Program Book

MONASH University
MALAYSIA

MONASH SCIENCE SYMPOSIUM

PASSIONS CONVERGE • IDEAS EMERGE

MONASH SCIENCE SYMPOSIUM 2018

21 – 23
NOVEMBER
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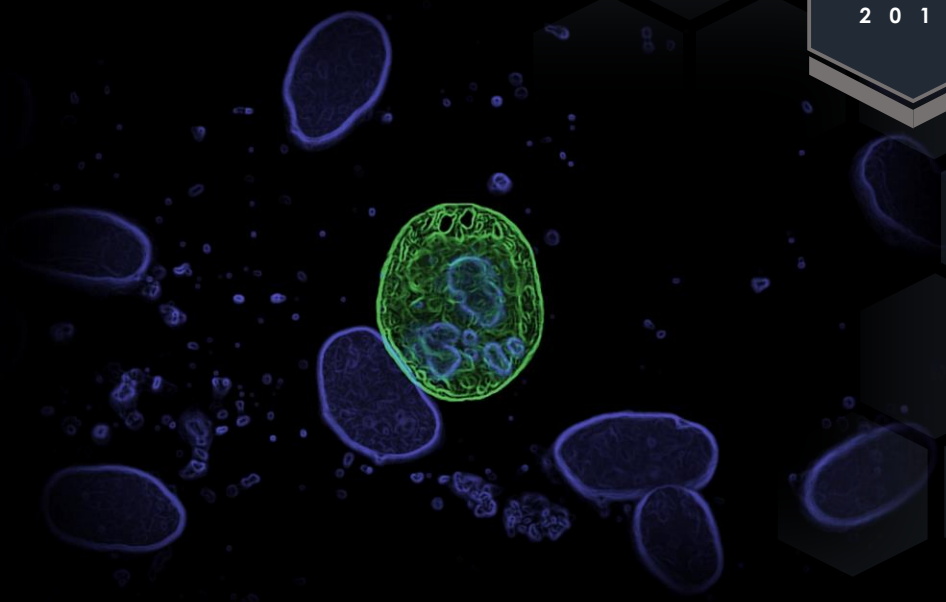

Monash University Malaysia is a joint venture

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HEAD OF SCHOOL

It is my pleasure to welcome you to the Monash Science Symposium 2018 organised by Science postgraduate students of Monash University Malaysia, for the fifth time.

The passion for science is the key to the launch of the Monash Science Symposium. “Passions Converge, Ideas Emerge” is the theme for this year.

Science is an essential discipline to explore the unknown and to find solution for various challenges in our daily lives. Sharing the advances in science and building networks at the symposium will be valuable especially among the younger generation who will be moving towards the academia or other industries.

The symposium will serve as a platform for emerging ideas in the area of applied microbiology, cell and molecular biology, chemistry and drug discovery, environmental and agricultural sciences, genomics and bioinformatics, and food science and technology. I look forward to seeing you at the symposium in Monash University Malaysia.

Associate Professor Emily Goh Joo Kheng
Head, School of Science
Monash University Malaysia

POST-GRADUATE COORDINATOR

A warm welcome to the Monash Science Symposium 2018!

This symposium where "Passions Converge, Ideas Emerge', aims to bring together like-minded and equally passionate scientist from various institutions, to engage in presentations, discussions and interactions related to various aspects and scope of science. It is also a good training ground for young scientists to go on to greater heights and excel in their chosen field.

I wish to congratulate the Organizing Committee, which comprise solely of the postgraduate students from the School of Science, for their outstanding enthusiasm, dedication and professionalism in making the symposium a success. And to the sponsors for their support to our commitment in grooming young scientists and leaders.

I hope that by the end of the symposium, you will have each acquired new knowledge, new friends and new networking opportunities. I wish you all, a rewarding experience throughout this symposium.

Let your *"Curiosity Unleashed"*!

Associate Professor Dr. Adeline Ting Su Yien
Advisor of Monash Science Symposium 2018
Monash University Malaysia

ORGANIZING COMMITTEE

On behalf of the Monash Higher Degree by Research postgraduates, we would like to formally welcome you to the 5th Monash Science Symposium 2018 from November 21-23, 2018 at Monash University Malaysia. To have all these inspiring scientists gather to share their journey and research makes this an exciting event indeed.

In this world we are living in, challenges are always on the rise, from bacterial resistance to genetic disorders, from food development to environmental destruction. Here, experts from various industrial and academic niches are called together to share their own profound ideas in aid of solving these issues.

As we continue to bring out the Monash's spirit since our first symposium in 2012, this year's symposium, themed "Passions Converge, Ideas Emerge", is geared towards the advancement and connectedness of scientific individuals from different parts of the world. We would like to thank each one of you for participating and sharing your expertise in this event. Your participation and contribution will help pave the future to a better world.

We welcome you to this symposium and look forward to your participation. We hope you enjoy a pleasant experience and with it obtain invaluable knowledge and benefits.

With great love and respect,

Krystle Angelique Santiago
Mah Wee Li
MSS18 Chairpersons

ORGANIZING COMMITTEE

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*** = Judging session may continue up to 1.30pm.

PLENARY SPEAKER PROFILES

Genomics & Bioinformatics

Associate Professor Qasim Ayub
Monash University Malaysia,
School of Science

Dr. Qasim Ayub joined Monash University Malaysia as Associate Professor and Director of the Genomics Facility in September 2017. He trained as a clinician in Pakistan and subsequently obtained his doctorate from the University of North Texas, Denton, USA.

He has worked in USA, Pakistan and at the world renowned Wellcome Sanger Institute located in Hinxton, United Kingdom. In Pakistan he assisted in setting up a state of the art molecular biology research facility in Islamabad, which was a focal point for the Human Genome Diversity Project. Several of the novel male specific markers that were identified during his studies of the Pakistani populations are now routinely used in forensic DNA identification. For this work he was awarded the President of Pakistan's Medal of Excellence for contributions to science in 2006. At the Sanger Institute he was part of the 1000 Genomes Project Consortiums and the gorilla sequencing efforts and published several high profile papers. He continues to maintain his interest in South Asian population genetics and exploring the functional basis for high-altitude adaptation in the Himalayas. He is currently leading the genomics research platform at Monash University Malaysia and developing projects in evolutionary and disease genomics.

The Abode of Snow: Population Demography and Adaptation in the Himalayas.

Associate Professor Qasim Ayub
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Modern humans have adapted to living at high altitudes and harsh climates in the Himalayan Mountain Ranges that separate the Indian sub-continent from China. In order to understand the population origins and identify genomic regions that enabled adaptations to living in this environment we genotyped and sequenced populations from Nepal, Bhutan, North India and Tibet and compared them with populations worldwide. The results indicate that high altitude adaptation occurred once in the region and subsequently spread. The strongest signals of high-altitude adaptation were located near genes involved in response to low oxygen levels in the atmosphere and we replicated the selection signal in *EPAS1* intronic region. This region is believed to be a classic example of adaptive introgression from an archaic human species. However, identification of the causal variants underlying this selection signal are confounded due to the extensive linkage disequilibrium and lack of functional data that we are trying to address. This talk will discuss what we know and what needs to be discovered.

Cell & Molecular Biology

Professor Mary Beth Bacano-Maningas
University of Santo Tomas

Dr. Mary Beth Bacano-Maningas, was one of the pioneer in perfecting the technique for RNA interference (RNAi) in shrimp as part of her Ph.D. dissertation from Tokyo University of Marine Science and Technology (TUMSAT).

This technique is now being adapted by other students and researchers in several laboratories in the country and around the world. The aquaculture industry is highly vulnerable to infection by pathogens, which if left unchecked can lead to rapid staggering slump in production. Her team developed a low cost diagnostic kit that is quick, affordable and easy to use so that big and small scale aquaculture farmers can detect infecting pathogens at an early stage, enabling them to take necessary measures against the proliferation of pathogens before they can start potential damage. Dr. Mary Beth Bacano-Maningas is one of the most prolific scientists in the Philippines working on the detection of disease-causing microorganism in aqua-cultured shrimps through cutting edge and innovative molecular technologies. Her work deals with an issue of pressing national concern, owing to the impact of the aquaculture industry which contribute up to P10 Billion annually to the Philippine economy. Her scientific innovation is crucial for the Philippines to catch up with its ASEAN neighbors. She is fulfilling her dream as scientist to bring technology from “BENCH to FARM”.

Saving the Shrimp Industry through Innovative Molecular Technologies

Professor Mary Beth Bacano-Maningas
Department of Biological Sciences, College of Science/Research Center for Natural and Applied Sciences, University of Santo Tomas
mbmaningas@ust.edu.ph

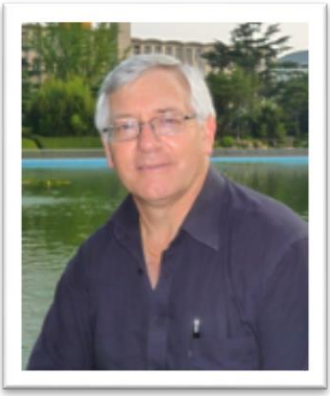
The shrimp aquaculture industry is a multi-billion dollar industry globally. But the industry is plagued by a lot of diseases which can be bacterial or viral in nature. Understanding the immune system of the shrimp and early disease diagnosis are essential in the management and sustainability of the shrimp industry.

RNA interference (RNAi) and Loop-mediated isothermal amplification (LAMP) are effective tools with applications in shrimp immunity. Delayed and reduced mortalities were observed in dsRNA-treated and WSSV- challenged shrimps which highlights the protective effect of gene-specific dsRNA against WSSV infection. Moreover, results showed that treatment of dsRNAs specific to viral genes such as VP9 and DNApol significantly increased survival rates of shrimps challenged with WSSV.

A loop-mediated isothermal amplification (LAMP)–based kit specific for WSSV was developed. The kit contains DNA extraction procedure and a LAMP assay master mix with specially designed primers for the detection of WSSV. A locally fabricated heat block was also designed compatible with the LAMP reaction. The results can also be viewed using a fitted black light in the heat block. The protocol and components of the kit makes it simple, affordable and time efficient, capable of DNA extraction and amplification without a high level of expertise. WSSV screening was performed on samples coming from different sites across the Philippines.

The future commercialization of the kit would greatly help in improving farm management practices and reduce the country's dependence on expensive and imported diagnostic kits.

Chemistry & Drug Discovery



Professor Dr. Philip J Marriott
Monash University Clayton, Australia
School of Chemistry

Professor Marriott obtained his PhD in Chemistry from LaTrobe University, Melbourne, and did postdoctoral research at the University of Bristol, UK, in Organic Geochemistry.

His first academic appointment was at the National University of Singapore, School of Chemistry for 5 years. He then returned to Australia (RMIT University). In 2010, he moved to his present position at Monash University, Melbourne. He received an Australian Research Council Discovery Outstanding Researcher Award in 2013. He has had extended Australian Academy of Science visits to China and Portugal, and received a World Class University Distinguished Professorship (Korean National Research Foundation). In 2015, he was awarded a CNPq Special Researcher Award (Federal University of Rio de Janeiro, and Embrapa, Brazil). His primary research is in gas chromatography and mass spectrometry, specifically comprehensive 2D GC and multidimensional GC, with MS, covering fundamental method development and a broad applications base. He has published 386 research papers and book chapters.

High Resolution Drugs Analysis: Separation and Mass Spectrometry

Professor Dr. Philip J Marriott
School of Chemistry, Monash University Clayton, Australia
Philip.Marriott@monash.edu

High resolution drug analysis usually requires chromatographic methodology, often with mass spectrometry. Using these technologies, we can determine quality of manufactured drugs; conduct forensic analysis for a variety of purposes; perform ADMET studies for pharmacology; study pharmaceuticals in the environment; and analyse drugs in doping control. Without the informing power of GC and LC (MS), such studies may be severely limited. We have evaluated various technologies for a variety of tasks; assessment of World Anti-Doping Agency (WADA) criteria for steroid analysis in doping control using GC×GC-MS; forensic analysis using UHPLC-Orbitrap-MS analysis; analysis of sildenafil and analogues 'contamination' in nutrient supplements by using GC-EIMS, GC-CIMS, GC-supersonic molecular beam MS; and distribution of pharmaceuticals in the environment using UHPLC-MS/MS. Our studies for authenticity assessment of natural materials is extended to essential oils, where we use chiral GCMS analysis to authenticate the source of oils. If 'wine' qualifies to be called a drug, then we have considerable interest in developing new approaches for wine analysis – but usually for aroma profiling. Included in methods that we developed is olfactometry assessment of odour-active constituents using a multi-parametric / multi-analysis approach based on GC, MDGC and GC×GC to permit high resolution analysis. These platforms prove to be powerful approaches for a multitude of analytical problems.

Environmental & Agricultural Sciences

Dr. Yek Sze Huei
Monash University Malaysia,
School of Science

Dr. Sze Huei Yek is currently a senior lecturer at School of Science. Previously, she worked as a Premier Assistant at the University of Lausanne, Switzerland. She is an evolutionary ecologist that use mainly ants to understand the working of the biological world.

She did her undergraduate in Malaysia (BSc in Biochemistry), then went to James Cook University, Australia for her Graduate Diploma (Tropical Zoology), the University of Texas at Austin, US for her MSc (Ecology, Evolution and Behaviour), the University of Copenhagen, Denmark for her PhD (Social Evolution). Prior to returning to Malaysia, she had worked in South Africa and Switzerland, on questions in biological control, invasive species, mating strategies, and symbiosis of hymenopteran insects. Earlier last year (2017) she founded a science outreach website where she provides translation and writing service to busy scientists that want to showcase their work to the general public.

The Diversity of Ant-Plant Symbioses in the Diminishing South East Asia Forests

Dr. Yek Sze Huei
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Ant-plant symbioses are complex between-species interactions found only in tropical environments. Typically, in such symbioses, plants provide housing structures and food to their ant symbionts. In return, the ants protect their plants' host against herbivore attack and provide supplementary nutrients to help with plants' growth. These win-win ant-plant interactions range from facultative to obligate mutualism. Ants and the trees have a tight evolutionary relationship, having co-evolved since the diversification and dominance of angiosperms 135-65 mya. In the present day, many of ant-plant mutualisms are ant species-tree host specific and are only found in the tropics, leading to a delicate between-species cooperative networks that together form the identity and diversity of the tropical forests' ecosystems. However, ant-plant symbioses are completely understudied, particularly in SE Asia. The first phase of our "diversity, mechanism and evolution of ant-plant symbioses in the diminishing South East Asia forests" project characterise the diversity of ant-plant symbioses across different forest habitat, from pristine- through varying degrees of degraded forest. Diversity survey are carried out from ants' perspective and from plants' perspective. Both candidate partners are morphologically identified to species and their identity re-enforced molecular barcoding, generating a comprehensive network interaction manual for ant-plants symbioses for SE Asia. This finding from first phase serve as baseline and resources for understanding the mechanisms and the context of how ant-plant interactions evolved and adapt to changing environment.

Applied Microbiology

Professor Dr. Yvonne Ai-Lian Lim
University of Malaya

Professor Dr. Yvonne Ai-Lian Lim is currently the Deputy Dean (Research) of the Faculty of Medicine, University of Malaya. She loves teaching and enjoys research. She has been teaching Parasitology to the medical, pharmacy, biomedical, nursing and medical laboratory technology students for the past 15 years.

Recently, she and her co-authors wrote a textbook on "Medical Parasitology: A textbook" which was published by Springer (2018). Her research focuses on neglected tropical diseases primarily among marginalised populations (e.g., Orang Asli communities, migrant workers) using tools such as GIS and next generation sequencing to map and understand these diseases among these populations. More recently, she began exploring the molecular mechanisms that underpin the interactions between parasitic infections, in particular gut worm infections, nutritional status, gut microbiota (bacteria) and the inflammatory responses. Her research has been funded by internal university grants and external grants from the Ministry of Science, Technology and Innovation (MOSTI), Ministry of Higher Education (MOHE) and Ministry of Health (MOH). This year, together with her collaborator at the New York University, they succeeded in securing a highly competitive US National Institutes of Health (NIH) grant for a period of 5 years to understand the interactions of gut worms and gut microbiota.

How Do Gut Worms Influence Gut Microbiota?

Professor Dr. Yvonne Ai-Lian Lim
University of Malaya
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Infections with gut worms cause great concern in the developing countries. These parasites live in the gut and may interact with the bacterial communities in the gut, also called the gut microbiota. To determine whether there are alterations to the gut microbiota that are associated with worm infections, we examined the types of bacteria present in faecal samples from rural Malaysians and unraveled the mystery of how worm colonization alters the gut microbiota for these rural Malaysians.

Food Science & Technology

Professor Tan Chin Ping
University Putra Malaysia

Prof. Tan received his degrees Bachelor of Food Science and Technology in 1998 and PhD in Food Processing in 2001, from Universiti Putra Malaysia (UPM). He began his career at the Department of Food Technology, Faculty of Food Science and Technology, Universiti Putra Malaysia in 2001. He then served as a JSPS Postdoctoral Fellow at the National Food Research Institute in Japan from 2002 to 2004. Currently, he is leading one of the major research programs at UPM, Fats and Oils Technology. To date, he has published one joint-edited book, ten book chapters and over 290 scientific articles in peer-reviewed journals, has filed more than 15 patents and has presented more than 270 papers at various national and international conferences. His areas of research specialisation are palm oil, food nanotechnology, food emulsions and the extraction of bioactive compounds from various agricultural by-products. His research in the area of edible oil focuses on new product development, the development of value-added processes and products and quality and safety issues related to fats and oils.

Lipid Nanodispersion in Food: An Overview of Their Preparation, Characterization, Stability Evaluation and Application

Professor Tan Chin Ping
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At the nanoscale, the range below 100 nm is important because at this small size, the laws of physics and chemistry for a bulk system change, resulting in novel properties that enable researchers to produce new materials with the exact characteristics they desire. The food industry has traditionally dealt with macro- or microscale lipid substances, but the introduction of the nanoscale may spur a paradigm shift within the field. The study of both fundamental and applied aspects of lipid nanodispersions has received increasing attention in recent years. Nanodispersion systems are widely used for the encapsulation of bioactive compounds to protect the compounds from degradation and improve their bioavailability. In this paper, the different methods used to prepare these systems are discussed. During the preparation of nanodispersions, two critical parameters which would determine the quality of the final samples are the processing and formulation parameters. Thus, an in-depth review of the processing and formulation parameters commonly used by researchers is included in this paper. Once a nanodispersion is formed, the characterization of its physicochemical properties is the next logical step. Depending on the research objectives, researchers frequently employ various analytical techniques to characterize nanodispersions. Thus, a summary of the different analytical techniques that are commonly applied for the purpose of nanodipersion characterization is included. A nanodispersion can only be useful and serve its purpose if it remains stable over a defined period of time. Therefore, the stability of nanodispersions against storage time and various environmental conditions are also discussed and reported in this paper. Finally, although limited, few examples of nanodispersion being applied into different food products and systems are highlighted.

KEYNOTE SPEAKER PROFILES

Genomics & Bioinformatics

Associate Professor Sarinder Kaur Kashmir Singh
University of Malaya

Dr. Sarinder was awarded a Bachelor of Computer Science from the Faculty of Computer Science and Information Technology, University Malaya (UM) in 2000 and a Masters in Computer Science in 2002. She then completed her PhD in the field of Bioinformatics at the Faculty of Science, University of Malaya in 2007. Currently she is an Associate Professor at the same department, as well as the Program Coordinator for Bachelor of Science in Bioinformatics program. She is also the Principal Investigator of the Data Science & Bioinformatics Laboratory in UM. Dr Sarinder's main interest is managing, representing and analysing biological data using computational tools and techniques. Her contribution towards these projects is mostly in building digital systems using visual analytics, databases and data mining techniques. She is also working on research projects to automate species recognition using image processing and machine learning techniques. Currently, she is engaged in a project on Electronic Medical Records (EMR) at the University Malaya Medical Center (UMMC), mainly for building automated systems using data science techniques. Dr Sarinder has published 70 over publications including books, journals and proceedings. Dr Sarinder is an Associate Editor of Malaysian Journal of Science (MJS) and a reviewer for many journals in her discipline. Dr Sarinder was also a Visiting Scholar at the Computer Laboratory, University of Cambridge, UK.

Bioinformatics Databases- The Current Trends and Future Perspectives

Associate Professor Sarinder Kaur Kashmir Singh
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Data is the most powerful resource in any field or subject of study. In Biology, data comes from scientists and their actions, while any institution that makes sense of the data collected, will be in the forefront in their respective research field. In the beginning of any data collection endeavour, it is critical to find proper management techniques to store data and to maximise its utilisation. This talk reflects upon current trends and techniques of data modeling, architecture with a highlight on the uses of database, focusing on Bioinformatics examples and case studies. Finally, the future of bioinformatics databases will be highlighted to give an overview of the modeling techniques to accommodate the biological data escalation in coming years.

Cell & Molecular Biology

Professor Cheah Yoke Kqueen
University Putra Malaysia, Department of Biomedical Sciences

Prof. Dr. Cheah Yoke Kqueen is the Deputy Director of the Centre for Industry Relations and Networks (CiRNeT), UPM.

He is also the Technical Advisor on Molecular Diagnostic to Subang Jaya Medical Centre. He is a Chartered Scientist, Fellow of Institute of Biomedical Science, UK and Chartered Biologist, Royal Society of Biology, UK. He holds the position as President for Malaysian Biomedical Science Association and BiomedKL. Prof. Dr. Cheah is an established scientist with more than 200 scientific publications, 5 patents, copyrights and won numerous awards in the research exhibitions. Prof. Dr. Cheah was awarded as the Top Research Scientist Malaysia in 2017.

Trends in the Molecular Diagnosis of Lung Cancer

Professor Cheah Yoke Kqueen
University Putra Malaysia
Department of Biomedical Sciences
ykcheah@upm.edu.my

Globally, lung cancer remains the leading cause of cancer-related mortality. Non-small cell lung cancer (NSCLC) accounts for majority of lung cancers, and huge fraction of patients have metastatic disease at presentation. Chemotherapy, the standard treatment of metastatic lung cancer, results in a modest survival benefit compared to best supportive care, and has reached a plateau with no meaningful differences among the many platinum-based regimens used. The discovery of Epidermal Growth Factor Receptor (EGFR) mutations that confer sensitivity to tyrosine kinase inhibitors in lung adenocarcinomas in 2004 signalled the beginning of the era of precision medicine for lung cancer.

A range of technologies are employed to perform molecular testing, from sophisticated genomic sequencing platforms to simpler single-marker assays. These tests, broadly referred to as molecular diagnostics, have quickly become an essential component of the treatment of advanced lung cancer. The simpler tests, which identify the presence of a single molecular marker, are often called “companion diagnostics” because they are developed and tested alongside targeted therapies in clinical trials.

The molecular profiling of lung cancer using molecular diagnostic approach is useful to diagnose specific EGFR mutations and subsequently prescribe tyrosine kinase inhibitors as part of the targeted therapy. Moreover, the advancement of molecular diagnostic also plays an important role in the progress monitoring of the emerging drug resistant lung cancer cells. At the molecular level, the most common mechanism of resistance is the EGFR T790M resistance mutation. This finding has led to the development of third generation mutant specific EGFR TKI’s to specifically target T790M.

