percentage of the degree qualification, 25% respondents. The survey showed the variables age ( $P \leq .004$ )\*\* and work status ( $P = .036$ )\* were significant and correlated with attitude on CRC. There were moderate significant association among religion and marital status which correlated with attitude or perception toward CRC. However, there is still a need to increase public awareness and knowledge to detect and treat CRC in early stage.

**Keywords:** Colorectal Neoplasms, Colorectal Cancer, Patient Medication Knowledge, Attitude to Health, Perception

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## Nisin Induces Apoptosis of MG63 Osteosarcoma Cells while Protecting Non-neoplastic Cells

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**Introduction:** Osteosarcoma is a primary bone tumour typically treated with neo-adjuvant chemotherapy, with its inherent adverse effects on normal cells. Hence targeted therapy is an area of concentrated research effort. Nisin, a polycyclic bacteriocin, has been shown to exhibit anti-cancer properties on epithelial malignancies by inducing apoptosis and inhibiting proliferation while sparing non-cancerous cells. Data on the effects of nisin on osteosarcoma cells is still lacking. This study aimed to investigate the effect of Nisin on osteosarcoma vs. non-neoplastic osteoblast cells. **Methods:** MG63 (osteosarcoma cells) and hfOB1.19 (human foetal osteoblast cells) were cultured at 37°C, 95% humidity and 5% CO<sub>2</sub>. They were divided into control, nisin (562µg/ml), doxorubicin at (500ng/ml) and nisin+doxorubicin treatment groups. The cell morphology, viability, apoptosis (Annexin V-FITC assay) and cell cycle arrest were recorded. **Results:** At 24-hour post treatment, nisin caused death of 50% MG63 cells, but spares 80% of the hfOB1.19 cells. For nisin-treated MG63 cells, 43.5% were in early and only 2.03% in late apoptosis. Doxorubicin caused approximately 34% cell death of both cancer and osteoblast cells which increased to 60% when combined with nisin. Nisin caused increased arrest at G2/M phase of the cell cycle (33.7% ± 1.6%) compared to control (25.9% ± 3.3%), p<0.05. However, doxorubicin exhibited greater effect (47.7% ± 4.3%). Microscopy confirmed more apoptotic bodies among MG63 cells treated with nisin, compared to hfOB1.19 cells. **Conclusion:** Nisin leads to increase apoptosis and cell death in osteosarcoma cells whilst sparing normal cells. This effect was enhanced when administered with doxorubicin.

**Keywords:** osteosarcoma, nisin, apoptosis, cell cycle arrest

## Air Pollution Skin Effects and Hospital Admissions for Eczema in Kuala Lumpur, Malaysia

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**Introduction:** Adverse health effects due to air pollution have become a major global public health concern over the decades. Epidemiological studies are suggestive of PM<sub>2.5</sub>'s adverse effect on human skin; however, the findings remain limited. This study aims to compare the association of ambient air PM<sub>2.5</sub> with skin dryness and itchiness among indoor and outdoor workers and also association between PM<sub>2.5</sub> concentration and hospital admission for eczema cases. **Methods:** A 2 cycle - 3 months cohort follow-up study was conducted involving 440 respondents being categorized as indoor and outdoor workers with 220 respondents on each arm. Weekly self-reporting questionnaire on skin dryness and itchiness using Visual Analogue Scale (VAS) were conducted. Demographic information was collected at recruitment stage. A DustTrak<sup>TM</sup> Aerosol Monitor Model 8520 was used to obtain PM<sub>2.5</sub> concentrations. Daily hospital eczema admission data were obtained from hospital records of University Malaya Medical Centre. **Results:** Between indoor and outdoor workers, change in mean score of skin dryness and itchiness were significantly different ( $p < 0.05$ ) for both cycles. Moderate to strong correlation for skin dryness and strong correlation for skin itchiness was established among indoor workers against PM<sub>2.5</sub> concentrations. Moderate negative correlation ( $r = -0.539$ ) was established for eczema admission against PM<sub>2.5</sub> concentration. **Conclusion:** Stronger correlation seen for indoor workers skin symptoms. Findings are suggestive of a potential relationship with PM<sub>2.5</sub> concentration and could serve as evidence for future studies though a causal link could not be established.

**Keywords:** Air pollution, skin dryness, skin itchiness, eczema

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## Real-Time Reverse Transcription Loop-Mediated Isothermal Amplification for Rapid Detection of SARS-CoV2

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**Introduction:** Real-time reverse transcription polymerase chain reaction (RT-PCR) methods have been developed for the detection of SARS-CoV2 as these methods are highly sensitive. However, they are costly. Loop-mediated isothermal amplification (LAMP) assay has emerged as a novel alternative isothermal amplification method for the detection of nucleic acid. **Methods:** A rapid, sensitive, and specific real-time reverse transcription LAMP (RT-LAMP) assay was developed for COVID-19 detection. **Results:** This assay was able to detect 10 copies of SARS-CoV2 RNA in 30 min. Both the clinical sensitivity and specificity of this assay were 100%. The RT-LAMP showed comparable performance with real-time RT-PCR. **Conclusion:** Combining simplicity and cost-effectiveness, this assay is therefore recommended for use in resource limiting settings.

**Keywords:** molecular diagnosis, rapid test, COVID-19

## Comparative Proteomics Profiling of Serum of Women with BI-RADS Scores of 1 to 5 Using Gel-Based Approaches

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**Introduction:** Mortality due BrCa can be greatly reduced through an early detection. Mammography, the gold standard technique used for breast cancer screening has few limitations including high false-positive and negative rates thus, leading to overdiagnosis. Currently, there are no protein biomarkers that is capable of detecting BrCa at an early stage. Thus, the present study aims to screen for the potential protein signatures in serum of women with BI-RADS scores of 1 to 5, using gel-based proteomics approach. **Methods:** Silver-stained two-dimensional gel electrophoresis (2-DE) profiles were generated from 34 neat serum samples of women with different BI-RADS scores. The levels of expression of proteins were analysed *via* image analysis. The proteins with significant altered abundance ( $p < 0.01$ ) were identified by MALDI-ToF/ToF and further analysed using appropriate bioinformatics analysis. **Results:** A total of twenty-one proteins (and/or protein species) were found significantly altered in abundance in the silver-stained 2-DE serum profiles of women with different BI-RADS scores ( $p < 0.01$ ). Majority of the proteins were acute-phase proteins. **Conclusion:** Serum protein signatures detected in the present study has the potential to complement mammography screening for providing an early and reliable indicator for detection of BrCa. This would in turn facilitates better patient management as well as prognosis. However, the data of the present study needs to be further validated in a larger representative population.

