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ABSTRACTS

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Oral Presentations

OP011: Chemopreventive potential of *Moringa oleifera* leaves and seed residues extract in xenograft mice model induced with breast cancer cells

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Chemoprevention is an approach of precision health to improve cancer patients' prognosis using agents which have milder side effects than conventional chemotherapy treatment. *Moringa oleifera* (MO) is a well-known miracle plant with anti-cancer properties. In this study, MO leaves (MOL) with antioxidant potential and MO seed residues (MOSr) with chemopreventive potential were combined as MOLSr extract to provide a wider spectrum of anti-cancer activities. Preliminary study showed that MOLSr extract exhibited potent cytotoxicity against breastcancer cell lines. To gain further insights, xenograft mice were established with aggressive MDA-MB-231 breast cancer cells to develop tumor before receiving MOLSr injection. Biochemical analysis (three protein markers) using ELISA method and human breast cancer gene expression analysis using RT2 Profiler PCR array (84 genes) were completed to investigate the biological effects of MOLSr in xenograft mice. For up to six weeks, body weights showed no significant changes while tumor volume exhibited dramatical decrease in MOLSr- treated xenograft mice compared to control mice, reaching up to 64.5% of tumor growth inhibition. MOLSr extract exhibited cytotoxic effects in tumor without inducing any toxiceffects on other organs. Expression of genes denoting CaN and VEGF as well as SLC39A6 and SFRP1 proteins were reduced significantly in MOLSr-treated xenograft mice, possibly through MAPK and ERK1/2 signaling pathways. These data provide evidence on the cytotoxicity activity of MOLSr extracts to treat aggressive breast cancer. However, further in-depth study of its biological effects are required to understand the mode of action of MOLSr.

Keywords: *Moringa oleifera*, breast cancer, MDA-MB-231, xenograft mice, PCR array

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OP012: Formulation and Evaluation of Mucoadhesive Gels of Clarithromycin for The Effective Treatment of Dental Infections

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Clarithromycin is a second-generation macrolide antibiotic used in the non-surgical treatment regimen of chronic periodontitis and gingivitis. Mucoadhesive gels have gained attention for targeted delivery of antibiotics in treating periodontitis and gingivitis. The study aimed to prepare and evaluate the mucoadhesive gel containing clarithromycin for sustained release of the drug at the site of action. Nine formulations were prepared by simple dispersion method using different ratios of polymers. The polymers used in the formulations were hydroxypropyl methylcellulose, chitosan, sodium carboxymethylcellulose and Carbopol 934P. Gel formulations were characterized for physical appearance, pH, spreadability, drug content, in-vitro diffusion, and drug release kinetics. All prepared gels were organoleptically acceptable and possessed good spreadability. The pH of the all formulated gels was between 6-7, which does not cause any irritation upon administration. The average percentage of drug content was 97% - 99%. In-vitro diffusion results showed that polymer content influenced the rate of drug release, and it may be due to the increased viscosity of the gels with anincreased of polymer concentration. The drug was entrapped in the polymer matrix and delayed the diffusion rate providing a sustained drug release. The drug diffusion followed first order kinetics, Fickian diffusion with Higuchi type release where the drug was entrapped in the polymer matrix and the drug release was diffusion-dependant. The results were found satisfactory for all the gel parameters studied suggesting further evaluation of the gels against susceptible microbes and stability studies.

Keywords: Oral mucoadhesive gel, clarithromycin, periodontitis, carbopol, HPMC. CMC

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OP017: Novel Variants Denoting Anti-Tuberculosis Drug Resistance Features of the Clinical Multi-Drug Resistant *Mycobacterium tuberculosis* Isolates in Malaysia

