VIRAL INFECTIONS

MSBMB - Taylor's
Virtual Focused Meeting 2020

ABSTRACT BOOK

An event organised by the
Malaysian Society for Biochemistry and Molecular Biology
and
Taylor's University Faculty of Health and Medical Science

19 NOVEMBER 2020
2.30 pm – 4.30pm

Persatuan Biokimia & Biologi Molekul Malaysia
msbmb
Malaysian Society for Biochemistry & Molecular Biology

TAYLOR'S UNIVERSITY
Wisdom · Integrity · Excellence

Contents

WELCOME MESSAGE

PRESIDENT OF THE MALAYSIAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY

Dear friends and colleagues,

On behalf of the Malaysian Society for Biochemistry and Molecular Biology (MSBMB), it is my honour to welcome you to the Malaysian Society for Biochemistry and Molecular Biology-Taylor's University Virtual Focused Meeting 2020, themed *Viral Infections*, with a special webinar on Covid-19: Understanding the Science.

The Covid-19 pandemic has created a new paradigm for us and changed our personal and professional lives dramatically. Nevertheless, this pandemic provides an opportunity to expand the interaction among scientific communities across the globe and more importantly, to reinforce scientific cooperation. MSBMB continues its effort to organise the annual conference for our members and participants. This year, MSBMB collaborates with Taylor's University to organise the MSBMB – Taylor's University Virtual Focused Meeting 2020. It is our privilege to have three renowned researchers to highlight their research findings on Covid-19. They are Professor Dr. Jamal I-Ching Sam, Associate Professor Dr. Tan Yee Joo and Dr. Ravindran Thayan.

On behalf of our society, I would like to accord our heartfelt appreciation to Taylor's University for joining MSBMB in organising this virtual meeting. I also would like to thank the Organising Committee chaired by Associate Professor Dr. Anthony Ho Siong Hock for their effort in organising this event.

Your participation will definitely make this first virtual meeting extraordinary!

Let's stay together to face the challenges amidst the pandemic and hope for the best. Stay healthy and be safe.

Professor Ts. Dr. Lim Yang Mooi
President
Malaysian Society for Biochemistry and Molecular Biology (MSBMB)

WELCOME MESSAGE

EXECUTIVE DEAN OF THE FACULTY OF HEALTH & MEDICAL SCIENCES, TAYLOR'S UNIVERSITY

Dear colleagues,

I am pleased to pen a short foreword for the abstract book for the MSBMB-Taylor's Virtual Focused Meeting 2020 with the theme *Viral Infections*.

Our nation and the world were unexpectedly hit with the Covid-19 pandemic in the first quarter of 2020. Educational institutions and the scientific community have had to adapt to new ways of providing education very quickly and conducting research in an environment where access to physical facilities was restricted or not possible. We are not yet at a stage where virtual meetings can exactly replicate face-to-face meetings, but we have done well, and this virtual meeting is one adaption to the pandemic.

Although we are not able to interact as in a normal conference (something that most of us look forward to) and discuss and forge collaborations, this virtual meeting still enables us to listen to leaders in the scientific community and affords an opportunity for us to share our research findings, both of which are important components in the advancement of science.

I wish to thank the plenary speakers for sparing their valuable time to share your insights with all of us. I also wish to thank all the participants for your support and participation.

Finally, I wish to thank the organizing committee made up of hardworking colleagues from MSBMB and Taylor's University for all the effort you have put in towards the success of this virtual meeting.

I wish all of you a fruitful and enjoyable meeting.

Emeritus Professor Dr. Paraidathathu Thomas A/L P.G. Thomas
Executive Dean
Faculty of Health & Medical Sciences, Taylor's University

FOREWORD

CHAIRPERSON OF THE MSBMB - TAYLOR'S VIRTUAL FOCUSED MEETING 2020

Dear friends,

What a year 2020 has turned out to be! Challenging, frustrating, anxiety-inducing, sadness and grief are perhaps some words that some of us may use to describe the year. Our thoughts and prayers to those who have lost loved ones. 2020 brings sharply into focus the continued need for humans to be vigilant against the threat of emerging and re-emerging diseases. While we now have glimmers of hope that therapeutics for COVID-19 are on the horizon, the road to recovery to our 'normal way of life' may take some time. In the meantime, we adapt and evolve how we live and work, even finding innovative ways to do things better than before, embracing a 'new normal'. Human ingenuity and spirit can be truly Inspirational!

This year, the MSBMB made the necessary decision to postpone our Annual Conference planned together with our co-organiser, Taylor's University, to August 2021. However, we wanted to continue some level of engagement with our members and the greater scientific community. Thus, we launched the MSBMB-Taylor's Virtual Focused Meeting and aptly chose the theme *Viral Infections* with a special webinar on COVID-19: Understanding the Science. A fully online event featuring 3 scientists who will speak on fundamental understanding of how this disease manifest manifests and how potential therapies may work. Taking advantage of this platform, we also attracted 32 abstracts submitted by participants in a broad array of topics to enable researchers to share their work via e-posters or short videos. I hope everyone checks out the scientific presentations that will remain on our website for 1 week after the 19th of November.

Regardless of the challenges faced, the Science must go on and I hope you will find the presentations engaging and stimulate new conversations, collaborations and spark new ideas.

Please join me in thanking and appreciating my organising committee who have volunteered their time and effort in bringing you this Focused Meeting. They have done a tremendous job in preparing this fully online experience. We wish everyone a pleasant day and do leave us a note to tell us how we did.

Finally, we hope to see you again in August of 2021!

Assoc. Prof. Dr. Anthony Ho Siong Hock
Chairperson
MSBMB-Taylor's Virtual Focused Meeting 2020

Program

TIME	EVENT
14.30 - 14.00	Admission of Attendees ePosters are available for viewing
14.30 - 14.35 14.35 - 14.40	Welcome address President, Malaysian Society of Biochemistry and Molecular Biology (MSBMB) **Professor Ts. Dr. Lim Yang Mooi** Executive Dean, Faculty of Health & Medical Sciences, Taylor's University **Professor Dr. Paraidathathu Thomas A/L P.G. Thomas**
14.40 - 15.00	Plenary 1 - *Seroprevalence and molecular epidemiology of SARS-CoV-2 in Malaysia* **Professor Dr. Jamal I-Ching SAM (University of Malaya, MALAYSIA)**
15.00 - 15.20	Plenary 2 - *Characterization of antibodies against the spike protein of SARS-CoV-2: implications for the development of COVID-19 vaccine and diagnostic assays* **Assoc. Prof. Dr. Yee-Joo TAN (National University of Singapore & A*STAR, SINGAPORE)**
15.20 - 15.40	Plenary 3 - *Updates on COVID-19- Virological Characterization and Impact of D614G mutation* **Dr. Ravindran THAYAN (Institute for Medical Research, MALAYSIA)**
15.40 - 16.25	**Q&A Forum**
16.25 – 17.00	Closing Remarks Chairperson, MSBMB-Taylor's Virtual Focused Meeting 2020 **Associate Prof. Dr. Anthony Ho Siong Hock**

PLENARY 1

SEROPREVALENCE AND MOLECULAR EPIDEMIOLOGY OF SARS-COV-2 IN MALAYSIA

JAMAL I-CHING SAM

Department of Medical Microbiology, Faculty of Medicine,
50603 Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia

Malaysia experienced its first wave of SARS-CoV-2 in March/April 2020, driven by spread associated with a Tablighi Jamaat religious mass gathering in Kuala Lumpur. We carried out two studies to better understand the local situation. The first is a seroprevalence study, which provides a more accurate idea of occurrence of COVID-19 than official reported acute cases. We used screening and confirmation assays to test for SARS-CoV-2 IgG in 588 residual serum samples from University Malaya Medical Centre, collected during and after the main wave. The direct age-standardized seroprevalence rate of 0.4% (95% CI, 0%-0.93%) was > 10× higher than the period prevalence of reported cases (0.05%) in Kuala Lumpur and Selangor. With little herd immunity, Malaysia remains highly susceptible to COVID-19. Continued surveillance and public health measures are critical pending availability of an effective vaccine. In our second study, we analysed whole genome sequences of 58 SARS-CoV-2 from UMMC and 57 other publicly available Malaysian sequences. The B.6 lineage appeared soon after the Tablighi and is epidemiologically linked. B.6 predominated (65.2%) in the community, despite being rare globally (1.4%). Increases in total cases, Tablighi-associated cases and B.6 sequences were temporally linked, as were B.6 increases in Asia-Pacific. Multiple non-B.6 lineages were introduced from different countries but showed limited spread in Malaysia. We also identified a C6310A mutation in nsP3 which reduced sensitivity in a well-known diagnostic PCR assay. Mass gatherings are important causes of spread of COVID-19. Genomic surveillance can identify transmission chains and monitor diagnostic assays.

PLENARY 2

CHARACTERIZATION OF ANTIBODIES AGAINST THE SPIKE PROTEIN OF SARS-COV-2: IMPLICATIONS FOR THE DEVELOPMENT OF COVID-19 VACCINE AND DIAGNOSTIC ASSAYS

YEE-JOO TAN

Infectious Diseases Translational Research Programme Department of Microbiology and Immunology, Yong Loo Lin School of Medicine, National University of Singapore
&
*Institute of Molecular and Cell Biology, Agency for Science, Technology and Research (A*STAR), Singapore.*

The Severe Acute Respiratory Syndrome (SARS) coronavirus is the etiological agent for SARS which emerged 18 years ago. In Dec 2019, another novel coronavirus (SARS-CoV-2) crossed species barriers to infect humans and was effectively transmitted from person to person, leading to a viral outbreak in Wuhan, China. In March 2020, COVID-19, which is caused by SARS-CoV-2, was declared as a pandemic and it is causing major health problems and socioeconomic disruption worldwide. Extensive research on SARS-CoV-2 is being performed in laboratories all over the world and this has led to the development of drugs and vaccine for COVID-19. To achieve this, multidisciplinary teams of scientists have employed a large variety of techniques including omics profiling, cryogenic electron microscopy, reverse genetics and animal models. In this talk, I will be highlighting some of the approaches that have been used to deepen our understanding of this newly emerged virus.