**Keywords:** Breast cancer, BI-RADS scores, Two-dimensional electrophoresis, Biomarkers, Lectin.

## Effect of R92L and R92P Mutations in Ornithine transcarbamylase (OTCase) Enzyme

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**Introduction:** Ornithine transcarbamylase (OTCase) is an enzyme that is responsible in urea cycle to synthesize urea from ammonia. Mutations found in *OTC* gene usually causes hyperammonemia, which leads to the occurrence of ornithine transcarbamylase deficiency (OTCD). Previous studies found the OTCase binding pocket undergoes an induced-fit conformational change during the binding of the first substrate, carbamoyl phosphate (CP). Several residues located close to the binding pocket have been identified important in this activity which include R92. Therefore, the aim of this study is to elucidate the effect of mutation at this residue using molecular dynamics (MD) simulations. **Methods:** The R92L-PALO and R92P-PALO mutant models were generated using PyMOL software based on reference structure (PDB ID: 1OTH). The validation of the mutant models was done with ProSA, ERRAT and PROCHECK web-servers. MD simulations were carried out and analysed using the GROMACS package. **Results:** The MD simulations analyses of the mutant complexes (R92L-PALO and R92P-PALO) exhibited both mutations caused a local effect to the OTCase structure. The simulations exhibited the substitution of L92 and P92 disrupted the intermolecular interactions between OTCase and PALO. Both mutations also disrupted hydrogen bond interactions with the neighbouring residue (E326) and also residue involved in the catalytic mechanism (C303). **Conclusion:** In conclusion, the findings indicated that mutations of R92 residue affect the catalytic activity of the OTCase, which may influence the occurrence of OTCD.

**Keywords:** Ornithine transcarbamylase, OTCase, mutation, catalytic

## Wnt Pathway Gene Expression in Oral Squamous Cell Carcinoma

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**Introduction:** Oral squamous cell carcinoma (OSCC) is the most common type of oral cancer worldwide. Uncharacteristic regulation of Wnt pathway has been associated with various cancers. Inhibition of Wnt pathway mechanism is efficiently blocked cancer growth in highlighting a great potential of therapeutics treatment. Several studies highlight the contribution of WNT signalling pathway activation in oral neoplastic transformation toward OSCC progression. **Methods:** ORL-48 (OSCC) cell line was derived from Cancer Research Malaysia. Normal gingival fibroblast (hGF) cell line was used for the control group. After cell culture and treatment with 5-aza-2'-deoxyxytidine, cells were preceded for PCR array profiling by Custom RT2 Profiler PCR Array. Data analysis was done by GeneGlobe software (Qiagen). **Results:** In comparison between the untreated control and OSCC, the genes of PPP2R1B, SENP2, Fzd1, PPP3R2, WIF1 and Wnt8a were significantly expressed. After treatment with 5-aza-2'-deoxyxytidine, Wnt8a was not longer extinct. In comparison between treated OSCC and untreated, RAC and SFRP4 genes are downregulated, while Wnt10B, Fzd10, Wnt1 and WIF1 genes show having upregulation role in oral cancer. **Conclusion:** Wnt8a has downregulation role in OSCC, while Wnt10b, Fzd10, Wnt1 and WIF1 have upregulation role in OSCC. Wnt pathway genes can be used as a targeted therapy in OSCC.

**Keywords:** oscc, pcr array, wnt pathway

## ***Mallotus mollissimus* and *Solanum erianthum* carries potential phytochemical with antimicrobial properties**

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**Introduction:** *Mallotus mollissimus* (*M. mollissimus*) and *Solanum erianthum* (*S. erianthum*) plants are underutilized plants with potential medicinal properties and has been used indigenous communities. However, the phytochemical constituents and antimicrobial activities of these plants remain under-reported. This study is aimed to investigate the phytochemicals contents and antimicrobial activities of *M. mollissimus* and *S. erianthum* plant extracts. **Methods:** Plant extracts were obtained and fractionated with column chromatography. Antimicrobial activity screening was performed against several Gram-positive and Gram-negative microorganisms by disk diffusion method. Qualitative phytochemicals were performed targeting alkaloid, saponins, steroids and tannins, flavonoids, terpenoid and phlobatannins, anthraquinones and cardiac glycosides. **Results:** *M. mollissimus* and *S. erianthum* plant extracts showed broad spectrum of antimicrobial activities against Gram-positive bacteria. Both plant extracts and their fractions contain alkaloid, steroids and cardiac glycosides. Interestingly, flavonoids, terpenoid, tannins were found in *M. mollissimus* only and correlated to the antimicrobial activity against *Streptococcus pneumoniae*. **Conclusion:** These findings suggested that *M. mollissimus* and *S. erianthum* contains potential antimicrobial agents.

**Keywords:** *Mallotus mollissimus*, *Solanum erianthum*, antimicrobial, phytochemical

## ***In Silico* Identification of Transcription Factor Families in *Curcuma alismatifolia* (Ornamental Ginger) Using Available Transcriptomic Resources**

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*Curcuma alismatifolia* is ornamental ginger from the Zingiberacea family that grows from rhizomes and originated from tropical and sub-tropical areas of northern Thailand and Cambodia. *Curcuma alismatifolia* flowering stems comprise showy inflorescence with several apical bracts on a long and stiff peduncle. The inflorescence comprises several of pink, white, red, and purple bracts in the upper part and green bracts in the lower part. Both types of bracts bear small axillary flower buds. Transcription factors are proteins that regulate the expression of genes involved in the anthocyanin pathway in ornamental plants. However, there is no information on transcription factor identification in *C. alismatifolia*. In this study, by transcriptome-wide mining of inflorescence of two *C. alismatifolia* cvs. 'Chiang Mai Pink' and 'UB Snow 701', 2,740 unigenes encoding 59 classes of transcription factor families were predicted. Based on TF classification, 625 and 130 unigenes encoded MYBs and NACs transcription factors, respectively. These findings provide a valuable resource for gene expression and genetic transformation studies and improvement of flower color in the ornamental *Curcuma*.