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Detecting drug-resistant *Mycobacterium tuberculosis* (DR-Mtb) is important to determine suitable anti-tuberculosis (anti-TB) regime for TB patients. DR-Mtb types can be profiled through genotyping of the variants that were reported to confer anti-TB drug-resistance. Advance in research technology allows scientists to profile Mtb genetic diversity and determine anti-TB drug-resistance pattern through next-generation sequencing (NGS) approach. Besides that, the opportunity to unveil the novel variants with a possible association with anti-TB drug-resistance and functional impact using computational modeling approach can be studied. In this study, we present the analysis of 23 local clinical Mtb genomes; in which 10 isolates were sensitive-Mtb, 10 were multi-drug resistant Mtb (MDR-Mtb) isolates, two (2) were rifampicin-resistant Mtb (RR-Mtb), and one, an extensively drug-resistant Mtb (XDR-Mtb). A total of 2,154 non-synonymous variants across the 13 resistant Mtb isolates were identified. Cross-check with the Genome-wide *Mycobacterium tuberculosis* Variants Database (GMTVD) has revealed a total of 81 novel variants, of which 24 were predicted to have deleterious effect. The frequency of the 24 novel variants was identified after screening them with the local Mtb genome database, Malaysian *Mycobacterium tuberculosis* Complex Genome Database (MyMtbG). Three homology models of novel variants with the highest frequency were modeled (*echA16*_Asp156Tyr, *nudC*_Pro239Arg, and Rv3837c_Gly15Asp). The target genes were found to be involved during the stationary-phase survival and pathogenicity of the Mtb during TB infection and suggested to be candidates of the new therapeutic targets in fighting TB infection.

Keywords: *Mycobacterium tuberculosis*, DR-Mtb, tuberculosis, NGS, non-synonymous variants.

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Poster Presentations

PP002: Cluster of differentiation (CD) antigens as biomarkers for prognosis of different subtypes of gastric cancer: a preliminary study

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Gastric cancer is still one of the leading causes of cancer-related death worldwide. Classification of gastric cancer subtypes is based on the anatomical site of the tumor and pathological findings. Different subtypes of gastric cancer have a different prognosis, in which a worse prognosis has been demonstrated in the cardia and diffuse subtypes than noncardia and intestinal subtypes. Cluster of differentiation (CD) antigens are cell surface antigens expressed on all cell types that can serve as a novel biomarker in the prognosis of cancer as the expression of these antigens change according to disease state. Therefore, this study was designed to determine the expression of CD antigens in different subtypes of gastric cancer using antibody microarray. Mixed cell population derived from gastric cancer patients' cancerous tissues with different subtypes of gastric cancer (intestinal, diffuse, cardia, and noncardia) were immunophenotyped using DotScanTM antibody microarray slide. Expression of CD antigens on cells was analyzed based on the binding density of cells to respective CD antibodies. Nineteen CD antigens, the majority of them were markers for B cells, were expressed higher in cardia than noncardia subtype. CD182 and CD125, the essential interleukin receptors, were expressed higher in noncardia than cardia subtype. Interestingly, CD56 which is an important marker for natural killer cells was highly expressed in intestinal subtype than diffuse subtype. This study showed different expressions of CD antigens in different subtypes of gastric cancer with distinct prognosis. Results from this study can be further examined for immunotherapy purpose that targets specific CD antigens for better prognosis of patients.

Keywords: Gastric cancer, CD antigens, Immunotherapy, Prognosis, Gastric cancer subtypes, Biomarker

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PP009: Gut Dysbiosis in Students with Depression, Anxiety and Stress

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The gut-brain axis (GBA) consists of a bi-directional communication between the central and the enteric nervous system. Several studies have shown links between the gut microbiota and mental health. Therefore, the present study aimed to identify the potential correlations between gut dysbiosis and depression, anxiety and stress (DAS) in a cohort of UiTM students. Faecal samples were collected from 45 participants who were experiencing DAS (n=30) and those without DAS (n=15). Gut microbial diversity was analysed by sequencing the V3–V4 region of the 16S rRNA gene using MiSeq and bioinformatics analysis was performed using QIIME2. Participants with depression showed a significantly lower distribution in *Bacteroides* compared to healthy controls, which had an increase in the distribution of *Eubacterium* and *Coprobacillus*. Participants experiencing anxiety and stress showed an overrepresentation of *Bacteroides*, *Parabacteroides*, *Lactococcus* and *Ruminococcus* compared to the healthy controls. A total of 24 potential microbial biomarkers ($P < 0.05$) were predicted using PICRUSt. Dysbiosis of the gut microbiome was identified in the students with DAS in comparison with the healthy controls. Transforming the dysbiosis of gut microbiomes is potentially a good strategy to help the students reduce symptoms of DAS.