Cell & Molecular Biology

Professor Fahrul Zaman Huyop
University of Technology, Malaysia
Faculty of Bioscience & Biomedical Engineering

Professor Fahrul Huyop obtained his Bachelor's degree in Biotechnology with honours from the University of Wales College of Cardiff, United Kingdom in 1995, and his PhD was from University of Leicester, United Kingdom in 2001.

He has extensive experience in the scientific research field as well as in administration. He has been either an active member or spearheading numerous committees and different taskforces related to the university management and development, including as a University level committee member for evaluation of research grants. His dedication to research has largely been on bacteria capable of decomposing toxic halogenated hydrocarbons, namely bacteria producing dehalogenase enzymes, an enzyme that catalyzes the removal of a halogen atom from a substrate. The toxic halogenated organic compounds in the environment can be reduced by the method of degradation via microbial metabolism, that is mediated by enzymes which remove the halogen substituents. Much of the work was due to interest in how toxic materials such as active components of herbicides or pesticides viz. Dalapon and Glyphosate, enter the bacterial cell membrane for the degradation process and consequently, are rendered harmless to the environment. These enzymes in the bacteria system are highly relevant or a greener approach to remove xenobiotic toxic and recalcitrant halogenated compounds from the environment. Much of his work has been related to Microbiology of Prokaryotic, concentrating on biotransformation and development of sustainable solutions for industrial and environmental pollutions. Due to his extensive research experience, he was invited by several local and international universities within the South-East Asian region as a "Visiting Professor" and as a mentor for undergraduate and postgraduate students as well as junior lecturers for opinion and knowledge sharing in the field of his expertise.

Contributions to academic his work have been well documented, reflected from extensive more than 100 articles published in reputable refereed journals, with a current cumulative citation of 861 and cumulative h-index of 14. He is also source of inspiration to hundreds of my former local and international students. Finally, his current study has primarily focused on the "Fundamental aspects" of the "Biochemistry and Molecular Biology of Pollutant Degradation".

Biochemistry & Molecular Biology of Pollutant Degradation

Professor Fahrul Zaman Huyop
University of Technology, Malaysia
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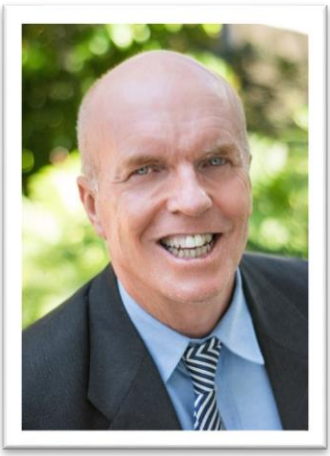
Organic pollutants are mostly anthropogenic and microbial degradation plays an important role to reduce the build-up of toxic chemicals in the soil and water systems. Degradation of halogenated organic compounds are highlighted because carbon-halogen bonds are the most recalcitrant materials. There are four basic criteria for a given halogenated compound to be utilized by an organism as a sole carbon and energy source. First, the halogenated compound should not be toxic to the organism at intracellular concentrations. Secondly, entry of halogenated compound into the organism should be either through passive or active transport and trigger a specialized genes in the operon. Thirdly, the organism should be able to synthesize enzyme (dehalogenase) which can remove the substituent halogen(s) from the compound and finally, the product of dehalogenation should be non-toxic and easily converted to an intermediate which can readily be absorbed in the microorganisms via central metabolic pathways. There were many dehalogenase producing bacteria were isolated so far. Among all these microbes, only Rhizobium sp. RC1 produce three kinds of dehalogenase DehD, DehE and DehL. Current study will focus on all these 4 criteria that allow biodegradation to occur.

Chemistry & Drug Discovery



Professor David James Young
University of The Sunshine Coast
School of Science and Engineering

Professor David Young is the Head of School, School of Science and Engineering at USC and previously held the positions of Head of the School of Science and Interim Head of the School of Arts and Social Sciences at Monash University Malaysia.

He is a chemist with an interest in new materials and has been awarded two national research medals by the Royal Australian Chemical Institute. Professor Young obtained his PhD from the University of Queensland before postdoctoral training at the University College of North Wales and at Oxford University. He joined University of Sydney as a Senior Tutor, from where he moved to the Queensland University of Technology and then to Griffith University. After 20 years at Griffith, he joined Universiti Brunei Darussalam and was appointed Dean of their Graduate Studies and Research Office. Professor Young holds the honorary post of Visiting Scientist at the A*STAR Institute for Materials Research and Engineering, Singapore, Visiting Professor at Soochow University, China and Adjunct Professor at Monash University. He is an Associate Editor of Journal of Molecular and Engineering Materials.

Designing for Selective Chemical Sensing

Professor David James Young
University of The Sunshine Coast, Australia
School of Science and Engineering
dyoung1@usc.edu.au

Mother nature detects individual molecules by their shape and functionality. Modern technology can do the same in some instances, but we have so much still to learn. This presentation will discuss how multiple, weak interactions can be used for the selective detection of metal ions, organic and biological molecules using carefully designed coordination polymers.

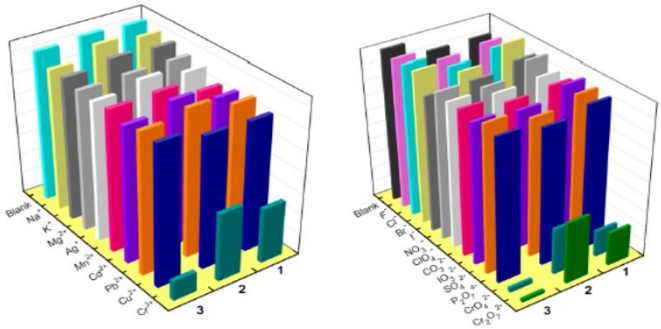


Figure 1. Selective detection of Cr(III) and Cr(VI) ions.

1. Gu, T.-Y.; Dai, M.; Young, D. J.; Ren, Z. –G.; Lang, J. –P. "Luminescent Zn(II) Coordination Polymers for Highly Selective Sensing of Cr(III) and Cr(VI) in Water" Inorg. Chem., 2017, 56 (8), 4668–4678.

2. Yuan, F. –L.; Yuan, Y.-Q.; Chao M. Y.; Young, D. J.; Zhang, W. –H.; Lang, J. –P. 'Deciphering the Structural Relationships of Five Cd-Based Metal–Organic Frameworks', Inorg. Chem., 2017, 56, 6522−6531.

3. Shi, Y. –X.; Li, W.-X.; Chen, H. –H.; Young, D. J.; Zhang, W.-H.; Lang, J. –P. "A crystalline zinc(II) complex showing hollow hexagonal tubular morphology evolution, selective dye absorption and unique response to UV irradiation" Chem. Commun., 2017, 53, 5515-5518.

Environmental & Agricultural Sciences

Associate Professor Dr. Sreeramanan Subramaniam
University of Science, Malaysia
School of Biological Sciences

Associate Professor Dr. Sreeramanan Subramaniam graduated in BSc (Hons) of Biochemistry from Universiti Putra Malaysia (UPM) in 2000 and PhD in Plant Biotechnology from the same university in 2005.

He worked as a lecturer at AIMST University Malaysia from July 2004 prior joining with the School of Biological Sciences, Universiti Sains Malaysia (USM) in March 2008. Currently, he is the Programme Manager for the Agrobiology, Entomology and Parasitology at the School of Biological Sciences, USM. He held this position since September 2011. His current research interests are on the plant tissue culture of various ornamental plants and horticultural crops, establishment of cryopreservation technology, secondary metabolites using cell culture system, genetic engineering of selected plants for fungal disease resistance, induction of hairy roots in selected medicinal plants, LED technology in plant tissue culture, somaclonal variation for crop improvement and studies on the vegetative crystal proteins from native Bacillus thuringiensis isolates. He has published more than 194 manuscripts in journals listed under Scopus/ISI, 11 book chapters, research reports, magazines and 1 academic book. At the moment, total of 13 PhD and 33 MSc students (both as main and co-supervisor) were graduated under his supervision. Currently he is supervising 22 postgraduate students. His primary research collaborators are Universiti Putra Malaysia (UPM), AIMST University, UAEU University Abu Dhabi, MARDI Malaysia, Universiti Malaysia Sabah (UMS), Universiti Malaysia Kelantan (UMK), Universiti Institut Teknologi Mara (UITM), Tamil Nadu Agriculture University, India (TNAU), Periyar University Tamil Nadu India, Institute of Biology of Mongolia (Mongolian Academy of Science), Rajshahi University of Agriculture Bangladesh, University of Dhaka Bangladesh, Tribhuvan University Nepal, Syiah Kuala University Aceh Indonesia, University of Yangdon Myanmar, United Plantations Sdn Bhd (Teluk Intan Malaysia), Figs Direct Sdn. Bhd. (Kedah), OSRAM, P-Plus Sdn Bhd (LED company in Penang), and Bioversity International's Banana and Plantain group (formerly known as INIBAP).

Development of Novel Plant Tissue Culture Systems

Associate Professor Dr. Sreeramanan Subramaniam
University of Science, Malaysia
School of Biological Sciences
sreeramanan@usm.my

Micropropagation known as plant tissue culture plays a pivotal role in the multiplication of orchid, super fruits such as figs and gac, rose, banana, mango, kiwano, cape gooseberries and medicinal plants. Tissue culture technology warrants a reliable and potent alternative in mass propagating plants *in vitro* at a consistent and faster rate yielding clones of parents from novel varieties. This aspect allows for the establishment of plantations leading to high quality and consistent production of these valuable crops in Malaysia. Thin cell layers (TCLs) technique is found useful in plant tissue culture through transverse and longitudinal systems. Remarkable advances in *ex situ* conservation of *in vitro* plant cultures such as cryopreservation provides an alternative for storage longevity of valuable germplasm at relatively low costs, once an appropriate protocol is designed and validated. It involves the storage of *in vitro* grown plant tissues at extremely low temperatures (-196°C) in liquid nitrogen, allowing conservation for a theoretically unlimited period of time. *In vitro* cell culture technology is also a sustainable approach for production of phytochemicals in pharmacognosy without resorting to collection of wild plants that may eventually threaten population in their natural habitat. The obvious advantage of employing cell culture technology is the short culture period to obtain secondary metabolites under sterile and controlled conditions, which eliminate the risk of environmental influence on *in vivo* plant growth and leading to ease of extraction of compounds from *in vitro* cultured cells. One such attempt is the production of 9-methoxycanthin-6-one from the hairy root cultures of *Eurycoma longifolia* (Tongkat Ali), alkaloids (narciclasine and tazettine) from *Hymenocallis littoralis*, betalain from reddish purple dragon plants (*Hylocereus costaricensis*), petunidin and dendrobine from *Dendrobium* Sabin Blue orchids, and anthocyanins from the Jewel orchids (*Anoectochilus* spp. and *Ludisia discolor*). Light is notably one of the crucial variables affecting growth and development of plant tissue cultures. The illumination system of lights for plant *in vitro* culture should supply light in the spectral region which is involved in photosynthesis and photomorphogenic responses. Development of the LED plant tissue culture technology system which incorporates intelligence to achieve function as well as cost efficiency, and utilizing different LED, operated spectra of uniform intensity determined for enhancing the production efficiency of superior quality of selected plantlets.

Environmental & Agricultural Sciences

Associate Professor Dr. Shyamala Ratnayeke
Sunway University
Department of Biological Sciences

Dr. Ratnayeke is an associate professor in the Department of Biological Sciences at Sunway University, Malaysia. She completed her doctoral work on the genetics and spatial organization of carnivores at the University of Tennessee, Knoxville, USA. In 2002, she received an International Research Fellowship award from the U.S. National Science Foundation to conduct carnivore field research in Sri Lanka, including a pioneering study on the subspecies of sloth bear endemic to the island. In 2011, she received a U.S. Fulbright Scholarship Award to work in Tanzania's largest public university, before coming to Sunway University in 2014. Her current research focuses on invasive species biology and the conservation ecology of tropical carnivores.

Carnivore Hotspots in Peninsular Malaysia and Their Landscape Attributes

Associate Professor Dr. Shyamala Ratnayeke
Sunway University
Department of Biological Sciences
shyamalar@sunway.edu.my

Mammalian carnivores play a vital role in ecosystem functioning. However, they are prone to extinction because of low population densities and growth rates, and high levels of persecution or exploitation. In Peninsular Malaysia, rapid conversion of natural habitats threatens the persistence of this vulnerable group of animals. We georeferenced 375 observations of 28 species of carnivore from 89 unique geographic locations using records spanning 1948 to 2014. Using the Getis-Ord Gi*statistic and weighted survey records by IUCN Red List status, we identified hotspots of species that were of conservation concern and built regression models to identify environmental and anthropogenic landscape factors associated with Getis-Ord Gi*z scores. Our analyses identified two carnivore hotspots that were spatially concordant with two of the peninsula's largest and most contiguous forest complexes, associated with Taman Negara National Park and Royal Belum State Park. A cold spot overlapped with the southwestern region of the Peninsula, reflecting the disappearance of carnivores with higher conservation rankings from increasingly fragmented natural habitats. Getis-Ord Gi*z scores were negatively associated with elevation, and positively associated with the proportion of natural land cover and distance from the capital city. Malaysia contains some of the world's most diverse carnivore assemblages, but recent rates of forest loss are some of the highest in the world. Concerted efforts to reduce poaching and maintain large contiguous tracts of lowland forests will be critical for the persistence of threatened carnivores including a diversity of mammals.

Applied Microbiology

Associate Professor Moritz Mueller
Swinburne University of Technology Sarawak Campus
Faculty of Engineering, Computing and Science

Upon graduation [PhD (Biogeochemistry) at the UK National Oceanography Centre in Southampton, UK], Moritz accepted a lectureship position at Swinburne Sarawak where he initially established the BSc (Biotechnology) program and later set up the Aquatic and Environmental Sciences (AquES) Research Group. The focus of our current research projects lies on tropical peat-draining rivers in Sarawak, Borneo; in particular the production, transport and burial of organic material from the rivers to the coast and the diversity and roles of microbes in these processes. We apply multidisciplinary techniques (i.e. field observations, laboratory experiments; analysis of trace gases (CO2, CH4), their stable C isotopes and radiocarbon content (14C-AMS), as well as high-throughput sequencing of microbial diversity) in collaboration with colleagues from China, Singapore, UK, Germany, and Australia. Collaboration with international colleagues is of great importance to us and has allowed us to publish in Nature Communications, as well as other A* category and leading journals in the respective fields such as Global Change Biology, Biogeosciences, and Geobiology. Besides peat-draining rivers, we work in coastal waters, coral reefs, as well as on endophytic fungi which live inside host plants. We assess their diversity and roles as well as their potential use as biosorbents for heavy metals and producers of novel antibiotics and anti-cancer compounds.

Microbes in Coral Reefs: Their Roles and Potential Applications

Associate Professor Moritz Mueller
Swinburne University of Technology Sarawak Campus
Faculty of Engineering, Computing and Science
mmueller@swinburne.edu.my

Coral reefs are complex and diverse ecosystems that provide habitats for thousands of marine species. Resilience of corals is highly dependent on the physiological capabilities of the coral itself as well as their symbiotic partners —associated *Symbiodinium* and other microbes.

This talk will provide an overview of research carried out in coastal waters of Sarawak, Borneo, with a focus on microbial diversity and their potential roles in the health of local coral reefs. In an extension, potential applications of these microbes will be discussed.

Studies carried out range from shotgun surveys of surface waters to isolation of coral mucus-associated bacteria and their role in the coral's defense against microbial pathogens to tagging coral pathogens (*Vibrio coralliilyticus*) with GFP for better visualization to the utilization of a microfluidic device for assessing chemotactic response of said *Vibrio* to the use of coral-associated bacilli in quorum quenching as potential probiotic agents against the Early Mortality Syndrome that is a major threat to shrimp aquacultures worldwide.

Food Science & Technology

Associate Professor Hii Ching Lik
University of Nottingham,
Malaysia Campus
Faculty of Engineering

Dr. Hii is currently Director of Food and Pharmaceutical Engineering Research Group, University of Nottingham Malaysia Campus.

His research interests are in the areas of modern drying & dehydration technologies, preservation of food antioxidants & nutrients, bio-products processing and computer simulation on heat & mass transfer processes. In the past and including to date, he has carried out research for several agriculture/food products such as cocoa beans, chocolates, star fruits, herbs, kedondong, chicken meat, papaya leaf and also investigated/developed several processing technologies such as heat pump drying, adsorption drying, stepwise drying, hybrid drying and solar drying. Particularly, he is interested to investigate the effect of processing on the nutritional and antioxidant properties of underutilized agriculture materials in his current research. He was awarded Drying Technology Top 30 Journal Referees and The University of Nottingham Vice Chancellor's Medal in 2017.

Emerging Drying and Dehydration Techniques for Food Products

Associate Professor Hii Ching Lik
University of Nottingham, Malaysia Campus
Faculty of Engineering
Ching-Lik.Hii@nottingham.edu.my

In the past, food products are dried solely for the purpose of preservation and this can be achieved simply by placing the products under direct sunlight and dry to an acceptable level of dryness. Conventionally, drying encompasses techniques that use convective hot air while dehydration uses dehumidified air or moisture removal through osmotic agents. Modern consumers demand high quality dried products with requirements ranging from acceptable visual appearance to retention of bioactive ingredients that could benefit human health. Several drying techniques have in the past able to overcome the drawbacks (e.g. quality aspects) of hot air drying such as freeze drying, vacuum drying and heat pump drying. However, such drying techniques (e.g. freeze drying) might requires extended drying time in order to achieve the required moisture level and quality. Recently, various studies have investigated the use of microwave assisted vacuum drying, intermittent drying, pulse combustion drying, multistage and hybrid drying to improve drying kinetics and to optimize product quality.

LIST OF PRESENTERS

GENOMICS & BIOINFORMATICS

Invited Speakers				
No.		**Date**	**Time**	**Venue**
1	**Associate Professor Qasim Ayub**	21 Nov	10.00-10.30	Plenary Theatre
	The abode of snow: population demography and adaptation in Himalayas			
2	**Associate Professor Sarinder Kaur Kashmir Singh**	21 Nov	01.00-01.30	LT-6007
	Bioinformatics databases -The current trends and future perspectives			
Oral Presenters				
OP-GB-01	**Dr. Faezah Mohd Salleh**	21 Nov	01.30-01.45	LT-6007
	An expanded mammal mitogenome dataset from Southeast Asia			

Poster Presenters				
PP-GB-01	**Yean Ru Ann**	23 Nov	12.00-01.00	Foyer
	Contemporary evolution of herbicide resistance in Malaysian weedy rice			
PP-GB-02	**Puteri Nur Syahzanani Jahari**	23 Nov	12.00-01.00	Foyer
	Honey metabarcoding: Tracking anthropod and botanical origins			
PP-GB-03	**Jayasyaliny Jayaraj**	23 Nov	12.00-01.00	Foyer
	Development of reduced-HiSeq genotyping-by-sequencing (GBS) on weedy rice			
PP-GB-04	**Farheena Iqbal**	23 Nov	12.00-01.00	Foyer
	Mitochondrial genome diversity and population structure of common house crow in South Asia			
PP-GB-05	**Rupini Yesudasan**	23 Nov	12.00-01.00	Foyer
	Origin and population genetics of weedy rice populations from Sabah using genotyping-by-sequencing			
Research in a Flash				
RF-GB-01	**Puteri Nur Syahzanani Jahari**	23 Nov	09.00-10.30	Plenary Theatre
	Honey metabarcoding: Tracking anthropod and botanical origins			

AN EXPANDED MAMMAL MITOGENOME DATASET FROM SOUTHEAST ASIA

Faezah Mohd Salleh[1]*, Mohd Shahir Shamsir Omar[1], M. Thomas P. Gilbert[2], Mohammad Shahfiz Azman[3]

[1]*Faculty of Science, Universiti Teknologi Malaysia, 81310 Johor Bahru, Johor, Malaysia*

[2]*Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade, 5-7, 1350, Copenhagen, Denmark*

[3]*Forest Biodiversity Division, Forest Research Institute Malaysia, 52109 Kepong, Selangor, Malaysia*

* Corresponding author: faezah@fbb.utm.my

Southeast (SE) Asia is one of the most biodiverse regions in the world, and it holds approximately 20% of all mammal species. Despite this, the majority of SE Asia's genetic diversity is still poorly characterized. The growing interest in using environmental DNA (eDNA) to assess and monitor SE Asian species, in particular threatened mammals—has created the urgent need to expand the available reference database of mitochondrial barcode and complete mitogenome sequences. We have partially addressed this need by generating 72 new mitogenome sequences reconstructed from DNA isolated from a range of historical and modern tissue samples. Approximately 55 gigabases of raw sequence were generated. From this data, we assembled 72 complete mitogenome sequences, with an average depth of coverage of ×102.9 and ×55.2 for modern samples and historical samples, respectively. This dataset represents 52 species, of which 30 species had no previous mitogenome data available. The mitogenomes were geotagged to their sampling location, where known, to display a detailed geographical distribution of the species. Our new database of 52 taxa will strongly enhance the utility of environmental DNA approaches for monitoring mammals in SE Asia as it greatly increases the likelihoods that identification of metabarcoding sequencing reads can be assigned to reference sequences. This magnifies the confidence in species detections and thus allows more robust surveys and monitoring programmes of SE Asia's threatened mammal biodiversity. The extensive collections of historical samples from SE Asia in western and SE Asian museums should serve as additional valuable material to further enrich this reference database.

CONTEMPORARY EVOLUTION OF HERBICIDE RESISTANCE IN MALAYSIAN WEEDY RICE

Yean Ru Ann[1], Song Beng Kah[1]*

[1]School of Science, Monash University Malaysia, Jalan Lagoon Selatan, 47500 Bandar Sunway, Selangor, Malaysia

* Corresponding email: Song.Beng.Kah@monash.edu

Weedy rice is a noxious weeds strain prevalent in most of the rice producing countries. As it belongs to the same biological taxon (*Oryza sativa*) with cultivated rice, eradication of weedy rice with herbicides will caused harm to the cultivated rice. It remains as a major challenge for rice growers until the introduction of Clearfield® technology by LSU AgCenter. The Clearfield® system consists of a new variety of cultivated rice, Clearfield® (CL) rice resistant to imidazolinone (IMI) herbicides allowed farmer to selectively control weedy rice. Although Clearfield® technology has gained popularity in weed management, implementation of this technique without long term planning and appropriate stewardship could potentially incur adverse implications, particularly the escape of the mutant ALS gene from CL rice to weedy rice. Recent years, Malaysian farmers started to complain about the reduced efficacy of IMI herbicides to control the growth of weedy rice. These observations and problems of the long term imidazolinone application on Clearfield® rice warrant investigation with ALS-based DNA sequencing and genome-wide analyses of Malaysian rice populations after widespread use of the IMI tolerant rice line. We identified ALS gene mutation in the herbicide-resistant weedy rice, resulting in a substitution of Ser^{653} with Asn. Genome-wide SNPs sharing between CL rice and coexisting weedy rice populations points to recent CL-to-weedy introgression associated with the weed's proliferation in Clearfield® plots in Sekinchan. Although no obvious signature of introgression in the STRUCTURE analysis, the CL cultivar was found to be heterozygotes, which possibly suggest a recent admixture with co-existing weedy rice in the fields. This problem must be taken into account for effective weed management.