**Keywords:** ulam, luminescent assay, CYP 3A4, inhibition, food-drug interaction

## Metabolome analysis of oil palm friable calli and its development

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**Introduction:** Plant development in *in vitro* culture system involves both growth and differentiation processes which depends on multiple factors such as genotype, nutrient availability and culture conditions. Growth, in size or biomass, is a quantitative change that is irreversible. **Methods:** Oil palm liquid culture system was initiated through the selection of friable calli induced from inoculated immature leave explants after 3 months in culture. The friable calli were mass propagated further in suspensions that were subjected to scheduled subculture routines and maintenance then were transferred into maturation stage for further development. The multiplication and transition of oil palm calli to cell aggregates has yet to be delineated from the biochemical perspective. The metabolite profiling and characterization of both calli and cell aggregates were conducted using liquid chromatography-mass spectrometry (LC-MS), while multivariate statistical analyses were employed to facilitate data interpretation. **Results:** At least 21 metabolite peaks were detected in friable calli, while 32 peaks were observed in cell aggregates at 7<sup>th</sup> subculture. Differential abundance of amino and organic acids were observed and identified from the friable calli tissues and the cell aggregates in parallel with the chemometrics data. **Conclusion:** The distinction of oil palm tissue culture materials by its phytochemical profiles is of major interest to better understand its biosynthesis for future performance and quality improvements. The discovery of phytochemicals in oil palm liquid culture system may provide added prospects in the production of high value compounds for the pharma and nutraceuticals sectors.

**Keywords:** *Elaeis guineensis*, metabolomics, LC-MS, tissue culture, liquid culture system

## Classification of Multifunctional and Multisubunit Oil Palm Acetyl-CoA Carboxylase (ACCase) via Domain Analysis

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**Introduction:** Acetyl-CoA carboxylase (ACCase) is considered one of the most important enzymes in the regulation of fatty acid synthesis, as it controls the carbon flux into lipids in plants. The enzyme catalyzes the first step of fatty acid synthesis by converting acetyl CoA to malonyl-CoA. There are four domains (alpha-carboxyl transferase (CT- $\alpha$ ), beta carboxyl transferase (CT- $\beta$ ), biotin carboxyl carrier protein (BCCP), biotin carboxylase (BC)) present in ACCase. These domains may be present in a single protein (multifunctional form) and/or as four separate proteins, in multisubunit form, each containing a different subunit. The multifunctional and multisubunit ACCase is found in the cytoplasm and plastid respectively. In oil palm, both the multifunctional and multisubunit forms of ACCase are present. Multisubunit ACCase is involved in oil palm fatty acid production. **Methods:** To identify the oil palm ACCase, the *Arabidopsis thaliana* ACCase gene sequence was downloaded from the KEGG pathway databases and used as a query sequence, resulting in the identification of an ACCase gene from the published oil palm gene models. **Results:** Seven domains were predicted to exist in oil palm ACCase using Interproscan (ACCA, ACC\_central, Carboxyl\_trans, CPSase\_L\_D2, CPSase\_L\_chain, Biotin\_carb\_C and Biotin\_lipoyl). Using the domains identified, a set of identified domain(s)-containing protein sequences were retrieved and annotated using Blastx. **Conclusion:** The oil palm ACCase genes were classified into multifunctional (2 copies) and multisubunit (CT-  $\alpha$  [3 copies], BCCP [2 copies], BC [2 copies]) forms.

**Keywords:** oil palm, acetyl-CoA carboxylase, fatty acid synthesis, multisubunit, multifunctional

## Variability in Yield Components and Vegetative Traits of 3-Way Crosses Oil Palm Progenies

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High yielding and dwarf planting materials has become a goal in oil palm breeding and improvement programmes. A total 30 progenies of MPOB-Nigeria *dura* x Deli *dura* were progeny tested with AVROS and Yangambi were initiated aiming at assessing their yield components and vegetative growth performance. The progenies were laid down in a Randomized Complete Block Design (RCBD) with four replicates in 2011 at the Malaysian Palm Oil Board (MPOB) Research Station, Ulu Paka, Malaysia. Analysis of variance (ANOVA) revealed highly significant results for yield components and vegetative traits, denoting there were substantial genetic variation for breeding and selection for the traits studied. Four progenies had exceeded FFB yield of more than 200 kg palm<sup>-1</sup> year<sup>-1</sup> where PKG 136 from MPOB-Nigeria *dura* x Deli *dura* x AVROS was the top scorer for having FFB yield of 207.36 kg palm<sup>-1</sup> year<sup>-1</sup>. The plant height varied from 1.91 (PKG 115) to 2.51 m (PKG 126), giving the height increment ranged from 31.8 to 41.8 cm year<sup>-1</sup>. In this study, the correlation analysis showed positive and highly significant between FFB yield with all other yield and vegetative traits except for frond production (FP). Both PKG 136 and PKG 105 from MPOB-Nigeria *dura* x Deli *dura* x AVROS *pisifera* have been identified as the potential parent and will be selected for further evaluation trial.

**Keywords:** oil palm, germplasm, advance population, progeny test

## Optimization of Protoplast Isolation From Oil Palm *In Vitro*-derived Leaf and Mesocarp

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**Introduction:** The protoplast represents a truly single-cell system which is useful and beneficial for *in vivo* gene functional study. The different source of protoplasts according to the gene of interest, together with robust isolation and cultivation procedure are beneficial for genetic improvement of the perennial crop, such as oil palm. **Methods:** Previously, a method has been published on the isolation of oil palm protoplast from suspension callus. This study serves as the extension of the previous research to optimize isolation of protoplasts from oil palm mature tissues such as *in vitro*-derived (*iv*) leaf and mesocarp. Isolation of mesophyll protoplasts from *iv* leaf was optimized by identifying the best parameters affecting protoplast yield and viability, such as enzyme combinations and procedure to obtain clean and vital protoplasts. **Results:** By doing this, an efficient protocol for isolation of oil palm mesophyll protoplasts that can produce up to  $2.5 \times 10^6$  protoplasts/g FW with up to 94.78% viability was developed. Then, optimization for isolation of protoplasts from the mesocarp of the age around 12 WAA was carried out with previously optimized enzyme mixture. After two hours of incubation time,  $3.98 \times 10^6$  protoplasts/g FW with 85% viability were recovered. **Conclusion:** Overall, we conclude that combination of cellulase R-10, macerozyme R-10, driselase, and pectolyase Y-23 enzymes improved isolation of oil palm protoplast from mature tissues.