PLENARY 3

UPDATES ON COVID-19- VIROLOGICAL CHARACTERIZATION AND IMPACT OF D614G MUTATIONS

RAVINDRAN THAYAN

Infectious Diseases Research Centre, Institute for Medical Research (IMR), Jalan Pahang, 50588 Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia.

Coronavirus disease 2019 or COVID-19 is caused by a coronavirus belonging to betacoronavirus genera, which include other important coronavirus associated with public health importance such as SARS-CoV and MERS-CoV. The disease first started in China in late 2019 while Malaysia reported the first case of COVID-19 on 25th January 2020. The virus which is zoonotic in nature had jumped species and infected human after successive genetic transfer among wild animals and mutations especially at the spike protein which is the binding point for the virus to infect human. Genetic characterization of the COVID-19 circulating in Malaysia has been carried out by comparing viruses isolated from different clusters and corresponding to the three different waves of infections in Malaysia. Results indicate that the strains widely spread during the third wave has D614G mutation. This mutation is associated with increased transmissibility due to efficient entry into host leading to increase replication ability, and thus increasing viral load. Many of the patients infected are infected with COVID-19 with D614G mutation have low Ct values. Hence, there must be effective measures to isolate and contain those infected to minimize risk of transmission.

RAPID ORAL 1

POTENTIAL OF HONEY IN COMBATING COVID-19 INFECTION

WAN IRYANI WAN ISMAIL[1, *], MUHAMMAD ASHRAF MOHD SALLEH[2] & ZOLKAPLI ESHAK[2]

[1] Cell Signaling and Biotechnology Research Group (CeSBTech), Faculty of Science and Marine Environment, Universiti Malaysia Terengganu, Terengganu, Malaysia; [2] Faculty of Pharmacy, Universiti Teknologi MARA Puncak Alam, Selangor, Malaysia.

*Corresponding author: waniryani@umt.edu.my

Honey is well-known for its medicinal effects, including as antimicrobial effects since a long time ago. However, the effects on severe acute respiratory syndrome (SARS) coronavirus (CoV) in causing COVID-19 disease are still unknown. Based on meta-analysis study using in-vitro, in-vivo, in-silico and clinical studies, honey has the potential to be used one of the supplements in combating the infection. Interestingly, based on our previous study as well, we coincidently found that honey has the ability to stimulate autophagy and apoptosis in inhibiting human breast adenocarcinoma (MCF-1) cell lines. The data may have become a starting point to study the effects of honey in combating COVID-19 infection.

RAPID ORAL 2

THYMOQUINONE-KINASES INTERACTION IN PERSPECTIVE OF COARSE-GRAINED MOLECULAR DYNAMICS (CGMD) SIMULATION

MOHAMMAD TASYRIQ CHE OMAR

Biology Section, School of Distance Education, Universiti Sains Malaysia, 11800 USM Minden, Pulau Pinang, Malaysia.

Corresponding author: mtasyriq@usm.my

Kinases are the enzymes responsible for the regulation of cell fate. In cancer, the overexpression of this protein that acts in the abnormal ways led to the progression of cancer and the inhibition of the cell death program. Currently, the unregulated growth can be monitored by the drugs against the kinases. Also, the use of natural compound like thymoquinone (TQ) in preclinical setups have shown to be a potential agent in inhibiting the growth of the kinases-dependent cancer cell lines. However, the specific interaction of this compound with the kinases has not been documented well. In this study, the kinases targeted by TQ were chosen and subjected to unbiased coarse-grained dynamics simulation (CGMD) to determine the interaction between thymoquinone and kinases. Atomistic simulation approaches successfully modelled coarse-grained parameter of TQ. One microsecond of simulation demonstrated that TQ could bind directly to particular sites of different kinases. Clustering analysis of trajectory frames showed that the complex forming interaction as exhibited by the kinase-drug complex pdbs. This finding suggested that the action of TQ observed *in vitro* studies may be influenced by the direct binding of TQ to kinases. A further experimental setup, such as site-directed mutagenesis will verify these computational findings.

RAPID ORAL 3

STRUCTURE AND FUNCTION OF A COLD SHOCK PROTEIN FROM *GLACIOZYMA ANTARCTICA*

JENNIFER CHARLES, MAKDI MASNODDIN, FARHAN NAZAIE & **NUR ATHIRAH YUSOF***

[1] Biotechnology Research Institute, Universiti Malaysia Sabah, Jalan UMS 88400 Kota Kinabalu, Sabah, Malaysia

*Corresponding author: nrathirah.yusof@ums.edu.my

Cold shock domain (CSD)-containing proteins are one of the groups of the evolutionarily conserved nucleic acid-binding proteins in all three domains of life consisting of an ancient beta-barrel fold that serves to bind nucleic acids. The cDNA of a novel protein-coding gene containing CSD was cloned from *Glaciozyma antarctica* designated as Ga16676. The full length of *Ga16676* gene with the size of 1335 bp encodes for an N-terminal CSD with conserved nucleic acids binding motif RNP1 and RNP2. The *Ga16676* gene was cloned in pET30 Ek/LIC, sequenced, expressed and its resistance towards cold was characterized. Recombinant protein expression of Ga16676 showed overexpressed soluble expression in both supernatant and pellet forms at 20 ℃. The effects of recombinant CSD protein overexpression on colony formation shows that E. coli cells were able to grow at 37 ℃ and 20 ℃ but not at 4 ℃ while *E. coli_Ga16676* cells were able to grow at all temperatures tested. In addition, E. coli_Ga16676 cells showed higher growth rate compared to empty *E. coli* cells at 10 ℃. Structural analysis of Ga16676 reveals some interesting findings such as more aromatic interactions for efficient binding in low energy environment, a longer loop that may contribute to structural flexibility and clustering of charged amino acids on the protein surface that is important for protein stability and flexibility.

RAPID ORAL 4

EFFECT OF TOCOTRIENOL RICH FRACTION ON RETINAL VESSELS DIAMETER IN DIABETIC RETINOPATHY RODENT MODEL

MUHAMMAD ZULFIQAH SADIKAN[1], NURLIYANA AIN ABDUL GHANI[2,3], LIDAWANI LAMBUK[1], IGOR NIKOLAYEVICH IEZHITSA[4], RENU AGARWAL[4], NURUL ALIMAH ABDUL NASIR[1, *]

[1] Centre for Neuroscience Research (NeuRon), Faculty of Medicine, University Teknologi MARA, Sungai Buloh, Selangor, 47000, Malaysia; [2] Universiti Malaya Eye Research Centre, Universiti Malaya, Malaysia; [3] Department of Ophthalmology, Faculty of Medicine, Universiti Teknologi MARA Malaysia, 47000 Sungai Buloh, Selangor, Malaysia; [4] School of Medicine, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia.

*Corresponding author: nurulalimah@uitm.edu.my

Purpose: Diabetic retinopathy (DR) is a common microvascular complication of diabetes. In this study, we investigated the effect of tocotrienol-rich fraction (TRF) on retinal vessel diameter in rats with streptozotocin (STZ)-induced DR as it was shown to preserve retinal morphological structure in diabetic rats. **Methods:** Male Sprague-Dawley rats, weighing 200-250 grams, were divided into normal and diabetic rats. Diabetes was induced by intraperitoneal (IP) injection of STZ, 55 mg/kg, whereas normal rats received IP citrate buffer (N). Diabetic rats were then divided into diabetic control group which received vehicle (DV) and diabetic treated group which received 100 mg/kg TRF (DT). Treatment was given orally for 12 weeks. Fundus images were captured at week 0, 6 and 12 post-induction to observe changes in retinal veins and arteries. Images were then analysed using Fiji Image J software. **Results:** Retinal venous diameter was increased in N, DV and DT at week 6 and 12 ($p<0.05$) compared to corresponding baseline measurement at week 0. Larger retinal venous diameter was observed in DV compared to N at week 6 and 12 by 1.37- and 1.35-folds ($p<0.001$), respectively. However, smaller retinal venous diameter was observed in DT compared to DV at week 6 (1.37-fold, $p<0.05$) and 12 (1.19-fold, $p<0.001$). Whereas, for retinal arteries, larger diameter was seen in DV and DT at week 6 and 12 compared to corresponding baseline. There were no intergroup differences for the arterial diameter at any time point. **Conclusion:** Oral TRF supplementation preserves retinal venous diameter of rats with STZ-induced diabetic retinopathy.

RAPID ORAL 5

USE OF ALBUMIN-BOUND BILIRUBIN FLUORESCENCE AS A PROBE TO STUDY DRUG-INDUCED DISPLACEMENT OF BILIRUBIN FROM HUMAN SERUM ALBUMIN

JACLYN TIO & SAAD TAYYAB*

Biochemistry Programme, Institute of Biological Sciences, University of Malaya,
50603 Kuala Lumpur, Malaysia

*Corresponding author: saadtayyab2004@um.edu.my

Drug binding to serum albumin could interfere with the bilirubin (BR) binding in jaundiced newborn infants due to competition of BR and drugs for albumin binding. In view of it, drug-induced BR displacement from human serum albumin (HSA) was investigated using albumin-bound bilirubin fluorescence as a spectral probe. Excitation of BR-HSA (1:1) mixture at 460 nm produced a fluorescence spectrum in the wavelength range, 480600 nm with the emission maxima at 533 nm. The BR displacing effects of five site markers, namely, warfarin (WFN), indomethacin (IDM), phenylbutazone (PBZ), ketoprofen (KTN) and hemin (HMN) were studied by monitoring the decrease in the fluorescence intensity at 533 nm ($FI_{533\ nm}$) with increasing concentrations of the site markers. Although all site markers produced a significant decrease in the $FI_{533\ nm}$ of BR-HSA complex, maximum decrease in the $FI_{533\ nm}$ value (~93%) was noticed with 80 µM HMN. These results indicated greater displacement of BR from HSA upon HMN addition. BR binding site has been reported to lie between subdomains IB and IIA of HSA. Since HMN binds to site III, located in subdomain IB of HSA, greater BR displacement upon HMN addition seems understandable. Varied BR displacement from HSA by site I (subdomain IIA) and site II (subdomain IIIA) markers also suggested either sharing of the BR binding site or through allosteric effect. All these results suggested that fluorescence of albumin-bound BR can be successfully used to study BR displacement from HSA.