HONEY METABARCODING: TRACKING ANTHROPOD AND BOTANICAL ORIGINS

Puteri Nur Syahzanani Jahari[1], Faezah Mohd Salleh[1]*, Mohd Zulkifli Mustafa[2], M. Thomas P. Gilbert[3]

[1]*Faculty of Science, Universiti Teknologi Malaysia, 81310 Johor Bahru, Johor, Malaysia*

[2]*Department of Neuroscience, School of Medical Science Universiti Sains Malaysia, 16150, Kubang Kerian, Kelantan, Malaysia*

[3]*Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade, 5-7, 1350, Copenhagen, Denmark*

* Corresponding author: faezah@fbb.utm.my

In Malaysia, honey products are usually collected from two major species; *Apis* honey bees and *Trigona* stingless bees. 'Kelulut' honey produced by stingless bees has been known to be a great health elixir. It is different from honey made by *Apis spp* in term of their taste, viscosity and color. Generally, honey is derived from plants nectar excreted by plant-sucking insects. This can be a source of environmental DNA (eDNA) that provide biological signature from extracted DNA. Previously, diagnostic phytochemicals and melissopalynology has been implemented to ascertain the entomological sources of honey. However, these methods are not reliable to determine the authenticity of 'unknown' honey and are not species-specific. Genetic DNA analysis can resolve this limitation by applying genetic marker to identify nectar, pollen and bees species in honey specimen. In a more advance approach, honey metabarcoding coupled with high throughput sequencing platform gives great advantage to analyse many samples, containing mixtures of plant-anthropod species, with extensive depth of sequencing coverage. This shows to be an invaluable tool for massive botanical, pollen and anthropod identification. In this study, we combined DNA markers (ITS2 and COI Zeale) with Illumina MiSeq platform to disclose entomological signature in DNA extracted from 'Kelulut' honey. The genetic identities of honey origin from *Trigona spp* and the herbaceous plant species that were regularly visited by stingless honey bees were successfully identified. Therefore, the study proves the potential of DNA metabarcoding as a potent technique to investigate plant, insect, fungal, bacterial communities in the honey specimen and could be used for honey product authentication. Although the study did not show fungal and bacterial communities, investigation by using other genetic marker should be made to explore the potential of 'Kelulut' honey.

DEVELOPMENT OF REDUCED-HISEQ GENOTYPING-BY-SEQUENCING (GBS) ON WEEDY RICE

Jayasyaliny Jayaraj[1], Wee Wei Yee[1], Song Beng Kah[1]*

[1]School of Science, Monash University Malaysia, Jalan Lagoon Selatan, 47500 Bandar Sunway, Selangor, Malaysia

* Corresponding author: song.beng.kah@monash.edu

Single nucleotide polymorphisms (SNPs) are the most common type of genetic variation among living organisms. With the advent of the next-generation sequencing (NGS) technology, rapid advance in high throughput SNP genotyping such as genotyping-by-sequencing (GBS) have significantly increased efficiency in simultaneous discovery and genotyping of SNPs in complex plant species. However, the current Illumina HiSeq-based GBS protocols have their own limitations in terms of complex, high capacity bioinformatics analyses prohibiting the use of GBS among small laboratories and small-scale users. This study aims to produce a smaller scale, bioinformatically simplified and more convenient reduced-HiSeq GBS method, which possesses advantages of GBS over other SNP genotyping methods, including the high reproducibility of markers and reduced representation of genome. Weedy rice (*Oryza Sativa*) was used as the model species. Rice samples from selected paddy fields in Malaysia were collected and genomic DNA was extracted, used for library construction and subjected to sequencing using Illumina HiSeq platform. Reduced-HiSeq GBS datasets were generated and subjected to various population genetic tests. Comparative analysis between reduced-HiSeq and full HiSeq-GBS datasets revealed that the former is potentially useful and sufficient for genetics analyses in rice.

MITOCHONDRIAL GENOME DIVERSITY AND POPULATION STRUCTURE OF COMMON HOUSE CROW IN SOUTH ASIA

Farheena Iqbal[1, 2]*, Qasim Ayub[1,2], Robyn Fay Wilson[1, 2], Muhammad Fahim[3], Beng Kah Song[1] and Sadequr Rahman[1, 2]

[1]*School of Science, Monash University Malaysia, Jalan Lagoon Selatan, 47500 Bandar Sunway, Selangor, Malaysia*

[2]*Tropical Medicines and Biological Multidisciplinary Platform, Monash University, Malaysia*

[3]*Institute of Biotechnology and Genetic Engineering, The University of Agriculture Peshawar, Pakistan*

* Corresponding author: farheena.iqbal@monash.edu

House crow (*Corvus splendens*) the native passerine bird of the south Asia is widely dispersed in urban environments in this whole region and known as an invasive bird species. Four and sometime five subspecies are described based on slight variation in neck plumage coloration without any genetic validation. The aim of the present study was to examine any genetic differentiation among these subspecies and estimate their phylogenetic relationship using complete mitochondrial genome sequences. 137 specimens were collected from culled birds and museum samples from five countries i.e. Pakistan, India, Bangladesh, Nepal and Sri-Lanka. Genetic diversity measurements identified substantial level of haplotype diversity (*Hd* 0.99) but limited nucleotide diversity (π 0.28%) and negative Fu's Fs test of neutrality. Phylogenetic analysis by maximum likelihood and Bayesian inference grouped 132 haplotypes into a monophyletic clade with two distinct lineages. A haplotype network was consistent with the phylogenetic trees. The genetic diversity indices elucidate the trend of rapid population expansion within all populations, however no mitogenomic features were diagnostic to subspecies characterization. The high invasive characteristics, no geographical barrier for the dispersal and a vast range of suitable bioclimate niches for the species may be responsible for the high gene flow among all populations in the whole Indian subcontinent.

ORIGIN AND POPULATION GENETICS OF WEEDY RICE POPULATIONS FROM SABAH USING GENOTYPING-BY-SEQUENCING

Rupini Yesudasan[1], Jayasyaliny Jayaraj[1], Beng Kah Song[1]*, Sadequr Rahman[1]

[1]School of Science, Monash University Malaysia, Bandar Sunway, 47500 Subang Jaya, Selangor, Malaysia

* Corresponding author: Song.Beng.Kah@monash.edu

The weedy rice (*Oryza sativa*), which is a conspecific form of cultivated rice that infests rice fields worldwide. Notorious for its easy-shattering biotype, weedy rice poses a significant threat to rice production. Despite being a serious problem in the rice industry, little is known about the genetics of weedy rice in the state of Sabah. Given that occurrence of Sabah weedy rice is chronologically later than the spread of the weedy rice in Peninsular Malaysia and the fact that some weedy rice forms were found to share phenotypic similarities for some wild traits with their weedy counterparts from the Peninsula, we hypothesized that emergence of these weeds in Sabah may likely to have an exotic origin outside of the state. In order to learn more about the Sabah weedy rice genetics, it is necessary to study the genetic diversity and structure of the weedy rice populations. Here, we attempt to identify the origin and population structure of weedy rice sampled from Sabah by addressing the following questions; 1) What is the relationship between Sabah weedy rice and its Peninsular counterparts? 2) What information does the genetic diversity and structure of Sabah weedy rice populations provide in relation to their counterparts in Peninsular Malaysia? Does Sabah weedy rice originate from Peninsular Malaysia? 3) What does the distribution of the alleles of the domestication candidate genes and associated phenotypes reveal about the origin and contemporary evolution of Sabah weedy rice? Using two complementary approaches: genotyping-by-sequencing (GBS) and candidate gene analysis on TAC1 domestication gene, we revealed that an independent origin for Sabah weedy rice despite their close phenotypic resemblance to Peninsular weedy rice. Our results suggest a considerable contribution of local Sabah cultivars to Sabah weedy rice evolution. Our finding also does not support the notion that Sabah weedy rice populations are directly evolved from Peninsular Malaysia weedy rice and wild relatives. The genetic constitutions of Sabah weedy rice populations are dynamic which influenced by ongoing introgression from domesticated local cultivars.

HONEY METABARCODING: TRACKING ANTHROPOD AND BOTANICAL ORIGINS

Puteri Nur Syahzanani Jahari[1], Faezah Mohd Salleh[1]*, Mohd Zulkifli Mustafa[2], M. Thomas P. Gilbert[3]

[1]Faculty of Science, Universiti Teknologi Malaysia, 81310 Johor Bahru, Johor, Malaysia

[2]Department of Neuroscience, School of Medical Science Universiti Sains Malaysia, 16150, Kubang Kerian, Kelantan, Malaysia

[3]Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade, 5-7, 1350, Copenhagen, Denmark

* Corresponding author: faezah@fbb.utm.my

In Malaysia, honey products are usually collected from two major species; *Apis* honey bees and *Trigona* stingless bees. 'Kelulut' honey produced by stingless bees has been known to be a great health elixir. It is different from honey made by *Apis spp* in term of their taste, viscosity and color. Generally, honey is derived from plants nectar excreted by plant-sucking insects. This can be a source of environmental DNA (eDNA) that provide biological signature from extracted DNA. Previously, diagnostic phytochemicals and melissopalynology has been implemented to ascertain the entomological sources of honey. However, these methods are not reliable to determine the authenticity of 'unknown' honey and are not species-specific. Genetic DNA analysis can resolve this limitation by applying genetic marker to identify nectar, pollen and bees species in honey specimen. In a more advance approach, honey metabarcoding coupled with high throughput sequencing platform gives great advantage to analyse many samples, containing mixtures of plant-anthropod species, with extensive depth of sequencing coverage. This shows to be an invaluable tool for massive botanical, pollen and anthropod identification. In this study, we combined DNA markers (ITS2 and COI Zeale) with Illumina MiSeq platform to disclose entomological signature in DNA extracted from 'Kelulut' honey. The genetic identities of honey origin from *Trigona spp* and the herbaceous plant species that were regularly visited by stingless honey bees were successfully identified. Therefore, the study proves the potential of DNA metabarcoding as a potent technique to investigate plant, insect, fungal, bacterial communities in the honey specimen and could be used for honey product authentication. Although the study did not show fungal and bacterial communities, investigation by using other genetic marker should be made to explore the potential of 'Kelulut' honey.

CELL & MOLECULAR BIOLOGY

Invited Speakers

No.		Date	Time	Venue
1	**Professor Mary Beth Bacano-Maningas**	21 Nov	10.30-11.00	Plenary Theatre
	Saving the shrimp industry through innovative molecular technologies			
2	**Professor Fahrul Zaman Huyop**	21 Nov	01.00-01.30	LT-6008
	Biochemistry and molecular biology of pollutant degradation			
3	**Professor Cheah Yoke Kqueen**	21 Nov	02.45-03.15	LT-6008
	Trends in the molecular diagnosis of lung cancer			

Oral Presenters

OP-CMB-01	**Winfrey Hoo Pui Yee**	21 Nov	01.30-01.45	LT-6008
	Immunological assessment of modified mutant G12V K-RAS mimotopes as potential peptide cancer vaccines			
OP-CMB-02	**Rowshan Ara Islam**	21 Nov	01.45-02.00	LT-6008
	Nanoparticle mediated delivery of PKM2 and SLC2A1 siRNAs inhibits tumor growth in a syngeneic mouse model via apoptotic pathway			
OP-CMB-03	**Teoh Ru Wei**	21 Nov	02.00-02.15	LT-6008
	Effects of miR-30c-2-3p on Influenza A infection through regulating NF-kB signalling pathway in A549 cell line			
OP-CMB-04	**Ishrat Jabeen**	21 Nov	02.00-02.15	LT-6008
	Genetic analysis of rice differing in glycemic index (GI)			

Poster Presenters

PP-CMB-01	**Amirah Fathin Ahmad Danian**	23 Nov	12.00-01.00	Foyer
	In silico molecular interactions study of pattern-recognition receptor Xa26 and plant pathogen-associated molecular patterns			
PP-CMB-02	**Eunice Yap Xin Le**	23 Nov	12.00-01.00	Foyer
	Study of extracellular vesicles in urine using IR spectroscopy for early detection of prostate cancer			
PP-CMB-03	**Yiing Jye Yap**	23 Nov	12.00-01.00	Foyer
	A novel ATP13A2 loss-of-function mutation model for Parkinson's disease			
PP-CMB-04	**Yong Yanning**	23 Nov	12.00-01.00	Foyer
	Cell-based and zebrafish (*Danio rerio*) phenotypic investigation of cytotoxic properties in *Arctium lappa*. L. root extract			
PP-CMB-05	**Lew Min Han**	23 Nov	12.00-01.00	Foyer
	MHC-restricted peptide vaccination enhances cellular immunity against latency tuberculosis antigen			
PP-CMB-06	**Janet Tan Jia Yin**	23 Nov	12.00-01.00	Foyer
	Molecular mechanisms of dioscin in oral squamous cell carcinoma			
PP-CMB-07	**Teoh Ru Wei**	23 Nov	12.00-01.00	Foyer
	Effects of miR-30c-2-3p on Influenza A infection through regulating NF-κB signalling pathway in A549 cell line			
PP-CMB-08	**Jamal Sajjad Mansuri**	23 Nov	12.00-01.00	Foyer
	An investigation of the effect of smoking on salivary exosomes			

Research in a Flash				
RF-CMB-01	**Winfrey Hoo Pui Yee**	23 Nov	09.00-10.30	Plenary Theatre
	Immunological assessment of modified mutant G12V K-RAS mimotopes as potenial peptide cancer vaccines			
RF-CMB-02	**Rowshan Ara Islam**	23 Nov	09.00-10.30	Plenary Theatre
	Nanoparticle mediated delivery of PKM2 and SLC2A1 siRNAs inhibits tumor growth in a syngeneic mouse model via apoptotic pathway			
RF-CMB-03	**Teoh Ru Wei**	23 Nov	09.00-10.30	Plenary Theatre
	Effects of miR-30c-2-3p on Influenza A infection through regulating NF-κB signalling pathway in A549 cell line			

IMMUNOLOGICAL ASSESSMENT OF MODIFIED MUTANT G12V K-RAS MIMOTOPES AS POTENTIAL PEPTIDE CANCER VACCINES

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To date, *KRAS* gene is the most frequently mutated oncogene in cancer with single point mutations at codons 12 or 13 being one of the most common causes of colorectal cancer progression. Mutant *KRAS* biomarkers are currently recognised clinically worldwide as ineligibility criteria for anti-EGFR therapies, and patients are therefore left with non-specific chemotherapies and a poor prognosis as their treatment options. An approach using peptide-based vaccines in immunotherapy is currently being studied, and in this study, it involves the use of *Lactococcus lactis* as a live delivery vector for safe oral immunisation. Modified mutant G12V K-ras epitopes fused with diphtheria toxoid (DT) were first cloned into *Lactococcus lactis* and immunogenicity of K-ras epitopes was then assessed *in vivo*. Mice were fed orally with recombinant *Lactococcus lactis* casted on edible films and immunoassessments were performed post-immunisation to evaluate: presence of T- and B-cell populations via immunophenotyping of whole blood, and levels of IgG and IgA antibodies via indirect enzyme-linked immunosorbent assay. Cell surface staining via flow cytometry has detected levels of regulatory T-cells ($CD3^+CD4^+CD25^+FOXP3^+$) and cytotoxic T-cells ($CD3^+CD8a^+$) induced by 68-V:DT, while 68-V showed no immunological responses. On the other hand, only specific-IgG sera titres against mutated K-ras antigens from 68-V immunised Balb/c mice were elevated post second boosters compared to wild-type and G12V controls. Immunological assessments showed that edible films delivering K-ras mimotopes were unable to initiate significant immunogenic responses at the intestinal region of a host. More studies to improve the delivery of K-ras mimotopes to the intestinal region can be performed, followed by oral immunisations *in vivo* with other mutant K-ras mimotopes to treat other *KRAS*-positive cancers in the future.

NANOPARTICLE MEDIATED DELIVERY OF PKM2 AND SLC2A1 siRNAs INHIBITS TUMOR GROWTH IN A SYNGENEIC MOUSE MODEL VIA APOPTOTIC PATHWAY

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Introduction: Tumour cells show many distinct features regarding signalling pathways and energy metabolism. Loss of function mutations in tumour suppressor genes, gain of function mutations in proto-oncogenes and aberrant expression of many regulatory signalling pathway proteins attribute some distinct features to cancer cells, one of which is the inordinate dependence on aerobic glycolysis and glutamine metabolism and uncoupling of glycolysis and mitochondrial respiration. Current chemotherapeutic treatment has strong side effects, causing severe discomfort to patients. Recently, researchers have been exploring siRNA as a potential therapeutic with very minimal side effect. As a medium of therapeutic delivery, carbonate apatite, an inorganic, pH sensitive nanoparticle formulated in our lab proved its efficiency to deliver drugs and genetic materials. **Objective:** To inhibit tumour growth by silencing metabolic enzymes with siRNAs delivered by carbonate apatite. **Result:** siRNAs targeting glycolytic enzyme pyruvate kinase M2 (PKM2) and glucose transporter 1 (GLUT1), a member of solute carrier family 2(SLC2A1) were delivered via carbonate apatite nanoparticles both in vitro and in vivo. For in vitro study, we did MTT assay in triple negative human MDA-MB-231 and murine 4T1 cell lines. For in vivo study, breast tumours were induced in the mammary fat pad of female balb/c mice, followed by intravenous delivery of carbonate apatite bound siRNA(s) when the tumour volume reached 13 mm^3. We found a statistically significant ($p<0.01$) reduction in tumour volume for GLUT1(SLC2A1) and for the combination of PKM2 and GLUT1, compared to the untreated group in vivo. Western blot analysis confirms cell death via apoptotic pathway. **Conclusion:** Pre-clinical trial showed that simultaneous silencing of glucose transporter and pyruvate kinase could be a potential molecular therapeutic approach in treating triple negative breast cancer.

EFFECTS OF MIR-30C-2-3P ON INFLUENZA A INFECTION THROUGH REGULATING NF-KB SIGNALING PATHWAY IN A549 CELL LINE

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NF-κB signalling pathway plays an important role in regulating immune response and the development of B cells. Influenza A virus (IAV) is known to activate this signalling pathway to promote replication. Inhibition of IAV replication through inhibiting NF-κB signalling pathway by chemical inhibitors was well characterized, but the role of miRNA in modulating IAV replication through modulating NF-κB signalling pathway was not well studied yet. Here, we found that miR-30c-2-3p upregulates IAV replication despite downregulating NF-κB signaling pathway. The effect of miR-30c-2-3p on non-IAV PR8 infected-A549 cells was determined. miR-30c-2-3p reduce the protein level of phospho-p65 and phospho-105. Therefore, NF-κB signalling pathway to be downregulated as both of these phosphorylated proteins are the key proteins in stimulating the target gene expression. This may be due to the downregulation TRADD, an adaptor molecule that involves in activating the downstream of NF-κB signalling pathway, by this miRNA. Moreover, in IAV PR8 infected-A549 cells, miR-30c-2-3p significantly reduce the phospho-p65 protein level. This also shows that miR-30c-2-3p can downregulates the IAV PR8 activated-NF-κB signalling pathway. However, plaque assay shown a significant increase in IAV replication with miR-30c-2-3p. We proposed that this phenomenon may be due to the impaired protective effect of NF-κB signaling pathway, whereby downregulation of NF- κB signalling pathway by miR-30c-2-3p render the A549 cells to be more susceptible to IAV infection. This is also probably due to the downregulation of immune-related proteins that are predicted targets of miR-30c-2-3p, based on bioinformatic analysis, such as Toll-like receptor 4 (TLR4).In conclusion, miR-30c-2-3p downregulates NF-κB signalling pathway but upregulates IAV replication. However, this is a preliminary study and requires more study to further confirm the effect of miR-30c-2-3p on IAV through NF-κB signalling pathway.

GENETIC ANALYSIS OF RICE DIFFERING IN GLYCEMIC INDEX (GI)

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Rice feeds more than half of the world's population. The physiochemical properties of starch, the major component of rice endosperm, determine both the eating and cooking qualities of rice. Rice with low glycemic index (GI) values and good palatability provide benefits in the prevention and management of chronic diseases including type II diabetes which is one of the major health concerns in Asia. Therefore, the objective of our study is to identify markers linked to the low GI trait using readily available rice lines in Malaysia and Bangladesh. RNA and protein expression of major starch biosynthesizing genes such as granule bound starch synthase I (*GBSSI*), starch synthase IIa (*SSIIa*) and starch branching enzyme IIb (*SBEIIb*) were also analysed. Eating trials revealed MR219 as high GI, BD192 and BRRI29 as low GI and MRQ74, UKMRC10 as intermediate GI rice cultivars. Nucleotide variations for *GBSSI* and *SSIIa* genes between high and low GI tested rice lines were uncovered which could provide markers for the introgression of alleles linked to low GI trait into high GI rice lines. Protein expression analysis revealed earlier accumulation of both *GBSSI* and *SSIIa* proteins in low GI rice than high GI rice lines which could be considered as a contributing factor to rice lines with low GI values. RNA-seq data analysis also indicated the enhanced expression of both *GBSSI* and *SSIIa* genes in low GI rice lines compared to high GI rice line at the early stage of grain development. The inconsistent variation of RNA expression of *SBEIIb* between high and low GI tested rice cultivars was supported by the protein expression analysis. The combination of results from genetic, protein expression and RNA-seq data analysis could provide useful insights into the genetic basis of low GI rice cultivars.

IN SILICO MOLECULAR INTERACTIONS STUDY OF PATTERN-RECOGNITION RECEPTOR XA26 AND PLANT PATHOGEN-ASSOCIATED MOLECULAR PATTERNS

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First line defense of plant innate immune system is known as pattern-triggered immunity (PTI). PTI is activated by pathogen-associated molecular patterns (PAMPs) of the host plant with the recruitment of co-receptor protein. There are numbers of studies on Xa26, but detail components involved in this mechanism is still not elucidated. The purpose of this study is to explore protein interactions between pattern recognition receptor (PRR) Xa26 with several PAMPs namely flg22 and RaxX21-sY. In this study, these two PAMPs were interacted with PRR Xa26 in presence of different co-receptor named BAK1, OsSerk2 (PDB:4Q3G) and its mutant (PDB:4Q3I). PRR Xa26 protein model was constructed by homology modelling using Modeller HHpred followed by docking and molecular dynamics (MD) simulation of PRR Xa26 with the PAMPs using Zdock and GROMACS respectively. The modelling of PRR Xa26 gave the best result with Verify 3D of 99.68%, ERRAT of 65.854% and 90.2% amino acid in allowed region of Ramachandran plot. Docking result showed that complex interaction of PRR Xa26, PAMP RaxX21-sY with co-receptor OsSerk2 (normal) bind at the concave portion of Xa26 leucine-rich repeat (LRR) which match with the FLS2 mediated PTI, the only crystallized structure in PTI till date. This is the best docking complex as it maintains protein conformational structure and provides stable binding interaction without any loss of bond after the simulation. Furthermore, MD simulation result showed that mutated protein complex of Xa26_RaxX21-sY_OsSerk2 reduced in hydrogen number from 767 to 0 which caused conformational changes of the proteins structure. Besides, the formation of salt bridge between Arg152 with the nearby residue Glu174 in the mutant caused the binding disruption among the protein complex. This study provides significant information about the interaction between Xa26 and multiple PAMPs, which emphasizes future perspectives to find the right PAMP for PTI mechanism of Xa26.