**Keywords:** protoplast isolation, oil palm *in vitro* leaf, oil palm mesocarp

## Preliminary Analysis of QTLs Associated with Yield Components in Oil Palm (*Elaeis guineensis* Jacq.) through Association Mapping

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**Introduction:** Oil palm (*Elaeis guineensis* Jacq.) is the most widely traded vegetable oil in the world, with the current yielding is about 4-6 t/ha. There is a large scope for increasing the oil yield by selecting elite planting material for breeding programs in germplasm evaluation and utilization. Through association mapping (AM), it is now possible to dissect complex quantitative traits and identify a single polymorphism within a gene that is responsible for phenotypic differences. **Methods:** In the present study, a diverse range of 116 Tanzania oil palm germplasm genotypes were characterized using 92K single nucleotide polymorphism (SNP) array through Illumina platform. After SNP filtering using ASSiST 1.01 and removing markers with minimum allele frequency (MAF) <0.05, a total of 49961 informative SNPs was obtained. These markers were analyzed using FarmCPU package embedded in R software for association mapping analysis. Analysis was combined with three top principal components (PC1-3) analyzed using GAPIT to control the population structure. **Results:** Results from the Manhattan plots revealed that seven quantitative trait loci (QTLs) each were significantly associated with yield components (bunch number and bunch weight). QQ plot showed that the model applied fitted best to the uniform distribution and appropriate for analyzing the association between the oil palm SNPs and trait studied. **Conclusion:** The detection of marker-traits associations will facilitate the implementation of marker assisted selection (MAS) and speed up breeding improvement programs in the future.

**Keywords:** association mapping, oil palm germplasm, SNP marker

## Oil Palm Tissue Culture System for Artificial Inoculation Study of *Ganoderma boninense*

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**Introduction:** One of the shortcomings of conventional pathogenicity studies is to achieve uniformity of infection in biological materials. The aim of this study was to investigate the possibility of developing a non-invasive tissue culture system that allows the infection of *Ganoderma boninense* to take place naturally in oil palm ramets with uniform infection. This methodology is suitable for the development of an artificial pathogenicity assay using pathogens of interest for the purpose of elucidating pathological responses. *Ganoderma boninense* is a pathogen that causes basal stem rot (BSR) in oil palm, was used in this study. **Methods:** Two different inoculum preparations were prepared; mycelial agar disc and mycelial colonized sawdust. The inoculums were carefully introduced to the ramets without imposing any pressure or wounding to allow the natural infection process to take place. **Results:** The *G. boninense* colonized sawdust inoculum achieved 100 % infection in the ramets tested, while less than 60 % infection was obtained using the mycelial agar disc inoculum. The physiological symptomology of *G. boninense* infected ramets by mycelial colonized sawdust inoculum resembled the typical BSR infection observed in the conventional nursery method, which include leaf wilting, necrotic and rotting of bole tissues. **Conclusion:** The developed *in vitro* tissue culture system to study pathogenicity is the first to establish a non-invasive *Ganoderma* infection in ramets using sawdust as inoculum.

**Keywords:** *Elaeis guineensis*, basal stem rot, sawdust, artificial infection, tissue culture ramets

## Production of Recombinant Iridovirus Coat Protein Using a Synthetic Biology Approach

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**Introduction:** Grouper iridovirus (GI) is a causative agent that is associated with the infection and disfigurement of groupers in aquaculture systems. The Iridovirus coat protein has been reported to be antigen with potential applications for the development of vaccines for the aquaculture industry, however the mass production of this protein is limited by the lack of availability of a suitable gene construct for its large scale production.

**Methods:** This study was directed towards engineering a synthetic gene construct of the GI major capsid protein (GI-MCP) followed by insertion into two different bacterial expression vectors, pET-22 and pGS21A. The vectors were transformed into chemically competent *E. coli* BL21 DE3 and expression was induced at 12°C, 25°C and 37°C. **Results:** The synthetic gene containing the synthetically designed GI-MCP was successfully expressed in both plasmids and was validated using protein spectroscopy. **Conclusion:** The gene construct can be applied for the large-scale production and commercial application of the GI-MCP as an antigen for diagnostic purposes as well as a vaccine for aquaculture.

**Keywords:** Iridovirus, Major Capsid Protein, Grouper Iridovirus, Synthetic Biology, Codon Optimization.

## ***In Vitro* Proliferation of Shoots and Callus of *Talinum paniculatum* (Jacq.) Gaertn.**

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**Introduction:** *Talinum paniculatum* also known as Javanese ginseng is an important medicinal plant that was used as traditional medicine to treat various illnesses. The present of oleanane-type saponins in this plant demonstrates antifertility, antibacterial, antifungal, antioxidant, and cytotoxic activities. The main goal of this study is to establish a protocol for *in vitro* propagation and callus induction of *T. paniculatum* as an alternative method to ameliorate the pharmaceutical potential of this species. **Methods:** Nodal explants and transverse thin cell layer from the aseptic seedlings of *T. paniculatum* were used in this study. Multiple shoots were induced in MS medium supplemented with BAP (0.5 – 1.5 mg/L) while callus formation was induced in MS medium supplemented with combination of 1.0 mg/L BAP and 2,4-D (0.5 – 2.5 mg/L). **Results:** The highest number of shoots ( $4.00 \pm 0.62$ ) was recorded in nodal explants cultured on MS medium supplemented with 1.0 mg/L BAP ( $p < 0.05$ ). Various concentration of auxins influenced the induction, proliferation, morphology and colour of the callus. Transverse thin cell layer explants cultured on MS medium supplemented with 1.0 mg/L BAP and 2.0 mg/L 2,4-D reached the maximum biomass production in callus induction stage. The highest proliferation of subcultured callus with whitish green colour was observed in MS medium supplemented with 1.0 mg/L BAP and 0.5 mg/L 2,4-D. **Conclusion:** The optimized conditions for shoot multiplication and callus proliferation of this underutilized medicinal plants potentially useful for biotechnological applications in pharmaceutical industry.