RAPID ORAL 6

ZIKA VIRUS-INDUCED ENDOPLASMIC RETICULUM STRESS: HOW DO HOST CELLS RESPOND?

MUHAMMAD IZZUDDIN BIN MOHD ROPIDI, AHMAD SUHAIL KHAZALI, NURSHAMIMI NOR RASHID* & ROHANA YUSOF

Department of Molecular Medicine, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia

*Corresponding author: nurshamimi@um.edu.my

A virus life cycle consists of a series of events beginning with its entry into a cell followed by viral translation, replication and assembly before it is released into the extracellular environment, in search for a new cell to infect and repeats the entire process. Along this pathway, the cell's endoplasmic reticulum (ER) bears an integral function in hosting the virus replication and assembly. Here, Zika virus (ZIKV) proteins interact with a myriad of ER factors and exploits the organelle's protein folding capability and membrane plasticity for the virus propagative benefit. As a result, unfolded/misfolded ZIKV proteins accumulate in the ER lumen and overwhelms the ER protein folding capacity leading to ER stress. Correspondingly, this stress activates several host cell responses, which are primarily focused on reducing the protein folding burden of the ER through halting protein translation, eliminating excess unfolded/misfolded peptides and increasing the protein folding capacity. Despite these initiatives, ZIKV is capable of suppressing these solutions for their selfish objective and eventually leads to cell death. Nevertheless, several pharmacological interventions against various ER and stress factors demonstrated positive signs of reducing virus propagation and preventing ZIKV-induced neurological complications *in vivo*.

RAPID ORAL 7

ANTIPROLIFERATIVE EFFECT OF ANTHRAQUINONES FROM *MORINDA CITRIFOLIA* ON COLORECTAL CANCER CELL LINES

CHEE CHEOK WUI[1], NURSHAMIMI BT NOR RASHID[1,3,*],
& NAJIHAH BT MOHD HASHIM[2,3]

[1] Department of Molecular Medicine, Faculty of Medicine, Universiti Malaya, 50603, Kuala Lumpur, Malaysia; [2] Faculty of Pharmacy, Universiti Malaya, 50603, Kuala Lumpur, Malaysia; [3] Centre for Natural Products Research and Drug Discovery (CENAR), Universiti Malaya, 50603, Kuala Lumpur, Malaysia.

*Corresponding author: nurshamimi@um.edu.my

Colorectal cancer (CRC) is ranked the second most common cancer in Malaysia. Crucial role of phytochemical compounds as chemoprevention for CRC is definite, as there is strong association between dietary factors and colorectal risk. Anthraquinone compounds which are found abundance in *Morinda citrifolia* were previously reported by having various pharmacological properties. In this study, three CRC cell lines, HCT116, LS174T, HT29 and normal colon cells, CCD841 CoN were treated with eight anthraquinone compounds obtained from the roots of *Morinda citrifolia* at various concentrations. Based on the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) analysis, damnacanthal and morindone exhibited significant antiproliferative effect in HCT116 and HT29 cells. The IC50 value of damnacanthal in both HCT116 and HT29 cells was at 0.74μM and 28.17μM, respectively, while the IC50 value of morindone for HCT116 cells is 10.70μM and 19.20μM for HT29 cells. Following this analysis, the impedance measurement of the cell proliferation of these two compounds, were monitored in real time using xCELLigence Real Time Cell Analyzer. The data showed that the proliferation rate of HCT116 and HT29 cells decreased in dose- and time-dependent manner. Therefore, based on these results, damnacanthal and morindone may act as competitive antiproliferative agents in treating CRC.

RAPID ORAL 8

VENOMICS OF THE MALAYAN PIT VIPER, *CALLOSELASMA RHODOSTOMA*: UNRAVELLING A COMPLEX TOXIN ARSENAL THROUGH A MULTI-STEP DECOMPLEXATION APPROACH

ESTHER TANG LAI HAR[1, *], TAN CHOO HOCK[2], FUNG SHIN YEE[1], TAN NGET HONG[1]

[1]Department of Molecular Medicine; [2]Department of Pharmacology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia.

*Corresponding author: esther_tanglh@yahoo.com

The Malayan pit viper (*Calloselasma rhodostoma*) is a medically important terrestrial snake in Southeast Asia. A comprehensive proteome profile of *C. rhodostoma* venom that details its toxin composition and abundance is essential for understanding the pathological roles of the different toxins and for effective antivenom development. This study unravelled the venom complexity of *C. rhodostoma* through a multi-step venomic approach. The proteins in *C. rhodostoma* venom were first de-complexed through serial chromatography and gel electrophoresis, followed by mass spectrometric protein identification. A comprehensive and quantitative profile of *C. rhodostoma* venom composition, detailing its toxin isoforms and/or complex subunits was successfully revealed. At least 96 distinct proteins (29 basic, 67 acidic) in 11 families were identified from the venom. The venom consists of mainly snake venom metalloproteinases (SVMP, 41.17% of total venom proteins), within which the P-I (kistomin, 20.4%) and P-II (rhodostoxin, 19.8%) classes predominate. This is followed by C-type lectins (snaclec, 26.3%), snake venom serine protease (SVSP, 14.9%), L-amino acid oxidase (7.0%), phospholipase A2 (4.4%), cysteine-rich secretory protein (2.5%), and five minor toxins (nerve growth factor, neurotrophin, phospholipase B, 5′-nucleotidase and phosphodiesterase, totaling 2.6%). Importantly, all principal hemotoxins unveiled correlate with the envenomation syndrome: SVSP ancrod causes venom-induced consumptive coagulopathy, aggravated by snaclec rhodocytin that causes thrombocytopenia, while P-II rhodostoxin mediates hemorrhage, exacerbated by P-I kistomin and snaclec rhodocetin that inhibit platelet plug formation. The findings indicate that these toxins are the principal targets for effective antivenom neutralization and should be addressed in the production of a pan-regional polyspecific antivenom.

RAPID ORAL 9

INFLUENCE OF *IsaA* GENE DISRUPTION ON STAPHYLOCOCCAL REPLICATION, ADHERENCE AND BIOFILM FORMING

MA PEI YEE[1], HO KET LI[2], CHONG CHUN WIE[3], LESLIE THAN THIAN LUNG[4], ANITA BINTI SULONG[5], LIEW YUN KHOON[2, *]

[1] School of Postgraduate Studies, International Medical University; [2] School of Pharmacy, International Medical University, Bukit Jalil, 57000 Kuala Lumpur, Malaysia; [3] School of Pharmacy, Monash University Malaysia, Bandar Sunway, 47500 Subang Jaya, Selangor, Malaysia; [4] Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia. [5] Department of Medical Microbiology and Immunology, Pusat Perubatan UKM, Malaysia.

*Corresponding author: LiewYunKhoon@imu.edu.my

The immunodominant staphylococcal antigen A (IsaA) is an antigenic protein that is consistently expressed by the coloniser and invasive pathogen of *Staphylococcus aureus*. Besides being a protein that is commonly found on the cell wall, it is also secreted by the staphylococcal cells of *S. aureus*. Its main function is in the remodelling of peptidoglycan structures during cell division. To further explore the influence of IsaA on staphylococcal phenotypes, we analysed the mutant *isaA* (*ΔisaA*) *S. aureus* strain in relation to i) growth kinetic in human plasma mimicking condition, ii) capability to bind extracellular matrix proteins, iii) autolytic activity and iv) biofilm forming. The *ΔisaA* mutant showed different growth pattern in human plasma mimicking condition, but with the similar maximum specific growth rate compared to its respective wild-type strain (*S. aureus* SH1000). Furthermore, it caused only slight changes to the adherence to extracellular matrix proteins of fibrinogen or fibronectin; the small difference in autolytic activity between them was not statistically significant. Interestingly, its ability to form biofilm was reduced significantly compared to the wild-type strain. Taken together, IsaA influences the cellular functions (replication, and autolysis) and extracellular proteins adherence, albeit most of the differences were not significant which could be attributed to genetic compensation, except for the radically attenuation of biofilm formation. All these suggest the need to look into more thorough investigation on the role of IsaA through proteomic and transcriptomic studies to gain new insight into the biological function of IsaA in relation to other genes or proteins.

RAPID ORAL 10

A PHYSICAL INTERACTION NETWORK OF ZIKA VIRUS AND HUMAN PROTEINS

THAMIL VAANI KOMARASAMY[1], NUR AMELIA AZREEN ADNAN[1], WILLIAM JAMES[2] & VINOD RMT BALASUBRAMANIAM[1,*]

[1] Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, Selangor, Malaysia; [2] Sir William Dunn School of Pathology, University of Oxford, United Kingdom.