STUDY OF EXTRACELLULAR VESICLES IN URINE USING IR SPECTROSCOPY FOR EARLY DETECTION OF PROSTATE CANCER

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Prostate cancer (PCa) is the third most frequent cancer in men and prostate-specific antigen (PSA) is currently the biomarker used despite its low sensitivity and specificity. Extracellular vesicles (EVs) which are secreted by all types of cells in the body have raised research interest for their association with cancer progression. Urinary EVs has emerged as a potential biomarker for PCa detection as it is non-invasive and urine samples are easily obtained from patients. Several studies have reported that prostate-related genes were detected in urinary EVs. Therefore, we hypothesize that PCa cells secrete EVs containing a unique set of biomolecules which can be exploited as a signature profile of the cancer. In this study, Attenuated Total Reflection-Fourier Transform Infrared (ATR-FTIR) spectroscopy is used for characterization of the EVs isolated from urine samples aiming to obtain a signature spectrum for early detection of PCa. The results of particle size analysis and Western blotting showed that EVs were successfully isolated from both healthy and PCa urine samples as their sizes ranged from 50-500 nm and the samples were found to express protein CD10, the marker for prostate-derived EVs. In the preliminary ATR-FTIR analysis, the spectroscopic protein-to-lipid ratio derived from the sample IR spectra demonstrated that urinary EVs from PCa patients may contain higher lipid content compared to healthy individuals. We anticipate that our finding on the unique IR spectrum of PCa urinary EVs can be used in the development of a non-invasive urine test for early diagnosis of prostate cancer.

A NOVEL ATP13A2 LOSS-OF-FUNCTION MUTATION MODEL FOR PARKINSON'S DISEASE

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Parkinson's disease (PD) is characterized by the selective loss of dopaminergic neurons and presence of Lewy Bodies that are enriched with filamentous α-synuclein in the substantia nigra of the patients. ATP13A2 gene which encodes lysosomal P5-type ATPase is mutated in autosomal recessive forms of early-onset parkinsonism, known as Kufor-Rakeb syndrome (KRS). ATP13A2 loss-of-function mutation causes lysosomal and autophagic dysfunction. Several studies have been conducted in animal models of PD as well as in fibroblasts and dopaminergic cells derived from KRS patients with ATP13A2 mutations to identify the physiological role of ATP13A2. Non-viral synthetic systems and lentiviral vector-mediated ATP13A2 knockdown in primary cultures of neurons have also been developed to study the loss of ATP13A2 function. Unfortunately, the use of current models has its drawback and limitation including toxicity, immunogenicity, recombination, high cost and restricted targeting of specific cell type. In this study, we created a novel cellular model by using carbonate apatite (CA) nanoparticle-associated ATP13A2 siRNAs transfection approach to mimic ATP13A2 loss-of-function mutation. pH-sensitive inorganic CA nanoparticle were fabricated as nanocarrier to deliver pre-designed ATP13A2 siRNAs and non-targeting siRNAs control. siRNAs with concentration range from 1 pM to 50 nM were used for transfection. Following the induction of defective ATP13A2 in SH-SY5Y cell model, western blot was used to check the transfection efficiency. Here, we showed that ATP13A2 protein expression was knocked down by approximately 40% in SH-SY5Y cells transfected with 20 nM of ATP13A2 siRNAs. The results suggest that this ATP13A2 knockdown cell model is useful for further study of ATP13A2-mediated lysosomal-autophagic impairment. The development of ATP13A2 loss-of-function mutation SH-SY5Y cells model via CA nanoparticles-associated ATP13A2 siRNAs would illustrate novel understanding of mechanisms associated with ATP13A2 mutations, providing an insight for the development of new therapeutic strategies to treat PD.

CELL-BASED AND ZEBRAFISH (*DANIO RERIO*) PHENOTYPIC INVESTIGATION OF CYTOTOXIC PROPERTIES IN *ARCTIUM LAPPA* L. ROOT EXTRACT

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The great burdock (*Arctium lappa* L.) has been used as traditional herbs due to its nutritive and therapeutic benefits. Its decoctions or herbal tea preparations were generally used to treat disease-related symptoms of allergy, inflammation and common illness. Recent studies revealed various pharmacological potential of the *A. lappa* root extract by showing anti-cancer, anti-oxidative and anti-inflammatory properties. This project aims to investigate the underlying mechanisms of its cytotoxic properties using cell-based and zebrafish phenotypic assay. The *A. lappa* root was authenticated by species barcoding. *Arctium lappa* root was extracted by decoction method. The bioactive constituents present in the hot aqueous *A. lappa* root extract were screened using LC/MS. The compounds were identified as amino acids (L-Arginine, D-Proline) chlorogenic acids (3,5-Dicaffeoyl-4-succinoylquinic acid), Quinic acid, and S-Propyl propane-1-sulfinothioate. Cell-viability (MTT) assay showed a dose-dependent cytotoxic effects on the cancer cell lines, HeLa and MCF-7, with an IC_{50} of 342.64 and 410.66 µg/ml, respectively. The root extract also displayed selective toxicity towards HeLa and MCF-7 with a selective index of >2. Combinatorial results from JC-1, Caspase-3/7 and Annexin-V/PI assays suggested that the root extract induced apoptosis through the intrinsic apoptotic pathway in a time-dependent manner. Zebrafish phenotypic assay was then performed to determine the targeted cancer-related signalling pathways as observable abnormal phenotypic changes. Zebrafish embryos treated with 315 µg/ml of extract showed the highest rate of reduced pigmentation at 48 hpf. The relative expression of genes related to reduce pigmentation exhibited significant down-regulation of the key genes (*SOX10, kita, β-catenin*) which involved in cell proliferation. Our findings suggest the *A. lappa* root extract could suppress cancer cell proliferation *via* modulation of cancer-related signalling pathways and activation of caspase-mediated intrinsic apoptosis.

MHC-RESTRICTED PEPTIDE VACCINATION ENHANCES CELLULAR IMMUNITY AGAINST LATENCY TUBERCULOSIS ANTIGEN

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Tuberculosis (TB) is a serious human pulmonary disease caused by the infection of *Mycobacterium tuberculosis*, typically with a higher mortality rate among population in developing countries. BCG vaccine confers adequate protection in children but with their immunity waning over time due to clonal exhaustion and suppression. To circumvent this issue, MHC-peptide vaccine was specifically designed to induce T-cell immunity against a latency-associated TB antigen, known as alpha-crystalline heat-shock protein (HspX). C57BL/6 mice (n = 5) were initially primed with recombinant HspX protein, followed by intradermal immunisation and re-stimulation of MHC I and II peptides in conjunction with the use of combined molecular adjuvant (CASAC). Peripheral blood mononuclear cells (PBMC) was then harvested for immunophenotyping assays, such as ELISA and Flow Cytometry. Immunisation with Major Histocompatibility Complex class I and II peptides (MHC I and II) triggered a significant increase of antigen-specific $CD8^+$ response, with 30% higher level of cell population compared to unstimulated control. MHC-restricted vaccines maintained the regulatory T-cell population ($CD4^+$ $CD25^+$ $FOXP3^+$) with reduced $KLRG1^+$ and $PD1^+$ T-lymphocytes in stimulated $CD8^+$ populations. MHC-peptide vaccination in combination with CASAC has shown elevated IFN-γ and TNF-α with low IL-4 and IL-10 release upon immunisation, suggesting a predominant Th1-mediated immunity. In conclusion, novel MHC-restricted peptide vaccination is useful to generate efficient T-cell responses with least hindrance from immunosuppression, which might be a potential therapeutic approach to treat TB infection in the future.

MOLECULAR MECHANISMS OF DIOSCIN IN ORAL SQUAMOUS CELL CARCINOMA

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Oral squamous cell carcinoma (OSCC) is the most prevalent head and neck cancer which has poor prognosis due to therapy-resistant locoregional recurrences and distant metastases. Recent years, natural products have increasing attention to be used against malignant invasive progression in the late stages of neoplastic diseases and as potent chemopreventive drugs. Dioscin, a compound naturally found in plant has been reported to have anti-tumour effect, but the molecular mechanisms of dioscin on human oral squamous cell carcinoma have not been clarified. The aim of this study was to investigate the effects of dioscin on OSCC cells and elucidate its mechanism of action. As previously proven in our lab, H314 are OSCC cells which is resistant to cisplatin treatment while H103 is the sensitive line. These two cell lines were chosen in this study and were treated with or without dioscin. Results showed that dioscin significantly inhibited cell viability of both H314 and H103 cells. Flow cytometry analysis indicates the compound induced cell cycle arrest of H314 cells at G1 phase. In addition, dioscin demonstrates significant suppressive effect on H314 cells motility in the transwell migration assay. At the same time, a quantitative proteomic study was carried out. A total of 498 differentially expressed proteins was identified in dioscin treated H314 cells. Analysis of networking between these proteins using KEGG pathway database showed dioscin significantly interferes metabolism of the cells with strongest effect on glycan biosynthesis. Taken together, the present work showed that dioscin may play a crucial role in glycan metabolism of H314 that regulates the viability and migration of OSCC cells. Findings of this study suggest that dioscin could be one of the potent therapeutic candidates for the treatment of oral cancer.

EFFECTS OF MIR-30C-2-3P ON INFLUENZA A INFECTION THROUGH REGULATING NF-KB SIGNALING PATHWAY IN A549 CELL LINE

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NF-κB signalling pathway plays an important role in regulating immune response and the development of B cells. Influenza A virus (IAV) is known to activate this signalling pathway to promote replication. Inhibition of IAV replication through inhibiting NF-κB signalling pathway by chemical inhibitors was well characterized, but the role of miRNA in modulating IAV replication through modulating NF-κB signalling pathway was not well studied yet. Here, we found that miR-30c-2-3p upregulates IAV replication despite downregulating NF-κB signaling pathway. The effect of miR-30c-2-3p on non-IAV PR8 infected-A549 cells was determined. miR-30c-2-3p reduce the protein level of phospho-p65 and phospho-105. Therefore, NF-κB signalling pathway to be downregulated as both of these phosphorylated proteins are the key proteins in stimulating the target gene expression. This may be due to the downregulation TRADD, an adaptor molecule that involves in activating the downstream of NF-κB signalling pathway, by this miRNA. Moreover, in IAV PR8 infected-A549 cells, miR-30c-2-3p significantly reduce the phospho-p65 protein level. This also shows that miR-30c-2-3p can downregulates the IAV PR8 activated-NF-κB signalling pathway. However, plaque assay shown a significant increase in IAV replication with miR-30c-2-3p. We proposed that this phenomenon may be due to the impaired protective effect of NF-κB signaling pathway, whereby downregulation of NF- κB signalling pathway by miR-30c-2-3p render the A549 cells to be more susceptible to IAV infection. This is also probably due to the downregulation of immune-related proteins that are predicted targets of miR-30c-2-3p, based on bioinformatic analysis, such as Toll-like receptor 4 (TLR4).In conclusion, miR-30c-2-3p downregulates NF-κB signalling pathway but upregulates IAV replication. However, this is a preliminary study and requires more study to further confirm the effect of miR-30c-2-3p on IAV through NF-κB signalling pathway.

AN INVESTIGATION OF THE EFFECT OF SMOKING ON SALIVARY EXOSOMES

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Exosomes are cell-derived vesicles that range in the size of 30-120 nm and are suggested to be present in almost all biological fluids (e.g. saliva, plasma etc.). These vesicles are the result of random invagination of intracellular vesicles, and often contain molecular cargos of their cell of origin, including mRNAs, microRNAs, and proteins. Several studies have reported the role of exosomes in the pathogenesis of several inflammatory diseases including cancers. As cigarette smoking is the number one risk factor for lung cancer, we hypothesize that exosomes from the saliva of the smokers should contain different molecular cargos when compared to those from healthy individuals. In this study, we aim to examine whether a smoking status of an individual influences their protein phenotype of salivary exosomes compared to a healthy cohort, using a list of inflammatory biomarkers. Whole unstimulated saliva samples were collected from both a smoking and healthy/non-smoking cohort and the abundant α-amylase was removed from the samples using affinity chromatography-based filter (ACCF) system. Differential centrifugation was employed on whole saliva samples to isolate the salivary exosomes. Bradford assay for protein quantification, Nanoparticle Tracking analysis (NTA) for measuring particle size, transmission electron microscopy (TEM) for morphology analysis and Western blot for verification of exosomal marker proteins (e.g. CD63) were used to optimize the method for isolation of exosomes from the whole saliva. Preliminary results showed an exosomal yield of 19.57 µg per mL of whole saliva, with the particle size distribution showing a bimodal distribution and the diameter of exosomes ranging from 20 nm-200 nm, indicating the isolation of salivary exosomes is successful. To conclude, we developed and optimized a salivary exosomes isolation methodology using differential centrifugation coupled with ACCF-system. Next, inflammatory biomarkers will be used to investigate the differences between a smoking and healthy/non-smoking cohort.

IMMUNOLOGICAL ASSESSMENT OF MODIFIED MUTANT G12V K-RAS MIMOTOPE AS POTENTIAL PEPTIDE CANCER VACCINES

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To date, *KRAS* gene is the most frequently mutated oncogene in cancer with single point mutations at codons 12 or 13 being one of the most common causes of colorectal cancer progression. Mutant *KRAS* biomarkers are currently recognised clinically worldwide as ineligibility criteria for anti-EGFR therapies, and patients are therefore left with non-specific chemotherapies and a poor prognosis as their treatment options. An approach using peptide-based vaccines in immunotherapy is currently being studied, and in this study, it involves the use of *Lactococcus lactis* as a live delivery vector for safe oral immunisation. Modified mutant G12V K-ras epitopes fused with diphtheria toxoid (DT) were first cloned into *Lactococcus lactis* and immunogenicity of K-ras epitopes was then assessed *in vivo*. Mice were fed orally with recombinant *Lactococcus lactis* casted on edible films and immunoassessments were performed post-immunisation to evaluate: presence of T- and B-cell populations via immunophenotyping of whole blood, and levels of IgG and IgA antibodies via indirect enzyme-linked immunosorbent assay. Cell surface staining via flow cytometry has detected levels of regulatory T-cells ($CD3^+CD4^+CD25^+FOXP3^+$) and cytotoxic T-cells ($CD3^+CD8a^+$) induced by 68-V:DT, while 68-V showed no immunological responses. On the other hand, only specific-IgG sera titres against mutated K-ras antigens from 68-V immunised Balb/c mice were elevated post second boosters compared to wild-type and G12V controls. Immunological assessments showed that edible films delivering K-ras mimotopes were unable to initiate significant immunogenic responses at the intestinal region of a host. More studies to improve the delivery of K-ras mimotopes to the intestinal region can be performed, followed by oral immunisations *in vivo* with other mutant K-ras mimotopes to treat other *KRAS*-positive cancers in the future.

NANOPARTICLE MEDIATED DELIVERY OF PKM2 AND SLC2A1 siRNAs INHIBITS TUMOR GROWTH IN A SYNGENEIC MOUSE MODEL VIA APOPTOTIC PATHWAY

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Introduction: Tumour cells show many distinct features regarding signalling pathways and energy metabolism. Loss of function mutations in tumour suppressor genes, gain of function mutations in proto-oncogenes and aberrant expression of many regulatory signalling pathway proteins attribute some distinct features to cancer cells, one of which is the inordinate dependence on aerobic glycolysis and glutamine metabolism and uncoupling of glycolysis and mitochondrial respiration. Current chemotherapeutic treatment has strong side effects, causing severe discomfort to patients. Recently, researchers have been exploring siRNA as a potential therapeutic with very minimal side effect. As a medium of therapeutic delivery, carbonate apatite, an inorganic, pH sensitive nanoparticle formulated in our lab proved its efficiency to deliver drugs and genetic materials. **Objective:** To inhibit tumour growth by silencing metabolic enzymes with siRNAs delivered by carbonate apatite. **Result:** siRNAs targeting glycolytic enzyme pyruvate kinase M2 (PKM2) and glucose transporter 1 (GLUT1), a member of solute carrier family 2(SLC2A1) were delivered via carbonate apatite nanoparticles both in vitro and in vivo. For in vitro study, we did MTT assay in triple negative human MDA-MB-231 and murine 4T1 cell lines. For in vivo study, breast tumours were induced in the mammary fat pad of female balb/c mice, followed by intravenous delivery of carbonate apatite bound siRNA(s) when the tumour volume reached 13 mm^3. We found a statistically significant ($p<0.01$) reduction in tumour volume for GLUT1(SLC2A1) and for the combination of PKM2 and GLUT1, compared to the untreated group in vivo. Western blot analysis confirms cell death via apoptotic pathway. **Conclusion:** Pre-clinical trial showed that simultaneous silencing of glucose transporter and pyruvate kinase could be a potential molecular therapeutic approach in treating triple negative breast cancer.

EFFECTS OF MIR-30C-2-3P ON INFLUENZA A INFECTION THROUGH REGULATING NF-KB SIGNALING PATHWAY IN A549 CELL LINE

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NF-κB signalling pathway plays an important role in regulating immune response and the development of B cells. Influenza A virus (IAV) is known to activate this signalling pathway to promote replication. Inhibition of IAV replication through inhibiting NF-κB signalling pathway by chemical inhibitors was well characterized, but the role of miRNA in modulating IAV replication through modulating NF-κB signalling pathway was not well studied yet. Here, we found that miR-30c-2-3p upregulates IAV replication despite downregulating NF-κB signaling pathway. The effect of miR-30c-2-3p on non-IAV PR8 infected-A549 cells was determined. miR-30c-2-3p reduce the protein level of phospho-p65 and phospho-105. Therefore, NF-κB signalling pathway to be downregulated as both of these phosphorylated proteins are the key proteins in stimulating the target gene expression. This may be due to the downregulation TRADD, an adaptor molecule that involves in activating the downstream of NF-κB signalling pathway, by this miRNA. Moreover, in IAV PR8 infected-A549 cells, miR-30c-2-3p significantly reduce the phospho-p65 protein level. This also shows that miR-30c-2-3p can downregulates the IAV PR8 activated-NF-κB signalling pathway. However, plaque assay shown a significant increase in IAV replication with miR-30c-2-3p. We proposed that this phenomenon may be due to the impaired protective effect of NF-κB signaling pathway, whereby downregulation of NF- κB signalling pathway by miR-30c-2-3p render the A549 cells to be more susceptible to IAV infection. This is also probably due to the downregulation of immune-related proteins that are predicted targets of miR-30c-2-3p, based on bioinformatic analysis, such as Toll-like receptor 4 (TLR4).In conclusion, miR-30c-2-3p downregulates NF-κB signalling pathway but upregulates IAV replication. However, this is a preliminary study and requires more study to further confirm the effect of miR-30c-2-3p on IAV through NF-κB signalling pathway.

CHEMISTRY & DRUG DISCOVERY

Invited Speakers

No.		Date	Time	Venue
1	**Professor Dr. Philip Marriott**	21 Nov	11.00-11.30	Plenary Theatre
	High resolution drugs analysis: separation and mass spectrometry			
2	**Professor David Young**	21 Nov	01.00-01.30	SR-6215
	Designing for selective chemical sensing			

Oral Presenters

OP-CDD-01	**Fatimah Alqadeeri**	21 Nov	01.30-01.45	SR-6215
	Phytochemical constituents and antibacterial activity of fractions of *Piper cubeba* L. extract against vegetative cell of *Bacillus* sp.			
OP-CDD-02	**Rahela Zaman**	21 Nov	01.45-02.00	SR-6215
	Fabrication of oral nano-insulin formulation for regulating blood glucose level			
OP-CDD-03	**A.K Mahmud Hasan**	21 Nov	02.00-02.15	SR-6215
	Optical and electrical characteristics of electron beam deposited nickel oxide films as a function of thickness			
OP-CDD-04	**Shafi Ullah Khan**	21 Nov	02.45-03.00	SR-6215
	In silico and *in vitro* identification of new G protein-coupled estrogen receptor-1 (GPER) modulators			
OP-CDD-05	**M. S. Jamal**	21 Nov	03.00-03.15	SR-6215
	Effects of defect states in perovskite layer on performance of perovskite solar cells by numerical simulation			

Poster Presenters

PP-CDD-01	**Sundus Khan**	23 Nov	12.00-01.00	Foyer
	The polymer modified sensors for the determination of GA using Voltammetric technique			
PP-CDD-02	**Fatimah Alqadeeri**	23 Nov	12.00-01.00	Foyer
	Phytochemical constituents and antibacterial activity of fractions of *Piper cubeba* L. extract against vegetative cell of *Bacillus* sp.			
PP-CDD-03	**Maryam Aisyah Abdullah**	23 Nov	12.00-01.00	Foyer
	New sulfonylated-diarylpentadienone analogues as dipeptidyl peptidase 4 (DPP-4) inhibitors			
PP-CDD-04	**M. Rashidi Abdull Manap**	23 Nov	12.00-01.00	Foyer
	Preparation of chemically modified and hypercrosslinked microspeheres of poly(acrylonitrile-co-divinylbenzene-80-co-vinylbenzylchloride) as sorbents to capture pharmaceutical residues			
PP-CDD-05	**Shenly Marie T. Gazo**	23 Nov	12.00-01.00	Foyer
	Utilization of hydroxyapatite from tilapia (*Oreochromis niloticus*) bones for photocatalytic degradation of methyl orange and rhodamine B			
PP-CDD-06	**Nabilah Ibnat**	23 Nov	12.00-01.00	Foyer
	Co-delivery of PTEN plasmid and siRNA against protein kinase C-α (PKC-α) gene persuaded synergistic effect of the treatment			
PP-CDD-07	**Ethel Jeyaseela Jeyaraj**	23 Nov	12.00-01.00	Foyer
	Effect of organic solvents and water (heat and ultrasound-assisted) extraction on the extract yield, anthocyanin composition and total phenolic content of *Clitoria ternatea* flowers			

PP-CDD-08	**Jahid Md Mahabub Islam**	23 Nov	12.00-01.00	Foyer
	Nano-fabrication of organic/inorganic hybrid drug carrier to selectively kill cancer cells			
PP-CDD-09	**Nuraina Anisa Dahlan**	23 Nov	12.00-01.00	Foyer
	Carboxymethyl cellulose grafted polyethylene glycol and properties tailored for tissue engineering applications			
PP-CDD-10	**Ha Zhe Ying**	23 Nov	12.00-01.00	Foyer
	Synthesis and evaluation of benzimidazole derivatives for Alzheimer's disease			
PP-CDD-11	**Tan Soo Suen**	23 Nov	12.00-01.00	Foyer
	Synthesis of dispiro compounds as cholinesterase inhibitors for Alzheimer's disease therapeutics			
PP-CDD-12	**Hammad Saleem**	23 Nov	12.00-01.00	Foyer
	Biological, chemical and toxicological perspectives on aerial and roots of *Filago germanica* (L.) huds: Functional approaches for novel phyto-pharmaceuticals			

Research in a Flash

RF-CDD-01	**Fatimah Alqadeeri**	23 Nov	09.00-10.30	Plenary Theatre
	Phytochemical constituents and antibacterial activity of fractions of *Piper cubeba* L. extract against vegetative cell of *Bacillus* sp.			
RF-CDD-02	**M. Rashidi Abdull Manap**	23 Nov	09.00-10.30	Plenary Theatre
	Preparation of chemically modified and hypercrosslinked microspeheres of poly(acrylonitrile-co-divinylbenzene-80-co-vinylbenzylchloride) as sorbents to capture pharmaceutical residues			
RF-CDD-03	**Shenly Marie T. Gazo**	23 Nov	09.00-10.30	Plenary Theatre
	Utilization of hydroxyapatite from tilapia (*Oreochromis niloticus*) bones for photocatalytic degradation of methyl orange and rhodamine B			
RF-CDD-04	**Nabilah Ibnat**	23 Nov	09.00-10.30	Plenary Theatre
	Co-delivery of PTEN plasmid and siRNA against protein kinase C-α (PKC-α) gene persuaded synergistic effect of the treatment			
RF-CDD-05	**Shafi Ullah Khan**	23 Nov	09.00-10.30	Plenary Theatre
	In silico and *in vitro* identification of new G protein-coupled estrogen receptor-1 (GPER) modulators			

RF-CDD-06	**Hammad Saleem**	23 Nov	09.00-10.30	Plenary Theatre
	Biological, chemical and toxicological perspectives on aerial and roots of *Filago germanica* (L.) huds: Functional approaches for novel phyto-pharmaceuticals			

PHYTOCHEMICAL CONSTITUENTS AND ANTIBACTERIAL ACTIVITY OF FRACTIONS OF *PIPER CUBEBA* L. EXTRACT AGAINST VEGETATIVE CELL OF *BACILLUS* SP.