**Keywords:** 6-benzylaminopurine, callus, shoot multiplication, *Talinum paniculatum*, transverse thin cell layer.

## Identification of putative olfactory proteins from a key palm oil pollinating weevil, *Elaeidobius kamerunicus*

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Olfaction is essential for the survival of many insects. Their sophisticated olfactory systems help them accomplish key tasks, such as seeking food resources, avoiding predators, locating mate partners and selecting egg-laying sites. The olfactory proteins, which are primarily expressed in the olfactory sensilla located in the antennae of insects, play vital roles in the responses triggered by external chemical stimuli. Recent advances in bioinformatics and molecular biological techniques have enabled the identification of numerous olfactory-related genes as well as their functions but information on the molecular chemoreception transduction mechanism is still very limited. A tiny weevil called *Elaeidobius kamerunicus* (*Ek*) of the Coleopteran order of the Curculionidae family that originated from West Africa is the most efficient pollinator of *Elaeis guineensis*. Due to the key role and economic importance of *E. kamerunicus* to the oil palm industry, scarcity of its genetic information should be addressed, particularly pertaining to its genome. Basic genomic features such as K-mer distribution prediction of diploid genome size supported by flowcytometry, heterozygosity ratio, repeats rate percentage and GC content percentage were obtained for both male and female *Ek*. Leveraging the genome survey data, a more targeted in silico characterization of the olfactory proteins such as the odorant-binding proteins (OBP) and odorant receptors (OR) was conducted. De novo functional annotation was performed on the assembled data through OmicsBox platform. A total of 35 to 47 and 24 to 28 scaffolds contained partial putative/candidate OR and OBP genes respectively. These results represent an early effort in providing the *Ek* genome with functional molecular information.

## Food Operators' Perceptions on Biodegradable Food Container Usage at Subang Jaya: The relationship of Environmental Knowledge, Concern, Attitude and Usage Intention

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Malaysia generated around 1 million tonnes of unmanaged plastic waste, putting the country as the eighth worst country worldwide for plastic waste. The waste management system is not efficient enough to address the pollution in the nation. In recent years, the government has taken steps to educate the citizen on biodegradable packaging, recycling and reduction of plastic usage. The study explores the perceptions on biodegradable food container usage among food operators in terms of sociodemographic characteristics, environmental knowledge, concern, and attitude and usage intention. A total of 113 food operators from Subang Jaya, Selangor were surveyed through self-administered questionnaire through convenience sampling method. The findings show that level of education has a significant impact on environmental knowledge and attitude. Besides, the results of Pearson correlation coefficient show medium positive relationship between environmental knowledge with both attitude and usage intention. Medium positive relationship is also observed between environmental attitude and usage intention. Meanwhile, weak positive relationship recorded between environmental knowledge and concern. Environmental concern demonstrates weak positive relationship with both attitude and usage intention. High level of environmental awareness among the food operators reflected that they are more conscious about the environment and the beneficial effects of biodegradable food container usage. However, high price and low product quality may be the reasons the purchase intention is not reflected in the actual purchase of biodegradable products. The collective measure to increase awareness among food operators' on proper waste management is crucial to effectively minimise the amount of waste in general.

**Keywords:** Environmental, biodegradable, Knowledge, Concern, Attitude

## Pharmaceuticals and Personal Care Products (PPCPs) Residues in Surface Water Bodies from Selangor (Malaysia): Occurrence and Environmental Risk Assessment

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**Introduction:** Pharmaceuticals and Personal Care Products (PPCPs) are classified as the new emerging class of pollutants by the United States Environmental Protection Agency. Its ubiquitous nature coupled with its high persistency in the environment is alarming. Moreover, some PPCPs are endocrine disrupting chemicals (EDC) responsible for feminization of male fishes via production of vitellogenin. Occurrences of antibiotics in the environment induce high bacterial resistance. PPCPs were widely manufactured and administered in Malaysia but little or no quantification was carried out. Thus, this study aims to investigate environmental occurrences of PPCPs in Langat River Basin and to conduct Environmental Risk Assessment (ERA). **Methods:** River water samples were collected from twelve sampling locations in the Langat Basin. Samples were extracted using Solid Phase Extraction (SPE) Oasis HLB cartridges and analysed using tandem Liquid Chromatography Mass Spectrometry (LC-MS/MS). Environmental Risk Assessment (ERA) was calculated and classified as no risk, low risk, medium risk and high risk. **Results:** All PPCPs were detected at sampling locations except gemfibrozil, levonorgestrel, naproxen, norethindrone, progesterone and trimethoprim whose frequency of detections were 97.2, 91.7, 91.7, 88.9, 83.3 and 63.9% respectively. Two PPCPs were quantified at concentrations more than 1000 ng/L; they were caffeine and naproxen. Thereafter, ERA was used to evaluate possible aquatic toxicities in Langat River. High risks of acute toxicities were found for naproxen and sulfamethoxazole. Several PPCPs exhibited high chronic ecological toxicities namely diclofenac and sulfamethoxazole. Naproxen exhibited medium ecological risk. Metoprolol and DEET exhibited low chronic ecological risk. **Conclusion:** More studies should be encouraged to safeguard the aquatic ecosystem and human health.

**Keywords:** Pharmaceuticals and Personal Care Products (PPCPs), Endocrine Disrupting Compounds (EDC), Environmental Risk Assessment (ERA)

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## Functionalization of Medium-Chain-Length Polyhydroxyalkanoates with Methyl Acrylate by Free Radical Copolymerization using Azobisisobutyronitrile

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**Introduction:** Chemical modifications of PHA and mcl-PHA are important to enhance their performance characteristics and add novel functionalities. **Methods:** Functionalization of mcl-PHA produced by *Pseudomonas putida* Bet001 with methyl acrylate (MA) using 2,2'-azobisisobutyronitrile (AIBN) as a radical initiator was carried out. **Results:** Optimum copolymerization was obtained at 30 mM AIBN, 50°C in 60 minutes. Spectroscopic analysis authenticated the successful grafting of MA to mcl-PHA. **Conclusion:** MA-grafted mcl-PHA exhibits improved flexibility from adjusted crystallinity behaviour.

**Keywords:** Polyhydroxyalkanoate, *Pseudomonas putida*, graft copolymerization, azobisisobutyronitrile, methyl acrylate

## Molecular Characterization and Phylogenetic Analysis of an *Enterococcus Faecium* Isolate from a Clinical Sample in Sabah, Malaysia

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**Introduction:** *Enterococcus faecium* is a gram-positive bacterium commonly found as a commensal which causes different infections in humans including hospital-acquired infections. We were interested in investigating the molecular characterization of local *Enterococcus* bacteria isolated from a clinical sample in a tertiary hospital in Kota Kinabalu, Sabah, based on the whole-genome sequencing approach. **Methods:** The collected sample was cultured for bacteria onto blood agar and characterized by using molecular methods. Bacterial DNA was extracted by using the Qiagen DNeasy Tissue Kit (Qiagen, Valencia, CA). The quantification of DNA was done using a Qubit fluorometer (Qubit 3.0, Thermo Fisher Scientific). The sample was then sequenced using the Illumina HiSeq 4000 platform. The quality of the sequence reads was checked using FastQC. This research was approved by the Medical Research Ethics Committee (MREC), Ministry of Health, Malaysia (No. NMRR-19-1770-48622) and University Malaysia Sabah ethical committee (JKEtika 1/19(26)). **Results:** There were 221 contigs, an estimated genome length of 2,890,784 bp, and an average G+C content of 37.73%. The N50 length is 38,963 bp and the L50 count is 22. Our phylogenetic tree analysis using comprehensive genome analysis service at PATRIC (a comprehensive bioinformatics resource tool) showed the isolate belongs to *Enterococcus faecium*. The raw reads were deposited in the NCBI SRA. This whole-genome data was deposited in DDBJ/ENA/GenBank under the accession number JAEFCY000000000. **Conclusion:** The molecular characterization data from our study might be useful in detecting pathogenic microorganism of *E. faecium* infections and would broaden the application of whole genome sequencing in clinical practice.