*Corresponding author: vinod.balasubramaniam@monash.edu

Zika virus (ZIKV) received worldwide attention over the past decade when outbreaks of the disease were found to be associated with adverse pregnancy and birth outcomes with numerous neurological complications, including microcephaly. The Zika epidemic peaked in 2016 and has affected over 80 countries worldwide. There are currently no antiviral drugs with proven efficacy or vaccines for its prevention. Identification of human proteins targeted by ZIKV is essential to decipher cellular pathways hijacked by the virus to replicate, escape innate immunity, and induce neuropathogenesis. To illuminate this, two selected ZIKV proteins, namely premembrane (prM) and NS4A of a Brazilian isolate were cloned and expressed. Both the prM and NS4A proteins of the Brazilian ZIKV strain have been found to play critical roles in ZIKV induced microcephaly and other neurological complications. The interacting human proteins were then identified through yeast two-hybrid system using Universal Human cDNA library. The virus-host interaction study identified 31 human proteins involved in distinct biological processes, as interactors to ZIKV prM and NS4A proteins. Among these, 10 proteins are associated with brain development, neural function, embryogenesis and various neurological disorders. These findings can be used as a resource for the future characterization of ZIKV neuropathogenesis and help to provide a basis for the discovery of host-directed antiviral drugs that may disrupt the interaction and overcome the neurological complications in newborns.

RAPID ORAL 11

INTERACTOMICS OF CHIKUNGUNYA VIRUS E1 AND E2 PROTEINS WITH HUMAN UNIVERSAL CDNA LIBRARY

NUR AMELIA AZREEN BINTI ADNAN[1], THAMIL VAANI KOMARASAMY[1], THAM HONG WAI[2], SHARIFAH SYED HASSAN[1] & VINOD RMT BALASUBRAMANIAM[1,*]

[1] Infection and Immunity Research Laboratory, Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, 47500, Subang Jaya, Selangor, Malaysia.
[2] Biopharmaceutical Research Unit, SEGI University, Jalan Teknologi, Taman Sains Selangor, Kota Damansara PJU 5, 47810 Petaling Jaya, Selangor Darul Ehsan, Malaysia.

*Corresponding author: vinod.balasubramaniam@monash.edu

Chikungunya virus (CHIKV) is an evolving arbovirus that is prevalent in tropical regions and spreads rapidly to temperate climates with recent epidemics in Africa, Asia, Europe and the Americas. The chikungunya virus genome is ~11.8kb nucleotides long and encodes for two polyproteins – the non-structural polyprotein consisting of four proteins (nsP1, nsP2, nsP3 and nsP4) and the structural polyprotein consisting of five proteins (Capsid, E3, E2, 6K and E1). Specifically, we are interested in the structural envelope proteins, E1 and E2 which play a crucial role in viral binding and entry to the host cell. Although it has been known to play a role in viral replication but the crosstalks between the viral E1 and E2 surface glycoproteins and host which may aid in virulence and pathogenesis still remains elusive. Thus, our aim is to elucidate the role played by envelope protein, E1 and E2 of CHIKV with the human host proteins. A high throughput yeast two-hybrid (Y2H) screening was used to identify the interaction of E1 and E2 proteins (bait plasmid) with human cDNA library (prey plasmid). Bait and prey plasmid were mated together to produce interactions. Thirty positives interactions were observed for E1 while sixty positives interactions were observed for E2 with human cDNA library. We have successfully obtained a few lists of human host proteins that might be crucial in CHIKV entry and pathogenesis. This could help in better understanding of viral pathogenesis and identification of host biological pathways involved in viral replication, maturation, and spread of infection.

RAPID ORAL 12

CYTOTOXIC EFFECTS OF POLYSACCHARIDE FROM *GANODERMA LUCIDUM* TOWARDS ORAL CANCER CELL LINE

SYAIRAH NABILA SUHAIMI[1], KHOR GOOT HEAH[1,2] & GABRIELE RUTH ANISAH FROEMMING

[1] Faculty of Dentistry, Universiti Teknologi MARA, Sungai Buloh Campus, Jalan Hospital, 47000 Sungai Buloh, Selangor, Malaysia.
[2] Oral and Maxillofacial Cancer Research Group, Faculty of Dentistry, Universiti Teknologi MARA, Sungai Buloh Campus, Jalan Hospital, 47000 Sungai Buloh, Selangor, Malaysia.
[3] Faculty of Medicine and Health Sciences, Jalan Datuk Mohammad Musa, 94300 Kota Samarahan, Sarawak, Malaysia.

*Corresponding author: gootheah@salam.uitm.edu.my

Introduction: Oral cancer is the sixth most common cancer worldwide with five-year survival rate of less than 50%. Current cancer therapies are known to possess many side effects that could lead to serious complications. The application of natural product as complementary and alternative treatment could be advantages in terms of reducing the side effects and increasing sensitivity of cancer therapies. *Ganoderma lucidum* (*G. lucidum*) has long been used in traditional Chinese and conventional medicine. Exopolysaccharide (EPS), which is one of the fractions of polysaccharides found in *G. lucidum* was identified to exhibit anti-cancer effects in many studies. Hence, in this study, cytotoxicity of EPS towards oral cancer was determined using an in vitro model study. **Methods:** The effects of EPS and cisplatin on cell viability of oral cancer cell line, ORL-48T and human normal gingival fibroblast cell line, HGF, were assessed using 4,5-dimethylthiazol-2-yl)-3,5-diphenylformazan (MTT) assay. Cell death of ORL-48T was analysed using DNA fragmentation ELISA assay. **Results:** After 72 h of treatment with EPS, the IC_{50} of ORL-48T analysed was 0.2297±0.06 mg/ml, while no IC_{50} of EPS obtained for hGF. **Conclusion:** This study shows a preliminary evidence of EPS from *G. lucidum* exerts cytotoxic activity towards oral cancer cell line, ORL-48T and no significant cytotoxicity towards human normal gingival fibroblast, hGF.

E-POSTER 1

IN SILICO IDENTIFICATION AND EVALUATION OF POTENTIAL FLAVONOIDS AS FLAVIVIRUS INHIBITORS

SYAKIRAH NIK ISMAIL & NURUL AZIRA ISMAIL*

Faculty Health and Life Sciences, Management & Science University, University Drive, Off Persiaran Olahraga, Section 13, 40100 Shah Alam, Selangor Darul Ehsan, Malaysia.

*Corresponding author: nurulazira_ismail@msu.edu.my

Dengue and Zika viruses are closely related mosquito-borne flaviviruses with similar transmission cycles, antigenically and disease manifestations including high fever, rash, severe muscle and joint pain. Dengue infection has become global epidemic health problem and the most rapidly spreading mosquito-borne viral disease in the world. Zika virus infections still remain at risk because of ongoing transmission and the potential for new outbreaks. Currently there is neither effective vaccine nor inhibitors for both viruses. Due to that, another effort to reduce the infection of both viruses is by interferes the interaction between the envelope (E) glycoprotein of the viruses to the host before the viral undergo the dramatic conformational changes during membrane fusion. Therefore, this study is attempts to suggest the entry inhibitors which can block the interaction between E protein to the host using DENVs serotypes and ZIKV strains from Malaysia. The 3D protein models of all DENVs serotypes and ZIKV isolated in Malaysia were developed by three different servers. The best stereochemical quality models were used as macromolecules structure for protein-ligand complex in molecular docking simulation. Ten potential flavonoids were selected to be docked to both dengue and zika E protein models. Impressively, the ten flavonoids were found to dock in the same pocket located in the E protein of each DENVs and ZIKV protein models. The consensus pocket was observed during the optimization of the grid box at 30Å. The size of the binding pocket for the DENV1, DENV3 and ZIKV are 25.28 Å, 23.53 Å and 19.08 Å, respectively. From the ten flavonoids, bromelain indicated the lowest binding energy (-9.8 kJ/mol) followed by EGCG (-9.3 kJ/mol), baicalin (-9.0 kJ/mol), isoquercitrin (-8.8 kJ/mol), baicalein, fisetin, quercetin, delphinidin and panduratin A (-7.5–6.7 kJ/mol) and papain showed the highest binding energy for all the protein-ligands complexes. The lower binding energy (-9.8 kJ/mol) between the ligands and protein models, indicated higher binding affinity. However, based on the pharmacokinetics and lipinski analysis, EGCG and isoquercitrin have lower GI (gastrointestinal) absorption and higher violation. Therefore, these two flavonoids results will be excluded to be suggested as potential flavonoids for the flavivirus inhibitors. The observation of this binding pocket is a promising as an antiviral development for both flavivirus since the interaction between E protein and the host that could lead to the maturation and fusion of the virus can be blocked by these flavonoids. Further molecular dynamics simulation for the protein-ligand complexes should be carried out to ensure the similar pocket was observed on all the structures hence the conformational dynamics change of each ligands can be addressed.

E-POSTER 2

PHENOTYPE AND TRANSCRIPTOME ANALYSIS PROPOSES *Burkholderia pseudomallei* BPSL2988 AS AN ADENOSINE KINASE

CHEE-HOO YIP, RUI-RUI WONG, YEE-CHIN WONG & SHEILA NATHAN*

Department of Biological Sciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Selangor, Malaysia

*Corresponding author: sheila@ukm.edu.my

Melioidosis is a fatal infectious disease caused by *Burkholderia pseudomallei* (*Bp*). Melioidosis is endemic in South East Asia and northern Australia whilst sporadic and imported cases have been reported worldwide. Currently, melioidosis treatment relies solely on antibiotics therapy but the disease remains difficult to treat due to high Bp intrinsic antibiotics resistance and incomplete understanding of how the bacterium affects the infected host. Previously, a list of *Bp* essential proteins required for *in vivo* survival was identified using Transposon Directed Insertion Sequencing (TraDIS). One of these proteins is BPSL2988, annotated as a putative sugar kinase. To further characterise the predicted protein function, a *bpsl2988*::Tn5 isogenic mutant was constructed. Virulence and organ colonisation by the isogenic mutant was significantly attenuated in *Caenorhabditis elegans* and BALB/c mice, respectively. Furthermore, a significant reduction in biofilm synthesis and motility was also noted with the mutant. Transcriptome analysis was then undertaken on the *bpsl2988*::Tn5 mutant and *Bp*R15 wild-type strain. A total of 179 genes were differentially modulated in the mutant with 27 up-regulated and 152 down-regulated genes. Analysis of these genes showed that both adenine salvage and DNA base excision repair pathways were highly expressed whilst metabolism-related genes were significantly down-regulated in the mutant. This enabled us to propose that BPSL2988 is an adenosine kinase that maintains the intracellular levels of adenosine and adenine to preserve the integrity of bacterial DNA. We suggest that drug targeting of BPSL2988 should disrupt bacterial DNA integrity and reduce cell metabolism leading to decreased *Bp* survival.