Fatimah Alqadeeri[1], Faridah Abas[1,2], Khozirah Shaari[1,3] and Yaya Rukayadi[1,2]*

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Piper cubeba L. is a medicinal plant that belongs to the Piperaceae family. Moreover, it is important as a source of pepper (the dried berries) for the worldwide spice market. Many species of genus Piper are used in traditional herbal medicine and have shown antifungal, insecticidal and antitumor activities. This study was done in order to analyze the phytochemical components and to investigate the antibacterial activity of *Piper cubeba* L. berries fractions. *Piper cubeba* L. berries were extracted using methanol as a solvent to get the crude extract. The methanolic crude extracts were then fractionated using n-hexane, dichloromethane, butanol and ethyl acetate. Meanwhile, the antibacterial properties of the samples were tested against four *Bacillus* strains ;- *B. cereus* ATCC 33019, *B. subtilis* ATCC 6633, *B. pumilus* ATCC 14884 and *B. megaterium* ATCC 14581 using the disk diffusion (DDA) method, minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) referring to standard method of Clinical and Laboratory Standards Institute (CLSI). Phytochemical screening was carried out to identify the presence of principal chemical components of the crude extracts and fractions. The results showed that *P. cubeba* L. extracts consist of phytochemical constituents, such as lignan, alkaloids, terpenoids and flavonoids which are responsible for the biological activities. Dichloromethane fraction showed the best activity against *Bacillus* sp. The bioactive compounds present in *P.cubeba.* extract were determined using Gas Chromatography-Mass Spectrometry (GC-MS) and Liquid Chromatography-Mass Spectrometry (LC-MS). GC-MS analysis showed that the crude methanolic extract and all the solvent fractions of *Piper cubeba* L. berries contained a diverse array of constituents. The major volatile bioactive compounds determined using GC-MS were β-cubebene, cubebol, β-Asarone, α-copaene, caryophyllene, and germacrene-D. Non- volatile compounds identified by LC-MS were α-Cubebene, yatein, Dihydroclusin, Spathulenol, β-Asarone and Hinokinin. The results revealed that *Piper cubeba* L. has a future potential as an antibacillus agent.

FABRICATION OF ORAL NANO-INSULIN FORMULATION FOR REGULATING BLOOD GLUCOSE LEVEL

Rahela Zaman[1]*, Md.Ezharul Hoque Chowdhury[1], Iekhsan Othman[1], Anuar Zaini Md Zain[1]

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Insulin, essentially used in treatment of diabetes melitus, is only available in injectable form. Being a peptide molecule, it is not resistant enough to withstand harsh environment in GIT making any oral form practically impossible. Here, we are introducing a new approach, carrier mediated insulin delivery through GIT. Carrier mediated drug delivery is considered as one of the most promising technologies for targeted delivery of therapeutics of wide range. Different precipitation based particulates formulated in our lab, have shown promising binding effinity towards small molecular drugs and genetic materials. We have tested CO_3Ap, Sr-CO_3Ap, Ba-salt NPs, Sr-salt NPs and Ca-salt NPs, *in vitro,* to observe their potential as macromolecular peptide therapeutic carrier, or more specificly, insulin carrier during oral delivery. At the sametime, tests were carried out to see whether these molecules can withstand low pH environement and therefore, can protect protein therapeutic molecules from harsh pH and enzymatic degradation. With two types of carbon apatite particles (CO_3Ap and Sr-CO_3Ap NP) and a total of 14 different NPs prepared from precipitation salt reaction were tested. From this list of NPs, CO_3Ap and Sr-CO_3Ap, 2 of the Ca salt particles ($CaSO_3$ and $CaCO_3$), 3 of the Ba salt particles ($BaSO_4$, $BaSO_3$ and $BaCO_3$) and 2 of the Sr-salt particles ($SrSO_4$ and $SrCO_3$) were selected based on their pH resistance and insulin binding profile. Selected insulin-NP formulations will be orally given to diabetic rats and blood analysis will be conducted to estimate bioavailability of the delivered insulin and to observe its effect on maintaining blood glucose level.

OPTICAL AND ELECTRICAL CHARACTERISTICS OF ELECTRON BEAM DEPOSITED NICKEL OXIDE FILMS AS A FUNCTION OF THICKNESS

A. K Mahmud Hasan[1], M.S. Jamal[1], Asmaa Soheil Najm[1], Nurhifiza. K[1], Fahia Tarannum Munna[1], Samiya Mahjabin[1], Muhamad Irsyam Uddin[1], Itaru Raifuku[2], Yasuaki Ishikawa[2], N. Amin[3], MD. Akhtaruzzaman[1]*

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The optical, electrical and crystallinity properties of NiO depend on deposition technique. Deferent thickness of Nickel oxide films were deposited at the same experimental condition by electron beam deposition technique without any intentional increment of temperature at vacuum pressure of 4.2 X 10^{-6} Torr on glass substrate. The optical properties were measure by UV-Vis. The results show that films transmittance decreased and band gap reduced upon the increasing of thickness. The X-ray diffraction was used to investigate crystalline properties of NiO films as dependence of film thickness in the range of 30° to 90° angle. NiO film without thermal annealing treatment still can exhibit clear and distinct diffraction peaks at 37.36°, 43.53°, 63.20°, 75.66° and 79.67°, which could be indexed to the (1 1 1), (2 0 0), (2 2 0), (1 1 3) and (2 2 2) planes of hexagonal NiO, respectively. A comparative reduction on the ionization potential or work function of NiO films was observed when measured by photoelectron yield spectroscopy. The valence band maxima were pushed towards Fermi level in a decimal scale.

IN SILICO AND *IN VITRO* IDENTIFICATION OF NEW G PROTEIN-COUPLED ESTROGEN RECEPTOR-1 (GPER) MODULATORS

Shafi Ullah Khan[1], Nafees Ahemad[1], Lay-Hong Chuah[1,2], Rakesh Naidu[3], Thet Thet Htar[1]*

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G protein-coupled estrogen receptor-1 (GPER-1, formerly known as GPR30) is a seven transmembrane receptor, mediates important pathophysiological signalling pathways induced by estrogens and is currently regarded as a promising target for ER-negative (ER-) and triple-negative (TN) breast cancer. Only a few selective GPER-1 modulators have been reported to date. The 3D structure of GPER-1 is essential for discovering novel inhibitors during high-throughput virtual screening. However, to date, the 3D structure ofGPER-1not been resolved. In this study, initially a series of intensive computational techniques, both ligand-based and structure-based virtual screening (VS) were performed for the identification of GPER-1 modulators. The obtained results strongly support the reliability of our VS procedure, as the topmost resulting compounds that survived the VS filtering procedure were very similar to already reported GPER-1 ligands. Two compounds, SKO and SKOP having tetrahydropyran and tetrahydrofuran moiety respectively, were found having higher chemguass4 score compared to the known selective GPER-1 modulator. These two compounds were then synthesised using microwave irradiation technique in a good yield of 74 and 66 % respectively and characterized by FTIR, ^{1}H NMR, ^{13}C NMR and mass spectral analyses. These compounds were also subjected to MTT cell viability assay for investigating their-cancer activities in GPER-1 expressing breast cancer cell line, MCF-7 and SKBr-3 cell line. Preliminary results provide valuable information towards the identification of promising scaffold for designing novel GPER ligands.

EFFECTS OF DEFECT STATES IN PEROVSKITE LAYER ON PERFORMANCE OF PEROVSKITE SOLAR CELLS BY NUMERICAL SIMULATION

M. S. Jamal[1], A K Mahmud Hasan[1], S. A. Shahahmadi[2, 3], P. Chelvanathan[1], Fahia Tarannum Munna[1], Samiya Mahjabin[1], Asmaa Soheil Najm[2], N. Amin[2,3], K. Sopian[1], Md. Akhtaruzzaman[1]*

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Metal halide perovskite solar cells (PSCs) have been recently identified as the most attractive photovoltaic technology for energy harvesting due to their exceptional semiconducting properties. Understanding of defect formation in absorption layer is crucial for successful development of stable and highly efficient PSCs. Here, we have studied the effect of defect density of absorber layer on the performance of PSCs by numerical simulation. SCAPS-1D software was used in this numerical simulation and studied the effect of defect densities of absorber and interface layer on the performance of inverted structure PSCs. The effect of defect density ranging from 10^{13} to 10^{19} cm^{-3} and defect energy level from -8 to +8 eV is probed to explore the device performance. The values of J_{sc} are linearly decreased with increasing defect densities of perovskite absorber layer and values are ranging from 22.0 to 23.3 mA/cm^2. At the same time, V_{oc} is substantially reduced from 1.15 to 1.00 V for the same range of defect density. Power conversion efficiency (PCE) is reduced from 24.0% to 14.0% when the defect densities increase from 1×10^{13} cm^{-3} to 1×10^{19} cm^{-3} but the PCE is linearly increased with increasing the defect energy level ranging from 0.0 to 0.5 eV of perovskite absorber layer.

THE POLYMER MODIFIED SENSORS FOR THE DETERMINATION OF GA USING VOLTAMMETRIC TECHNIQUE

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Electrochemical sensors are the smart devices used for the detection of electrochemically active compounds. Reviews in this field has shown that no research has been conducted for detection of gallic acid (GA) with polymer sensor. Electrochemical methods are the alternate, competent, inexpensive and sensitive methods for the estimation of antioxidant capacity. Polymer sensor is the unique electrochemical sensor modified with nanomaterials for fabricating a novel class sensor. The polymer modified sensor will be applied for the determination of oxidation of GA using voltammetric technique. The electrocatalytic process is shown by a well-defined peak of GA obtained with bare GCE. Investigation of experimental parameters for the determination of GA potential window, pH, scan rate and supporting electrolyte will also be done.

PHYTOCHEMICAL CONSTITUENTS AND ANTIBACTERIAL ACTIVITY OF FRACTIONS OF *PIPER CUBEBA* L. EXTRACT AGAINST VEGETATIVE CELL OF *BACILLUS* SP.

Fatimah Alqadeeri[1], Faridah Abas[1,2], Khozirah Shaari[1,3] and Yaya Rukayadi[1,2]*

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Piper cubeba L. is a medicinal plant that belongs to the Piperaceae family. Moreover, it is important as a source of pepper (the dried berries) for the worldwide spice market. Many species of genus Piper are used in traditional herbal medicine and have shown antifungal, insecticidal and antitumor activities. This study was done in order to analyze the phytochemical components and to investigate the antibacterial activity of *Piper cubeba* L. berries fractions. *Piper cubeba* L. berries were extracted using methanol as a solvent to get the crude extract. The methanolic crude extracts were then fractionated using n-hexane, dichloromethane, butanol and ethyl acetate. Meanwhile, the antibacterial properties of the samples were tested against four *Bacillus* strains ;- *B. cereus* ATCC 33019, *B. subtilis* ATCC 6633, *B. pumilus* ATCC 14884 and *B. megaterium* ATCC 14581 using the disk diffusion (DDA) method, minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) referring to standard method of Clinical and Laboratory Standards Institute (CLSI). Phytochemical screening was carried out to identify the presence of principal chemical components of the crude extracts and fractions. The results showed that *P. cubeba* L. extracts consist of phytochemical constituents, such as lignan, alkaloids, terpenoids and flavonoids which are responsible for the biological activities. Dichloromethane fraction showed the best activity against *Bacillus* sp. The bioactive compounds present in *P.cubeba.* extract were determined using Gas Chromatography-Mass Spectrometry (GC-MS) and Liquid Chromatography-Mass Spectrometry (LC-MS). GC-MS analysis showed that the crude methanolic extract and all the solvent fractions of *Piper cubeba* L. berries contained a diverse array of constituents. The major volatile bioactive compounds determined using GC-MS were β-cubebene, cubebol, β-Asarone, α-copaene, caryophyllene, and germacrene-D. Non- volatile compounds identified by LC-MS were α-Cubebene, yatein, Dihydroclusin, Spathulenol, β-Asarone and Hinokinin. The results revealed that *Piper cubeba* L. has a future potential as an antibacillus agent.

NEW SULFONYLATED-DIARYLPENTADIENONE ANALOGUES AS DIPEPTIDYL PEPTIDASE 4 (DPP-4) INHIBITORS

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Type 2 diabetes mellitus (T2DM) is an epidemic disease occurred worldwide and is currently a major cause of morbidity and mortality. Several drugs such as sulfonylureas and biguanides are presently available to reduce hyperglycemia in T2DM, however, these medicines possess several side effects and thus searching for a new class of compounds is essential to overcome this problem. A series of aminated-1,5-diphenylpenta-2,4-dien-1-ones were synthesized by treating aminoacetophenones with differently substituted cinnamaldehydes *via* aldol condensation reaction, further completion by sulfonylation reaction with trifluorobenzenesulfonyl chloride to afford the sulfonylated-diarylpentadienone analogues. The purified final compounds were collected and subjected to confirmatory structural elucidation *via* established spectroscopic techniques comprising high field nuclear magnetic resonance (NMR), gas chromatography-mass spectroscopy (GC-MS), high-resolution mass spectroscopy (HRMS), and infrared spectroscopy. These new derivatives were screened for their anti-diabetic properties on dipeptidyl peptidase (DPP-4) *in vitro* assay. It was found that N-(4-((2E,4E)-5-(4-methoxyphenyl)penta-2,4-dienoyl)phenyl)-4-(trifluoromethyl) benzenesulfonamide, compound **15** show the most potent DPP-4 inhibitor exhibiting IC_{50} of 25.5 µM. The structure-activity relationship (SAR) and molecular docking of these bioactive compounds on DPP-4 will be summarized to provides evidence supporting the development of amino-substituted and sulfonamide-substituted diarylpentadienone as molecules to treat T2DM.

PREPARATION OF CHEMICALLY MODIFIED AND HYPERCROSSLINKED MICROSPEHERES OF POLY(ACRYLONITRILE-*co*-DIVINYLBENZENE-80-*co*-VINYLBENZYLCHLORIDE) AS SORBENTS TO CAPTURE PHARMACEUTICAL RESIDUES

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Residues of pharmaceutical are potentially hazardous contaminants to aquatic life and human. Pharmaceutical residues have been detected in Malaysian tropical wastewaters. A challenge therein is the development of enrichment techniques able to extract polar pharmaceutical residues, since these compounds are widely found in aqueous samples yet present particular difficulties in their extraction due to their polar character. Acrylonitrile (AN)-divinylbenzene-80 (DVB-80)-vinylbenzylchloride (VBC) porous terpolymer material was prepared in the present research *via* precipitation polymerisation method. The porous terpolymer (MNA1) containing chlorine pendant groups was hypercrosslinked *via* a Friedel Crafts reaction to develop 3D network structure within the terpolymer chains. FT-IR spectrum of MNA1 showed that the chloromethyl groups derived from VBC were consumed, which was consistent with successful hypercrosslinking. The hypercrosslinked porous material was then chemically modified with ethylenediamine (EDA) (MNA2) to develop active functional groups (diamine moisties) along terpolymer chains. FT-IR spectrum showed that a new diamine absorption band appeared after the chemical modification, indicating the nitrile group was successfully converted into diamine moieties. Both experimental spectra was validated and proved by the calculated transmittance spectra. The mono-disperse spherical particles of MNA1 and MNA2 were observed using SEM analysis. Their high specific surface area and polar character (arising from AN residues), make them as potential materials to extract pharmaceutical residues.

UTILIZATION OF HYDROXYAPATITE FROM TILAPIA (*OREOCHROMIS NILOTICUS*) BONES FOR PHOTOCATALYTIC DEGRADATION OF METHYL ORANGE AND RHODAMINE B

Reinzo Vittorio B. Cardenas[1], Shantel Gayle Q. Tayag[1], Danielle A. Moreno[1], Chienne Andrei P. Regodon[1], Aaron John M. Supan[1], Judee Anne D. Enriquez[1], Dannah Salcedo[1], Tyrone Sundiam[1], Janielle Seen[1], Nicole Saltarin[1], Michael Lucido[1], and Shenly Marie T. Gazo[1]*

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Synthetic dyes are widely used in industrial companies. Improper disposal of these dyes can pose harmful effects in the water systems. Therefore, wastewater treatment prior to its disposal is vital in regulating its adverse effects. This research assessed the photocatalytic degradation of Rhodamine B (RhB) and Methyl Orange (MO) using Hydroxyapatite (HAp) from *Oreochromis niloticus* (tilapia) fish bones. The HAp was synthesized via calcination at 900˚C for three hours under simple heat treatment and was then characterized using X-ray Diffractometer. The degradation of RhB and MO was determined using UV-Vis spectrophotometer under varying parameters that included the amount of catalyst (500, 750, and 1000 mg) and UV irradiation time (20, 40, 60, 80 and 100 minutes). Results in the X-ray diffractometer revealed that distinct peaks at (2θ) 31.70˚, 32.84˚, and 32.12˚ were in line with the HAp standards that indicated the potential of tilapia bones as a source of HAp. Results as well showed that the highest percent degradation was obtained in 1000 mg HAp for Rhodamine B (24.02%) and 750 mg HAp for methyl orange (48.58%) with an initial concentration 8 ppm and 100 minutes of UV irradiation. The study suggested the potential of HAp from tilapia fish bones as a photocatalyst for Rhb and MO.

CO-DELIVERY OF PTEN PLASMID AND SIRNA AGAINST PROTEIN KINASE C-α (PKC-α) GENE PERSUADED SYNERGISTIC EFFECT OF THE TREATMENT

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PTEN (Phosphatase and tensin homolog deleted on chromosome ten) is a tumor suppressor protein and loss of expression of PTEN and it's promoter methylation is noticed in breast cancer patients. In addition, PKC-α, is an isoform of protein kinase C family of protein kinases and contribute to cellular differentiation and proliferation. Elevated PKCα is associated with endocrine resistance and poor prognosis in ER-positive (ER+) breast tumors. We developed carbonate apatite nanoparticles as a delivery system to deliver PTEN tumor suppressor gene in the form of plasmids as well as to deliver siRNA against PKC-α, to interrupt PKC-α, expression in breast cells. We designed carbonate apatite nanoparticles (NPs) and complexed with PTEN plasmid (pPTEN) and / PKC-α siRNA and performed transfection of breast cancer cell lines to assess cellular proliferation by MTT. Treated cells were also subjected to western blot experiment to assess expression of phospho-AKT (P-AKT) protein. Upon cytotoxic assessment we observed a novel synergistic effect of PTEN expression and PKC-α silencing, particularly in MCF-7 and MDA-MB-231 (TNBC) cells. The cell viability data demonstrated that co-delivery of PTEN plasmid and PKC-α siRNA by means of NPs exhibited a synergistic effect compared to the specific delivery of the components. The expression level of phospho-AKT protein in pPTEN+NP and PKC-α siRNA+NP treated cells is lower than the NP control. Interestingly, the band is almost faded or invisible in the cell lysate, receiving both treatments, pPTEN + PKC-α siRNA +NP formulation. Significantly reduced amount of P-AKT protein is a direct indication of the successful co-delivery effect of the treatment. Since less AKT is activated in these cells, the proliferation signal is reduced and cancer cell growth is also retarded.

EFFECT OF ORGANIC SOLVENTS AND WATER (HEAT AND ULTRASOUND-ASSISTED) EXTRACTION ON THE EXTRACT YIELD, ANTHOCYANIN COMPOSITION AND TOTAL PHENOLIC CONTENT OF *CLITORIA TERNATEA* FLOWERS

Ethel Jeyaseela Jeyaraj[1], Yau Yan Lim[1] and Wee Sim Choo[1]*

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Clitoria ternatea flowers are commonly used as a traditional medicinal herb and as a food colourant in Southeast Asia. *C. ternatea* is rich in anthocyanins and this study investigated the effect of extraction conditions to extract anthocyanins. Two extraction techniques which were aqueous organic solvent (50%, 80% or 100% of methanol, ethanol or acetone) and water (heat and ultrasonic-assisted) were used. Total anthocyanin content (TAC), total phenolic content (TPC) and extraction yield were determined. Anthocyanin composition was determined using LC-MS. Among the organic solvent extraction, 50% ethanol was determined to be the best solvent for the extraction of *C. ternatea* with an extract yield of 57.3 ± 7.9%, TAC of 6.1 ± 2.5 mg cyanidin-3- glucoside equivalent/g dry weight of extract (CGE/g) and TPC of 59.4 ± 3.5 mg gallic acid equivalent/g dry weight of extract (GAE/g) while 50 °C for 1 h was the best extraction condition for water (heat or ultrasound) extraction with an extract yield of 56.1 ± 3.0%, TAC of 4.0 ± 0.9 mg CGE/g extract and TPC of 57.5 ± 2.6 mg GAE/g extract. A total of 10 ternatin anthocyanins were identified with different composition in the aqueous organic solvent and water extract in which the former was found to have higher amount of anthocyanins. C18-OPN and Amberlite XAD-16 open column chromatography were used to obtain anthocyanin-rich extract of *C. ternatea*. Amberlite XAD-16 column chromatography yielded a higher ratio of TAC:TPC.