**Keywords:** *Enterococcus faecium*, Hospital-acquired infections, Whole genome sequencing, phylogenetic analysis

## Prevalence and Genetic Diversity of PVL-Positive *Staphylococcus aureus* Nasal Carriers among Patients and Healthcare-Workers in a Tertiary Hospital in Selangor - Malaysia

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**Introduction:** The virulence of *Staphylococcus aureus* (*S. aureus*) is associated with the presence of various toxins including Panton-Valentine leukocidin (PVL) toxin gene. The PVL toxin encodes for extracellular cytotoxin. These toxins interrupt the permeability barrier of leukocytes and erythrocytes by making pores in their cell membranes. The PVL-positive *S. aureus* is a main cause of nosocomial and community-acquired infections. The aim of the present study is to determine the percentage rate, associated risk factors and the phylogenetic relationship of PVL-positive *S. aureus* nasal carriers among patients and nurses. **Methods:** collectively, 315 nasal swabs were collected from inpatients and nurses from Hospital Sungai Buloh. Isolation and identification of *S. aureus* was performed by using Staphylase test kit. Multiplex PCR assay was used to confirm *S. aureus* isolates with positive PVL toxin gene. Antimicrobial susceptibility of PVL-positive *S. aureus* was identified by the disk diffusion method. Phylogenetic analysis of PVL-positive *S. aureus* was determined using pulsed-field gel electrophoresis (PFGE). **Results:** One hundred-sixty out of 315 (50.8%) isolates were *S. aureus*. About 7/160 (4.4%) harboured *lukS* gene (six MSSA and one MRSA). The patients with a nasogastric intubation, fever past 2 weeks, runny nose, nose itching and longer hospital stay had a significantly high risk of being PVL-positive *S. aureus* nasal carriers. The phylogenetic of all seven PVL isolates presented five patterns of isolates and they were distantly related. **Conclusion:** The current study provided awareness to the hospital authority to act for prevention and control.

**Keywords:** *S. aureus*; nasal carriers; PVL; multiplex PCR and PFGE

## Identification of Lactic Acid Bacteria through Phenotype and Genotype Based Method

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**Introduction:** Lactic acid bacteria are a group of Gram-positive, non-sporulating and microaerophilic bacteria that have similar nutritional and growth requirements among their group members. They occur naturally in certain environment including in several type of food products. Due to their many application including for industrial and food processing purposes, isolation and identification work of LAB were continuously done to find a better strain. Identification of LAB was usually done using phenotype and/or genotype identification methods. **Methods:** In this study, preliminary identification of 22 LAB isolates originated from 127 local pickled fruits samples was done based on their morphological characteristics on agar and physiological analysis (Gram staining and catalase reaction) followed by identification based on biochemical reactions (phenotype) using API 50 CHL system and polymerase chain reaction (PCR) amplification of 16S rRNA gene and sequencing (genotype). **Results:** The 22 LAB isolates have been successfully identified as LAB group members based on both methods. Through genotype identification, majority of the isolates were of the *Lactobacillus* genus (19 isolates), while another three belongs to the genus *Leuconostoc* (two isolates) and *Enterococcus* (one isolate) respectively. The identification using API 50 CHL was not able to identify the *Enterococcus* as it has been identify as *Lactobacillus* sp. Identification results between both methods at species level was not in agreement for certain isolates as seven of the isolates were identified differently by both methods. **Conclusion:** All 22 presumptive LAB isolates based on their morphological characteristics on agar and also physiological analysis have been identified as LAB genus based on both phenotype and genotype identification. However, there were differences in identification result by both methods especially at species level.

**Keywords:** Lactic acid bacteria, identification, genotype, phenotype, API

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## WINNERS OF MSMBB EDUSTEM GRANT

The MSMBB EduSTEM Grant was set up to support projects working with STEM (Science, Technology, Engineering, and Mathematics) education, and to fund activities which are aligned with UNESCO Sustainable Development Goals (SDGs), such as, to improve the quality of education, life, health, and well-being. Two grants, with each amounting up to RM5,000, are available for MSMBB members. The project must bring direct benefit to the community. Assessment criteria for the grant include research background, objectives, methodology, community impact, feasibility, and being a member of MSMBB. The grant was opened on 31<sup>st</sup> July 2019, closed on 30<sup>th</sup> September 2019, and the results were announced on 27<sup>th</sup> November 2019.

Project Title : Are You Human Or AI? See Your DNA!  
Project Leader : Assoc. Prof. Dr. Siti Sarah Othman (Universiti Putra Malaysia)  
Project Members : Assoc. Prof. Dr. Chia Suet Lin (Universiti Putra Malaysia)  
Dr. Muhammad Zamir Othman (Universiti Sains Islam Malaysia)  
Duration : 01 November 2019 – 31 October 2021  
Grant awarded : RM5,000.00

Project Title : Evoking An Interest In STEM Through The Mysterious World Of The Unseen  
Project Leader : Dr. Adelene Song Ai Lian (Universiti Putra Malaysia)  
Project Members : Dr. Suriana Sabri (Universiti Putra Malaysia)  
Dr. Saila Ismail (Universiti Putra Malaysia)  
Duration : 01 November 2019 – 31 October 2021  
Grant awarded : RM5,000.00



## WINNERS OF MSMBB EDUSTEMX GRANT

The **MSMBB EduSTEMX Grant** is a seed fund available to support MSMBB members for activities that are aligned with UNESCO Sustainable Development Goals (SDGs), such as improving the quality of education, life, health, and well-being. Funding is available between RM1,000-4,000 to support projects working with **Virtual STEM** (Science, Technology, Engineering, and Mathematics) education. Preference is given to projects which demonstrate innovative approaches and techniques to solve community issues and build individual, neighbourhood, and/or community capacity. The project must bring direct benefit to the community. Assessment criteria for the grant include research background, objectives, methodology, community impact, feasibility to conduct virtually, and being a member of MSMBB. The grant was opened on 28<sup>th</sup> September 2020, closed on 31<sup>st</sup> December 2020, and the results were announced on 2<sup>nd</sup> February 2021.