E-POSTER 3

IDENTIFICATION AND EVALUATION OF INHIBITORS FOR HAND FOOT MOUTH DISEASE (HFMD)

INTAN IDASHAFIRA MOHD SHAFIRI & NURUL AZIRA ISMAIL*

Faculty Health and Life Sciences, Management & Science University, University Drive, Off Persiaran Olahraga, Section 13, 40100 Shah Alam, Selangor Darul Ehsan, Malaysia.

*Corresponding author: nurulazira_ismail@msu.edu.my

Hand, foot, and mouth disease is a common paediatric disease and continuing endemic in Asia especially Malaysia. Currently there is neither effective vaccine nor inhibitors and no specific cure for HFMD. The HFMD disease is trigger primarily by human Enterovirus 71 (EV-A71) and Coxsackievirus A16 (CVA-16). One of the effort to reduce the infection, is by interferes with the interaction between both viruses to the host before the viruses undergo the replication process. The 3D protein models of CVA-16 and EV-A71 isolated in Malaysia were developed by three different servers. The best stereochemical quality models were used as macromolecules structure for protein-ligand complex in molecular docking simulation. Ten potential flavonoids were selected to be docked to both CVA-16 and EV-A71 models. Based on the pharmacokinetics analysis all the ligands have higher GI (gastrointestinal) absorption, however, Lipinski analysis shows that, bromelain exhibit violated against the rule of five of Lipinski rule. Bromelain was therefore excluded from being suggested as potential flavonoids. Remarkably, the ideal ten flavonoids were found to dock in the same pocket of each CVA-16 and EV-A71 protein models, with baicalin indicating the lowest binding energy (-11.3 kJ / mol) in each of the protein models. Conclusion: Further simulation of molecular dynamics for the protein-ligand complexes should be conducted to ensure that the same pocket was observed on all the structures hence the change in the conformational dynamics of each ligand can be addressed.

E-POSTER 4

IN SILICO SCREENING OF EXTRACTED CHEMICAL COMPOUNDS FROM *CLEOME ARABICA* AS ENZYME INHIBITOR

SEGLAB FATIHA*, IHCEN KHACHBA & YOUSFI MOHAMED

Laboratory of Fundamental Sciences, University Amar Telidji, Laghouat, Algeria.

*Corresponding author: f.seglab@lagh-univ.dz

Background: *Cleome arabica* belongs to the family of Capparaceae has attracted wide attention in recent years for its pharmaceutical potential due to their antioxidant, antihypercholisterolemic, Anti-cancer and chemoprotective activities. **Objective:** The objective of this study was to predict the α-amylase inhibitory activity of certain secondary metabolite ligands found with HPLC–SM of *Cleome arabica* leaves extract, using *in silico* docking studies. Methods: The 3D structure of PDB ID (6taa) from the Protein Data Bank (www.rcsb.org/pdb/home.do) and pyrx software was used to screen the 15 compounds (secondary metabolite) investigated by (HPLC-MS) of *Cleome arabica*. **Results:** Three secondary metabolites found to have best docking interaction with the target proteins. amblyone ,diosmine and luteoluside.amblyone showed highest binding affinity with alpha amylase, with binding energies -9.2kcal/mol, -9.1 kcal/mol and -8.7 kcal/mol from nine poses model respectively. Calycopterin has the least binding energy of -6.5 kcal/mol with the target alpha amylase. Among all these metabolites diosmine is also an interesting ligand by its high binding affinity with much lesser binding energy of -8.6 kcal/mol,-8.1 kcal/mol and -8.0 kcal/mol respectively with target enzyme when compared with that of the standard (-7.6kcal/mol). **Conclusions:** These *in silico* approach analyses of the selected flavonoids and terpene could lead to the further development to find the potent α-amylase inhibitors for the treatment of diabetes.

E-POSTER 5

INTERACTION OF STEROIDAL SAPOGENIN, DIOSGENIN WITH HUMAN SERUM ALBUMIN AND α_1-ACID GLYCOPROTEIN: MULTISPECTROSCOPIC ANALYSES AND MOLECULAR MODELLING

KHAIRUL AZREENA BAKAR[1], SU DATT LAM[2], HASIDAH MOHD SIDEK[1] & SHEVIN RIZAL FEROZ[1, *]

[1] Department of Biological Sciences and Biotechnology; [2] Department of Applied Physics, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, 43600 Bangi, Selangor, Malaysia.

*Corresponding author: shevin@ukm.edu.my

Diosgenin (DIO), a steroidal sapogenin and commonly used as precursor for synthesizing synthetic steroidal drugs. This phytochemical compound has been reported to exhibit various of pharmacological activities. The efficacy of bioactive compounds as a promising drug are highly influenced by its interaction with proteins in the circulatory system. Hence, the interaction of DIO with the major carrier proteins in humans, i.e. human serum albumin (HSA) and α_1-acid glycoprotein (AAG), was characterized using multispectroscopic approach and molecular docking simulations. Moderate binding affinity for both DIO–HSA and DIO–AAG interactions were determined from analysis of fluorescence enhancement data. Far-UV and near-UV CD spectral results suggested minimal conformational alterations in HSA upon DIO binding, but the effect on AAG was more significant. Site marker competitive experiments concluded that DIO binds weakly to the main drug binding sites of HSA. However, results obtained from molecular docking was found DIO to docked near subdomain IB of HSA. For variant A of AAG, the binding site was located in the central binding pocket of the protein, while in variant F1*S, DIO was accommodated to a cleft on the protein surface using molecular docking. Involvement of hydrophobic interactions and van der Waals forces in the complex formation for both protein, but hydrogen bond only involved for both variants of AAG.All these results suggest that AAG as the more prefer transporter for DIO. These findings were useful in the design of new analogues for drug development derived from DIO.

E-POSTER 6

AN EXPLORATION INTO THE GUT OF URBAN AND RURAL POPULATIONS ACROSS THE GLOBE: ANALYZING THE EFFECTS OF SOCIO-DEMOGRAPHIC, LIFESTYLE BEHAVIORS, DIETARY HABITS, AND LIVING ENVIRONMENT ON GUT MICROBIOME

FARHAT ABJANI[1], PRIYA MADHAVAN[2, *], PEI PEI CHONG[1]; KARUTHAN CHINNA[2] CHARLES ANTHONY RHODES[3] & YVONNE A. L. LIM[4]

[1] School of Biosciences; [2] School of Medicine, Faculty of Health and Medical Sciences, Taylor's University, Subang Jaya, Malaysia; [3] Department of Biomedical Science, Division of Applied Biomedical Sciences and Biotechnology, International Medical University, Malaysia; [4] Department of Parasitology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia

*Corresponding author: priya.madhavan@taylors.edu.my

It is a well-established fact that a balanced community of the gut microbiota is crucial for human health. Abrupt changes in gut microbiota can cause dysbiosis, which can potentiate several health disorders. In the 21st century, urbanization represents a major demographic shift in developed and developing countries. The gut microbiota profiles of the citizens of a developed country are quite different when compared with the profiles of the people living in either developing or underdeveloped countries. Studies based on the comparative analysis between urban and rural population have proved that healthy adults from rural societies such as Papua New Guinea, Amerindia and Malawi and hunter-gatherers from Tanzania and Amazon have higher gut bacterial species richness compared to urban populations in Italy and US. Similarly, children from rural communities have more diverse gut microbiota compared to children from Western populations. The World Allergy Organization" (WAO) has proposed that the increase in the incidence of inflammatory diseases are linked to a lack of biodiversity in modern urbanised environments, resulting in a reduced range of gut microbiota and an inappropriate immune response. This suggest that a biodiverse environment that is microbe-rich may promote the development of healthy gut microbiota and lower disease risk. Factors such as living environment, socio-demographics, lifestyle behaviours and dietary habits are likely to influence the gut microbiota. Unfortunately, not much data has been gathered (especially from Asia) that explains the relationship between the above-mentioned factors with respect to its microbial composition. Therefore, it highly significant to collect and analyse data from rural and indigenous communities living in a unique biodiverse location whose lifestyle and environment are in complete contrast to that of the people living in western world. This will allow us how biodiversity influences health and diseases, particularly diseases of the post-modern era.

E-POSTER 7

EFFECTS OF FRESH GARLIC EXTRACT (FGE) ON 'MASTER REGULATOR' GENES IN *CANDIDA ALBICANS*

DAVE ARANKA THOMAS[1], JOSHUA LEE VOON KAI[1], CHOO SULIN[1], HARINASH RAO[2] AND CHONG PEI PEI[1,*]

[1] School of Biosciences; [2] School of Medicine, Faculty of Health and Medical Sciences, Taylor's University, No. 1, Jalan Taylor's, 47500 Subang Jaya, Selangor, Malaysia

*Corresponding author: peipei.chong@taylors.edu.my

Candida-associated nosocomial infections are a persistent problem which have been steadily increasing over the years. The emergence of resistant strains has narrowed the spectrum of effective antifungals and indicated the need for alternative therapeutics. Garlic, a spice with unique characteristics has been widely researched for its antimicrobial properties. Allicin, a thiosulfinate that makes up approximately 70% of the total thiosulfinates extracted from garlic attributes for most of its antimicrobial properties. This study aimed to determine the effects of fresh garlic extract (FGE) towards *C. albicans*' biofilms and the expression of two major transcription factors, Flo-8 and Ndt80 involved in biofilm formation, which enables phenotypic switching from planktonic cells to biofilm. Minimum inhibitory concentration (MIC) of FGE towards *C. albicans* was observed at 100 mg/mL through agar well and disc diffusion assays. Preformed *C. albicans* biofilms treated with ¼× to 2× MIC of FGE and Amphotericin B exhibited a statistically significant disruption of its biofilms with FGE at ¼× MIC. Effects of FGE on the expression of Flo-8 and Ndt80 at 5 mg/mL and 10 mg/mL quantitatively by real-time polymerase chain reaction (RT-PCR) indicated an upregulation of both genes with a marked increase in Flo-8. It is surmised that the upregulation is a survival mechanism in the presence of FGE. The findings from this study indicate that FGE exhibit antifungal and antibiofilm properties that makes it a promising alternative therapeutic to address *C. albicans*-associated nosocomial infections. Further research is required to understand the mechanism behind this phenomenon.