Keywords: 16S rRNA gene sequencing, gut microbiome, stress, anxiety, depression

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PP010: Football players with *NOS3* TT genotype have a stronger postural stability: a cohort study of UiTM FC

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Nitric oxide synthase enzyme affects the growth of muscle cells. Performances of the elite athletes have been associated with the polymorphisms of the *NOS3* gene. Strong postural stability is an important feature among the athletes and has a huge effect on their sports performance particularly in football. The study aimed to investigate the effects of *NOS3* -786 T/C polymorphism (rs2070744) on the postural stability among the Malaysian elite football players. A total of 23 elite football players (age = 18.09 ± 0.42) were recruited from Universiti Teknologi MARA Football Club (UiTM FC). The players were genotyped for the *NOS3* (rs2070744) variant. The postural stability scores between the players with different *NOS3* genotypes were evaluated using Student t-test for independent samples. The players who carried the *NOS3* TT genotype had better postural stability performance. Significant differences were discovered between the players with *NOS3* CT and TT genotypes (M = 2.51, SD = 0.16 vs. M = 1.55, SD = 0.12; $P < 0.05$, $d = 1.48$) for the means of right overall postural stability scores. In addition, significant differences were also observed between the players with *NOS3* CT and TT genotypes for the means of right mediolateral postural stability scores (M = 1.91, SD = 0.21 vs. M = 0.89, SD = 0.16; $P < 0.01$, $d = 1.76$). Therefore, the results highlighted that *NOS3* TT genotype is beneficial for postural stability performance of the football players.

Keywords: Polymorphism, nitric oxide synthase, performance, football, stability

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PP014: Reliability Test of the Questionnaires used for a study on Executive Function and Academic Achievement among the University Students

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The executive function covers people's capability to control their thoughts, emotions and actions. In the academic context, executive function performance is often linked with the achievement of university students generally. In this study, we aimed to investigate the executive function performance in a cohort of UiTM students using validated questionnaires. A total of 357 students from Universiti Teknologi MARA participated in the survey. The reliability of the data obtained for executive function performance was analyzed using descriptive statistics and Cronbach's alpha by Statistical Package for Social Science (SPSS) version 23. From twelve elements of executive skills questionnaire, only four of total elements showed low Cronbach's alpha; working memory (M =10.70, $\alpha = 0.579$), emotional control (M =10.32, $\alpha = 0.537$), task initiation (M =9.81, $\alpha = 0.508$), goal-directed persistence (M =10.46, $\alpha = 0.536$). Other than that, personality test on extraversion (M =31.0056, $\alpha = 0.652$) and intellect/imagination (M =31.7283, $\alpha = 0.648$) from a total of five personality traits also showed weak reliability result. Meanwhile, learning styles show good reliability for all the elements from virtual, auditory, tactile and kinesthetic. In a nutshell, a reliability test is required to be done on a validated questionnaire before it is used to ensure the data collected is valid. The reliable questionnaire can now be used for a bigger study that investigates the relationship between human genetic variants and executive function performance.

Keywords: Executive function performance, Big-Five Personality Traits, Learning styles, Academic achievement, University students.

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PP017: Medication Adherence Among Non-Communicable Diseases Patients in A Primary Care Setting

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Non-communicable diseases (NCDs) kill 41 million people each year, equivalent to 71% of all deaths globally according to World Health Organization. In Malaysia, almost two-thirds of the adult population in Malaysia has at least one of three NCDs such as diabetes mellitus, hypertension, or hypercholesterolemia. It is estimated that 73% of total mortality in Malaysia were caused by NCDs. Medication adherence is important in the management of NCDs. However, the problems related to low medication adherence were prevailing in Malaysia. To assess the medication adherence level among the chronic disease patients such as diabetes mellitus, chronic kidney disease, respiratory disease and cardiovascular diseases. A cross sectional descriptive study was carried out at a private primary care setting in Negeri Sembilan, Malaysia**.** A validated questionnaire Medication Adherence Rating Scale (MARS) was used to evaluate patients' medication adherence level. A total of 74 patients participated in the study with various demographic characteristics. Slightly more than half of the participants (59.5%) agreed that they forgot to take medication while 30 participants (40.5%) denied. About half of the participants (52.7%) was categorized at low medication adherence group. The duration of illness was not significantly associated with medication adherence levels in this study. The various demographic characteristics of the NCDs patients were not statistically significant to medication adherence level ($p>0.05$) in this study. The low adherence rate was noticed among half of the participants. There was no significantly difference of medication adherence level among patients with various chronic diseases.