Project Title : STEM FOOD FUN – Learning the Art of Science through the Science of Food: Future-casting the Science “Classroom” through an Inquiry-based Pedagogy

Project Leader : Associate Professor Dr Crystale Lim Siew Ying (UCSI University)

Project Members : Dr. Alan Tan Yee Hock (UCSI University)  
Dr. Gurion Ang (University of Queensland)  
Mr. John Ooi (CEO and Founder of Pathfinder)

Duration : 15 February 2021 – 14 February 2022

Grant awarded : RM4,000.00

Project Title : Enhancing Students’ STEM Knowledge and Language Proficiency through Flipped Classroom Method in Online Learning Platform

Project Leader : Dr. Kew Si Na  
Dr. Nor Hasniza Ibrahim (Universiti Teknologi Malaysia)  
Professor Dr. Zaidatun Tasir (Universiti Teknologi Malaysia)  
Associate Professor Dr. Koh Tieng Wei (Universiti Putra Malaysia)

Project Members : Associate Professor Dr. Crystale Lim Siew Ying (UCSI University)

Duration : 15 February 2021 – 14 February 2022 (12 months)

Grant awarded : RM2,600.00



## WINNERS OF MSMBB TIKTOK VIDEO CHALLENGE

MSMBB STEM “TIKTOK” VIDEO CHALLENGE aims to create public interest in Science, Technology, Engineering, and Mathematics (STEM) through social media platforms. STEM bridges the gap between society and scientific knowledge, by not only designing and creating new things but also in providing solutions for everyday hurdles to provide a sustainable living environment. Social media platforms provide millions of subscribers that are either influencers or observers across gender, generation or location. By employing these approaches, STEM awareness can be empowered in a more approachable yet savvy manner. The competition was opened on 20<sup>th</sup> September 2020, closed on 30<sup>th</sup> October 2020, and the results were announced on 16<sup>th</sup> November 2020.

### Top 2 videos with the best content (by MSMBB invited judges)

Video Title : Scorbage  
Project Leader : Chan Mui Mui (Universiti Putra Malaysia)  
Project Members : Nur Aqilah Nadhirah Binti Affendie  
Nurhannah Nabyllah Binti Ramizan

Video Title : Spray, spray and get protected  
Project Leader : Nur Iqmaliza Akmal Binti Mohd Kamal (Universiti Putra Malaysia)

### Top 2 videos with the most likes on Instagram

Video Title : Chronic Wasting Disease  
Project Leader : Adam Danieal Bin Ariffin  
Project Members : Universiti Putra Malaysia (UPM)

Video Title : Eyes Wide Shut  
Project Leader : Sharon Tiang Qin Yee  
Project Members : Wong Pui Man  
Yoo Jia Hao  
Elvia Jemima Tanaka





**BEST CONTENT**

Nur Iqmaliza Akmal  
Binti Mohd Kamal  
Universiti Putra Malaysia (UPM)  
Spray, spray and  
get protected

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**MOST LIKES**

Adam Danieal Bin Ariffin  
Universiti Putra Malaysia (UPM)  
Chronic Wasting Disease

SILENT KILLER  
CHRONIC WASTING DISEASE  
DISEASE

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**MOST LIKES**

Sharon Tiang Qin Yee  
UCSI University  
Eyes Wide SHUT  
Team members:  
Wong Pui Man, Yoo Jia Hao,  
Elvia Jemima Tanaka

Sleep Tight  
As You & Your bed are perfect to each other  
you let alarm clock keeps trying to break you up

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## WINNERS OF MSMBB BEST SCIENTIST AWARDS 2021

The Malaysian Society for Molecular Biology and Biotechnology (MSMBB) established the Best Scientist Award in 2021 to recognise outstanding scientists who have made significant contributions to the field of molecular biology and biotechnology. There are two categories of Awards, namely, Young Scientist Award, for members who are at the age of 40 or below; and Distinguished Scientist Award, for members who are above 40 years old. The proposer and nominee must be a member of MSMBB. Assessment criteria for awards include, Academic achievements (scientific leadership and engagement with academic and university research; quality of high impact peer-reviewed publications; significant mentoring of graduate students, postdocs, staff members, visiting scientists, peers, industry training etc.), Professional appointments (service to the research community through agency, professional society, or advisory work), honours and awards received, and contributions (service to the community and impact of research on Society). The nomination was opened on 22<sup>th</sup> February 2021, closed on 15<sup>th</sup> April 2021, and the results are to be announced during ICMBB 2021.

**BEST SCIENTIST AWARDS**  
MALAYSIAN SOCIETY FOR MOLECULAR BIOLOGY AND BIOTECHNOLOGY

**Distinguished Scientist Award**  
**PROF. DR. KOH CHONG LEK**  
Gene Express Sdn Bhd

**Young Scientist Award**  
**A/P DR. LIONEL IN LIAN AUN**  
UCSI University

*Congrats!*

WINNER ANNOUNCEMENT

## MSMBB DISTINGUISHED SCIENTIST AWARD 2021

Professor Dr. Koh Chong Lek (Gene Express Sdn Bhd)



### Biography

Dr Koh Chong Lek hails from Penang, Malaysia, although born in Singapore on 27.7.1948. After completing his secondary education in Penang, he entered, in 1966, the University of Malaya (UM) where he graduated with BSc (Hons) and MSc degrees in Genetics. In 1981, he graduated with PhD (Biochemistry) and DIC from the University of London and Imperial College of Science and Technology, England, respectively. From July 1970 to June 2018, he had 48 years of eminent academic record at UM, Osaka University (Japan), Florida International University (USA), Nanyang Technological University (Singapore), UTAR Sungai Long Campus, and Xiamen University Malaysia. From July 2018, he is the Chief Scientific Officer of Gene Express Sdn Bhd, which provides direct-to-consumer gene variant profile test for health, wellness, and predisposition risk of certain health conditions.