E-POSTER 8

NEWLY SYNTHESIZED HAp/Al_2O_3/TiO_2 COATINGS ONTO Ti-6Al-4V ALLOY EXHIBITS IMPRESSIVE BIOCOMPATIBILITY FOR MEDICAL RELEVANCE APPLICATIONS

ERIC TZYY JIANN CHONG[1], JUN WEI NG[1], NISHAT ANAN[1], DUNYA ABDULSAHIB HAMDI[2], LINH NGUYEN THI TRUC[3], ZHONG-TAO JIANG[4] AND PING-CHIN LEE[1]

[1] Biotechnology Programme, Faculty of Science and Natural Resources, Universiti Malaysia Sabah, Jalan UMS, 88400 Kota Kinabalu, Sabah, Malaysia; [2] Department of Prosthetics & Orthotics Engineering, Al Nahrain University, Iraq; [3] Department of Chemistry, Ho Chi Minh City University of Pedagogy, Vietnam; [4] School of Engineering & Information Technology, Murdoch University, Murdoch, WA 6150, Australia.

*Corresponding author: eric_ctj@live.com

Ti-6Al-4V alloy is a metallic biomaterial that has been widely used to make devices in biomedical applications such as orthopaedic and dental implants. However, the leached heavy metals such as aluminium and vanadium from the alloy can result in severe side effects to humans. To extend this concern, this study synthesized a potential biomaterial with HAp/Al_2O_3/TiO_2 coatings onto Ti-6Al-4V alloy via radio frequency magnetron sputtering technique and assessed its biocompatibility using *in vitro* and *in vivo* tests in animal model. The structural and morphological formations of the newly synthesized biomaterial coatings showed a high crystallinity and improvement of corrosion behavior after immersion in simulated body fluid for 1 month, indicating a high degree of biocompatibility. Assessment of the biomaterial's extract on 3T3 fibroblast cells using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay revealed no cytotoxic effect. In addition, the biomaterial's extract also showed an incredibly low genotoxicity effect in rec-assay and Ames test using different bacterial strains. *In vivo* studies using the Spraque Dawley rats exhibited no hypersensitivity reaction in both primary dermal irritation and sensitization tests as well as no toxicity effect in both subchronic and systemic toxicity tests. In conclusion, the newly synthesized biomaterial with HAp/Al_2O_3/TiO_2 coatings onto Ti-6Al-4V alloy in this study shows superior biocompatibility for medical relevance applications.

E-POSTER 9

IMMUNOREACTIVITY AND NEUTRALIZATION EFFICACY OF GREEN PIT VIPER ANTIVENOM AGAINST HETERO-SPECIFIC PIT VIPER VENOMS

MUN YEE YONG[1], KAE YI TAN[2] & CHOO HOCK TAN[1, *]

[1] Department of Pharmacology; [2] Department of Molecular Medicine, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia.

*Corresponding author: tanch@um.edu.my

The arboreal pit vipers of *Trimeresurus* complex are medically important venomous snakes in Asia. These pit vipers are highly diverse, comprising more than ten different species. Species-specific antivenoms, however, are limited, and only one product i.e. the monovalent Thai Green Pit Viper Antivenom (GPVAV, raised against *Trimeresurus albolabris* of Thailand) is commercially available in the region. GPVAV is often used to treat snakebite envenomation caused by various *Trimeresurus* pit vipers, but its hetero-specific efficacy has been questionable. To address the problem, this study evaluated the immunological binding and neutralizing activities of GPVAV against the venoms of nine hetero-specific *Trimeresurus* pit vipers from different localities. On enzyme-linked immunosorbent assay, GPVAV demonstrated moderate-to-strong immunological binding activities (>70%) to the venoms of species from Southeast/East Asia, but relatively low activities (~50%) to that of *Trimeresurus trigonocephalus*, an endemic species distantly distributed in Sri Lanka (South Asia). The immunoreactivity finding implied that the *Trimeresurus* pit vipers of Southeast/East Asia share more closely related venom antigenicity compared to the species from South Asia. Further functional studies showed that all *Trimeresurus* pit viper venoms were strong procoagulant to human plasma, verifying the coagulotoxicity of these venoms that leads to consumptive coagulopathy during envenomation. GPVAV was found effective in cross-neutralizing the procoagulant effects of these venoms to different extents, despite the lack of correlation between the neutralizing potency and immunoreactivity. Together, the study indicates that GPVAV is potentially an effective antivenom treatment in the management of envenomation caused by hetero-specific *Trimeresurus* pit vipers in the region.

E-POSTER 10

EFFECTS OF FRESH GARLIC EXTRACT (FGE) ON *LACTOBACILLUS* SP.

JOSHUA LEE VOON KAI[1], DAVE ARANKA THOMAS[1], CHOO SULIN[1], HARINASH RAO[2] AND CHONG PEI PEI[1, *]

[1] School of Biosciences; [2] School of Medicine, Faculty of Health and Medical Sciences, Taylor's University, No. 1, Jalan Taylor's, 47500 Subang Jaya, Selangor, Malaysia.

*Corresponding author: peipei.chong@taylors.edu.my

Fresh garlic extract (FGE) contains a range of bioactive components that allows it to indiscriminately inhibit the growth of pathogenic microorganisms. Its broad-spectrum antimicrobial properties has made it a promising alternative therapeutic particularly, in light of antimicrobial resistance. Human commensals play a role in various essential functions including protecting the host from opportunistic microorganisms. The effects exerted by FGE towards these commensals have to be determined before it can be utilised as an alternative therapeutic. This study aimed to understand the effects of FGE towards one of the dominant members of the human commensals, *Lactobacillus* sp. Antibacterial effect of FGE towards *Lactobacillus casei* ATCC 393, *Lactobacillus fermentum* ATCC 14931 and *Lactobacillus rhamnosus* ATCC 53103 were determined through agar well and disk diffusion assays. No observable inhibition was noted for all strains at 100 to 300 mg/mL. A closer evaluation of FGE effects on the gene expression of *L. rhamnosus* quantitatively by real-time polymerase chain reaction (RT-PCR) indicated that the stress proteins, DnaK and GroEL were significantly upregulated at 300 mg/mL and downregulated at 100 to 300 mg/mL, respectively. It is surmised that the upregulation of DnaK is an attempt by the lactobacilli strains to protect its proteins from damage whilst the downregulation of GroEL is an attempt to adapt. The current findings indicate that while FGE triggers the stress proteins at high concentrations, it does not affect the growth of lactobacilli. Further studies involving other stress proteins is required to determine the extent of the treatment with FGE.

E-POSTER 11

ATTENUATION OF *MACROBRACHIUM ROSENBERGII* NODAVIRUS THROUGH CODON DEOPTIMIZATION OF THE VIRUS FUNCTIONAL GENOME

SITI NOOR FATIMAH ISMAIL[1], CHEE HUI YEE[2], SYARUL NATAQAIN BAHARUM[1] & LOW CHEN FEI[1, *]

[1] Institute of Systems Biology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Selangor, Malaysia; [2] Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia

*Corresponding author: low@ukm.edu.my

Macrobrachium rosenbergii nodavirus (MrNV) belongs to the proposed gammanodavirus of the family *Nodaviridae*. It is a non-enveloped icosahedral virus, containing a bipartite positive-sense single stranded RNA genome, namely RNA1 and RNA2. The discovery of this virus as the result from the white tail disease (WTD) in giant freshwater prawn, *Macrobrachium rosenbergii*, which causes up to 100% mortality in larva, post-larval and early juvenile stages. The objective of this study is to attenuate MrNV through codon deoptimization of the virus functional genome. A mutated infectious clone of the RNA2 genome was synthesized, consists of a total number of 125 synonymous codon substitutions. The mutated RNA2 is deoptimized based on the reduction in Codon Adaptation Index (CAI) value from 0.802 to 0.646 and increase in Relative Codon Deoptimization Index (RCDI) from 1.346 to 1.997. Nucleotide sequences of wild type RNA1, RNA2 and mutant RNA2 were synthesized *de novo* and transcribed *in vitro* using T7 promoter. The viral genes were then transfected into confluent *sf9* cells. Wild-type MrNV-infected sf9 cells showed an increment in size due to cytoplasmic swelling, and aggregation of the infected cells into clumps of various sizes. While the mutant MrNV-infected *sf9* cells exhibited a degree of cytoplasmic swelling with insignificant aggregation. The RNA viral genome of both wild type and mutant clones were successfully extracted from the transfected *sf9* cells at 92 hours post transfection, confirmed the infectivity of these infectious clones. The potential of live attenuated MrNV as the vaccine against WTD is currently being investigated.

E-POSTER 12

PRECLINICAL ASSESSMENT OF PAKISTAN VIPER ANTIVENOM (PVAV): PHYSICOCHEMICAL PROFILING AND IMMUNOLOGICAL BINDING ACTIVITY TO SAW-SCALED VIPER VENOMS

ANDY SHING SENG LIM[1], CHOO HOCK TAN[1,*] & KAE YI TAN[2,*]

[1]Department of Pharmacology, Faculty of Medicine, University Malaya, 50603 Kuala Lumpur, Malaysia; [2]Department of Molecular Medicine, Faculty of Medicine, University Malaya, 50603 Kuala Lumpur, Malaysia.