NANO-FABRICATION OF ORGANIC/INORGANIC HYBRID DRUG CARRIER TO SELECTIVELY KILL CANCER CELLS

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Non-selective targeting and tendency to destroy the healthy cells of the body are the major challenges of treating cancer by cytotoxic drugs. In this research a target specific nano-carrier is developed to entrap cytotoxic model drug i.e. 5-flurouracil (5-FU) and deliver it to the targeted cancer site. Low molecular weight chitosan and thermally degraded carboxymethyl cellulose (CMC) were mixed in several ratios with varying concentrations. Particle size was found to vary with variable concentrations of chitosan and CMC, with decreasing concentrations leading to particles of smaller sizes. Zetasizer study showed that average size of the particles formed with 500 µg/mL chitosan mixed with 500 µg/mL CMC was 435.06±15.20 nm, whereas mixing of 200 µg/mL chitosan with 200 µg/mL CMC resulted in particle size of 178.76±6.35 nm. These nanoparticles were also found to be biocompatible with human forehead fibroblast cell line (Hs-68), which suggested their compatibility with healthy human tissues. In the cytotoxicity study it was found that drug-loaded nanoparticles were more effective to kill cancer cells compared to the free drugs. Besides, as the nanoparticle was fabricated with organic polymers with free functional groups, it is possible to conjugate it with a cancer selective targeting ligand, such as folic acid to induce cancer specificity into the drug-loaded nanoparticle.

CARBOXYMETHYL CELLULOSE GRAFTED POLYETHYLENE GLYCOL AND PROPERTIES TAILORED FOR TISSUE ENGINEERING APPLICATIONS

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Tissue engineering, a rapidly evolving area within regenerative medicine focuses on the utilization of tissue engineering scaffolds to repair human organs. This work aims to synthesize a novel carboxymethyl cellulose grafted polyethylene glycol (CMC-*g*-PEG) for potential tissue engineering applications. The hydroxyl end terminal of PEG was converted into an amine group (-NH_2) prior to grafting onto the CMC backbone in the presence of *N*-ethyl-*N*'-(3-dimethylaminopropyl)carbodiimide (EDC) and *N*-hydroxysuccinimide (NHS). The -NH_2 conversion efficiency was found to be 92% with an absorption peak at 1652 cm^{-1} corresponded to -NH group was observed in the FT-IR spectroscopy. Furthermore, the grafting efficiency and percentage yield of CMC-g-PEG were found to be 71% and 86%, respectively. The novel grafted polymer was further characterized in terms of thermal behavior and crystallinity. Electrospinning is a versatile technique of producing fibrous polymers ranging from micron- to the nanoscale. However, natural polymer is very difficult to electrospin due to low conductivity, limited solubility in suitable solvents for electrospinning, hence cannot form fibers for themselves. These problems can be solved through emulsion electrospinning approach. Core-shell nanofibers were fabricated by emulsion electrospinning from PCL/CMC-*g*-PEG. The morphology of the prepared PCL/CMC-*g*-PEG was observed by field emission electron microscope (FESEM). Therefore, the synthesized PCL/CMC-*g*-PEG nanofibers lay a foundation for further development as a scaffold in tissue engineering applications.

SYNTHESIS AND EVALUATION OF BENZIMIDAZOLE DERIVATIVES FOR ALZHEIMER'S DISEASE THERAPEUTICS

Ha Zhe Ying[1] & Yeong Keng Yoon[1]*

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Alzheimer's disease is a chronic and progressive neurodegenerative disease that affects the brain. Efforts in understanding the disease have led to the discovery of cholinesterase inhibition as a viable treatment to increase the brain acetylcholine levels. Recent studies have implicated butyrylcholinesterase (BuChE) in late-stage Alzheimer's disease, prompting a shift in focus from acetylcholinesterase (AChE)-targeting inhibitors. This study aims to evaluate benzimidazole compounds for their cholinesterase inhibitory properties, analyse the structure-relationship activity, and asses the inhibition kinetics and cytotoxicity. Two series of 2-substituted benzimidazole derivatives were synthesized and confirmed using ^{1}H NMR spectroscopy. The compounds were screened for AChE and BuChE inhibition, and their structure-activity relationship was postulated. **5IIa** showed the highest inhibition, with a sub-micromolar BuChE IC_{50} 0.40 µM and selectivity index of 13.83 over AChE. Enzyme kinetics studies showed **5IIa** to be a competitive inhibitor, with $a_i$of 0.113 µM. The activity-time plot indicated a reversible binding at the BuChE active site, supporting the hypothesis of a competitive inhibition. Cytotoxicity assays using SH-S5Y5 and BEAS-2B cell lines showed no significant toxicity up to 50 µM ($p < 0.001$), giving **5IIa** a selectivity index of > 125. **5IIa** shows potential as a potent and selective BuChE inhibitor that can be employed for therapeutic or research purposes.

SYNTHESIS OF DISPIRO COMPOUNDS AS CHOLINESTERASE INHIBITORS FOR ALZHEIMER'S DISEASE

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Evaluated by Alois Alzheimer, Alzheimer's disease is a disease that affects a majority of older adults, determined by the gradual decline and deterioration of neurons and atrophy of the brain, which leads to a diminishing memory, a loss in cognitive function and a disruption in daily activities. The cost of being an Alzheimer's patient is tremendous, not only in monetary terms, but also in social terms. The disease is a multifactorial disease, with its hallmarks being senile amyloid plaques and neurofibrillary tangles. Cholinesterase inhibitors make up three out of four drugs for Alzheimer's disease on the market, but side effects are not uncommon, and there is almost no difference in efficacy. This project ventures into dispiro compounds as inhibitors for cholinesterases through exploitation of the rigidity and orthogonality that the structures offer. A series of dispiro compounds were synthesized, with compounds DEF, OHF and TOF showing inhibitory activity for AChE, and compound DMF and BZF were found to show inhibitory activity for BuChE. It was found that electron donating groups increased the potency of the compounds in terms of cholinesterase activity. In the antiproliferative studies, it was found that compounds OHF and DMF were cytotoxic to the cell line SH-SY5Y, but was not towards BEAS-2B cells. Molecular docking studies showed interactions of the Tyr70, Tyr334, Tyr121, Trp84, Phe330 and Phe331 amino acid residues in AChE with the compounds selected, and interactions with Ala328, Ser198 and His438 in BuChE for the compounds selected. The best performing compounds, OHF and DMF, had the shortest bond lengths when compared to compounds that were docked against the same enzyme.

BIOLOGICAL, CHEMICAL AND TOXICOLOGICAL PERSPECTIVES ON AERIAL AND ROOTS OF *FILAGO GERMANICA* (L.) HUDS: FUNCTIONAL APPROACHES FOR NOVEL PHYTO-PHARMACEUTICALS

Hammad Saleem[1,2], Thet Thet Htar[1], Rakesh Naidu[3] and Nafees Ahemad[1]*

[1]*School of Pharmacy, Monash University, Jalan Lagoon Selatan, 47500 Bandar Sunway Selangor Darul Ehsan, Malaysia*

[2]*Institute of Pharmaceutical Sciences (IPS), University of Veterinary & Animal Sciences (UVAS), Lahore-54000, Pakistan*

[3]*Jeffrey Cheah School of Medicine and Health Sciences, Monash University, Jalan Lagoon Selatan, 47500 Bandar Sunway Selangor Darul Ehsan, Malaysia*

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We investigated into the effects of methanol and dichloromethane extracts from aerial and roots of *Filago germanica* (L.) Huds (Astearaceae) on key enzymes (cholinesterases, α-glucosidase and urease), antioxidant capabilities, cytotoxic potential and secondary metabolomics profile. Total phenolic and flavonoids were determined *via* spectrophotometric technique and individual secondary metabolites composition was assessed by UHPLC-MS analysis. Antioxidant activities were evaluated employing free radical scavenging (DPPH and ABTS), ferric reducing power (FRAP and CUPRAC), phosphomolybdenum and metal chelating assays. The cell-toxicity was evaluated by MTT assay against breast (MCF-7, MDA-MB-231), cervix (CaSki), prostate (DU-145) and colon (SW-480) cancers cell lines. Overall, methanol extracts were found to have higher total bioactive contents and antioxidant potential. UHPLC-MS analysis revealed significant variation in the secondary metabolites in the methanol extracts. The most common derivatives belong to seven groups i.e. alkaloids, benzoic acids, flavones, flavonols, flavan-3-ols, terpenoids and saponins. The major polyphenolic compounds were found to be kampferol, robinin, luteolin, ferulic acid, benzoic acid and salicylic acid. All the extracts showed moderate cholinesterases inhibition, whereas methanol extracts exhibited highest urease inhibition and all extracts presented a relatively high inhibition against α-glucosidase. Similarly, all extracts showed strong to moderate cytotoxicity with IC_{50} values ranging from 53.02 to 382.7 µg/mL. Overall, results have suggested *F. germanica* to be a lead source for novel natural bioactive products with antioxidant and enzyme inhibitory potential.

PHYTOCHEMICAL CONSTITUENTS AND ANTIBACTERIAL ACTIVITY OF FRACTIONS OF *PIPER CUBEBA* L. EXTRACT AGAINST VEGETATIVE CELL OF *BACILLUS* SP.

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Piper cubeba L. is a medicinal plant that belongs to the Piperaceae family. Moreover, it is important as a source of pepper (the dried berries) for the worldwide spice market. Many species of genus Piper are used in traditional herbal medicine and have shown antifungal, insecticidal and antitumor activities. This study was done in order to analyze the phytochemical components and to investigate the antibacterial activity of *Piper cubeba* L. berries fractions. *Piper cubeba* L. berries were extracted using methanol as a solvent to get the crude extract. The methanolic crude extracts were then fractionated using n-hexane, dichloromethane, butanol and ethyl acetate. Meanwhile, the antibacterial properties of the samples were tested against four *Bacillus* strains ;- *B. cereus* ATCC 33019, *B. subtilis* ATCC 6633, *B. pumilus* ATCC 14884 and *B. megaterium* ATCC 14581 using the disk diffusion (DDA) method, minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) referring to standard method of Clinical and Laboratory Standards Institute (CLSI). Phytochemical screening was carried out to identify the presence of principal chemical components of the crude extracts and fractions. The results showed that *P. cubeba* L. extracts consist of phytochemical constituents, such as lignan, alkaloids, terpenoids and flavonoids which are responsible for the biological activities. Dichloromethane fraction showed the best activity against *Bacillus* sp. The bioactive compounds present in *P.cubeba.* extract were determined using Gas Chromatography-Mass Spectrometry (GC-MS) and Liquid Chromatography-Mass Spectrometry (LC-MS). GC-MS analysis showed that the crude methanolic extract and all the solvent fractions of *Piper cubeba* L. berries contained a diverse array of constituents. The major volatile bioactive compounds determined using GC-MS were β-cubebene, cubebol, β-Asarone, α-copaene, caryophyllene, and germacrene-D. Non- volatile compounds identified by LC-MS were α-Cubebene, yatein, Dihydroclusin, Spathulenol, β-Asarone and Hinokinin. The results revealed that *Piper cubeba* L. has a future potential as an antibacillus agent.

PREPARATION OF CHEMICALLY MODIFIED AND HYPERCROSSLINKED MICROSPEHERES OF POLY(ACRYLONITRILE-*co*-DIVINYLBENZENE-80-*co*-VINYLBENZYLCHLORIDE) AS SORBENTS TO CAPTURE PHARMACEUTICAL RESIDUES.

Nur Nida Syamimi Subri[1], Siti Nurul Ain Md. Jamil[1]* Mohd Farid Ismail[1] & M. Rashidi Abdull Manap[1,2]**

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IN SILICO AND *IN VITRO* IDENTIFICATION OF NEW G PROTEIN-COUPLED ESTROGEN RECEPTOR-1 (GPER) MODULATORS

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G protein-coupled estrogen receptor-1 (GPER-1, formerly known as GPR30) is a seven transmembrane receptor, mediates important pathophysiological signalling pathways induced by estrogens and is currently regarded as a promising target for ER-negative (ER-) and triple-negative (TN) breast cancer. Only a few selective GPER-1 modulators have been reported to date. The 3D structure of GPER-1 is essential for discovering novel inhibitors during high-throughput virtual screening. However, to date, the 3D structure ofGPER-1not been resolved. In this study, initially a series of intensive computational techniques, both ligand-based and structure-based virtual screening (VS) were performed for the identification of GPER-1 modulators. The obtained results strongly support the reliability of our VS procedure, as the topmost resulting compounds that survived the VS filtering procedure were very similar to already reported GPER-1 ligands. Two compounds, SKO and SKOP having tetrahydropyran and tetrahydrofuran moiety respectively, were found having higher chemguass4 score compared to the known selective GPER-1 modulator. These two compounds were then synthesised using microwave irradiation technique in a good yield of 74 and 66 % respectively and characterized by FTIR, ^{1}H NMR, ^{13}C NMR and mass spectral analyses. These compounds were also subjected to MTT cell viability assay for investigating their-cancer activities in GPER-1 expressing breast cancer cell line, MCF-7 and SKBr-3 cell line. Preliminary results provide valuable information towards the identification of promising scaffold for designing novel GPER ligands.

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ENVIRONMENTAL & AGRICULTURAL SCIENCES

Invited Speakers

No.		Date	Time	Venue
1	**Dr. Yek Sze Huei**	22 Nov	10.30-11.00	Plenary Theatre
	The diversity of ant-plant symbioses in the diminishing South East Asia forests			
2	**Associate Professor Dr. Shyamala Ratnayeke**	22 Nov	01.00-01.30	LT-6007
	Carnivore hotspots in Peninsular Malaysia and their landscape attributes			
3	**Associate Professor Dr. Sreeramanan Subramaniam**	22 Nov	02.30-03.00	LT-6007
	Development of novel plant tissue culture systems			

Oral Presenters

OP-EAS-01	**Soon Chu Yong**	22 Nov	01.30-01.45	LT-6007
	Electrospun bioadsorbent membrane: poly(hydroxylalkanoate) emulsified with nanocellulose and chitosan for dye removal			
OP-EAS-02	**Taneswarry Sethu Pathy**	22 Nov	01.45-02.00	LT-6007
	Effect of human activity associated with different land-use on mosquito composition and diversity			

Poster Presenters				
PP-EAS-01	**Jennie Unnikrishnan**	22 Nov	03.00-05.00	Foyer
	Systematic analysis of reproductive development in normal and mantled oil palm flowers and fruit			
PP-EAS-02	**Danielle Moreno**	22 Nov	03.00-05.00	Foyer
	Utilization of hydroxyapatite from tilapia (*Oreochromis niloticus*) bones for photocatalytic degradation of methyl orange and rhodamine B			
Research in a Flash				
RF-EAS-01	**Soon Chu Yong**	23 Nov	09.00-10.30	Plenary Theatre
	Electrospun bioadsorbent membrane: poly(hydroxylalkanoate) emulsified with nanocellulose and chitosan for dye removal			

ELECTROSPUN BIOADSORBENT MEMBRANE: POLY(HYDROXYLALKANOATE) EMULSIFIED WITH NANOCELLULOSE AND CHITOSAN FOR DYE REMOVAL

Soon Chu Yong[1], Norizah Abdul Rahman[2], Tee Yee Bond[3], Tan Choon Hui[1], Rosnita A. Talib[4], Khalina Abdan[5], Eric Chan Wei Chiang[1]*

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The enormous production in the textile industry worldwide had generated huge amount of dyes that leads to pollution and endangers ecosystems. The current developed nanoabsorbents from natural biomass show notable adsorption capabilities but is difficult to be collected in wastewater treatment. Electrospinning can be used to produce high surface-to-volume ratio bioadsorption composite membrane to enhance the colour dye adsorption and removal from waste effluent. In our study, the nanocellulose (NCC) suspension and acidified chitosan (Cts) solution as bioadsorptive fillers in different weight loadings were incorporated to the poly(hydroxylalkanoate) (PHA) that was dissolved in chloroform. The formation of Pickering emulsions were further stabilized with Tween 80 before electrospinning. The electrospun bioadsorbent membranes were characterized by Scanning Electron Microscope (SEM), Fourier transform-infrared (FTIR) spectroscopy, X-ray Diffraction (XRD), and Thermogravimetric Analysis (TGA). The electrospun bioadsorbent membranes were in high porosity. The addition of bioadsorptive fillers had no effect to the FTIR spectra but significantly increased the crystallinity of the bioadsorbent membranes. The adsorption of Congo red dye for both PHA-nanocellulose and PHA-chitosan biocomposite meshes fitted well with the Langmuir isotherm model and pseudo-second order kinetics, indicating a chemisorption nature. This research shows the facile and inexpensive method to produce a homogenous electrospun bioadsorbent membranes from different biodegradable and renewable organic polymers in immiscible solvents.

EFFECT OF HUMAN ACTIVITY ASSOCIATED WITH DIFFERENT LAND-USE ON MOSQUITO COMPOSITION AND DIVERSITY

Taneswarry Sethu Pathy[1]*, Lee Jin Min[1], Yek Sze Huei[1]

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Malaysia is a tropical country that has consistently been facing a prevalent threat of mosquito- borne diseases. Among the plethora of diseases, the most common mosquito-borne disease in the country is the dengue fever, transmitted by the *Aedes* mosquito. The aim of this research is to examine the effects of human activity associated with different land-use on mosquito composition and diversity. Our study site is Lake Chini, a naturally occurring lake and the second largest freshwater body in Malaysia. The areas surrounding the lake have been subjected to various human activities while some areas remain pristine, making Lake Chini an ideal location to examine a gradient of human effect on mosquito composition and diversity. We sampled adult mosquito and larva breeding sites across a range of areas with different levels of human activity. As expected, adult mosquito diversity was reduced while abundance was higher in the areas with high human activity. Conversely, adult mosquito diversity was higher while abundance was reduced in the areas with low human activity. Mosquito larva habitat survey revealed a higher number of larvae habitat and reduced larvae species diversity in areas with higher human activity. Areas with moderate or low human activity had fewer larvae habitats but higher larvae diversity. It is evident that some mosquito species, such as the *Aedes* mosquito, showed a strong positive correlation with human activity. This could be due to the altered landscape, where conditions favor such species in terms of breeding grounds and access to resources, enabling them to outcompete other mosquito species in the surrounding area. The results show that an increase in artificial breeding grounds at high human activity areas contribute to the increased abundance of diseases-transmitting mosquito species, suggesting that a more vigilant waste-disposal practice could have an impact on the population size of such species.

SYSTEMATIC ANALYSIS OF REPRODUCTIVE DEVELOPMENT IN NORMAL AND MANTLED OIL PALM FLOWERS AND FRUIT

Jennie Unnikrishnan*[1,2,3], Prof. Zoe Wilson[1], Prof. Festo Massawe[2], Dr. Sean Mayes[1], and Dr. Wei Chee Wong[3]

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Oil palm (*Elaeis guineensis Jacq*.) is one of the most important oil crops in the world. Since the introduction of oil palm tissue culture in the 70s, clonal propagation has been useful in producing uniform planting materials and developing the genetic engineering programme. However, one of the stumbling blocks for oil palm tissue culture is the occurrence of somaclonal variants in the form of the 'mantled' phenotype. After over 30 years of extensive efforts, in 2015 loss of *Karma* transposon methylation was found to be the underlying cause, effecting expression of the floral homeotic gene, *deficiens*. The current study investigates the mantled abnormality by detailed analysis of reproductive development in normal and mantled palms. The project utilises microscopy and molecular analysis of key genes over different developmental stages, to allow a comparative analysis of the changes occurring during flower development. Here we present preliminary results on male reproductive development in oil palm. The results will supplement current knowledge and the search for predictive techniques for tissue culture to eliminate the mantled variant, and help make oil palm a more sustainable crop in the context of environmentally sensitive land resources.

UTILIZATION OF HYDROXYAPATITE FROM TILAPIA (*OREOCHROMIS NILOTICUS*) BONES FOR PHOTOCATALYTIC DEGRADATION OF METHYL ORANGE AND RHODAMINE B

Reinzo Vittorio B. Cardenas[1], Shantel Gayle Q. Tayag[1], Danielle A. Moreno[1], Chienne Andrei P. Regodon[1], Aaron John M. Supan[1], Judee Anne D. Enriquez[1], Dannah Salcedo[1], Tyrone Sundiam[1], Janielle Seen[1], Nicole Saltarin[1], Michael Lucido[1], and Shenly Marie T. Gazo[1]*

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Synthetic dyes are widely used in industrial companies. Improper disposal of these dyes can pose harmful effects in the water systems. Therefore, wastewater treatment prior to its disposal is vital in regulating its adverse effects. This research assessed the photocatalytic degradation of Rhodamine B (RhB) and Methyl Orange (MO) using Hydroxyapatite (HAp) from *Oreochromis niloticus* (tilapia) fish bones. The HAp was synthesized via calcination at 900˚C for three hours under simple heat treatment and was then characterized using X-ray Diffractometer. The degradation of RhB and MO was determined using UV-Vis spectrophotometer under varying parameters that included the amount of catalyst (500, 750, and 1000 mg) and UV irradiation time (20, 40, 60, 80 and 100 minutes). Results in the X-ray diffractometer revealed that distinct peaks at (2θ) 31.70˚, 32.84˚, and 32.12˚ were in line with the HAp standards that indicated the potential of tilapia bones as a source of HAp. Results as well showed that the highest percent degradation was obtained in 1000 mg HAp for Rhodamine B (24.02%) and 750 mg HAp for methyl orange (48.58%) with an initial concentration 8 ppm and 100 minutes of UV irradiation. The study suggested the potential of HAp from tilapia fish bones as a photocatalyst for Rhb and MO.

ELECTROSPUN BIOADSORBENT MEMBRANE: POLY(HYDROXYLALKANOATE) EMULSIFIED WITH NANOCELLULOSE AND CHITOSAN FOR DYE REMOVAL

Soon Chu Yong[1], Norizah Abdul Rahman[2], Tee Yee Bond[3], Tan Choon Hui[1], Rosnita A. Talib[4], Khalina Abdan[5], Eric Chan Wei Chiang[1]*

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The enormous production in the textile industry worldwide had generated huge amount of dyes that leads to pollution and endangers ecosystems. The current developed nanoabsorbents from natural biomass show notable adsorption capabilities but is difficult to be collected in wastewater treatment. Electrospinning can be used to produce high surface-to-volume ratio bioadsorption composite membrane to enhance the colour dye adsorption and removal from waste effluent. In our study, the nanocellulose (NCC) suspension and acidified chitosan (Cts) solution as bioadsorptive fillers in different weight loadings were incorporated to the poly(hydroxylalkanoate) (PHA) that was dissolved in chloroform. The formation of Pickering emulsions were further stabilized with Tween 80 before electrospinning. The electrospun bioadsorbent membranes were characterized by Scanning Electron Microscope (SEM), Fourier transform-infrared (FTIR) spectroscopy, X-ray Diffraction (XRD), and Thermogravimetric Analysis (TGA). The electrospun bioadsorbent membranes were in high porosity. The addition of bioadsorptive fillers had no effect to the FTIR spectra but significantly increased the crystallinity of the bioadsorbent membranes. The adsorption of Congo red dye for both PHA-nanocellulose and PHA-chitosan biocomposite meshes fitted well with the Langmuir isotherm model and pseudo-second order kinetics, indicating a chemisorption nature. This research shows the facile and inexpensive method to produce a homogenous electrospun bioadsorbent membranes from different biodegradable and renewable organic polymers in immiscible solvents.