Dr Koh is the acknowledged doyen of genetics, molecular biology, and biotechnology in Malaysia and the Asia-Pacific region. Since 1981, he has, with much passion and dedication, pioneered, championed, and provided dynamic leadership in the advancement and development of molecular biology and biotechnology in Malaysia. He achieved it through different levels of taught courses, lectures, formal and informal oral presentations, training courses, hands-on workshops, seminars, interviews (newspapers, magazines, national TV and radio stations), journal articles, popular articles in newspapers and magazines, social media, and motivating his students and coworkers. He was featured in many Malaysian newspapers and magazines. He was referred to as “the DNA man” (Tatler Malaysia, 22.1.2002), “Bapak DNA” (‘Demystifying DNA Magic’, Theresa Manavalan, New Straits Times, 20.6.2004), and “the genetics man” (‘Our own genetics man from UM’, Sharon Kam, The Sun, Weekend, 26-27.6.2004). A special Momentum 2 Documentary Series: Episode 19, ‘The Blueprint of Life’ by Prof Koh Chong Lek (UM) was produced and filmed. It was first screened on 13.12.2001 at 9.30 pm on ASTRO’s RIA channel.

Dr Koh and his research associates used molecular biology and genetic techniques to investigate the genetic materials of humans, plants, animals, bacteria, and viruses from different sources. He has published actively by himself or with his students and collaborators. He has mentored many undergraduate and postgraduate students. In 1993, he was the first scientist in Malaysia to provide DNA typing service for human identification and parentage testing, based on chromosomal and mitochondrial markers. In 2000, he was a member of the team that discovered Malaysian Island flying-foxes as the natural animal reservoir of Nipah virus. The team included SK Lam and KB Chua, who discovered the Nipah virus.

Dr Koh has used his expertise to serve academia, community, government, and industry. He has served on many national and international committees and organizations. He was elected as Fellow of the Academy of Sciences Malaysia in 1999 and as Founder Member of the Asia-Pacific International Molecular Biology Network in 1998. He has received many awards and fellowships, including the ‘2001 MSMBB–Applied Biosystems Award’, the Malaysia Toray Science Foundation’s ‘1996 Science & Technology Award’, and the K Prathap Memorial Lecture Award, 2006. Currently, he is actively promoting biotechnopreneurship.

## MSMBB YOUNG SCIENTIST AWARD 2021

Associate Professor Ts. Dr. Lionel In Lian Aun (UCSI University)



### **Biography**

Assoc. Prof. Ts. Dr. Lionel In Lian Aun obtained his BSc in Biotechnology from University Putra Malaysia in 2003, and a MSc in Biotechnology from the Malaysian University of Science and Technology in 2005. Upon completing his MSc degree, he was employed by Merck Malaysia as a Product Specialist in the Microbiology and Microscopy division. In 2007, Dr. Lionel continued on with his Doctoral degree, specializing in the field of Molecular Oncology. He obtained his PhD from the University of Malaya in 2011, after which he started off his research career as a Post-Doctoral Research Fellow in the field of anti-cancer drugs and cancer immunology, together with the late Prof. Dr. Noor Hasima Nagoor.

Dr. Lionel's career as an academician began officially in 2013 when he joined UCSI University as a lecturer in the Department of Biotechnology. In 2017, he was appointed as the Head of Research & Postgraduate Studies, and soon after received his Associate Professorship. In 2018, Dr. Lionel was appointed as the Deputy Dean and received his Professional Technologist title from the Malaysian Board of Technologists. In 2019, Dr. Lionel was appointed as the Dean for the Faculty of Applied Sciences where he spearheaded the establishment of various academic programmes, including the Forensic Science and Applied Microbiology programmes. Dr. Lionel was also instrumental in initiating the Faculty's first StarTrek programme involving the research attachment of students at top ranked universities such as Harvard and Yale University. Additionally, he is also the Chairman of the Institutional Ethics Committee (IEC), a KPT appointed MyRA auditor, and the Head of the Research Programme for STI on Environment & Sustainability under the Tan Sri Omar Center for Science, Technology and Innovation Policy.

Being an active researcher, Dr. Lionel specializes in the area of cancer immunotherapeutics, and in 2015, he established the Cancer Immunotherapy Research Group (CIRG) at UCSI University. He has graduated over 15 postgraduate students and is currently supervising 11 MSc and PhD candidates. His current research involves the development of cancer vaccines, antibody engineering technologies and cancer diagnostics. In 2017, he was awarded the US InnoCentive Premium Challenge Award for the Delivery of Biomolecules through the Gastrointestinal Tract. He has actively published over 30 research articles, reviews, and book chapters, with a H-index of 13. He has also successfully secured several government and industry research grants amounting to RM1.4 million, and currently holds 2 patents involving cancer therapeutics and vaccines.

Dr. Lionel also plays an active role in furthering the advancement of STI in Malaysia. He has been a member of the Malaysian Society for Molecular Biology and Biotechnology (MSMBB) since 2011 and was co-opted into its council in 2013. He then served two terms as the Honorary Treasurer from 2015-2019 and is currently an auditor of the Society. He is also an active handling editor of the society's journal, the Asia Pacific Journal of Molecular Biology and Biotechnology (APJMBB). In 2017, Dr. Lionel became a member of the Young Scientist Network (YSN) under the Academy of Sciences Malaysia (ASM), and is engaged in many of its activities, including the Science Integrity working group and the Science in Exile initiative, in collaboration with The World Academy of Sciences (TWAS).

**ASIA PACIFIC JOURNAL OF MOLECULAR BIOLOGY & BIOTECHNOLOGY**  
(ISSN:0128-7451, eISSN: 2672-7277)

Asia Pacific Journal of Molecular Biology and Biotechnology (APJMBB) is an open access journal publishing research findings in the fields of Biotechnology and Molecular Biology. The Journal aims to promote research in all relevant areas of molecular & cellular biology in prokaryotes & eukaryotes (including methodology) and biotechnology (microbial, agricultural, animal, forensic, aquatic, medical, bioremediation, and regulatory biotechnology) in the Asia Pacific region through publication of research articles, both basic and applied.

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

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# MALAYSIAN SOCIETY FOR MOLECULAR BIOLOGY AND BIOTECHNOLOGY

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# **Acknowledgements**

The Organizing Committee of the 4<sup>th</sup> ICMBB2021 would like to thank the following:

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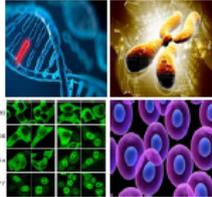
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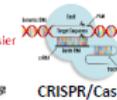
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