*Corresponding author: tanch@um.edu.my (CHT); kytan_kae@um.edu.my (KYT)

Snakebite envenomation is an important neglected tropical disease classified by WHO. It results in high morbidity and mortality particularly in South Asian countries, e.g., Pakistan. For decades, Pakistan relies heavily on imported Indian antivenoms to treat snakebite envenomation, but the Indian antivenoms have been found less effective against the snake species native to Pakistan. To overcome the problem, Pakistan Viper Antivenom (PVAV), which is an antivenom prototype raised against the native Pakistani saw-scaled vipers, has been recently produced from horses. This study aims to evaluate the physicochemical purity of PVAV and its immunological binding activity to the venoms of *Echis carinatus sochureki* (ECS) and *Echis carinatus multisquamatus* (ECM), two saw-scaled viper species endemic in Pakistan. Size-exclusion chromatography showed that PVAV composed of primarily high molecular weight protein (~150 kDa), consistent with equine immunoglobulin G, and the presence of contaminant proteins were minimal. This was further verified with sodium dodecyl sulfate-polyacrylamide gel electrophoresis under reducing and non-reducing conditions. On enzyme-linked immunosorbent assay, PVAV demonstrated potent immunological binding activities to ECS and ECM venoms toward the respective venoms. In comparison to the Indian antivenom product, the immunoreactivity of PVAV was significantly much higher by ~1.5-fold, suggesting higher efficacy in neutralizing the toxicity of Pakistani viper venoms. The findings show that PVAV has a relatively pure protein profile and is efficacious in immunological binding to the venoms of Pakistani saw-scaled vipers. PVAV is therefore a promising antivenom to undergo clinical trial of snakebite management in Pakistan.

E-POSTER 13

MIR-129-3P IS OVEREXPRESSED IN MALAYSIAN ORAL CANCER CELL LINE

KHOR GOOT HEAH[1,2 *], NUR RAWAIDAH MOHD SHOBRI[1] & GABRIELE RUTH ANISAH FROMMING[3]

[1] Centre of Preclinical Science Studies, Faculty of Dentistry, Universiti Teknologi MARA, Sungai Buloh Campus, Jalan Hospital, Sungai Buloh, Selangor, Malaysia.
[2] Oral and Maxilofacial Cancer Research Group, Faculty of Dentistry, Universiti Teknologi MARA, Sungai Buloh Campus, Jalan Hospital, Sungai Buloh, Selangor, Malaysia.
[3] Faculty of Medicine and Health Sciences, University Malaysia Sarawak. Malaysia

*Corresponding author: gootheah@uitm.edu.my

In recent years, oral cancer in Malaysia contributes 7.72 per 10,000 of death rate with world cancer death ranking number of 14. Current research has shown that the deregulation of miRNAs occur in most of the cancer. The accumulating research evidences indicate the miR-129-3p, could play a vital role in carcinogenesis. This study aimed to eluciadate the expression of miRNA-129-3p in Malaysian oral cancer cell line. MicroRNA of oral cancer cell line and normal cell line were extracted and prepared for real-time PCR process to check the microRNA expression level of miR-129-2 gene. The levels of microRNA expression of the oral cancer cell and normal fibroblast samples were compared using Mann-Whitney Test by SPSS version 22.0. Results demonstrated that the microRNA expression level of mir-129-3P in oral cancer cell line was upregulated with fold change value of 1.3433, while the normal cell line was downregulated with fold change value of 0.8285 ($p<0.05$). Thus, miR-129-3p is overexpressed in oral cancer in our study. It implicated that miR-129-3p can be applied as a diagnostic and prognostic biomarker for Malaysian oral cancer.

E-POSTER 14

HYPERFORIN INDUCES *IN VITRO* CELL DEATH IN MCF-7 AND MDA-MB-231 CELLS BY INDUCING INFLAMMATION

BARATHAN MUTTIAH[1], KUMUTHA MALAR VELLASAMY[1], SEE MEE HONG[2] & JAMUNA VADIVELU[1, *]

[1]Department of Medical Microbiology; [2]Department of Surgery, Faculty of Medicine, University of Malaya, Lembah Pantai, Kuala Lumpur 50603, Malaysia

*Corresponding author: jamuna@um.edu.my

Globally, current chemotherapy for breast cancer has become a major issue of concern, especially with that can increase in toxicity of drugs in the patient's body. Hence, innovations in the cancer treatment are still needed to address these issues. An earlier report confirmed the anticancer properties of hyperforin, an extract produced from St John's wort on other types of cancer cells. The potential consequences of hyperforin on various breast carcinoma cells in terms of regulation of immune mediators especially cytokines remains unclear. In this study, the cytotoxic effect of hyperforin on different types of breast cancer cells, MCF-7 and MDA-MB-231 was determined using the MTT assay and further confirmed investigating apoptosis, LDH, COX-2, MMP, ROS, cell cycle, DNA fragmentation and cytokine assays. Paclitaxel was used as positive control. Hyperforin demonstrated IC50 (6.15µg/mL) and (7.18 µg/mL) in inhibiting growth of MCF-7 and MDA-MB 231 cells respectively. No toxicity effect was found on normal breast. Hyperforin was able to arrest the proliferation of MCF-7 cells and MDA-MB-231 particularly G0/G1 and S phase of the cells in the cell cycle assay respectively. Excessive intracellular ROS, LDH, COX-2 and nuclear DNA fragmentation was also triggered besides a decrease in MMP in MCF-7 and MDA-MB-231 cell culture indicating occurrence of apoptosis. Furthermore, secretion of proinflammatory cytokines revealed induction of inflammation and potentially immunogenic cell death. The results demonstrated that hyperforin has almost similar chemotherapeutic properties as paclitaxel in inhibiting breast cancer cells hence suggesting further experiments on *in vivo* aspect.

E-POSTER 15

IN SILICO DESIGN OF BIOLOGICALLY ACTIVE ANTICANCER PEPTIDES DERIVED FROM ROYAL JELLY, ROYALISIN

STEPHANIE CHEAH HSIU EN[1] & TANG YIN QUAN[1,2,*]

[1] School of Biosciences, Faculty of Health and Medical Sciences, Taylor's University, 47500 Subang Jaya, Selangor Darul Ehsan, Malaysia.
[2] Centre for Drug Discovery and Molecular Pharmacology, Faculty of Medical and Health Sciences, Taylor's University, 47500 Subang Jaya, Selangor Darul Ehsan, Malaysia.

*Corresponding author: yinquan.tang@taylors.edu.my

Cancer treatment mainly employs the use of anticancer drugs which can cause negative side effects due to their toxicity and low specificity. Anticancer peptides (ACPs) are a promising cancer treatment approach due to their low toxicity, high tumour specificity, low labour costs and short production time. Our study identified several biologically active anticancer peptides derived from royalisin (defensin-1), an antimicrobial peptide (AMP) found in royal jelly produced by honeybees, *Apis mellifera*. Royalisin's anticancer effects were still unknown prior to our investigation. In this present study, 37 overlapping peptides were identified spanning the whole royalisin sequence, out of which 23 of them were predicted to be ACPs from data produced by three softwares; AntiCP, iACP and ACPred. Modification by single amino acid substitution on the highest SVM-scoring ACP produced 7 peptides with greater SVM scores, cationicity and amphipathicity than their parental peptide while possessing low toxicity and haemolytic activity. These peptides were also predicted to have α-helical structures which may be a contributing factor in their predicted cell-penetrating property, causing membrane perforation and cancer cell apoptosis. Future research should be conducted *in vivo* and *in vitro* to further explore their potential as therapeutic agents in cancer treatment.

E-POSTER 16

ANTICANCER ACTIVITY OF DENTATIN IN COLORECTAL CARCINOMA

AHMAD K. ZULPA*, BARATHAN MUTTIAH, KUMUTHA M. VELLASAMY & JAMUNA VADIVELU

Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Lembah Pantai, Kuala Lumpur 50603, Malaysia

*Corresponding author: khusairyahmad@gmail.com

Colorectal cancer (CRC) is blameworthy for more than 881 000 thousands of mortality which came up as third causes of entire cancer-related deaths worldwide. Drug resistance (DR) in existing CRC chemotherapy urge the search for new cytotoxic drugs majorly from natural compounds which are cost effective and have low level of resistance. Dentatin (DTN) is a types of coumarin isolated from *Clausena excavate*, a wild shrub of the Rutaceae family which has been used as folk medicine in South East Asia. Preliminarily, we found that DTN is cytotoxic towards colorectal carcinoma HCT-116 cell lines at low concentration assessed by MTT assay. Later by Acridine orange/Propidium iodide staining we found that DTN induces apoptosis in CRC cells and further analysis with agarose gel electrophoresis DTN also drives DNA fragmentation which a crucial feature of apoptosis. As a hallmark of cancer, targeting apoptosis is an attractive tool in combatting DR. Thus, our aim is to further assess anticancer activity of DTN as a possible cytotoxic agent in CRC. Reactive oxygen species (ROS) and mitochondrial membrane potential, caspases 3, 8 and 9 will be measured fluorometrically. While cell cycle arrest will be determine using flow cytometry. Relevant apoptotic and autophagic proteins expression will be determined using western blotting. We also will compare anticancer activity of DTN with first-line CRC chemotherapy drug, notably 5-fluororacil (5-FU). We expected a better understanding of anticancer activity of DTN, along with specific target molecules of apoptosis and ability to modulate autophagy for potential development of CRC drugs.

E-POSTER 17

TUALANG AND KELULUT HONEY MODULATE MICROGLIAL ROS PRODUCTION AND SURFACE MARKERS EXPRESSIONS

OOI YIN YIN[1,2,*], ROMEL MARIO SOYZA[1], LOW ZHAO XUAN[1] & TAN KAI LI[1]

[1] School of Biosciences, Faculty of Health and Medical Sciences, Taylor's University, No. 1 Jalan Taylor's, 47500 Subang Jaya, Selangor Darul Ehsan, Malaysia.
[2] Centre for Drug Discovery and Molecular Pharmacology, Faculty of Medical and Health Sciences, Taylor's University, 47500 Subang Jaya, Selangor Darul Ehsan, Malaysia.