Keywords: Non-communicable diseases (NCDs), medication adherence, primary care setting

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PP018: Transgenerational effects of heroin addiction: DNA methylation and metabolomics profiles in a rat model

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Heroin addiction is a psychiatric disorder that affects the socio-economic development of many countries. Repeated use of heroin causes alteration in gene expression and long-term behavioural changes. The epigenetic effects on gene expression could be reversed by pharmacotherapeutic agents such as DNA methylase which removes heroin-induced hypermethylated DNA. The preliminary study showed that male progenies of F1 and F2 sustained higher levels of anxiety and aggression, which are inherited from fathers with heroin addiction. To investigate the mechanism underpinning the transgenerational effects in heroin addiction, both serum-based untargeted metabolomics and medial prefrontal cortex tissue-dependent DNA methylation profiles were performed using liquid chromatography-mass spectrometry/quadrupole time of flight (LC/MS Q-TOF) and reduced representation bisulfite sequencing (RRBS), respectively. In F1, F2 and F3 generations, a total of 283, 41 and 55 of the known metabolites were significantly differentiated, respectively. These metabolites play important roles in lipid and nucleotide metabolism. Between control and heroin-treated rats, our findings demonstrated that higher hypermethylation regions were found in the F0, F2 and F3 generations while higher hypomethylation regions were found in the F1 generation. Each generation showed strong clustering effects, in which F1, F2 and F3 offspring shared similar pathways that are thought to be involved in the molecular mechanism of opioid receptors-dependent signalling, including calcium-, MAPK-, cAMP-, Rap1-signaling pathways, adrenergic signalling in cardiomyocytes, focal adhesion, glutamatergic synapse, cholinergic synapse and circadian entrainment. These studies concluded that DNA methylation could influence the metabolism of rats in response to paternal heroin addiction.

Keywords: Heroin, transgenerational, DNA methylation, metabolomics

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PP019: Intergenerational epigenetic changes of *Garcinia atroviridis* (MeGa)-treated obese rats

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Obesity is the fifth leading risk resulting in global death affecting almost 600 million people. In this study, the anti-obesity effect of *Garcinia atroviridis* was investigated. A preliminary study showed that the methanolic extract of *Garcinia atroviridis* (MeGa) is a safe slimming agent that reduces weight gain and improves lipid profiles in obese rats. We investigated the epigenetic and metabolic changes in F0 female (F0F) and the intergenerational effects to F1 female (F1F) and F1 male (F1M), respectively. To investigate the intergenerational slimming effects, obesity- associated phenotypes such as body weight and lipid profiles were examined while the mechanisms of action were studied using untargeted metabolomics and DNA methylation-based epigenomics approaches. Body weights of MeGa-treated obese rats in all groups were higher than their respective lean rats, but showed no significant difference. In addition, improvement of lipid profiles was observed specifically in F1F offspring. The distinct separation of the metabolite profiles was observed in F0F and F1F. Differential DNA methylation profiles related to adipogenesis, lipid metabolism, and inflammation were observed. The integrative analysis of DNA methylation and metabolomics data showed a powerful approach to elucidate the pathways significantly affected by MeGa. MeGa plays a role in being a methyl-donating agent resulting in different metabolisms which improve the obesity complications, specifically in F1 offspring female rats. These MeGa-induced epigenetic changes are the underlying mechanism for the anti-obesity effects observed. Therefore, epigenetic changes induced by herbs consumed by the communities is an important aspect to be studied in the effort of the country in building a healthy nation.