APPLIED MICROBIOLOGY

Invited Speakers				
No.		**Date**	**Time**	**Venue**
1	**Professor Dr. Yvonne Ai-Lian Lim**	22 Nov	10.00-10.30	Plenary Theatre
	How do gut worms influence gut microbiota			
2	**Associate Professor Moritz Mueller**	22 Nov	01.00-01.30	SR-6216
	Microbes in coral reefs: their roles and potential applications			
Oral Presenters				
OP-AM-01	**Mohammadhossein Zamani**	22 Nov	01.30-01.45	SR-6216
	Synthesis of polyurea capsules to encapsulate bacteria for self-healing of concrete			
OP-AM-02	**Mary Victory E. Gutierrez**	22 Nov	01.45-02.00	SR-6216
	Phylogenetic analysis of isolated Philippine Myxobacterial strain MB008 inferred from 16S rRNA gene sequence			

Poster Presenters				
PP-AM-01	**Ooi Teng Sin**	22 Nov	03.00-05.00	Foyer
	Effect of yeast as starter culture on the antioxidant properties of Malaysian cocoa beans produced using a simulation study			
PP-AM-02	**Ahmad Tarmizi bin Abdul Halim**	22 Nov	03.00-05.00	Foyer
	Characterization of KW-E bacteriophage isolated from Kuala Woh hot spring in Malaysia			
PP-AM-03	**Gan I-Ning**	22 Nov	03.00-05.00	Foyer
	A synthetic small regulatory RNA increases the antibiotic susceptibility of *Shigella sonnei*			
PP-AM-04	**Marie Andrea Laetitia Huët**	22 Nov	03.00-05.00	Foyer
	Bioremediation of heavy metals from aquatic environment through microbial processes: A potential role for probiotics?			
PP-AM-05	**Nurul Hidayah Adenan**	22 Nov	03.00-05.00	Foyer
	Actinobacteria and their potential in removal of triphenylmethane dyes			
PP-AM-06	**Teo Yong Kiat**	22 Nov	03.00-05.00	Foyer
	Potentiation of oxytetracycline via synergism with phenylpropanoids			
PP-AM-07	**Wong Li Wen**	22 Nov	03.00-05.00	Foyer
	Human intestinal eukaryotes in the gut microbiodata of the Segamat community in Johor, Malaysia			

Research in a Flash				
RF-AM-01	**Yeo Li-Fang**	23 Nov	09.00-10.30	Plenary Theatre
	Why Orang Asli's saliva and poop are my lifeline			
RF-AM-02	**Ho Jia Min**	23 Nov	09.00-10.30	Plenary Theatre
	Looking beyond antibiotics: A macromolecular approach to fight against multidrug-resistant pathogens			
RF-AM-03	**Mary Victory E. Gutierrez**	23 Nov	09.00-10.30	Plenary Theatre
	Phylogenetic analysis of isolated Philippine Myxobacterial strain MB008 inferred from 16S rRNA gene sequence			

SYNTHESIS OF POLYUREA CAPSULES TO ENCAPSULATE BACTERIA FOR SELF-HEALING OF CONCRETE

Mohammadhossein Zamani[1], Saeid Nikafshar[2]*, Ahmad Mousa[1]

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Concrete is the second most consumable material in the world after water. Cracking in concrete is the main drawback which can appear at any stage of service life. Although micro-cracks do not necessarily affect concrete strength, but they can impair its durability. Cracks may increase the permeability of concrete and allow penetration of oxygen, carbon dioxide and aggressive chemical substances (e.g. chloride, sulfate) into the concrete which facilitate degradation of structure and corrosion of reinforcement bars. Currently, there are different repair techniques and materials used to seal the detected cracks including chemicals and polymers such as epoxy, acrylic and polyurethane are used for sealing cracks and biotechnological methods by precipitating limestone which is the most compatible material with concrete matrix. In this method, suitable bacteria and nutrition are added into the concrete mixture. Once cracking is occurred, the bacteria will be active in presence of oxygen and moisture, then precipitated calcium carbonate crystals will seal the cracks. However, the efficiency and performance of self-healing by bacteria are strictly depended on the viability of bacteria in the concrete matrix. In addition, nutrition may have adverse effect on the mechanical properties of concrete. In the present work, polyurea polymer is proposed as a suitable carrier for the bacteria and nutrition due to its excellent properties including fast and simple curing reaction, great mechanical properties and versatility to change different properties. Bacteria and nutrition were encapsulated in polyurea through in-situ polymerization. The chemical characterization of polyurea capsules were evaluated by FT-IR, Raman spectroscopy and XRD. Also, TGA, DSC, FE-SEM and EDX analyses were carried out to prove encapsulation of healing agents. The results revealed that healing agents were successfully encapsulated in polyurea capsules and they were able to heal induced artificial cracks. Self-healing of cement paste by addition of encapsulated capsules was achieved.

PHYLOGENETIC ANALYSIS OF ISOLATED PHILIPPINE MYXOBACTERIAL STRAIN MB008 INFERRED FROM 16S rRNA GENE SEQUENCE

Mary Victory E. Gutierrez[1,3*], Ronald Garcia[2], Esperanza Cabrera[3], and Irineo Dogma[4]

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Myxobacteria are Gram-negative, proteolytic-bateriolytic and “social prokaryotes”. They belong to the so called, purple bacteria known as *Proteobacteria* under class Deltaproteobacteria alongside with the Bdellovibrio, Delsulfovibrio and Delsulfonema. This study aimed into profiling the unknown three Myxobacterial strains MB008 (2a, 3a, 4a) isolated from dried rice straw using the molecular data inferred from 16S rRNA gene sequence. Phylogenetic analyses based on NJ and ML tests, the three strains of myxobacteria isolated from this study were grouped within the family Sorangiinae (ingroup), genus *Chondromyces*. Closest to them was the *C. crocatus* strain Cm c5 (GU207874) with pairwise sequence divergences of 0.003, 0.005, and 0.006 for isolates 2a, 3a and 4a, respectively. The topological position of these three isolates, having strong bootstrap values of 95% (NJ analysis) and 99% (ML test) within the *C. crocatus* complex was highly supported. One of its highlights is the characterization of the matrix of the three Myxobacterial strains which exhibited singleton sequences. The current discovery efforts implies that there is high possibility of having a diverse population of Myxobacteria in the Philippines. Currently, the majority of unexplored Myxobacterial resource remains yet to be cultivated. To date, only three reported and published Philippine Myxobacterial 16SrRNA gene sequences are in the GenBank. Previous studies reaffirmed that Sorangiineae is one the richest sources of secondary metabolites and considered to exhibit bacteriolytic nutritional type, broad-spectrum antibiotic resistance, and possess major diverse and unusual fatty acids profile. This understanding provides the foundation for a very promising research on the bioactive compound since all newly sequenced isolates Mb008 belonged to family Sorangiineae. Phylogenetic analyses based on NJ and ML tests inferred from 16S rRNA gene sequences position the three strains myxobacterial *Mb008* in the family Polyangiaceae, suborder Sorangiineae.

EFFECT OF YEAST AS STARTER CULTURE ON THE ANTIOXIDANT PROPERTIES OF MALAYSIAN COCOA BEANS PRODUCED USING A SIMULATION STUDY

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Cacao fermentation is a fundamental process by which chocolate flavors are formed in cocoa beans. Previous studies have shown that yeast species initiate the cacao fermentation process and are key influencers in the final flavor profile. However, limited studies had investigated the influence of these yeast species on the antioxidant profile of the resultant cocoa beans. This research studied the effects of 13 yeast isolates obtained from spontaneous cacao fermentation on the antioxidant content of cocoa beans produced under simulated fermentation conditions. Each isolate was applied as a starter culture to freshly harvested cacao seeds mixed with fermentation simulation media. The total polyphenols content (TPC) was then determined using the Folin-Ciocalteau reagent method, while total flavonoids content (TFC) was determined using the aluminium chloride method. The 2, 2-Diphenyl-1-picrylhydrazyl (DPPH) content was subsequently determined using DPPH free radical scavenging reagent. The results indicated that all cocoa beans were well fermented after 96-h. Cocoa beans fermented with yeast showed higher TPC and TFC content ($p=0.05$) by the end of fermentation as compared to the Control. The TPC, TFC and DPPH of dried cocoa beans between isolates ranged from 21.82 to 64.95 mg/g Gallic acid (GAE), 1.68 to 6.33 mg/g Catechin and 113.85 to 328 µmoles/g Trolox (TE) respectively, which were consistent with literature. However, it was further discovered that there was no significant change of the TPC, TFC and DPPH within each isolate when compared at fixed 24-h intervals throughout the 120-h fermentation process. Based on these findings, it was therefore concluded that yeast isolate 6 and 33 had good potential as starter culture in field application, as both isolates demonstrated high TPC and TFC content throughout the fermentation process.

CHARACTERIZATION OF KW-E BACTERIOPHAGE ISOLATED FROM KUALA WOH HOT SPRING IN MALAYSIA

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Despite the abundance of bacteriophage on Earth, the bacteriophage community from hot springs in Malaysia is poorly documented. Therefore, the aim of this study was to isolate and characterize bacteriophage lytic to *Escherichia coli* BL21(DE3). Furthermore, the endolysin properties produced by this bacteriophage were also investigated. Bacteriophage samples were obtained from Kuala Woh hot spring in Perak, Malaysia. One phage isolate, KW-E, was amplified and characterized. Based on transmission electron micrograph, the phage can be categorized under the *Myoviridae* family. The phage host range was determined against different strains of *E. coli* and several *Shigella* species. Crude endolysin was also prepared and its activity was tested on the same bacterial species to compare the endolysin activity with the phage activity. The results showed that the phage and endolysin exhibited different lytic capabilities. In addition, the endolysin's stability at different pH and temperature was also tested and compared to lysozyme. The endolysin showed lytic activity on EDTA-treated *E. coli* cells and was thermostable up to 73°C. Furthermore, the endolysin demonstrated a stronger lytic activity at a lower concentration compared to lysozyme. The phage genome was sequenced and analyzed using bioinformatics tools. The size of the phage genome was 45 kb. Open reading frame prediction returned 67 genes for putative phage proteins, and one gene was identified as the endolysin gene. The endolysin was predicted to be 18 kDa in size with a pI of 9.46. Therefore, this study has demonstrated that this endolysin has a potential to be an alternative to the commercially available lysozyme for cellular lysis applications.

A SYNTHETIC SMALL REGULATORY RNA INCREASES THE ANTIBIOTIC SUSCEPTIBILITY OF S*HIGELLA SONNEI*

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Bacteria have evolved to become resistant against antibiotics through various mechanisms such as upregulation of the efflux pump. TolC is a multidrug efflux pump that confers bacteria the ability to survive in various antibiotic condition and be multidrug resistant. Interestingly, the expression of TolC was found to be regulated at the post-transcriptional level by a small regulatory RNA (sRNA) known as SdsR. Overexpression of SdsR in the model bacterium, *E. coli* represses the levels of TolC protein. However, the role of SdsR in *S. sonnei* is still not clear. In this study, we studied the effects of SdsR against the expression levels of *tolC* in *S. sonnei*. Similar to that observed in *E. coli*, overexpression of native SdsR represses the expression levels of *tolC* by 1.6 fold in *S. sonnei*. Interestingly, the synthetic version of SdsR (SdsR_v2) which incorporated additional point mutations to increase the stability of SdsR_V2 and *tolC* mRNA leads to 2.5 fold down-regulation in the expression levels of *tolC*. Moreover, the presence of SdsR_v2 significantly decreases bacterial growth rate during challenge with antibiotics. This study is the first to demonstrate that synthetic SdsR can increase regulation on target mRNA and to show that SdsR regulates *tolC* as well as antibiotics resistance in *S. sonnei.*

BIOREMEDIATION OF HEAVY METALS FROM AQUATIC ENVIRONMENT THROUGH MICROBIAL PROCESSES: A POTENTIAL ROLE FOR PROBIOTICS?

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The use of heavy metals for industrial purposes is still predominant in the developing world. These metals can cause disastrous effects on living organisms by entering aquatic environments through natural and anthropogenic sources. These contaminants may easily dissolve in waters and bioaccumulate in aquatic organisms. Probiotic bacteria have the ability to reduce metal toxicity within the human body. Bioremediation of polluted waters using these bacteria could be an alternative to conventional ineffective remediation methods. The aim of this study was to isolate and characterise heavy metal-resistant probiotics, mainly lactic acid bacteria, from three different metal-polluted soils in Mauritius and to determine their absorbing or binding potential to four different heavy metals namely, cadmium, chromium, lead and mercury. Soil samples were collected for isolation of such microorganisms followed by morphological determination via staining and morphological assessments alongside biochemical, molecular and probiotic characterisations. A preliminary heavy metal minimum inhibitory concentration (MIC) test was done followed by atomic absorption spectroscopy (AAS) analysis. Four *Enterococci* (BT1, BT2, MC1 and MC2) and two *Bacillus acidiproducens* (SM1 and SM2) were isolated with all manifesting key probiotic characteristics. They were acid and bile tolerant and produced lactic acid via glucose metabolization. These isolates have moderately hydrophobic cell surface with similar antibiotic susceptibility profiles. However, no antibacterial activity was observed against two indicator strains; *Escherichia coli* (ATCC 25922) and *Staphylococcus aureus* (ATCC 29213). BT1 and BT2 were able to tolerate mercury, cadmium, lead and chromium treatment with however, poor mercury-removal abilities (0.75 to 1.42%). MC1 and MC2 isolates were able to tolerate cadmium, lead and chromium treatment. respectively. MC1 showed the highest level of lead (43.00 ± 0.776%) and cadmium (46.19 ± 7.651%) removal. Yet, SM1 and SM2 isolates tolerated only lead and chromium. SM2 had the ability to remove the highest amount of chromium (43.06 ± 7.991%). These reasonable heavy metal removal abilities could be further studied for efficient use in bioremediation.

ACTINOBACTERIA AND THEIR POTENTIAL IN REMOVAL OF TRIPHENYLMETHANE DYES

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Actinobacteria used in this study was isolated from soil, known with an ability to produce several bioactive metabolites and degrading reactive dyes. Triphenylmethane dyes are highly toxic not only to living organism, but also to the environment. The discharge of these dyes to the environment can affect the penetration of sunlight into the water and reduce photosynthetic activity of living things. Actinobacteria was obtained from stock cultures, National Botanical Garden, Shah Alam and Tanah rata, Cameron Highland. The bacteria are studied for biosorption and biodegradation activities towards triphenylmethane dyes (TPM), which are Malachite Green (MG) and Methyl Violet (MV). Phenotypic characterization and phylogenetic analysis of the 16S rDNA sequence indicated that 12 isolated bacterial strains belonged to the genus *Streptomyces*, *Nocardiopsis* and *Rhodococcus*. *Nocardiopsis* sp. was found to be the most effective in decolorizing MG and MV at concentration of 100 mg l^{-1} with means of 97% and 95.1% respectively. Four strains that showed highest decolorization of triphenylmethane dyes used in this study were chosen to carry out optimization study on the influence of oxygen on TPM dyes decolorization. The result obtained in this study showed most isolates used decolorize better under aerobic condition except *Rhodococcus* sp.

POTENTIATION OF OXYTETRACYCLINE VIA SYNERGISM WITH PHENYLPROPANOIDS

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Rapid emergence of antibiotic-resistant bacteria has urged the need of new approaches to prolong the effectiveness of existing antibiotics. The large diversity of secondary metabolites endowed by plants have provided us a vast supply of bioactive compounds. Although most of these metabolites are weak antimicrobial, they can be used as antibiotic enhancer via combination approach. In this project, eight structurally-similar phenylpropanoids were combined with oxytetracycline for synergy screening against eight different bacterial strains via checkerboard assay. It was found that the presence of substituents on the aromatic ring of phenylpropanoids greatly influenced their potentiating ability with oxytetracycline. For instance, caffeic acid, a phenylpropanoid with two adjacent hydroxy substituents attached on its aromatic ring, demonstrated the broadest oxytetracycline's potentiating ability. Further time-kill analysis revealed the enhancement of caffeic acid on the bacteriostatic action of oxytetracycline which not only prolonged its efficacy, but also resulted in bactericidal effect. Structure-activity relationship drawn from these combinations therefore provides a useful insight to further investigate their mechanism. This study also demonstrates the potential use of caffeic acid as oxytetracycline enhancer.

HUMAN INTESTINAL EUKARYOTES IN THE GUT MICROBIOTA OF THE SEGAMAT COMMUNITY IN JOHOR, MALAYSIA

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Gut eukaryotes such as intestinal parasites are often correlated with the lack of sanitation and poor healthcare delivery. Conversely, yeasts have long been part of the gut microbiota, but the significance of their roles remain poorly studied. Collectively, the present study aims to determine the prevalence of intestinal parasites and *Candida albicans* along with their associated risk factors among the Chinese, Malays, Indians, and Jakun groups of the Segamat community in Johor, Malaysia. This is the first community-based study conducted in Segamat, taking account of all races in Malaysia for intestinal parasite of the human microbiota. Additionally, this is the first Asian study looking specifically into yeast and *C. albicans* in gut microbiota. Stool samples with completed survey questionnaires from 224 participants in Segamat were included in the study. Formalin-ether concentration and Kato-Katz were performed to detect the presence and to quantify the load of helminthic infection in the stool samples. PCR was performed to confirm the identity of the STHs. Lactophenol cotton blue staining was used to visualise the morphology of yeast colonies, followed by germ tube formation as a presumptive identification test for *C. albicans*. Risk factors associated with the prevalence of these organisms was performed using chi-square test. Overall, 1.79% (n = 224) of participants were infected with soil-transmitted helminths with no detected protozoa infection. All STH-infected individuals belonged to the Jakun tribe with barefoot walking and elementary level education being the two suggestive risk factors. Additionally, 19.2% of the participants were positive for *C. albicans* in their guts, in which the prevalence rate was found to be lower as compared to the western studies. As this is the first study conducted in Malaysia, the findings are important as there might some underlying factors which influences the different prevalence in two different continents, so warrant further study.

WHY ORANG ASLI'S SALIVA AND POOP ARE MY LIFELINE

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Orang Asli are the indigenous people of Peninsular Malaysia. They comprise only 0.5% of the total Malaysian population and their numbers are dwindling. Their unique culture and livelihood are threatened by urbanization and deforestation. There are urbanized communities living near large cities, semi-urbanized tribes that have been resettled by government development schemes and nomadic hunter-gatherers who live deep within the rainforest. I study the oral and gut microbiome of the Orang Asli. Microbiome is a term meaning all microbes found living in and on a human body. A healthy microbiome appears to have a high diversity of bacteria species whereas a diseased microbiome (in an obese or diabetic person) appears to have lower diversity. These findings were reported in westernized and urbanized populations. My research aims to explore the human microbiome of urbanized, semi-urbanized and rural Orang Asli tribes in association with their health. Microbiome of western population generally exhibited no difference among gender. My work showed that the oral microbiome of Temiar men had higher abundance of *Lactobacillus*, a "healthy" bacteria found in dairy products. Temiar women had higher abundance of opportunistic pathogens such as *Streptococcus, Capnocytophaga, Neisseria, Leptotrichia* and *Prevotella.* The differences in living environment, social standing and lifestyle practices, such as food taboos among the Orang Asli may have contributed to the differences observed in men and women microbiome. The next stage of my project would be to collect poop and study the gut microbiome for more insight.

LOOKING BEYOND ANTIBIOTICS: A MACROMOLECULAR APPROACH TO FIGHT AGAINST MULTIDRUG-RESISTANT PATHOGENS

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Antibiotics have saved millions of lives and helped shape modern medicine. However, the emergence of multidrug-resistant pathogens such as methicillin-resistant *Staphylococcus aureus* (MRSA) and *Mycobacterium tuberculosis* has become a global health problem, and novel approaches to antimicrobial therapy are urgently needed. To address this problem, an unconventional class of antimicrobial agents comprising of peptides and synthetic polymers have recently been developed. Antimicrobial peptides have been known to have multiple targets, thus making them less likely to impose selective pressure on bacteria. Because of this property they are considered to be excellent candidates for further development as a new class of antimicrobials to combat the emerging threat of multidrug-resistant bacteria. In this research project, we aim to characterize the antimicrobial properties of bortezomib and some peptidyl chloromethyl ketones, such as z-L-CMK and z-GLF-CMK on various Gram-positive, Gram-negative and anaerobic bacteria. Minimum inhibitory concentration (MIC), which is defined as the lowest concentration of antimicrobial agent required to inhibit bacterial growth, is one of the primary methods for determining and comparing the efficacy of antimicrobial agents. The MIC was measured using broth dilution method, whereby a standardized inoculum of bacteria was incubated in serial dilutions of the antimicrobial compounds. Our preliminary results showed z-L-CMK to be effective in inhibiting a wide range of Gram-positive bacteria including MRSA. We speculate that this peptide acts on a membrane-disruption mechanism to weaken the bacteria. Our next objectives are to find out if repeated use of these compounds leads to drug resistance and to elucidate the mechanism of action of these compounds. We hope that this project would help to gain insight into the development of new antibacterial strategies.

PHYLOGENETIC ANALYSIS OF ISOLATED PHILIPPINE MYXOBACTERIAL STRAIN MB008 INFERRED FROM 16S rRNA GENE SEQUENCE

Mary Victory E. Gutierrez[1,3]*, Ronald Garcia[2], Esperanza Cabrera[3], and Irineo Dogma[4]

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Myxobacteria are Gram-negative, proteolytic-bateriolytic and “social prokaryotes”. They belong to the so called, purple bacteria known as *Proteobacteria* under class Deltaproteobacteria alongside with the Bdellovibrio, Delsulfovibrio and Delsulfonema. This study aimed into profiling the unknown three Myxobacterial strains MB008 (2a, 3a, 4a) isolated from dried rice straw using the molecular data inferred from 16S rRNA gene sequence. Phylogenetic analyses based on NJ and ML tests, the three strains of myxobacteria isolated from this study were grouped within the family Sorangiinae (ingroup), genus *Chondromyces*. Closest to them was the *C. crocatus* strain Cm c5 (GU207874) with pairwise sequence divergences of 0.003, 0.005, and 0.006 for isolates 2a, 3a and 4a, respectively. The topological position of these three isolates, having strong bootstrap values of 95% (NJ analysis) and 99% (ML test) within the *C. crocatus* complex was highly supported. One of its highlights is the characterization of the matrix of the three Myxobacterial strains which exhibited singleton sequences. The current discovery efforts implies that there is high possibility of having a diverse population of Myxobacteria in the Philippines. Currently, the majority of unexplored Myxobacterial resource remains yet to be cultivated. To date, only three reported and published Philippine Myxobacterial 16SrRNA gene sequences are in the GenBank. Previous studies reaffirmed that Sorangiineae is one the richest sources of secondary metabolites and considered to exhibit bacteriolytic nutritional type, broad-spectrum antibiotic resistance, and possess major diverse and unusual fatty acids profile. This understanding provides the foundation for a very promising research on the bioactive compound since all newly sequenced isolates Mb008 belonged to family Sorangiineae. Phylogenetic analyses based on NJ and ML tests inferred from 16S rRNA gene sequences position the three strains myxobacterial *Mb008* in the family Polyangiaceae, suborder Sorangiineae.