*Corresponding author: yinyin.ooi@taylors.edu.my

Microglia, the resident macrophages in the central nervous system, secrete various pro-inflammatory factors and undergo proliferation upon activation in various neurodegenerative diseases. Activation of microglia has been implicated in exacerbation of neurodegenerative diseases. Hence, suppressing microglial cell activation may be a solution to control the progress of neurodegenerative disorders. In recent decades, researchers are more interested in raw materials that have anti-inflammatory properties and have been used from generations to generations. Since flavonoids and its metabolites are readily transport across BBB, honey which contain high concentration of these active compounds successfully caught the attention of neuroscientists worldwide. Honey therapeutic effects are widely documented due to its varied pharmacological activities. While the medicinal properties of honeys such as Manuka honey are well established, further investigation is required to elucidate the medicinal properties of locally sourced honeys, namely Tualang (TH) and Kelulut (KH) honeys. BV2 cells, an immortalized microglial cell line, incubated with TH at concentrations of 0.1% and 0.5%, and KH at concentrations of 0.1% and 0.25% for 24 and 48 hours showed cell survivability above 75%. Both TH and KH decreased ROS production significantly on LPS-induced BV2 cells, but increased ROS production on unstimulated BV2 cells. Additionally, the expression levels of CD40, CD11b and CD86 were also slightly reduced on honey-treated LPS-induced BV2 cells. These results have demonstrated that both TH and KH are capable of suppressing microglial activation. Therefore, we propose the idea of utilizing these honeys as a complementary treatment to suppress the progression of neurodegenerative diseases.

E-POSTER 18

TRANSCRIPTOME LANDSCAPE INDUCED BY *MELICOPE PTELEFOLIA* EXTRACT IN HUMAN FIBROBLAST (HS27) CELLS

JOHARI BIN MOHD ALI[1, *] & MOHAMMAD FAUJUL KABIR[1,2]

[1] Department of Molecular Medicine, Faculty of Medicine, University of Malaya, MALAYSIA.
[2] Fels Institute for Cancer Research and Molecular Biology, Temple University, Philadelphia, PA 19140, USA

*Corresponding author: johari@um.edu.my

We previously reported anticancer and antioxidant activities of *Melicope ptelefolia* hexane (MP-HX) and ethyl acetate (MP-EA) extracts, including cellular antioxidant activity in human skin fibroblast cell line (Hs27). In the present study, the transcriptional effect of MP-EA on Hs27 cells was investigated through microarray profiling. Based on cut-off fold change (FC) value of > ±1.50, MP-HX induced differential expression of 15,529 genes. MP-HX treatment induced upregulation of numerous genes that are involved in antioxidant response and promotion of proliferation and cell cycle. The treatment induced downregulation of numerous psoriasis-associated genes and genes that are associated with cell cycle arrest and programmed cell death. The treatment modulated several aging-associated genes in directions that could potentially exert anti-aging effect.

E-POSTER 19

A CROSS-SECTIONAL EVALUATION ON TYPE 2 DIABETES RISK AND THE POSTPRANDIAL BLOOD GLUCOSE LEVEL AMONG UNDERGRADUATE PHARMACY STUDENTS

SITI AISYAH BINTI BURHAN[1] & MAY KHIN SOE[2, *]

[1] B.Pharm (International Islamic University Malaysia (IIUM)); [2] Department of Basic Medical Sciences, Kulliyyah of Pharmacy, (IIUM), Jalan Sultan Ahmad Shah, 25200 Kuantan, Pahang, Malaysia.

*Corresponding author: may_soe@iium.edu.my

Most of university students usually underestimate the risk of diabetes mellitus though a recent statistic reported an estimated 3.9 million Malaysians aged 18 and above are suffering from diabetes. This cross-sectional study aimed to heighten the awareness of risk of diabetes mellitus among future pharmacists and to assess their diabetes risk score (DRS) with postprandial glucose level (PPG). To conduct this study, two batches of undergraduate first year pharmacy students, total (n=221); 107 from 2018/2019 (Group A) and 114 from 2019/2020 (Group B) intake were recruited. Both male and female students were 19-21 year- old. Anthropometric measurement, self-assessed DRS and PPG level were collected and analysed descriptively using SPSS version 22. Pearson's correlation coefficient was used to measure any differences between two groups. There were no differences in body mass index (BMI) and DRS between both groups; mean BMI for A were 22.23 kg/m^2 versus 21.81 kg/m^2 for B (p=0.149) and mean TRS for A was 8.93 versus 8.39 for B (p=0.172). Mean (TRS) of all students was 8.65 ± 2.97. Overall, majority of students (n=132, 59.72 %) have slightly elevated risk of diabetes and 33 students (14.93%) are under the moderate and high-risk categories despite being young. Mean PPG of group A (5.55 ± 0.78 mmol/L) was slightly higher than that of group B (5.43 ± 0.68 mmol/L), p=0.194. However, small sample size may be a limitation of this study. The students successfully obtained their risk score and learned the causes which contributed to the diabetes mellitus.

E-POSTER 20

POTENTIAL NOVEL DRUG BINDING POCKETS OF SARS-CoV-2 MAIN PROTEASE

NURUL ASYIQIN MOHD NARUDIN, NUR SAMSINAR FADILAH ABD RAHMAN & **SITI AZMA JUSOH***

Structural Bioinformatics & Molecular Modeling Lab, FF2-Level 8, Faculty of Pharmacy, Universiti Teknologi MARA (UiTM), Kampus Puncak Alam, Bandar Puncak Alam, 42300 Selangor, Malaysia.

*Corresponding author: sitiazma@uitm.edu.my

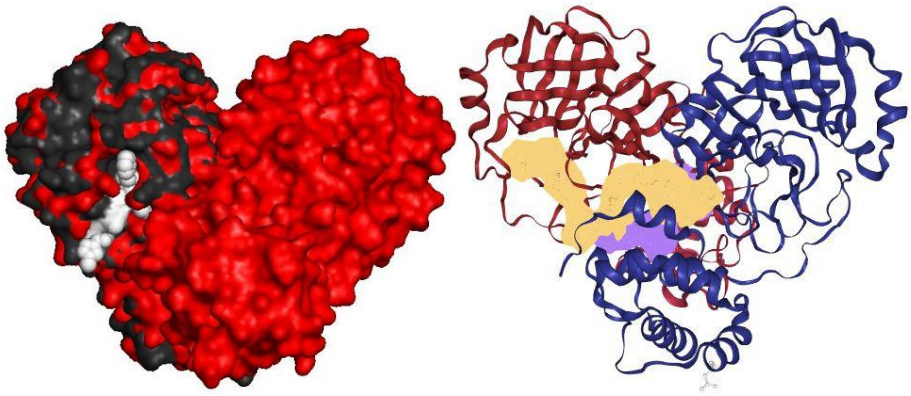

Figure (above) shows the potential druggable pockets of SARS-CoV-2 main protease (right) other than the known N3 binding pocket (left).

The current drug therapies for the coronavirus disease-19 (COVID19) are not target specific. Most of the drugs are broad range type and were priorly developed for other diseases. There are now more than 200 drug and 300 vaccine developments aimed to be the solution for COVID19. Unfortunately, the treatments can take some years to reach everyone on the planet. One of the drug development strategies is to create an inhibitor targeting the SARS CoV-2 main protease. Furthermore, it is shown that a small molecule named N3 bound to the protease and inhibited the function. However, the N3 binding pocket is conserved among many types of viruses. In this work, we explore other drug binding pockets on the SARS CoV-2 protease. The DogSiteScorer program was utilized to predict druggable pockets using several crystallographic structures of SARS-CoV2 main protease (PDBID: 2DUC, 6LU7, 6ZRD). The pockets that have druggability scores more than 0.7 were selected and further analysed for the consensus locations. We found four unique potential druggable pockets other than the known N3 binding pocket. In the next stage, we will perform virtual docking screening to these pockets for further analysis.

Organizing Committee of MSBMBTU.VFM 2020

CHAIRPERSON	*: Anthony Ho Siong Hock (Taylor's University)*
SECRETARIAT	*: Ng Chyan Leong (Chair) (Universiti Kebangsaan Malaysia)* *: Fong Lai Yen (Universiti Tunku Abdul Rahman)* *: Muhammad Fazril Razif (University of Malaya)*
SCIENTIFIC	*: Fung Shin Yee (Chair; University of Malaya)* *: Chong Pei Pei (Chair; Taylor's University)* *: Sheila Nathan (Universiti Kebangsaan Malaysia)* *: Yeannie Yap Hui Yeng (MAHSA University)* *: Tang Yin Quan (Taylor's University)* *: Looi Chung Yeng (Taylor's University)* *: Priya Madhavan (Taylor's University)*
TECHNICAL/SOCIAL	*: Muhammad Fazril Razif (University of Malaya)* *: Hwang Jung Shan (Sunway University)* *: Azzreena Mohamad Azzeme (Universiti Putra Malaysia)* *: Kok Yih Yih (International Medical University)* *: Adeline Chia Yoke Yin (Taylor's University)* *: Yap Wai Sum (UCSI University)*
FINANCE	*: Noor Azmi Bin Shaharuddin (Chair) (Universiti Putra Malaysia)* *: Izyanti Ibrahim (Universiti Kebangsaan Malaysia)* *: Jason Lee Khai Wooi (Taylor's University)*
PARTNERSHIP/ NETWORKING	*: Lim Yang Mooi (Universiti Tunku Abdul Rahman)* *: Renee Lim Lay Hong (UCSI University)* *: Fung Shin Yee (University of Malaya)* *: Hwang Jung Shan (Sunway University)*