Keywords: Obesity, *Garcinia atroviridis*, Intergenerational, DNA methylation, Metabolomics

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PP020: Preliminary Phytochemical Screening and Comparison Yield of Extracts of *Padina Australis Hauck* Collected from Coastal Area of Port Dickson

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Nature derived phytochemicals have been frequently investigated as medicinal substances. One potential source is nutrient-rich seaweeds. However, the quantitative extraction and analysis work of the seaweeds found in the seacoast area in Negeri Sembilan has not been much studied. The aim of this study was to compare extracts of *Padina australis Hauck* obtained using different solvents in terms of percentage yield and their phytoconstituents by preliminary phytochemical analysis. In this study, the specimen used is *Padina australis Hauck* from the brown algae variety. Maceration was conducted using solvents such as ethanol, methanol, and water. The mixture of extract/solvent was separated using a rotary vacuum evaporator. The yield (%) obtained were 14.73%, 9.47%, 18.47%, and the colour of extracts observed was greenish-black, yellowish-brown, reddish-brown of the extracts for ethanol, methanol and water respectively. Proteins, quinones, flavonoids, tannin, phenolic compounds were detected in all of the extracts while no trace of glycoside was found. The findings signify the importance of isolation of these phytochemicals and investigation of possible mechanisms of action to develop novel antibacterial agents from *Padina Australis Hauck*.

Keywords: Brown algae, *Padina australis Hauck*, Phytochemical screening

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PP021: Perturbated Amino Acid Metabolism Pathways in Chronically Stress Zebrafish

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Anxiety disorders affected 284 million of population globally in 2017, while in Malaysia, 4.34% were affected. Our understanding of the molecular mechanisms of anxiety however, remains largely unclear. Uncovering the underlying causes of anxiety and stress will allow scientists to identify potential treatment for anxiety. A comprehensive analysis of the metabolome of the brain of zebrafish with chronic anxiety will provide valuable information for understanding the perturbated pathway underlying anxiety. In this study, we had successfully developed a stress zebrafish model and the metabolomes were established. The zebrafish were first, induced with chronic unpredictable stress (CUS) and treated with fluoxetine at 5 mg/L concentration for 14 days. Each of the individual zebrafish were induced with two types of stressor daily. Upon the end of day 14, zebrafish was sacrificed, and the brain was immediately harvested and prepared for metabolomic study using LC/MS-QTOF. The changes in metabolite profiles and anxiety related pathways involved in anxiety and response to fluoxetine were studied. The data showed upregulation of metabolites, including inosine-5'-monophosphate, spermine, spermidine and L-glutamate that potentially reduce anxiety in the zebrafish. Metaboanalyst analysis had identified several pathways related to anxiety and stress, including purine, proline and arginine as well as glutamate metabolism. In conclusion, we had successfully identified perturbated metabolism in the stress zebrafish and the pathways involved.

Keyword: Anxiety, stress, animal model, metabolomic, pathway

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PP023: The Application of Body Area Sensor Network (BASNs) in Health Precision: A Mini Review

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Fourth Industrial Revolution (IR 4.0) highlights the wide application of implants, devices as well as the Internet of Things in medical fields. The use of sensor network to smoothen the wireless link and data integration is highly relevant and applicable for disease prevention and early disease detection under the scope of precision health. Herein, the application of nanostructured materials as a sensor in biomedical systems was reviewed as it has received a pronounced attention as a diagnostic tool. Body Area Sensor Networks (BASNs) emerges as a novel smart material consisting of several interconnections of nodes or tiny wireless sensors on or within a human body that deliver sensing, processing, and communication. Several devices have been successfully developed using this sensor technology. They include pulse oximetry which indirectly measures oxygen saturation levels (SpO2) using two wavelengths of light which passes through the blood in a human body to the detector. Another successful example is monitoring of heart condition through electrocardiography (ECG) that characterizes the propagation of electric potentials through the heart muscle with regard to time. Besides, implantable glucose sensor is capable of reducing hypoglycaemics excursions in patients with diabetes mellitus caused by high level of insulin by placing an implantable sensor in the abdomen tissue. Moreover, electrical activity of the brain represented by electroencephalography (EEG) which diagnoses epilepsy also has been recognized as one of the great models of the BASNs. BASNs offer many advantages that can be exploited for design and development of more devices that provide precise monitoring of health conditions which is in line with IR 4.0.