FOOD SCIENCE & TECHNOLOGY

Invited Speakers

No.		Date	Time	Venue
1	**Professor Tan Chin Ping**	22 Nov	11.00-11.30	Plenary Theatre
	Lipid nanodispersion in food: an overview of their preparation, characterization, stability evaluation and application			
2	**Professor Hii Ching Lik**	22 Nov	01.00-01.30	LT-6008
	Emerging drying and dehydration techniques for food products			

Oral Presenters

OP-FST-01	**Chien Lye @ Mervin Chew**	22 Nov	01.30-01.45	LT-6008
	Effect of steriliser condensate and empty fruit bunch's liquor restreaming on the physicochemical properties of crude palm oil			
OP-FST-02	**Nur Kamariah Rosni**	22 Nov	01.45-02.00	LT-6008
	Physiochemical characteristics, microbiological safety and sensory acceptability of coconut dregs during fermentation using *Rhizopus oligosporus*			
OP-FST-03	**Jing Ying Yap**	22 Nov	02.30-02.45	LT-6008
	Effects of drying on the total phenolics content and antioxidant properties of papaya leaves			

Poster Presenters				
PP-FST-01	**Priyanka Parhi**	22 Nov	03.00-05.00	Foyer
	Effect of inulin on the growth of *Lactobacillus casei* in model sugar systems			
PP-FST-02	**Dr. Thed Swee Tee**	22 Nov	03.00-05.00	Foyer
	Development of high-protein algae dark chocolate using *Arthrospira platensis*			
PP-FST-03	**Chan Siew Meng**	22 Nov	03.00-05.00	Foyer
	Product development of coconut energy gel and its effect on physical endurance performance			
PP-FST-04	**Wong Hong Jie**	22 Nov	03.00-05.00	Foyer
	Effects of different drying treatment on the antioxidant activity, oxidase enzyme activity and phytochemicals composition of *Salvia officinalis* (sage) leaves			
PP-FST-05	**See Kiat Wong**	22 Nov	03.00-05.00	Foyer
	Effects of volume of water and air on the oxidation rate of crude palm oil- an accelerated oxidation study			
Research in a Flash				
RF-FST-01	**Jing Ying Yap**	23 Nov	09.00-10.30	Plenary Theatre
	Effects of drying on the total phenolics content and antioxidant properties of papaya leaves			

EFFECT OF STERILISER CONDENSATE AND EMPTY FRUIT BUNCH'S LIQUOR RESTREAMING ON THE PHYSICOCHEMICAL PROPERTIES OF CRUDE PALM OIL

Chien Lye @ Mervin Chew[1,2]*, Syed Mohd Hadi Syed Hilmi[2], Norliza Saparin[2], Nik Suhaimi Mat Hassan[2], Yosri Mohd Siran[2], Ahmad Jaril Asis[2], Eng Seng Chan[1], Siah Ying Tang[1]

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Significant oil loss persists in palm oil mill processes and maximising the oil recovery is essential to minimise the losses. The re-streaming of oil containing liquors from mill processes, the condensate generated from the sterilisation process and the liquid extracted from empty fruits bunch (EFB) press into CPO is an alternative way to recover oil. In the present works, the effect of the liquors re-streaming on oil quality and stability has been examined. Remarkably, no significant ($P > 0.05$) difference between of re-streamed CPOs and normal CPO in term of oxidative stability and oil quality. The same finding was observed for its refined oil quality where there is no significant ($P > 0.05$) difference between the oils. It was suggested that the quality of a relatively low amount of oil in the liquors was diluted by the CPO quality that constitutes more than 95% of the total oil. No significant ($P > 0.05$) difference in oxidative and hydrolytic reaction up to 15 days retention time with mid heat exposure. However, the results show that the level of total chlorine in CPO and 3-monochloropropane-1,2-diol (3-MCPD) in RBDPO are in increasing trend from water, steriliser condensate, and the mixture of steriliser condensate and EFB liquor dilutions. Due to the water solubility of the chloride, this compound tends to be concentrated in the condensate stream and liquor stream.

PHYSICOCHEMICAL CHARACTERISTICS, MICROBIOLOGICAL SAFETY AND SENSORY ACCEPTABILITY OF COCONUT DREGS DURING FERMENTATION USING *RHIZOPUS OLIGOSPORUS*

Nur Kamariah Rosni[1], Maimunah Sanny[1,2], Nor Syahida Amalin Bahranor[1], Yaya Rukayadi[1,3]*

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A fermented coconut dregs is one of the Indonesia traditional fermented foods. The scientific studies regarding the quality and safety of fermented coconut dregs are still lacking. The aims of this study were to determine physicochemical characteristics, microbiological safety and sensory acceptability of fermented coconut dregs during fermentation using *Rhizopus oligosporus*. Fermentation of coconut dregs was done using *R. oligosporus* as starter culture for three days. The physicochemical analysis; internal temperature, pH, total soluble solid (TSS), water activity (a_w), colour determination, proximate analysis and texture profile, microbiological analysis; total plate count (TPC), *Escherichia coli*, *Salmonella* spp., *Pseudomonas aeruginosa*, *Bacillus cereus*, *Staphylococcus aureus* and lactic acid bacteria (LAB) and sensory acceptability were carried out in this study. The results showed that internal temperatures were increased and the pH showed a decreased trend along the fermentation day. The TSS and a_w show no significant differences from day 0 to day 3. The colour determination for final product has the highest lightness and yellowness but has the lower redness. A gradual increased in hardness, cohesiveness, chewiness and resilience were observed. Moisture content, crude protein and crude fat were slightly increased while ash, fibre and carbohydrate showed the decreasing trend during the fermentation day. The results for microbial count show the reducing number of *S. aureus* and *B. cereus* while increasing number of TPC and lactic acid bacteria. Interestingly, *E. coli*, *Salmonella* spp. and *P. aeruginosa* were not detected in fermented coconut dregs. The non-fermented coconut dregs was preferred more by the panellists as it achieved highest and overall acceptability on sensory attributes evaluation which is it has white colour and nice smell.

EFFECTS OF DRYING ON THE TOTAL PHENOLICS CONTENT AND ANTIOXIDANT PROPERTIES OF PAPAYA LEAVES

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Dengue fever causes mortality and morbidity around the world, specifically in the tropics and subtropics regions. It was reported that carpaine, which is the major bioactive compound extracted from papaya leaves, contributes to the antithrombocytopenic activity. Therefore, carpaine plays an important role in treating dengue patient by raising the platelet count in a patient's blood. This research focused on the study of drying papaya leaves using different drying methods such as oven drying (60° C, 70° C and 80° C), shade drying and freeze drying. The total polyphenol content in papaya leaves, which were dried by using oven drying, shade drying and freeze drying, was investigated by using the Folin-Ciocalteu spectrophotometric method. Freeze dried samples presented the highest phenolic content (2158 mg GAE/100 g). The papaya leaves were also investigated for their antioxidant properties using DPPH and ABTS radical scavenging capacity assay. That was found the freeze dried samples possessed the highest antioxidant capacities in both methods used. A significant relationship between antioxidant properties and total phenolic content was found, indicating that phenolic compounds are the major contributors to the antioxidant properties of these plants. The effects of different drying processes on carpaine are important to develop a better preparation protocol that produces a more stable papaya leaves extract with higher carpaine retention. The dried papaya was coarsely ground followed by an acid-base treatment in order to extract the carpaine. The qualification of carpaine was carried out by using Nuclear Magnetic Resonance (NMR) spectroscopy. The carpaine extracted was in high purity and to be used as a standard in liquid chromatography-mass spectrometry (LC-MS) analysis in the future.

EFFECT OF INULIN ON THE GROWTH OF *LACTOBACILLUS CASEI* IN MODEL SUGAR SYSTEMS

Priyanka Parhi[1], Keang Peng Song[1] and Wee Sim Choo[1]*

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Prebiotics are substrates that is selectively utilized by host microorganisms conferring a health benefit and inulin and fructooligosaccharide are few of the well-established ones. Probiotics have been known for their ability to utilize both simple and complex saccharides for their energy production. The effect of prebiotic such as inulin and fructooligosaccharide on the growth and viability of probiotics are reported to be inconsistent, which may be due to the presence of different sugar in the products. In this study single factor experiment was designed in which inulin concentrations were varied to study the effect on the growth of *Lactobacillus casei* in model glucose, fructose, lactose and sucrose systems during 24 hr growth assay. In glucose, fructose, sucrose and lactose model systems (3% and 4% sugar concentrations) without inulin supplementation, *L. casei* showed remarkable growth. However, 3% and 4% inulin supplementation in these systems showed partial inhibition where else 0.5% and 1% inulin supplementation showed no effect on the growth of *L. casei*. But in fructose and lactose model systems (2% sugar concentration), 0.5%, 1%, and 2% inulin supplementation showed growth-promoting effect on *L. casei.* In conclusion, inulin supplementation showed different effects on the growth of *L. casei* depending on the type and concentration of sugar and concentration of inulin used.

DEVELOPMENT OF HIGH-PROTEIN ALGAE DARK CHOCOLATE USING *ARTHROSPIRA PLATENSIS*

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[1]Tunku Abdul Rahman University College, Jalan Genting Kelang, 53300 Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur.

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Algae have been declared by World Health Organization as “Food for the Future” due to its high nutrient density and fast-growing rate. Algae contain up to 70% protein and rich in health-promoting micronutrients. This project aims to develop high-protein algae dark chocolate through the incorporation of *Arthrospira Platensis* (Spirulina powder). Proximate analysis and sensory evaluation were conducted on the developed algae dark chocolate. The results of proximate analysis were: protein (13.5%), fat (52.9%), crude fibre (14.9%), carbohydrate (18.4%) and moisture content (0.3%). Protein and fiber content were significantly higher ($p<0.05$), while carbohydrate content was significantly lower ($p<0.05$) than that of the control. The percentage of panellists (N=50) who like the various sensory attributes of algae dark chocolate were: color (98%), aroma (74%), taste (74%), smooth mouthfeel (82%) and melting mouthfeel (82%). A total of 58% of the panellists preferred algae dark chocolate over the control without algae. In conclusion, dark chocolate could serve as a potential carrier to deliver the nutrient dense algae to consumers. The algae dark chocolate can be claimed as high protein and high fiber foods. This project has implications on functional foods and global malnutrition.

PRODUCT DEVELOPMENT OF COCONUT ENERGY GEL AND ITS EFFECT ON PHYSICAL ENDURANCE PERFORMANCE

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[1]Tunku Abdul Rahman University College, Jalan Genting Kelang, 53300 Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur.

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Most energy gels in the market contain mainly maltodextrin and sugars. This study aims to develop energy gel by using coconut as the base ingredient. Coconut kernel contains high percentage of medium chain fatty acids (MCFAs) that can be easily metabolized to yield energy while coconut water is rich in minerals that replenish electrolytes loss during exercise. Two flavoured gels (natural coconut flavour and cocoa flavour) were developed. Proximate analysis, sensory evaluation (appearance, flavour, taste, gumminess, viscosity and overall acceptability) and the effect of coconut gel intake on physical endurance performance were conducted. Out of the two flavoured coconut gels, 54% of the panellists (N=50) preferred the cocoa flavoured coconut gel. The overall acceptability score of the cocoa flavoured coconut gel was 5.2 out of 7 using a hedonic scale (1: Dislike very much to 7: Like very much). Cocoa flavoured coconut gel contained 26.4% carbohydrate, 1.7% protein, 3.0% fat, 1.0 % ashes, 0.7% fibre and 392 mg potassium. A 20-meters beep test was conducted on 8 human subjects (with cross over) to determine the effect of coconut gel intake on the endurance performance. Blood glucose, heart rate, time to exhaustion and Borg scale Rated Perceived Exertion were recorded. Overall, subjects were found to endure longer time to exhaustion after consuming coconut gel, demonstrated 8% improvement on physical endurance performance as compared to the control. MCFAs are absorbed directly into portal circulation and transported to the liver for rapid oxidation to yield ATPs. Moreover, MCFAs are fully saturated fat, thus contribute to the oxidative stability of the product. In conclusion, coconut energy gel provides a potential alternative for nutritional ergogenic aids.

EFFECTS OF DIFFERENT DRYING TREATMENT ON THE ANTIOXIDANT ACTIVITY, OXIDASE ENZYME ACTIVITY AND PHYTOCHEMICALS COMPOSITION OF *SALVIA OFFICINALIS* (SAGE) LEAVES

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The leaves of *Salvia officinalis* have been used as a traditional medicine and it has been reported to have health beneficial properties such as anti-inflammatory and antioxidant properties. There is a rise in demand for herbal plants all over the world. The processing of herbal plant leaves is required to preserve the important phenolic compounds before exportation. Degradation of the phenolic compounds is mainly due to the thermal degradation and enzyme oxidation during the processing process. This research studied the effects of the microwave, freeze-drying, air-drying, oven 50°C and oven 100°C drying treatments on the polyphenol oxidase (PPO) and peroxidase (POD) enzymes activity and the antioxidant properties of *S. officinalis*. The result shows that there is an increase of phenolic content in the microwave and freeze-drying treatment, no changes of phenolic content in air-drying treatment and a decrease of phenolic content in the oven 50°C and oven 100°C drying treatment. PPO and POD enzymes show complete inactivation in all the drying treatment except freeze-drying treatment. The PPO activity of freeze-dried leaves shows no change compared to the fresh leaves of *S. officinalis* but the POD activity of the leaves decreases after freeze-drying treatment. Rosmarinic acid has been identified using RP-HPLC as the major chemical compound in the leaves of *S. officinalis*. The changes in the rosmarinic acid content are consistent with the TPC changes of different drying treatment. Factors that caused the changes in the antioxidant properties in different drying treatment have been discussed in this thesis. The best drying treatment for *S. officinalis* leaves is microwave treatment as it shows the greatest increase of phenolic compounds as well as the inactivation of both PPO and POD enzymes.

EFFECTS OF VOLUME OF WATER AND AIR ON THE OXIDATION RATE OF CRUDE PALM OIL – AN ACCELERATED OXIDATION STUDY

See Kiat Wong[1], Chien Lye Chew[1,2], Beng Ti Tey[1,3], Siah Ying Tang[1,3,4]*

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Oil oxidation remains a pressing problem where it lowers the overall stability and shorten the shelf-life of the lipid contained products. Both hydrolysis (by water) and oxidation (by oxygen) processes contributed to the breakdown of triglycerides into smaller molecules such as glycerol and fatty acid which could lead to oil rancidity. Herein, we evaluated the effects of water (hydrolysis) by employing different ratio of water-oil and air (oxidation) by using different ratio of air-oil on the oxidative stability of crude palm oil (CPO). In this study, accelerated oxidation test was utilized and the free fatty acid (FFA) value, deterioration of bleachability index (DOBI), total oxidation value (UV Totox) and carotene value of the CPO were analysed and discussed. Our results showed that FFA and UV Totox values increased considerably while DOBI and carotene values declined moderately for both hydrolysis and oxidation studies throughout 72 hours of storage period. The oxidation rate of CPO was found to be moisture dependent where higher total surface contact between oil and water/air layer increased the rate of oxidation. It has been observed that the oxidation rate of capped samples and uncapped samples were similar due to the low moisture content in the oven which operated at 90°C. The comparative study showed that the rapid oil oxidation was mainly attributed to the higher content of water molecules which increased the rate of hydrolysis. Our preliminary findings demonstrated that water is the dominant factor governing the rate of CPO oxidation and further study is required to validate the results at the storage conditions of different temperature.

EFFECTS OF DRYING ON THE TOTAL PHENOLICS CONTENT AND ANTIOXIDANT PROPERTIES OF PAPAYA LEAVES

Jing Ying Yap[1], Ching Lik Hii[1]*, Sze Pheng Ong[1], Kuan Hon Lim[2], Kar Yong Pin[3], Faridah Abas[4]

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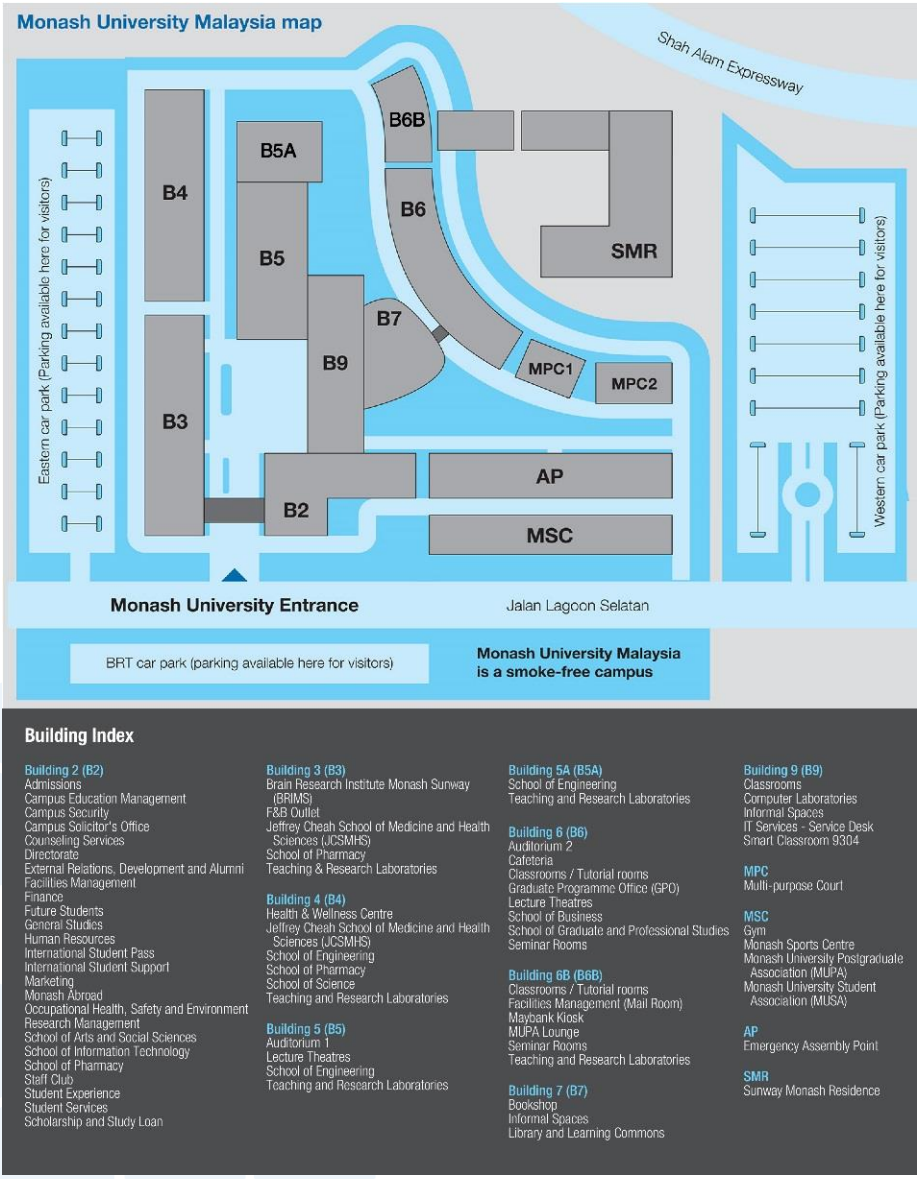
Dengue fever causes mortality and morbidity around the world, specifically in the tropics and subtropics regions. It was reported that carpaine, which is the major bioactive compound extracted from papaya leaves, contributes to the antithrombocytopenic activity. Therefore, carpaine plays an important role in treating dengue patient by raising the platelet count in a patient's blood. This research focused on the study of drying papaya leaves using different drying methods such as oven drying (60° C, 70° C and 80° C), shade drying and freeze drying. The total polyphenol content in papaya leaves, which were dried by using oven drying, shade drying and freeze drying, was investigated by using the Folin-Ciocalteu spectrophotometric method. Freeze dried samples presented the highest phenolic content (2158 mg GAE/100 g). The papaya leaves were also investigated for their antioxidant properties using DPPH and ABTS radical scavenging capacity assay. That was found the freeze dried samples possessed the highest antioxidant capacities in both methods used. A significant relationship between antioxidant properties and total phenolic content was found, indicating that phenolic compounds are the major contributors to the antioxidant properties of these plants. The effects of different drying processes on carpaine are important to develop a better preparation protocol that produces a more stable papaya leaves extract with higher carpaine retention. The dried papaya was coarsely ground followed by an acid-base treatment in order to extract the carpaine. The qualification of carpaine was carried out by using Nuclear Magnetic Resonance (NMR) spectroscopy. The carpaine extracted was in high purity and to be used as a standard in liquid chromatography-mass spectrometry (LC-MS) analysis in the future.

Monash Campus Map



Building Index

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International Student Support
Marketing
Monash Abroad
Occupational Health, Safety and Environment
Research Management
School of Arts and Social Sciences
School of Information Technology
School of Pharmacy
Staff Club
Student Experience
Student Services
Scholarship and Study Loan

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F&B Outlet
Jeffrey Cheah School of Medicine and Health Sciences (JCSMHS)
School of Pharmacy
Teaching & Research Laboratories

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School of Pharmacy
School of Science
Teaching and Research Laboratories

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Lecture Theatres
School of Engineering
Teaching and Research Laboratories

Building 5A (B5A)
School of Engineering
Teaching and Research Laboratories

Building 6 (B6)
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Cafeteria
Classrooms / Tutorial rooms
Graduate Programme Office (GPO)
Lecture Theatres
School of Business
School of Graduate and Professional Studies
Seminar Rooms

Building 6B (B6B)
Classrooms / Tutorial rooms
Facilities Management (Mail Room)
Maybank Kiosk
MUPA Lounge
Seminar Rooms
Teaching and Research Laboratories

Building 7 (B7)
Bookshop
Informal Spaces
Library and Learning Commons

Building 9 (B9)
Classrooms
Computer Laboratories
Informal Spaces
IT Services - Service Desk
Smart Classroom 9304

MPC
Multi-purpose Court

MSC
Gym
Monash Sports Centre
Monash University Postgraduate Association (MUPA)
Monash University Student Association (MUSA)

AP
Emergency Assembly Point

SMR
Sunway Monash Residence

For Muslim attendees,
Male prayer room : Building 6, Level 3, Room 11
Female prayer room : Building 6, Level 3, Room 12

Public Transports Around Monash

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Taxi elsewhere run by meter, with the rate starting from RM3. For example, the taxi fare from the Monash campus to the Sunway Pyramid shopping mall is approximately RM6.

Canopy Walkway

A secure canopy walkway links Monash University Malaysia directly to Sunway Pyramid, one of Malaysia's most popular shopping complexes.

Bus Rapid Transit (BRT)

The BRT station is just outside our door, providing a convenient mode of transport around Sunway. The stations are listed below:

1. Setia Jaya - Interchange station connects to Setia Jaya KTM (train) station.
2. Mentari
3. Sunway Lagoon - This station grants access to The Pinnacle, Sunway Lagoon, Sunway Resort and Spa Hotel, Sunway Pyramid Tower Hotel, Menara Sunway and Sunway Pyramid shopping mall.
4. SunMed
5. **SunU-Monash** - This station is situated in front of Monash University. It also provides access to Sunway College, Sunway University and Sunway International School.
6. South Quay
7. USJ 7 - Interchange station connects to the Kelana Jaya Light Rail Transit (LRT) line.

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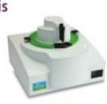
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