Keywords: Precision health, nanotechnology, BASNs, Health care

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PP025: A Nutrigenetics Study on the Eating Behaviours and Risks of Nutritional Deficiencies among the Orang Asli and Malays

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Nutrigenetics is a rapidly emerging field of study that explores nutrient requirements based on the genetic make-up of individuals. Personalizing diet based on analysis of genetic composition may help to prevent nutrition-related diseases. This study aimed to identify the SNPs associated with the risks of nutritional deficiencies and eating behaviours of the Orang Asli and Malays. A total of 163 genetic risk markers related to nutritional deficiencies and eating behaviours were identified from the GWAS. A nutrigenetics database was created. SNPs associated with the risks of nutritional deficiencies and eating behaviors of the Orang Asli and Malays were mined from the whole genome sequences using bioinformatics approach. Three bioinformatics tools (VCFtools, ANNOVAR and VEP) were used for the identification and annotation of the SNPs. The genetic risks of the nutritional deficiencies and eating behaviours of a cohort of 98 Orang Asli and 96 Malays were profiled. The Orang Asli and the Malays genomes have an average of 82% and 86% of the 163 SNPs associated with nutritional deficiencies as well as eating behaviours. The genetic markers that were identified in this study provided the basis for phenotype-genotype studies to be conducted in the Malaysian populations so that an association between genetic markers and nutritional status as well as eating behaviours can be established. Besides that, this bioinformatics approach can complement the healthcare providers to offer appropriate preventive or corrective measures for individuals at risk.

Keywords: Nutritional deficiency, Eating behavior, Genetic risks, Orang Asli, Malays

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PP034: Malaysian Mycobacterium *tuberculosis* Complex Genome Database (MyMtbG): a Whole Genome Sequence Database for Surveillance

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Tuberculosis (TB) has yet to find an end since it was first discovered in 1882. TB is recognized as one of the communicable diseases which poses a continuous threat globally due to the rise of multidrug-resistant *Mycobacterium tuberculosis* (MDR-Mtb) isolates. Whole genome sequencing (WGS) approach has been used to uncover the genetic make-up of the MDR-Mtb genome. Currently, thousands of Mtb genomes have been sequenced and several TB databases have been set up to allow scientists to share and assess the Mtb genome worldwide. At iPROMISE, we had initiated the setting up of a Malaysian *Mycobacterium tuberculosis* Complex Variants Database (MyMtbG). The database houses the whole genome sequence data of 164 MTBC isolates from Malaysia, 69 MTBC isolates from Nigeria, and 2 MTBC isolates from Mexico. Snippy (http://github.com/tseemann/snippy), a variant calling software, was used to map the query genome against the reference genome *Mycobacterium tuberculosis* H37Rv strains. A total of 54,643 variants across the 235 MTBC genomes were identified. Besides that, MyMtbG provides data on the sample background, MTBC lineages, time and isolation sites, and the phenotypic and next-generation sequencing-based drug susceptibility profiles. Curation of the Mtb sequences would allow us to understand the diversity and the anti-TB drug-resistant pattern among the local MTBC isolates and contribute to global surveillance of the MTBC population. In addition, the database will be useful for scientists who work on discovery of new therapeutic targets for TB treatment and development of TB diagnostic kits.

Keywords: Tuberculosis, *Mycobacterium tuberculosis*, whole genome sequencing, MDR-Mtb, MyMtbG, variants.

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PP035: Fargesin protects RAW264.7 cells from cytotoxicity induced by hydrogen peroxide

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The imbalance level of reactive oxygen species (ROS) in the body can lead to oxidative stress towards the cells, thus, leading to the progression of chronic diseases. Fargesin is a bioactive lignan which can be found in *Flos magnoliae* and widely used in Chinese herbal medicines. Hydrogen peroxide is one of the major ROS and used as an experimental model in oxidative stress study. In this study we investigated the protective effect of fargesin against hydrogen peroxide-induced cytotoxicity in murine macrophage cell line (RAW264.7). RAW 264.7 macrophage cells were pre-treated with fargesin for 20-hour prior to the exposure to the hydrogen peroxide for another 4-hour. The cells viability was assessed through 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assay. The MTT assay showed non-toxic doses of fargesin (1.56, 3.13, 6.25, 12.5 and 25 µM) significantly reduced hydrogen peroxide-induced cytotoxicity in hydrogen peroxide-treated cells as compared to control. Conclusion: The results indicated that fargesin has the potential to be developed as an antioxidant agent. However, further studies are required to clarify the underlying mechanism of fargesin in protecting cell from oxidative stress mediated cytotoxicity.

Keywords: fargesin, RAW264.7, hydrogen peroxide, cytotoxicity

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